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**A “ceasefire” model to explain efficient seed transmission of *Xanthomonas citri* pv. *fuscans* to common bean.**

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Other Keywords:	Seed, <i>Xanthomonas</i> , transmission, <i>Phaseolus vulgaris</i>
Abstract:	<p>Although seed represents an important means of plant pathogen dispersion, the seed-pathogen dialogue remains largely unexplored. A multi-omic approach ( <i>i.e.</i> dual RNAseq, plant small RNAs and methylome) was performed at different seed developmental stages of common bean ( <i>Phaseolus vulgaris</i> L.) during asymptomatic colonization by <i>Xanthomonas citri</i> pv. <i>fuscans</i> ( <i>Xcf</i>). In this condition, <i>Xcf</i> did not produce disease symptoms, neither affect seed development. Although, an intense molecular dialogue, via important transcriptional changes, was observed at the early seed developmental stages with down-regulation of plant defense signal transduction, via action of plant miR, and upregulation of the bacterial Type 3 Secretion System. At later seed maturation stages, molecular dialogue between host and pathogen was reduced to few transcriptome changes, but marked by changes in DNA methylation of plant defense and germination genes, in response to <i>Xcf</i> colonization, potentially acting as defense priming to prepare the host for the post-germination battle . This distinct response of infected seeds during maturation, with a more active role at early stages refutes the widely diffused assumption considering seeds as passive carriers of microbes. Finally, our data support a novel plant-pathogen interaction model, specific to the seed tissues, which differs from others by the existence of distinct phases during seed-pathogen interaction with seeds first actively interacting with colonizing pathogens, then both belligerents switch to more passive mode at later stages. We contextualized this</p>

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	observed scenario in a novel hypothetical model that we called "ceasefire", where both the pathogen and the host benefit from temporarily laying down their weapons until the moment of germination.
Note: The following files were submitted by the author for peer review, but cannot be converted to PDF. You must view these files (e.g. movies) online.	
Supplementary Data S1.xlsx Supplementary Data S3.xlsx	



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3 1 **A “ceasefire” model to explain efficient seed transmission of *Xanthomonas citri* pv.**  
4 ***fuscans* to common bean.**

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25 21  
26 22 **Summary**

- 27 23
- 28 • Although seed represents an important means of plant pathogen dispersion, the seed-pathogen dialogue remains largely unexplored.
  - 29 • A multi-omic approach (*i.e.* dual RNAseq, plant small RNAs and methylome) was performed at different seed developmental stages of common bean (*Phaseolus vulgaris* L.) during asymptomatic colonization by *Xanthomonas citri* pv. *fuscans* (*Xcf*).
  - 30 • In this condition, *Xcf* did not produce disease symptoms, neither affect seed development. Although, an intense molecular dialogue, via important transcriptional changes, was observed at the early seed developmental stages with down-regulation of plant defense signal transduction, via action of plant miR, and upregulation of the bacterial Type 3 Secretion System. At later seed maturation stages, molecular dialogue between host and pathogen was reduced to few transcriptome changes, but marked by changes in DNA methylation of plant defense and germination genes, in response to *Xcf* colonization, potentially acting as defense priming to prepare the host for the post-germination battle. This distinct response of infected seeds during
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3 37 maturation, with a more active role at early stages refutes the widely diffused  
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7 40 tissues, which differs from others by the existence of distinct phases during seed-  
8 41 pathogen interaction with seeds first actively interacting with colonizing pathogens,  
9 42 then both belligerents switch to more passive mode at later stages. We contextualized  
10 43 this observed scenario in a novel hypothetical model that we called “ceasefire”, where  
11 44 both the pathogen and the host benefit from temporarily laying down their weapons  
12 45 until the moment of germination.  
13 46

14 47 **Key words:** Seed, *Xanthomonas*, transmission, dialogue, epigenome, *Phaseolus*  
15 48 *vulgaris*, dual transcriptomics.  
16 49

## 17 50 Introduction

18 51 Legumes provide a sustainable source of proteins for human and livestock diet,  
19 52 moreover their symbiotic nitrogen fixation capacity contributes to soil preservation and reduces  
20 53 the need for chemical fertilizers (Stagnari et al., 2017; Ferreira et al., 2021). An important  
21 54 factor limiting legume utilization is their relatively high yield variability, greatly due to their  
22 55 susceptibility to environmental factors such as biotic and abiotic stresses (Cernay et al., 2015;  
23 56 Martins et al., 2020). While legumes are expected to better perform under changing climatic  
24 57 conditions in relation to other crops thanks to higher biomass accumulation under increased  
25 58 atmospheric CO<sub>2</sub> levels and higher photosynthetic efficiency under increased irradiation  
26 59 levels, other traits are predicted to be negatively affected, such as seed quality and resistance  
27 60 to pathogens (Myers et al., 2014).

28 61 Pathogens are responsible for 35-70% yield losses on grain legumes (Martins et al.,  
29 62 2020). An important determinant of disease outbreak is pathogen dispersal through infected  
30 63 seeds (Denancé and Grimault, 2022). The mode of transmission of pathogens to the seed can  
31 64 be schematically summarized in three non-exclusive pathways: internal (*via* the host xylem),  
32 65 floral (*via* the pistil) and external as a consequence of contact of the seed with symptomatic  
33 66 fruit tissues or with threshing residues (Maude, 1996). For instance, *Xanthomonas citri* pv.  
34 67 *fuscans* (*Xcf*), causal agent of common bacterial blight of bean (CBB), can use these three  
35 68 pathways for its transmission to common bean seeds (Darsonval et al., 2008; Darrasse et al.,  
36 69 2018). Contaminated seeds can be symptomatic or asymptomatic, and are generally  
37 70 associated with high or moderate bacterial population sizes, respectively, moreover  
38 71 symptomatic seeds often fail to germinate (Darrasse et al. 2018; Chen et al., 2021a) and no  
39 72 viable pathogen control method to counteract bacterial seed infections exists.

Decades of research led to a comprehensive overview of the genetic (for review Dodds and Rathjen, 2010; Wirthmueller et al., 2013) and epigenetic (for review Hannan Parker et al., 2022) mechanisms involved in plant-pathogen interactions during vegetative growth. However, the molecular dialogue that takes place between seeds and pathogens was overlooked to date. On the plant side, in the event of an incompatible interaction between *Medicago truncatula* and *X. campestris* pv. *campestris* (*Xcc*), seed transcriptome exhibited an activation of defense response and a repression of seed maturation pathways (Terrasson et al., 2015). From the bacterial side, some specific genetic determinants such as the type 3 secretion system (T3SS, Darsonval et al., 2008) and adhesins (Darsonval et al., 2009) were shown to be involved in the transmission of *Xcf* to common bean seeds. Involvement of the T3SS in seed transmission was also documented for *Acidovorax citrulli* in watermelon (Dutta et al., 2014). However, a global view of bacterial transcriptomic changes occurring during seed transmission is currently missing. This lack of knowledge is partly due to the difficulties of collecting enough bacterial RNA from the seeds. Indeed seed-associated bacterial population sizes are usually very low (from 10 to 1,000 CFU per bean seed; Chesneau et al., 2022) and follow a Poisson distribution, which complicates the sampling of contaminated seeds and prevent molecular analysis of seed-pathogens interactions (Gitaitis and Walcott, 2007).

Since knowledge regarding molecular interactions occurring during bacterial seed infections is currently lacking, the objective of this work was to decipher the molecular dialogue between the common bean (*Phaseolus vulgaris* L.) seed and a seed pathogen at several stages of seed development in order to identify major molecular factors involved in seed infection establishment and pathogen transmission to the seedling. A dual RNAseq approach to identify both the host seed and the *Xcf* pathogen transcriptomes was performed at three stages of seed development during seed filling, seed maturation and seed maturity. The technical limitation of low bacterial population within seeds was successfully bypassed using bacterial transcript enrichment. This transcriptomic analysis was complemented by the analysis of small RNAs and DNA methylation changes in infected seeds to reveal the role of these mechanisms in the seed-pathogen interaction, which allowed us to propose a novel model in plant-pathogen interactions specific to seed developmental stage and explaining the efficiency of pathogen seed transmission.

## Materials and Methods

### Bacterial strain and inoculum preparation

The *Xcf* bacterial strain 7767R (Rif<sup>R</sup>, Darrasse et al., 2018) was grown for 24h at 28°C in Tryptic Soy Agar at 10% (1.7 g.L<sup>-1</sup> tryptone, 0.3 g.L<sup>-1</sup> soybean peptone, 0.25 g.L<sup>-1</sup> glucose, 0.5 g.L<sup>-1</sup> NaCl, 0.5 g.L<sup>-1</sup> K<sub>2</sub>HPO<sub>4</sub> and 15 g.L<sup>-1</sup> agar) supplemented with 50 mg.L<sup>-1</sup> rifamycin.

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3 109 Bacterial cells were suspended in sterile distilled water, calibrated at  $10^8$  CFU.mL<sup>-1</sup> ( $OD_{600}$  =  
4 110 0.1) and adjusted to  $10^6$  CFU.mL<sup>-1</sup> for spray-inoculation.

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### 8 112 **Plant materials and production of contaminated seeds**

9 113 Experiments were performed with *Phaseolus vulgaris* L. cv. Flavert, a cultivar  
10 114 susceptible to CBB (Darrasse et al., 2007). Seeds were sown in one liter of Tray substrate  
11 115 (NF U 44–551, Klasmann- Deilmann GmbH, Rippert France). Plants were grown in a controlled  
12 116 growth chamber with 16h of light at 23°C and 8h of dark at 20°C and a relative humidity (RH)  
13 117 of 70%. Plants were watered twice a week during the first three weeks, then with a nutrient  
14 118 solution (N/P/K=15/10/30). Plants were staked and pinched after the third leaf.

15 119 Plants were spray-inoculated at the flower bud stage (R5, Michael 1994) with either  
16 120 *Xcf* bacterial suspension ( $10^6$  CFU.mL<sup>-1</sup>) or water as control. The day prior to inoculation,  
17 121 temperature (day 25°C/night 23°C) and RH (95%) were increased. Inoculation was performed  
18 122 using a two-step protocol. First, small green flower buds were sprayed. Three days later,  
19 123 flower buds at the pollination stage were tagged. Then, a second inoculation was performed  
20 124 at one day after pollination (DAP) when tagged organs turned into open flowers. Then  
21 125 afterward, RH was reduced to 70% to limit pathogen symptom development and seed  
22 126 abortion. Three independent replicates of five plants ( $n=15$ ) were inoculated. Tagged pods  
23 127 were harvested at 24, 35 and 42 DAP. Seeds were collected aseptically from pods to avoid  
24 128 contamination by external bacterial populations (Darsonval et al., 2008).

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### 26 130 **Monitoring of bacterial population sizes**

27 131 For each sample, *Xcf* population sizes were determined from ten individual seeds and from  
28 132 five pools of three seeds. Seeds were soaked in 0.5 mL of sterile water per seed overnight at  
29 133 4°C under shaking (150 rpm). Then, 50 µL of serial dilutions were plated on 10% TSA.  
30 134 Colonies were monitored five days after incubation at 28°C. The contamination rate of a  
31 135 sample (p) was calculated from the analysis of N sub-samples according to the formula  $p = 1 -$   
32 136  $(Y/N)^{1/n}$  (Maury et al., 1985), where n is the number of seeds in each group and Y the number  
33 137 of healthy groups.

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### 35 139 **Seed physiological analyses**

36 140 Three sub-samples of ten seeds were used to determine dry weight and water content. Each  
37 141 sub-sample was weighed before and after incubation (3 days) in a 96°C incubator (Mettler).

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### 39 143 **Plant and bacterial RNA extraction and RNA sequencing**

40 144 Seed samples harvested at 24, 35 and 42 DAP were flash-frozen in liquid nitrogen.  
41 145 Samples were ground in liquid nitrogen using a mechanical grinder (Retsch MM300

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3 146 TissueLyser) during 1 min at 30 Hertz. Total RNAs were extracted using the NucleoSpin® RNA  
4 147 Plant and Fungi Kit (Macherey-Nagel, Düren, Germany), according to the manufacturer  
5 148 instructions. RNA quantity and integrity were assessed respectively using a NanoDrop  
6 149 ND-1000 (NanoDrop Technologies, Wilmington, DE, USA) and a 2100 Bioanalyzer (Agilent  
7 150 Technologies, Santa Clara, CA, USA). Library constructions and single-end sequencing  
8 151 (SE50, 20M) were outsourced to the Beijing Genomics Institute (BGI, <https://www.bgi.com>)  
9 152 using the Illumina Hiseq 2500 technology. Raw reads are available at GSE226918.  
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11 154 Using the same seed lots as for plant RNAs, bacterial macerates were collected after  
12 155 soaking contaminated seeds (2 mL per gram of seed) overnight in KPO<sub>4</sub> buffer, (50 mM, pH  
13 156 6.8), supplemented with 20% of blocking agent (RNAlater, ThermoFisher scientific, Carlsbad,  
14 157 CA, United States). After centrifugation (15 min at 15,000 g) and removal of the supernatant,  
15 158 total RNAs were extracted as previously described (Darsonval et al., 2009). Concentration  
16 159 and integrity of RNAs were assessed with Qubit (Invitrogen, Carlsbad, CA, USA) and a 2100  
17 160 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA), respectively. As total RNA  
18 161 extracted from bacterial macerates corresponded mainly to plant transcripts (not shown), we  
19 162 designed a procedure of bacterial transcript enrichment. Bacterial mRNAs were captured  
20 163 using the SureSelectXT RNA Direct technology (Agilent, Santa Clara, CA, USA). A total of  
21 164 54,548 probes of 120-nts length were designed based on the predicted mRNAs of *Xcf7767R*  
22 165 genome sequence (GCA\_900234465; Chen et al., 2018). Quality and quantity of sequencing  
23 166 libraries were evaluated and quantified using Bioanalyzer and KAPA Library Quantification  
24 167 assay (Roche, Basel Switzerland). Paired-end sequencing (2 × 75 bp) was performed with a  
25 168 NextSeq 550 System High OutPut kit (Illumina, San Diego, CA, USA). Raw reads are available  
26 169 at GSE227386.

27 170 After quality control, high-quality reads were mapped either on *Xcf7767R* transcriptome  
28 171 (Briand et al., 2021) ([https://bbric-  
29 172 pipelines.toulouse.inra.fr/myGenomeBrowser?browse=1&portalname=Xcf7767Rpb&owner=  
30 173 armelle.darrasse@inrae.fr&key=TwzQ08DA](https://bbric-pipelines.toulouse.inra.fr/myGenomeBrowser?browse=1&portalname=Xcf7767Rpb&owner=armelle.darrasse@inrae.fr&key=TwzQ08DA)) or on *P. vulgaris* transcriptome version 2.1  
31 174 ([https://phytozome-next.jgi.doe.gov/info/Pvulgaris\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1)) using quasi-mapping alignment and  
32 175 quantification methods of Salmon algorithm v.1.2 (Patro et al., 2017). RNA-Seq data were  
33 176 normalized as transcripts per million (TPM). Differentially expressed genes (DEGs) were  
34 177 determined using DESeq2 v1.22.2 (Love et al., 2014), using an adjusted p-value <5%. *Xcf*  
35 178 DEGs were analyzed between sampling dates. *P. vulgaris* DEGs were obtained by comparing  
36 179 *Xcf*- versus H<sub>2</sub>O-inoculated seeds at each developmental stage. Gene annotations were  
37 180 provided with the *P. vulgaris* version 2.1 genome and Mapman functional categories v.4 were  
38 181 determined using Mercator tool from the predicted protein sequences (Schwacke et al., 2019).  
39 182 Bacterial Type III effectors were predicted using the automated machine-learning based web

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3 183 server Effectidor (Wagner et al., 2022). Over representation analyses of MapMan or COG  
4 184 terms were performed, respectively for plant and bacteria DEGs, using Clusterprofiler (Yu et  
5 185 al., 2012) package in R by applying an adjusted  $p$ -value cut-off  $<0.05$  obtained after the  
6 186 Bonferroni-Hochberg procedure.

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9 187 Differentially expressed genes during seed germination were identified using the data  
10 188 generated by Narsai et al. (2017) available in the SRA database (accession GSE94457). Raw  
11 189 reads were downloaded and mapped against the Arabidopsis transcriptome using Salmon  
12 190 algorithm and DEGs during germination kinetic were determined using ImpulseDE2 algorithm  
13 191 (Fischer et al., 2018) following an adjusted  $p$ -value  $<1\%$ .

14 192 To determine genes involved in post-germination defense, we inoculated healthy  
15 193 seeds with  $10^7$  of *Xcf* CFU.mL<sup>-1</sup> or H<sub>2</sub>O during 25 min followed by 3 min of vacuum infiltration  
16 194 before seed drying at room temperature. Inoculated dried seeds displaying between  $10^4$  and  
17 195  $10^5$  CFU.seed<sup>-1</sup> of *Xcf* were used for germination assay on Whatman paper in 16h-light growth  
18 196 chamber at 25°C. *Xcf*- and H<sub>2</sub>O-inoculated seeds were collected at 3 and 7 Days After  
19 197 Imbibition (DAI) and dissected as separated cotyledons and radicles for real-time qRT-PCR  
20 198 experiments. RNA were extracted at different germination timepoints and in different tissues  
21 199 using the NucleoSpin® RNA Plant and Fungi Kit (Macherey-Nagel, Düren, Germany) as  
22 200 described above but including a DNase treatment (Macherey-Nagel, rDNase set, Düren,  
23 201 Germany). RNA were quantified using a using a NanoDrop ND-1000 (NanoDrop  
24 202 Technologies, Wilmington, DE, USA) and cDNA was synthesized from 1 µg of total RNA using  
25 203 the Reverse Transcription system (iScript™ cDNA synthesis kit, Bio-Rad). Quantitative Real  
26 204 time PCR was performed using Sybr Green Master Mix (SYBR Green master mix, Bio-Rad)  
27 205 on a CFX96 real-time detection system (Bio-Rad Laboratories). *EF1* and *UBI* genes were used  
28 206 as housekeeping genes as described in Darrasse et al. (2010). Primers used for Real-time  
29 207 PCR are listed in Supplementary Table S4.

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#### 44 209 **small RNA extraction and analysis (sRNA-seq)**

45 210 Using the same frozen powders obtained from *Xcf*- and H<sub>2</sub>O-inoculated seeds from 24  
46 211 DAP and 42 DAP, we extracted small RNA using the NucleoSpin® miRNA Kit  
47 212 (Macherey-Nagel, Düren, Germany), according to the manufacturer's instructions. Small RNA  
48 213 enrichment was validated using Bioanalyzer small RNA analysis. Small RNAs were  
49 214 sequenced using DNBseq sequencing technology (SE50 40M, BGI) and Unique Sequence  
50 215 identifiers (UMI) to correctly quantify unique reads. Reads of 20 to 24 nucleotides were  
51 216 extracted and mapped on the reference mature miRNA database available in miRBase version  
52 217 22 (Kozomara et al., 2019) using bowtie (Langmead et al., 2009) and quantified using  
53 218 SAMtools (Li et al., 2009). Differentially expressed small RNA between *Xcf*-inoculated versus  
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3 219 H<sub>2</sub>O-inoculated seeds at 24 and 42 DAP were determined using DESeq2 following a *p*-value  
4 220 threshold < 5% from the SARTools R package (Varet et al., 2016). Known and putative novel  
5 221 small RNAs were mapped to the *P. vulgaris* genome sequence using ShortStack4 algorithm  
6 222 (Johnson et al., 2016) and displayed in the dedicated Jbrowse  
7 223 [https://iris.angers.inrae.fr/pvulgaris\\_v2](https://iris.angers.inrae.fr/pvulgaris_v2) in the 'small RNA tracks' section. Transcripts  
8 224 potentially targeted by miRNAs were predicted via analyzing complementary matching  
9 225 between sRNA and target and evaluating target site accessibility using psRNATarget tool (Dai  
10 226 and Zhao, 2011; Dai et al., 2018) and a threshold of expectation below 5 was set to consider  
11 227 transcripts as putative miRNA targets. Raw reads are publicly available at GSE226920.  
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### 219 **Plant DNA extraction and Bisulfite sequencing experiments (BS-seq)**

20 230 From the same frozen seed powders used for RNA extractions, we performed DNA  
21 231 extraction, on the three biological replicates of *Xcf*- and H<sub>2</sub>O-inoculated seeds at 42 DAP,  
22 232 using the NucleoSpin® DNA Food Kit (Macherey-Nagel, Düren, Germany), according to the  
23 233 manufacturer's instructions. DNA samples were sent to the BGI Genomics (Hong Kong) for  
24 234 bisulfite treatment using a ZYMO EZ DNA Methylation-Gold kit, library construction and  
25 235 paired-end sequencing using BGISEQ-500 sequencing technology (PE100 45M). FastQC  
26 236 was used to check sequencing quality and clean reads were mapped to the *P. vulgaris*  
27 237 genome version 2.1 using Bismark software (Krueger and Andrews, 2011). After mapping,  
28 238 deduplication of sequences and quantification of cytosine methylation were performed using  
29 239 Bismark\_deduplicate and Bismark\_methylation\_extractor. Each context of methylation was  
30 240 considered independently: CG, CHG, or CHH and corresponding bigwig files were generated  
31 241 using bismark\_to\_bigwig python script and displayed in the dedicated Jbrowse:  
32 242 [https://iris.angers.inrae.fr/pvulgaris\\_v2](https://iris.angers.inrae.fr/pvulgaris_v2). Putative differentially methylated regions (DMRs)  
33 243 were identified in each independent methylation context using DMRCaller algorithm available  
34 244 in R (Catoni et al., 2018). Raw reads are publicly available at  
35 245 <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226919>.  
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## 247 **Results**

### 248 ***Seed transmission of moderate Xcf population sizes does not impact seed*** 249 ***development***

250 Seed transmission of *Xcf* 7767R was investigated following spray-inoculation of *P.*  
251 *vulgaris* L. cv Flavert. Three stages of seed development were targeted: (i) 24 DAP (seed  
252 filling), (ii) 35 DAP (seed maturation) and 42 DAP (seed maturity). Seed water content (Fig.  
253 1A) and dry seed weight (Fig. 1B) were not significantly impacted by *Xcf*-inoculation. As

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3 254 described in Darsonval et al. (2008), we used  $10^6$  CFU.mL<sup>-1</sup> for *Xcf* spray-inoculation at  
4 255 flowering time to allow seed bacterial transmission without apparition of symptoms during seed  
5 256 development. Otherwise, higher concentration could generate symptomatic seed bacterial  
6 257 transmission leading to defect in germination of infected seeds. Following this mild treatment,  
7 258 about 80% of seeds were contaminated with *Xcf* with an average population size of  $10^5$  CFU.g<sup>-1</sup>  
8 259 of seeds at 24 DAP (Fig. 1C). Over the course of seed development, the frequency of  
9 260 detection of *Xcf* decreased from 80% to 50%. This was accompanied by a significant decrease  
10 261 in *Xcf* population size from 35 to 42 DAP, down to an average of  $10^3$  CFU.g<sup>-1</sup> of seeds at  
11 262 maturity (Fig. 1C).

### 18 263 ***Changes in the Xcf bacterial transcriptome during seed development***

21 264 To explore the genetic determinants involved in *Xcf* seed transmission, dual (host and  
22 265 pathogen) transcriptome sequencing was performed at 24, 35 and 42 DAP. An essential step  
23 266 to obtain sufficient bacterial transcript data was to enrich RNA-Seq libraries for *Xcf* transcripts  
24 267 using 54,656 capture-probes. Among a total of 27.7 to 61.3 M sequenced reads that were  
25 268 obtained for each sample, 4.7 to 55.1 M mapped on the predicted transcriptome of *Xcf* strain  
26 269 7767R (Supplementary Table S1). A total of 4,372 mRNA were detected in at least one sample  
27 270 (count  $\geq 10$ ), which corresponded to >96% of the 4,537 predicted mRNA, thus validating our  
28 271 *Xcf* transcriptome enrichment strategy. Extensive changes in *Xcf* transcriptome were  
29 272 observed between seed filling (24 DAP) and the two other seed maturation stages (35 and 42  
30 273 DAP). Indeed, 865 and 1,674 DEGs were detected between 24 and 35 DAP and 24 and 42  
31 274 DAP, respectively, (Fig. 2A). On the other hand, only 17 DEGs were detected between 35 and  
32 275 42 DAP, indicating that transcriptomic levels stabilized between seed maturation and maturity  
33 276 stages. In line with this result, over-representation analyses of COG terms associated to  
34 277 bacterial DEGs were performed and revealed that intracellular trafficking and secretion terms  
35 278 were enriched at 24 DAP and post-translational modification at 35 and 42 DAP (Fig. 2B). The  
36 279 other enriched categories were translation and repair, both enriched at 42 DAP,  
37 280 and extracellular structure and cell motility, both enriched at 24 DAP (Fig. 2B).

38 281 A focus on the COG related to secretion processes revealed that all T3SS encoding  
39 282 genes and several *xps* genes involved in the T2SS were up-regulated at the seed filling stage,  
40 283 but not later during seed maturation (Supplementary Table S1). This was consistent with the  
41 284 observed up-regulation of the master regulator *hrpG* that is known to control many genes  
42 285 involved in the interaction with the host plant (Teper et al., 2021) such as the T3SS  
43 286 transcriptional activator *hrpX* and cognate effectors (T3Es) but also the *xps* genes involved in  
44 287 the secretion of cell wall degrading enzymes (Szczyzny et al., 2010). In line with this result,  
45 288 26/40 (65%) of T3E-encoding genes and several genes encoding pectin lyase (1), pectate  
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3 289 lyases (2), glycoside hydrolases (34) and proteases (40) were only up-regulated at early stage  
4 290 (Supplementary Table S1). As demonstrated in Darsonval et al. (2008), T3SS encoding  
5 291 genes, including *hrpG* and *hrpX* are essential genes for efficient bacterial seed transmission.  
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7 292 Together, these results suggested that bacteria were actively interacting with the host plant  
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9 293 only at early seed maturation stages, but not later.

### 294 ***Transcriptomic analysis of bean seeds in response to pathogen colonization***

295 Changes in *P. vulgaris* transcriptome were assessed using the same seed lots as for  
296 the *Xcf* transcriptome analyses described above. All results from this RNA-Seq analysis are  
297 displayed in the dedicated Jbrowse ([https://iris.angers.inrae.fr/pvulgaris\\_v2](https://iris.angers.inrae.fr/pvulgaris_v2)) and in  
298 Supplementary Table S1. Similar to what was observed in *Xcf* transcriptome changes, RNA-  
299 Seq analysis revealed that the plant response to the bacteria was higher at early than later  
300 stages of seed maturation, with 1,826 DEGs at 24 DAP, 1,351 at 35 DAP and only 105 at 42  
301 DAP (Fig. 2C). Only 137 DEGs (7.5% of 24 DAP DEGs) were shared between 24 and 35 DAP,  
302 indicating that the plant's response was different between these stages, ending up with almost  
303 no response in mature seeds. Only one DEG, encoding a CHAPERONE PROTEIN DNAJ-  
304 LIKE PROTEIN, was found to be in common between all the three stages  
305 (*Phvul.001G262000*) and could reflect a cellular stress in seeds inoculated with *Xcf*. This low  
306 overlap in DEGs across different seed developmental stages was also reflected at the level of  
307 functional category enrichments, which were different between 24, 35 and 42 DAP (Fig. 2D).  
308 The 24 DAP timepoint displayed the most complex response, with six up-regulated and nine  
309 down-regulated Mapman functional categories detected through functional enrichment  
310 analysis of DEGs. Some categories had well characterized roles in the plant-microbe  
311 molecular dialogue, such as Leucine Rich Repeat protein kinases (LRRs), which were up-  
312 regulated in *Xcf*-inoculated seeds (*i.e.* up-regulation of 15 annotated LRR related proteins),  
313 whereas the Mitogen-Activated Protein Kinases (MAPKs) and transcription factors (TF) of the  
314 bZIP, TIFY and AP2/ERF classes were down-regulated. At 24 DAP, in parallel to the down-  
315 regulation of MAPKs known to be involved in defense signal transduction such as MAPKKK3,  
316 MAPK3 or MAPK4, we also identified down-regulation of defense related genes such as two  
317 encoding thaumatin pathogenesis-related (PR) proteins, five JAZ and one JAR genes involved  
318 in the jasmonic acid pathway, but also *PAD4*, a central regulator of the salicylic acid pathway  
319 (Supplementary Table S1). At 35 DAP, functional ontology enrichment detected four up-  
320 regulated categories related to peptidase/protease activities and transfer of carbon skeletons.  
321 At 42 DAP, only two up-regulated categories (chromatin regulation and calcium-permeable  
322 channel) were detected.

### 323 ***Small RNAs associated with Xcf seed colonization***



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3 324 To further characterize the molecular dialogue between the colonized seeds and *Xcf*  
4 and the changes in plant transcript expression we focused our analysis on small RNA changes  
5 325 between colonized and healthy seeds at two contrasted stages, at 24 DAP to decipher if  
6 326 transcriptome changes due to plant response to pathogen could be mediated by small RNAs  
7 327 and at 42 DAP to reveal if specific small RNA could be stored at seed maturity to mediate  
8 328 defense response at post-germinative stage. Following sequencing and mapping against the  
9 329 mature miRNA database (miRBase release 22), we observed a total of 255 and 112 mature  
10 330 miRNAs differentially expressed ( $p < 0.05$ ) between *Xcf*-colonized and healthy seeds at 24 and  
11 331 42 DAP, respectively. At 24 DAP, mature miRNA up-regulated in *Xcf*-colonized seeds  
12 332 belonged to six miRNA families (miR162, miR172, miR396, miR482, miR6478 and miR8175),  
13 333 while four miRNA families showed down-regulation (let7, miR21, miR2111 and miR482)  
14 334 (Supplementary Table S2, Table 1). Similarly, at 42 DAP, we observed up-regulation of only  
15 335 one miRNA family (miR31) and down-regulation of two miRNA families (miR164 and miR451)  
16 336 (Supplementary Table S2, table 1). These data further confirmed that the molecular dialogue  
17 337 was more intense at early stages compared to later stages. Moreover, several miRNA families  
18 338 differentially regulated in *Xcf*-inoculated seeds were known to be involved in plant defense  
19 339 response such as miR482 (Shivaprasad et al., 2012), miR396 (Soto-Suárez et al., 2017) and  
20 340 miR172 (Holt et al., 2015). Known and unknown identified small RNAs were mapped to the  
21 341 genome using ShortStack version 4 and are available in the dedicated *P. vulgaris* Jbrowse  
22 342 ([https://iris.angers.inrae.fr/pvulgaris\\_v2](https://iris.angers.inrae.fr/pvulgaris_v2)).  
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27 344 To reveal the potential response mediated by these miRNAs, we identified putative  
28 345 transcript targets using (i) psRNATarget predictive tool (Dai et al. 2018) combined with (ii) our  
29 346 generated transcriptomic data at these two stages (Supplementary Table S2). To clarify, a  
30 347 transcript was considered as putative miRNA target if (i) its expectation (E) score from  
31 348 PsRNATarget was below 5 and if (ii) its expression was down-regulated when miRNA was up-  
32 349 regulated or inversely. Following these criteria, we identified between one to 11 putative  
33 350 miRNA target transcripts depending on miRNA families (Table 1). Among miRNAs up-  
34 351 regulated at 24 DAP in *Xcf*-inoculated, there were target transcripts related to defense such  
35 352 as miR8175 that could down-regulate key defense genes such as *PAD4-LIKE* involved in the  
36 353 defense pathway mediated by salicylic acid or more generic ones potentially involved in  
37 354 defense signaling such as a calcium-dependent-lipid-binding domain gene (CalB) or  
38 355 phospholipase A1 (Table 1). At the opposite, in the *Xcf*-inoculated seeds, we observed down-  
39 356 regulation of miRNA families such as let7, miR21, miR2111 and miR482 that potentially  
40 357 enhanced expression of developmental/growth genes such as TOR-LIKE, MED15, MED13,  
41 358 NOC1/SWA2. At 42 DAP, only three miR families, miR31, miR451 and miR164, showed  
42 359 significant expression changes between *Xcf*-infected and healthy seeds. An unique putative

transcript target was identified associated with miR451, which encodes a UBP26-LIKE protein potentially involved in the heterochromatin silencing at the end of the seed maturation (Luo et al., 2008). In conclusion, these results suggested that miRNA did mediate seed growth by silencing defense response at 24 DAP during early seed development. On the other hand at maturity, even if miR164 up-regulation was already shown to be involved in plant defense against fungi in cotton (*Gossypium hirsutum*) and *Populus tomentosa* (Hu et al., 2020; Chen et al., 2021b), in our susceptible host this miR was down-regulated at 42 DAP, which did not support the hypothesis that specific miRNA were accumulated in *Xcf*-inoculated seeds to prepare plant defense during germination. Interestingly, at 24 and 42 DAP, we observed that plant miRNA could support seed defense silencing probably due to the bacteria infection arsenal such as its T3Es activated early during seed development.

### 371 ***Seed methylome dynamics associated with Xanthomonas seed colonization***

372 To better understand the plant defense response and the impact of the bacterial  
373 colonization during seed development, we analyzed the changes in the seed methylomes of  
374 healthy and *Xcf*-colonized bean seeds at seed maturity (42 DAP). Indeed, DNA methylation  
375 was already described as a relevant mechanism in defense priming and plant immunity (for  
376 review see Deleris et al., 2016; Espinas et al., 2016). By focusing on the mature stage, we  
377 intended to capture the cumulative impact on DNA methylation of the bacterial colonization  
378 throughout seed development. The comparison of *Xcf*-colonized **versus healthy seeds**  
379 **samples** revealed 954 Differentially Methylated Regions (DMRs), of which 61.95% were  
380 hypomethylated (loss of methylation due to bacterial colonization) and 38.05%  
381 hypermethylated (gain of methylation due to bacterial colonization) (Supplementary Table S3).  
382 Not surprisingly, DMRs were predominantly localized on sequences containing transposable  
383 elements or repeats (74.1% of total DMRs), while 7.9% and 4.5% were located within gene  
384 and promoter sequences, respectively (Fig. 3A). Regarding the methylation context, we mainly  
385 observed DMRs in the CHH (*i.e.* 481 DMRs) and CHG (*i.e.* 394 DMRs) contexts, while only  
386 79 were related to the CG context. The complete list of the differentially methylated genes can  
387 be found in Supplementary Table S3 and in the dedicated Jbrowse  
388 ([https://iris.angers.inrae.fr/pvulgaris\\_v2](https://iris.angers.inrae.fr/pvulgaris_v2)).

389 We identified a total of 102 DMRs located within either coding (n=66) or promoter  
390 regions (n=36) of annotated genes, affecting 99 unique genes. Among coding sequences, 33  
391 genes resulted in hypomethylation and 33 hypermethylation, while among promoter regions  
392 27 genes were hypomethylated and 9 hypermethylated (Fig. 3B). To understand the role of  
393 genes differentially methylated in promoter and coding sequences at seed maturity, we  
394 compared with their changes in expression and did not observe any overlap with the DEGs

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3 395 between *Xcf*-colonized and non-colonized mature seeds, suggesting that differentially  
4 396 methylated regions did not regulate gene expression during seed development. To understand  
5 397 the potential role of these DMRs in the host-pathogen interaction, we looked at genes involved  
6 398 both in the germination and defense processes. First, from the dataset generated from Narsai  
7 399 et al. (2017) during ten early stages of *A. thaliana* seed germination, we identified 21,015  
8 400 genes showing a differential expression (adjusted *p*value <1% using ImpulseDE2) during  
9 401 germination process, therefore potentially involved in germination. By mapping *P. vulgaris*  
10 402 transcripts on Arabidopsis transcripts, we identified potential homologous transcripts in these  
11 403 two species and revealed a statistically significant enrichment (Fig. 3B, Fisher's Exact test *p*-  
12 404 value < 2.2e-16) of *P. vulgaris* genes displaying DMRs following pathogen colonization with  
13 405 those differentially expressed during germination. Indeed, out of the 90 homologous genes  
14 406 identified in *A. thaliana* and displaying DMR, 78 were genes differentially expressed during  
15 407 germination (Fig. 3C). Second, by analyzing the list of 99 unique genes displaying changes in  
16 408 methylation levels following bacterial colonization, we compiled a list of genes with putative  
17 409 roles in defense. We identified 17 genes, 10 hypomethylated and 7 hypermethylated following  
18 410 bacterial infection (Table 2). As example, we observed five LRR-related protein kinases, two  
19 411 PR proteins, and some genes identified as involved in immune response such as *PUB13-*  
20 412 *LIKE*, *CES11-LIKE* or *WRKY72* (complete list in Supplementary Table S3). As it is known that  
21 413 changes in the methylation state of transposable regions can also spread to adjacent regions  
22 414 and regulate nearby gene expression (Ahmed et al., 2011), we extended our search to coding  
23 415 sequences that are 5kb nearby DMRs located in transposable regions. This analysis detected  
24 416 additional 280 genes potentially associated with DMRs located in transposable regions (61.4%  
25 417 with hypomethylated regions and 38.6% with hypermethylated regions). Among these genes,  
26 418 we observed a subgroup coding for disease resistance proteins, with 5 additional putative TIR-  
27 419 NB-LRR proteins (*Phvul.004G105600*, *Phvul.004G100300*, *Phvul.010G026400*,  
28 420 *Phvul.010G027900*, *Phvul.010G028000*), 3 putative NB-ARC proteins (*Phvul.002G130300*,  
29 421 *Phvul.002G130400*, *Phvul.004G076100*) and 4 putative LRR kinases (*Phvul.008G164500*,  
30 422 *Phvul.008G164600*, *Phvul.005G162100*, *Phvul.005G162000*) (Table 2, Supplementary Table  
31 423 S3 and in the dedicated Jbrowse). In total, we listed 17 DMRs nearby genes associated with  
32 424 defense processes (Table 2). A comparison between these two lists revealed that 5 genes  
33 425 encoding three *LRR related proteins* (*Phvul.008G164600*, *Phvul.005G162000* and  
34 426 *Phvul.005G163000*), one *TIR NBS LRR protein* (*Phvul.010G026400*) and *WRKY72 TF*  
35 427 (*Phvul.003G068700*), displayed DMRs both within their gene sequences and in transposable  
36 428 elements located in proximal genomic regions. To define if these DMRs present in defense  
37 429 genes could be associated to a mechanism of defense priming induced by the presence of  
38 430 the pathogen during seed development, we selected the most differentially methylated, the  
39 431 *WRKY72* gene, and validated its implication in *Xcf* response during germination. By qRT-PCR,

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3 432 we analyzed the expression profile of *WRKY72* during germination in healthy seeds that  
4 433 germinated in presence of water versus *Xcf*. We clearly observed an over-expression of  
5 434 *WRKY72* at 7 days after imbibition in radicle of germinated seeds in presence of *Xcf*, showing  
6 435 the role of this gene in the defense response to *Xcf* infection during germination (Fig. 3D).

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10 436 Together, these results suggested that DMRs due to the presence of *Xcf* were mainly  
11 437 located in genes that could serve during the germination process and/or to the plant immune  
12 438 response to *Xcf*. In other word, pathogen-specific DNA methylations occurring during seed  
13 439 development could serve as defense priming to regulate gene expressions during the  
14 440 germination process, including a resumption of the molecular dialogue with the pathogen.

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## 20 442 **Discussion**

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23 443 Seeds are essential components of plants fitness and represent an important means  
24 444 of pathogen dispersion. To date, seed-pathogen interactions have been understudied at the  
25 445 molecular level, with, to our knowledge, only one plant-orientated study describing the  
26 446 transcriptomic response of *Medicago truncatula* seeds to bacterial pathogens of the  
27 447 Xanthomonadaceae family (Terrasson et al., 2015). We thus attempted to mitigate this  
28 448 knowledge gap by describing the molecular dialogue between common bean seeds and *Xcf*  
29 449 in conditions that seed bacterial transmission was asymptomatic. A first central result  
30 450 regarding this interaction is that *Xcf* was able to colonize seeds without major impact on seed  
31 451 physiology parameters, which was reflected by similar dry weights and water contents in  
32 452 healthy- and infected-seeds (Fig. 1). Consequently, we could not observe any obvious  
33 453 morphological changes in *Xcf*-colonized seeds compared to mock treated samples. Such  
34 454 findings indicate that asymptomatic *Xcf* colonization does not impact seed development or  
35 455 alter seed growth. This is consistent with previous report in *M. truncatula* during compatible  
36 456 interaction with *X. euvesicatoria* pv. *alfalfae*, while incompatible interaction with *X. campestris*  
37 457 pv. *campestris* resulted in developmental defects alongside a strong activation of defense  
38 458 pathways (Terrasson et al., 2015).

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43 459 To look into molecular dialogue, transcriptomic changes were assessed using dual  
44 460 RNAseq, which implies that we profiled both bacterial and plant transcripts during seed  
45 461 development generating the first dual transcriptomic analysis of a seed-pathogen interaction  
46 462 ever made. Profiling of bacterial transcripts represented the main challenge we faced due to  
47 463 the low concentration of bacterial cells within seeds. In this study, we successfully achieved  
48 464 this technological breakthrough by an enrichment step of bacterial transcripts using an RNA  
49 465 capture technology provided by Agilent. Our study revealed that *Xcf* and common bean seeds  
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3 466 establish an intense molecular dialogue at the early stages of seed development that appears  
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5 467 to become less intense as seed maturity approaches (Fig. 2).

6 468 On the pathogen side, the up-regulation of the T3SS genes and cognate effectors  
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8 469 observed in the early stages in comparison with 42 DAP suggests they could play a role in the  
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10 470 host defense silencing during the early step of seed colonization (Buttner, 2016). Indeed,  
11 471 **Xanthomonads** T3SS and T3Es are known to play two crucial roles in allowing efficient  
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13 472 bacterial seed transmission (Darsonval et al., 2008) and in suppressing plant innate immunity  
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15 473 and modulate plant pathways for the benefits of the bacteria (Büttner, 2016). Interestingly,  
16 474 down-regulated categories at early stages include basic biological processes such as  
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18 475 translation, protein turnover and DNA replication. This might suggest that *Xcf* multiplication is  
19 476 hampered, consistently with the observation that number of *Xcf* cells in seeds does not  
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21 477 increase significantly throughout seed developmental stages (Fig. 1C). Fewer functional  
22 478 categories were enriched at 35 DAP (Fig. 2D). The up-regulated ones (4 out of 5) included  
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24 479 peptidases, glycosylases and methyl transferases. Such functions can be associated with both  
25 480 suppression of defense (peptidases, Figaj et al., 2019) and cell wall remodeling, which could  
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27 481 help bacterial colonization of seed tissues, with no detectable impact on the seed physiology  
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29 482 and morphology, although more subtle microscopical effects cannot be excluded (Fig. 1).

30 483 On the host side, we also observed intense gene expression changes at early seed  
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32 484 developmental stage (24 DAP) in comparison to later ones, concomitantly with the intense  
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34 485 bacterial secretion activity. We observed an enrichment of up-regulated Leucine Rich Repeat  
35 486 (LRR) protein kinases (2 categories out of 6, LRR class VIII and class Xb), which are known  
36 487 to have prominent roles in microbe perception and defense activation **in non-seed tissues**  
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38 488 (Chakraborty et al., 2019), suggesting that the host may be able to recognize the pathogen.  
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40 489 On the other hand, RNA-Seq data highlighted a down-regulation of gene categories with well  
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42 490 characterized roles in the transduction of defense signaling pathways, including Mitogen-  
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44 491 Activated Protein Kinases (MAPKs such as MAPKKK3, MAPK3 or MAPK4) and transcription  
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46 492 factors of the bZIP (basic leucine ZIPper), TIFY, and AP2/ERF (APETALA 2/ Ethylene  
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48 493 Responsive Factor) families (Bethke et al., 2009; Bai et al., 2011; Tintor et al., 2013; Noman  
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50 494 et al., 2017). In line with this, we observed down-regulation of transcription factor families  
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52 495 known to have wider functions in plant stress signaling, such as the TUB or TLP (TUBBY-Like  
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54 496 Proteins) and the HSF (Heat Shock Transcription factor), as well as genes encoding PR  
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56 497 proteins, including *JAZ* and *JAR* genes involved in the jasmonic acid pathway, and *PAD4*  
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58 498 involved in the salicylic acid pathway. Such data suggest that even the transduction  
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60 499 components of the defense pathway are inhibited, potentially due to the bacterial T3E,  
500 ultimately avoiding a defense response.

501 Similar to transcriptomic data, changes in expression of small RNA at 24 DAP and 42  
502 DAP were consistent with silencing of downstream defense gene response. Indeed, analysis



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3 503 of the differentially expressed miRNA at 24 DAP and their putative target genes suggest a  
4 504 growth/defense trade-off mechanism in favor of growth in *Xcf*-inoculated seeds, with down-  
5 505 regulation of defense-associated transcripts (e.g. putative ortholog of PAD4  
6 506 (*Phvul002G274500*, Phyto Alexin Deficient 4, involved in salicylic acid signaling in *A. thaliana*  
7 507 (Pruitt et al., 2021)), a pepsin-type protease (*Phvul001G229200*) and up-regulation of  
8 508 development-associated transcripts (e.g. TOR-LIKE (*Phvul011G050300*) and  
9 509 MED15 (*Phvul010G157900*, MEDIATOR 15, required for correct embryogenesis in *A. thaliana*  
10 510 (Kim et al., 2016)). Interestingly, a heat shock protein (HSP70, *Phvul003G154800*) was  
11 511 detected as down-regulated genes at 24 DAP in *Xcf*-inoculated seeds and potential target of  
12 512 miR396, which complete the observed downregulation of HSF and smallHSP from our infected  
13 513 host transcriptome data (Fig. 2D). Recently it was showed that heat shock proteins are the  
14 514 most represented family among the down-regulated DEGs in leaf in a resistant common bean  
15 515 genotype towards common bacterial blight (caused by *Xcf* and *Xanthomonas phaseoli* pv.  
16 516 *phaseoli*) in comparison to a susceptible one (Foucher et al., 2020). On the other hand, data  
17 517 obtained at 42 DAP revealed only down-regulation of one miRNA family miR451, potentially  
18 518 regulating the up-regulation of its predicted target gene (*Phvul009G100000*) (Table 1). Its *A.*  
19 519 *thaliana* homolog (AT3G49600.1) deubiquitinates the histone H2B and is required for  
20 520 heterochromatin silencing during seed development (Luo et al., 2008). It is worth noting that  
21 521 chromatin reorganization processes due to histone modifications are among the categories  
22 522 enriched at 42 DAP (Fig. 2D), therefore suggesting that epigenetic regulation is a relevant  
23 523 component of the seed-pathogen molecular dialogue at this stage, potentially acting as  
24 524 priming for post-germination phase. Globally, the transcriptomic response of the susceptible  
25 525 host plant suggests that developing seeds are able to perceive the pathogen, and that defense  
26 526 responses might be largely inhibited by the bacterial T3SS arsenal. Consistent with  
27 527 suppression of the plant defense, up-regulation of photosynthesis and down-regulation of cell  
28 528 wall organization enzymes (Fig.2D) were also previously observed in leaves of susceptible  
29 529 common bean plants upon infection (Foucher et al., 2020). On the other hand, down-regulation  
30 530 of HSP and HSF, and AP2/ERF transcription factors (Fig.2D) were the hallmark of resistant  
31 531 plants. This suggests that a balance between susceptibility and resistance exist in *Xcf*-infected  
32 532 seeds, which could explain why, despite active bacterial colonization, the seeds were  
33 533 asymptomatic and presented no obvious physiological impact.

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535 In this study, we also revealed that DNA methylation changes in *Xcf*-inoculated seed  
536 may also act as defense priming for post-germination phase. Indeed, the seed host methylome  
537 analysis at 42 DAP revealed significant changes in methylation status in 826 different genomic  
538 regions, affecting a total of 99 different genes, which did not display any change in gene  
539 expression during seed maturation. Of these, 17 can be associated to defense processes in

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3 540 a relatively straightforward manner (Table 2). As hypomethylation of defense genes has been  
4 541 widely associated with increased resistance to biotic stress (Downen et al., 2012; Annacondia  
5 542 et al., 2021), the hypomethylated genes of this list (10 out of 17) can be considered as  
6 543 candidates for epigenetic-dependent defense priming. The concept of defense priming  
7 544 postulates that plants conserve the memory of previous encounters with pathogens by  
8 545 preparing their defense networks to respond more rapidly and strongly to a future aggression  
9 546 (Martinez-Medina et al., 2016). Enhanced chromatin access to defense genes through  
10 547 hypomethylation is one of the best characterized mechanisms in this sense (Hannan Parker  
11 548 et al., 2022). Furthermore, epigenetic defense priming can be transmitted to the next  
12 549 generations (Slaughter et al., 2012). This would be consistent with a scenario where *Xcf*  
13 550 colonization does not directly induce defense gene activation in common bean seeds, but  
14 551 rather triggers a primed state that prepare defense networks for the moment when the  
15 552 pathogen will again become virulent (after germination). Hypomethylation of transposable  
16 553 elements is another well-characterized mechanism of epigenetic regulation of plant defenses,  
17 554 as it can lead to the euchromatisation of wide genomic regions, both proximal and distal (López  
18 555 Sánchez et al., 2016; Halter et al., 2021). The five defense genes present in Table 2 are thus  
19 556 likely to be good candidates for relevant roles in bean resistance against *Xcf*. They include  
20 557 three genes affected by hypomethylation (*Phvul.008G164600*, *Phvul.005G163000*,  
21 558 *Phvul.010G026400*), namely two putative LRR kinase receptors and one effector receptor, all  
22 559 uncharacterized. The other two genes affected by hypermethylation are another  
23 560 uncharacterized LRR kinase receptor (*Phvul.005G162000*) and the putative bean homolog of  
24 561 WRKY72 (*Phvul.003G068700*). This transcription factor has the highest methylation gain  
25 562 among all the genes detected (fold change of +4,3), suggesting that its methylation status  
26 563 might be important in response to *Xcf* infection. Indeed, the role of WRKY72 orthologs is  
27 564 contradictory in different species. A positive role on defense responses was showed in *A.*  
28 565 *thaliana* and tomato (*Solanum lycopersicum*) against oomycetes and bacteria, respectively  
29 566 (Bhattarai et al., 2010), but regarding the interaction between rice (*Oryza sativa*) and  
30 567 *Xanthomonas oryzae* pv. *Oryzae*, it was showed to negatively regulate rice defense responses  
31 568 by repressing jasmonate biosynthetic genes (Hou et al., 2019). In our study, we validated its  
32 569 role as *Xcf*-response genes during germination by highlighting its over-expression at 7 DAI in  
33 570 radicles of germinated seeds in presence of *Xcf*. Another consideration regarding our  
34 571 methylome data is the high overlap between DMRs-containing genes and germination-DEGs  
35 572 (Fig. 3B). This suggests that the DMR-containing genes following bacterial infection detected  
36 573 in this study may serve during the germination process through a defense priming mechanism.  
37 574 More investigation will be required to define if these methylation changes will have positive or  
38 575 negative impacts on defense- and/or germination-related gene expressions and will require  
39 576 extensive transcriptomic analyses.

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4 578 All together, these results indicate that the molecular mechanisms involved in the  
5 579 pathogen-seed dialogue change radically across the developmental stages for both the host  
6 580 and the pathogen side, potentially suggesting the existence of distinct phases in the  
7 581 considered seed-pathogen interaction. It would be interesting to explore whether such **pattern**  
8 582 takes place in other seed-pathogen interactions. By summing our physiological and molecular  
9 583 observations, with the previous findings of Terrasson et al. (2015), we can propose a model  
10 584 where the recognition of a host-specific pathogen at the early stages of seed development  
11 585 fails to trigger seed defense activation, as if the presence of the pathogen was “accepted” by  
12 586 the host. Even if we cannot define whether this suppression is caused by the pathogen or by  
13 587 the host, two *Xanthomonas* studies would support the role of bacterial T3SS in host defense  
14 588 silencing. Darsonval et al. (2008) showed the essential role of T3E for an efficient seed  
15 589 colonization in the *X. citri* pv. *fuscans*-bean seed interaction and Terrasson et al. (2015)  
16 590 showed that *X. euvesicatoria* pv. *Alfalfae* was able to silence some defense genes in a  
17 591 compatible interaction, but not in an incompatible one. In any case, the result is a situation  
18 592 where the seed develops normally without any obvious fitness costs associated to an eventual  
19 593 defense activation, while the host-specific pathogen displays a non-aggressive behavior  
20 594 throughout all the seed development and limits its proliferation (Fig. 4). Such “ceasefire”  
21 595 scenario might be advantageous for both parts: the seed is able to reach maturity, which would  
22 596 potentially be beneficial for the pathogen as well by allowing it to infect the future germinated  
23 597 seedling, therefore giving it access to nourishment and facilitating its dispersal. On the other  
24 598 hand, data at 42 DAP suggest a relevant role for epigenetic modifications in the host. It is  
25 599 tempting to speculate that such modifications contribute to prepare the host to face a novel  
30 600 pathogen assault after germination (Fig. 4). Detailed analysis of the transcriptome and  
31 601 epigenome of the bean-*Xcf* interaction during the germination process would be a promising  
32 602 future research direction in this sense. Recent data from the compatible interaction *Alternaria*  
33 603 *brassicicola*-*A. thaliana*, used as seed transmission model, showed that host defense  
34 604 pathways are subjected to drastic changes during the germination process (Ortega-Cuadros  
35 605 et al., 2022). It would be interesting to explore whether such rearrangements take place in  
36 606 other compatible interactions such as *Xcf*-bean and if a link with epigenetic modifications  
37 607 exists.

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54 609 To summarize, the present study adds novel elements to the current knowledge gap  
55 610 of seed-pathogen interactions. The dual transcriptomic analysis allowed for the first time to  
56 611 describe the molecular dialogue from both host and pathogen sides, while methylome and  
57 612 sRNAs profiling added further indications on the potential regulatory mechanisms and the  
58 613 genes involved. A dedicated Jbrowse containing all these generated data will serve as



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3 614 baseline tool for the scientific communities and will be enriched by future related studies. An  
4 615 important general conclusion that we can draw is that seeds have primarily an active role in  
5 616 this interaction at early seed maturation stage, contrary to the widely diffused assumption  
6 617 considering seeds as passive carriers of microbes (Dutta et al., 2014). As the role of  
7 618 seedborne pathogens in causing yield losses receives relatively little attention, we hope that  
8 619 the present study can stimulate novel research efforts in this sense to shed light on the many  
9 620 obscure points still shrouding seed-pathogen interactions.  
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## 15 622 **Supplemental data**

16 623 Supplementary Data S1: Result tables of RNA-seq data

17 624 Supplementary Data S2: Result tables of sRNA-seq data

18 625 Supplementary Data S3: Result tables of BS-seq data

19 626 Supplementary Data S4: Primers used for qPCR experiments.  
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## 25 628 **Acknowledgements**

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## 42 637 **Author contributions**

43 638 AD, MBarret and JV designed the research. AD, MBarret and JV supervised the  
44 639 experiments; AD, LPT, DL, NC, MBriand, MBarret, JV performed and analysed the  
45 640 experiments. AD, LPT, NC, MBarret and JV wrote the manuscript and all co-authors  
46 641 reviewed and edited the manuscript.  
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## 52 643 **Data availability**

53 644 The data that support the findings of this study have been deposited in NCBI Gene Expression  
54 645 Omnibus and are accessible through GEO Super Series accession number GSE227421  
55 646 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE227421>) or individually through  
56 647 GEO accession numbers GSE227386 (bacterial RNA-seq,  
57 648 <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE227386>), GSE226918 (plant

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3 649 RNAseq, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226918>), GSE226919  
4 650 (plant methylome, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226919>) and  
5 651 GSE226920 (sRNA-Seq, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226920>).

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## 25 848 **Legends**

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27 849 **Figure 1. Transmission of *Xcf* to bean seeds.** (A) Seed water content (B) Seed dry weight  
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29 850 (gram) and (C) *Xcf* population size ( $\log_{10}$  CFU per gram of seed) at the different sampling  
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31 851 stages (24DAP, 35DAP and 42DAP). Differences between the sampling stage and the  
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33 852 treatment ( $H_2O$ - or *Xcf*-inoculated) were assessed by Kruskal-Wallis test followed by post-hoc  
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35 853 Dunn's test. The percentages of observed contaminated seeds at different seed  
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37 854 developmental stages are indicated (expressed as averages with SD between brackets). P-  
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39 855 values are indicated as \* <5%, \*\* <1% and \*\*\* <0.1%.

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41 857 **Figure 2. Dual transcriptomic analysis of the *Xcf*-*P. vulgaris* seed interaction.** (A) & (C)  
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43 858 Histograms summarizing the number of differentially expressed genes (DEGs) detected  
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45 859 comparing datasets from different seed development stages from *Xcf* samples (A) and DEGs  
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47 860 from different development stages from *P. vulgaris* samples (C). The number of DEGs is  
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49 861 indicated on the bars. (B) & (D) Dot plots showing category enrichment results obtained  
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51 862 through gene ontology analysis of DEGs from *Xcf* (B) and *P. vulgaris* (D). Gene ontology  
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53 863 analysis was performed with the Clusterprofiler package for R.

54 864 **Figure 3. Summary of methylome analysis data generated by comparing *Xcf*-colonized  
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56 865 and uncolonized seeds at 42 DAP.** (A) Pie chart illustrating the repartition of differentially  
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58 866 methylated regions (DMRs) following *Xcf* colonization on *P. vulgaris* genome at 42 DAP. (B)  
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60 867 Venn diagram illustrating the overlap between gene sequences containing DMRs at 42 DAP  
868 and differentially expressed genes (DEGs) during germination (see details in text).

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3 869 **Figure 4. Schematic model of the *Xcf*-bean seed dialogue.** Left panel: at early seed  
4 870 development stages (24 DAP), *Xcf* is recognized by the host. Despite the bacterial recognition,  
5 871 defense transduction pathways based on MAP kinases cascades (MAPKs) and transcription  
6 872 factors (TFs) activation are suppressed in seeds, thus failing to induce a defense reaction.  
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8 873 Red dotted lines with flat end indicate hypothetical inhibition. Middle Panel: at 35 DAP, both  
9 874 the bacterial pathogen and the host plant are still transcriptionally active. Bacterial populations  
10 875 continue to grow, but the T3SS is no longer active, suggesting that the bacteria lowered its  
11 876 weapons, keeping the seed alive and healthy. Right panel: at seed maturation (42 DAP), the  
12 877 dialogue between *Xcf* and seed is much less detectable in comparison to earlier stages but  
13 878 epigenetic mechanisms such as DNA methylation could be active, which was observed at  
14 879 seed maturity by the changes in the methylation status of genes identified as involved in both  
15 880 defense and germination processes. This change in DNA methylation could prime genes  
16 881 involved in defense/germination, ultimately preparing the host for the post-germination battle  
17 882 with the virulent *Xcf* (see text for more details).

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## Tables

**Table 1. Summary of differentially accumulated small RNAs (up- or down-regulated) detected at 24 and 42 DAP in *Xcf*-colonized *P. vulgaris* seeds with their putative target genes according to psRNAtarget.**

Seed developmental stages	DEseq2		psRNAtarget combined with corresponding significant expression changes from RNAseq data	
	Up- or down-regulation in <i>Xcf</i> -colonized seeds	mature miR	variants	
			<b>putative targets using psRNAtarget (= miRNA potential target genes )</b>	
24DAP	Up	miR162	a,b	Phvul.007G067800 (HSF), Phvul.008G055500 (TGD3), Phvul.006G176000 (trihelix DNA-binding), Phvul.008G114700 (Rab-GDP)
	Up	miR172	a,c,d,e,f,g,h,i,l	Phvul.009G014600 (cardiolipin deacylase), Phvul.001G212400 (RING-domain E3 ligase), Phvul.005G068800 (Probable E3 ubiquitin-protein ligase), Phvul.003G053000 (glycosyltransferase)
	Up	miR396	a,b,c,d,e,i	Phvul.009G246000 (SNF4-like), Phvul.001G229200 (pepsin-type protease), Phvul.002G026300 integrin-like protein, Phvul.003G154800 (HSP70)
	Up	miR482	3p, b-3p, d-3p	Phvul.011G149100 Transducin/WD40 repeat-like, Phvul.008G055500 (ATPase component TGD3 of TGD), Phvul.003G295800 (ATG2-like), Phvul.011G082700 (P-loop NTPase), Phvul.010G141400 (DOF1-like TF), Phvul.002G261500 (RNA polymerase regulatory protein)
	Up	miR6478	-	Phvul.003G155500 (component SR-alpha of SRP)
	Up	miR8175	-	Phvul.002G059000 (Phospholipase A1), Phvul.002G274500 (PAD4-like), Phvul.010G082300 (UDP-D-glucuronic acid 4-epimerase), Phvul.005G035400 (mRNA-splicing factor 18), Phvul.001G240600 (CaLB domain)
	Down	let7	a,c,d,f	Phvul.001G022700 (REMORIN-LIKE), Phvul.003G119100 (calcium-dependent lipid-binding), Phvul.011G061600 (PTAC16-like), Phvul.003G035400 (XYL1-like), Phvul.004G121666 (subunit of CF1 of ATP synthase), Phvul.008G163350 (cohesin cofactor (PDS5)), Phvul.011G050300 (protein kinase (PIKK) TOR-like ), Phvul.003G050600 (catalytic protein (CER2)), Phvul.007G069900, Phvul.011G001200 (SAC1-like), Phvul.002G185150 (sodium:proton antiporter (SOS1))
	Down	miR21	a	Phvul.010G157900 (MED15-like), Phvul.007G191600 (CHR8-like)
	Down	miR2111	a,b,c,d,e,f,g,h,i,j,k,m,n,o	Phvul.001G269300 (MED13-like), Phvul.001G179300 (PGP1-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G168500 (Solute transport channels)
	Down	miR482	5p	Phvul.004G170000 (STT3-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G244066, Phvul.002G189700 (UPL1-like)
42DAP	Up	miR31	-	-
	Down	miR451	a	Phvul.009G100000 (UBP26-like)
	Down	miR164	a,b,c,d,e,f,g,h,i,j,k	-

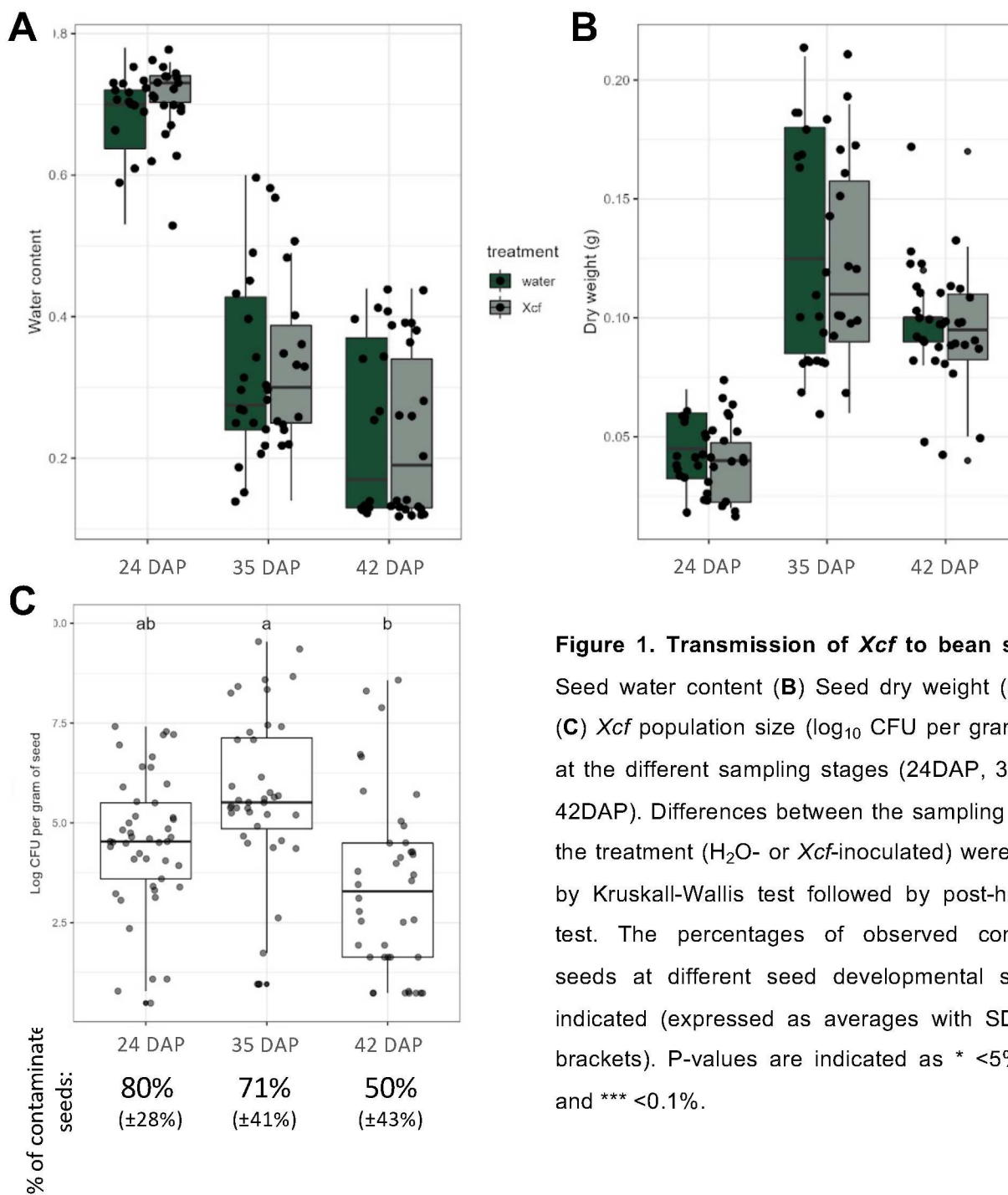
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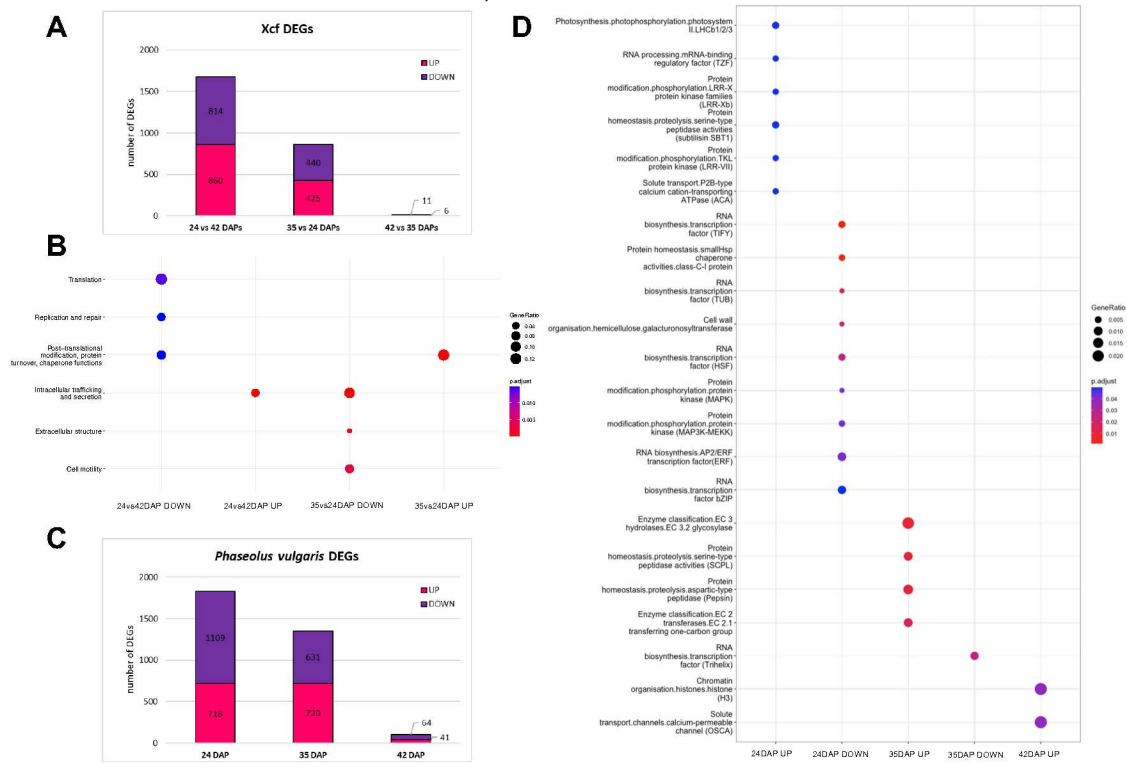
**Table 2. List of differentially methylated regions located in defense-associated genes in of *P. vulgaris* seeds following *Xcf* colonization at 42 DAP. DMRs were located in promoter or gene sequences, but also in transposable elements located within 5kb of genic regions. The *P. vulgaris* annotation column was filled according to the *P. vulgaris* genome (v2.1). The location indicates whether the region is localized in a coding region (gene) or in the promoter (1kbprom) or in TE within 5kb of genic regions (within 5kb). The putative ortholog was assigned as best hit based on sequence similarity in the *A. thaliana* genome (v.11). The “gain or loss” column shows whether the differentially methylated region associated with the corresponding *P. vulgaris* gene is hypo- (loss) or hypermethylated (gain) in response to *Xcf* colonization at 42 DAP. FC, fold change of methylation between *Xcf*- versus H<sub>2</sub>O-treated seeds. FC ratios are not indicated for DMRs within 5kb of genic regions because they correspond to multiple DMRs.**

<i>P. vulgaris</i> locus ID	Location	<i>P. vulgaris</i> annotation	<i>A. thaliana</i> putative ortholog	<i>A. thaliana</i> symbol	<i>A. thaliana</i> annotation	Methylation FC (Xcf vs H <sub>2</sub> O)	Gain or loss of methylation in <i>Xcf</i> -treated seeds
Phvul.001G233000	gene	protein kinase (SD-1)	AT3G16030	CES101	lectin protein kinase family protein	0.52	loss
Phvul.002G125500	within 5kb	not annotated	AT5G08315		Defensin-like (DEFL) family protein		loss
Phvul.002G130300	within 5kb	not annotated	AT3G14470		NB-ARC domain-containing disease resistance protein		gain
Phvul.002G130400	within 5kb	not annotated	AT3G14470		NB-ARC domain-containing disease resistance protein		gain
Phvul.003G021700	1kbprom	transferase transferring phosphorus-containing group	AT1G07040		Protein kinase superfamily protein	0.51	loss
Phvul.003G040300	1kbprom	6-deoxocasterone 6-oxidase	AT3G03180	BR6OX2	brassinosteroid-6-oxidase 2	2.98	gain
Phvul.003G056900	within 5kb	systemic acquired resistance (SAR) regulator protein (SN1)	AT4G18470	SN1	negative regulator of systemic acquired resistance (SN1)		loss
Phvul.003G068700	gene	transcription factor (WRKY)	AT5G15130	WRKY72	WRKY DNA-binding protein 72	4.30	gain
Phvul.003G068700	within 5kb	transcription factor (WRKY)	AT5G15130	WRKY72	WRKY DNA-binding protein 72		gain
Phvul.003G175700	gene	DRB4-DRB7.1 regulator complex component DRB7	AT5G20320	DCL4	dicer-like 4	0.37	loss
Phvul.004G076100	within 5kb	not annotated	AT3G14470		NB-ARC domain-containing disease resistance protein		loss
Phvul.004G105600	within 5kb	not annotated	AT2G34930		disease resistance family protein / LRR family protein		loss
Phvul.005G162000	1kbprom	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein	2.36	gain
Phvul.005G162000	within 5kb	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein		gain
Phvul.005G162100	within 5kb	transferase transferring phosphorus-containing group	AT1G51800		Leucine-rich repeat protein kinase family protein		gain
Phvul.005G163000	gene	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein	0.38	loss
Phvul.005G163000	within 5kb	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein		loss
Phvul.006G006800	gene	TKL protein kinase superfamily protein kinase (DUF26)	AT4G05200	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	0.18	loss
Phvul.006G033200	gene	not annotated	AT5G38280	PR5K	PR5-like receptor kinase	0.52	loss
Phvul.007G187700	1kbprom	not annotated	AT3G04720	PR4	pathogenesis-related 4	0.37	loss
Phvul.007G241200	gene	transcription factor (MYB-related)	AT5G47390		myb-like transcription factor family protein	3.25	gain
Phvul.007G241200	within 5kb	transcription factor (MYB-related)	AT5G47390		myb-like transcription factor family protein		gain
Phvul.007G241300	within 5kb	Ser/Thr protein kinase	AT1G50240	FU	Protein kinase family protein with ARM repeat domain		gain
Phvul.008G164500	within 5kb	transferase transferring phosphorus-containing group	AT3G21340		Leucine-rich repeat protein kinase family protein		loss
Phvul.008G164600	gene	not annotated	AT1G05700		Leucine-rich repeat transmembrane protein kinase protein	0.45	loss
Phvul.008G164600	within 5kb	not annotated	AT1G05700		Leucine-rich repeat transmembrane protein kinase protein		loss
Phvul.008G228714	gene	S8-class protease (subtilisin) families protease (SBT4)	AT3G46850		Subtilase family protein	4.29	gain
Phvul.008G229400	gene	S8-class protease (subtilisin) families protease (SBT4)	AT5G59100		Subtilisin-like serine endopeptidase family protein	0.48	loss
Phvul.010G026400	1kbprom	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family	0.35	loss
Phvul.010G026400	within 5kb	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family		loss
Phvul.010G027900	within 5kb	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family		loss
Phvul.010G028000	within 5kb	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family		loss
Phvul.010G062500	within 5kb	WRKY33-dependent plant immunity transcription factor	AT2G38470	WRKY33	WRKY DNA-binding protein 33		loss
Phvul.011G064700	gene	U-Box E3 ligase activities E3 ubiquitin ligase (PUB)	AT3G46510	PUB13	plant U-box 13	4.06	gain
Phvul.011G108300	gene	transferase transferring phosphorus-containing group	AT1G29730		Leucine-rich repeat transmembrane protein kinase	2.32	gain
Phvul.011G176100	gene	transferase transferring one-carbon group	AT3G11480	BSMT1	S-adenosyl-L-methionine-dependent methyltransferases family protein	2.56	gain

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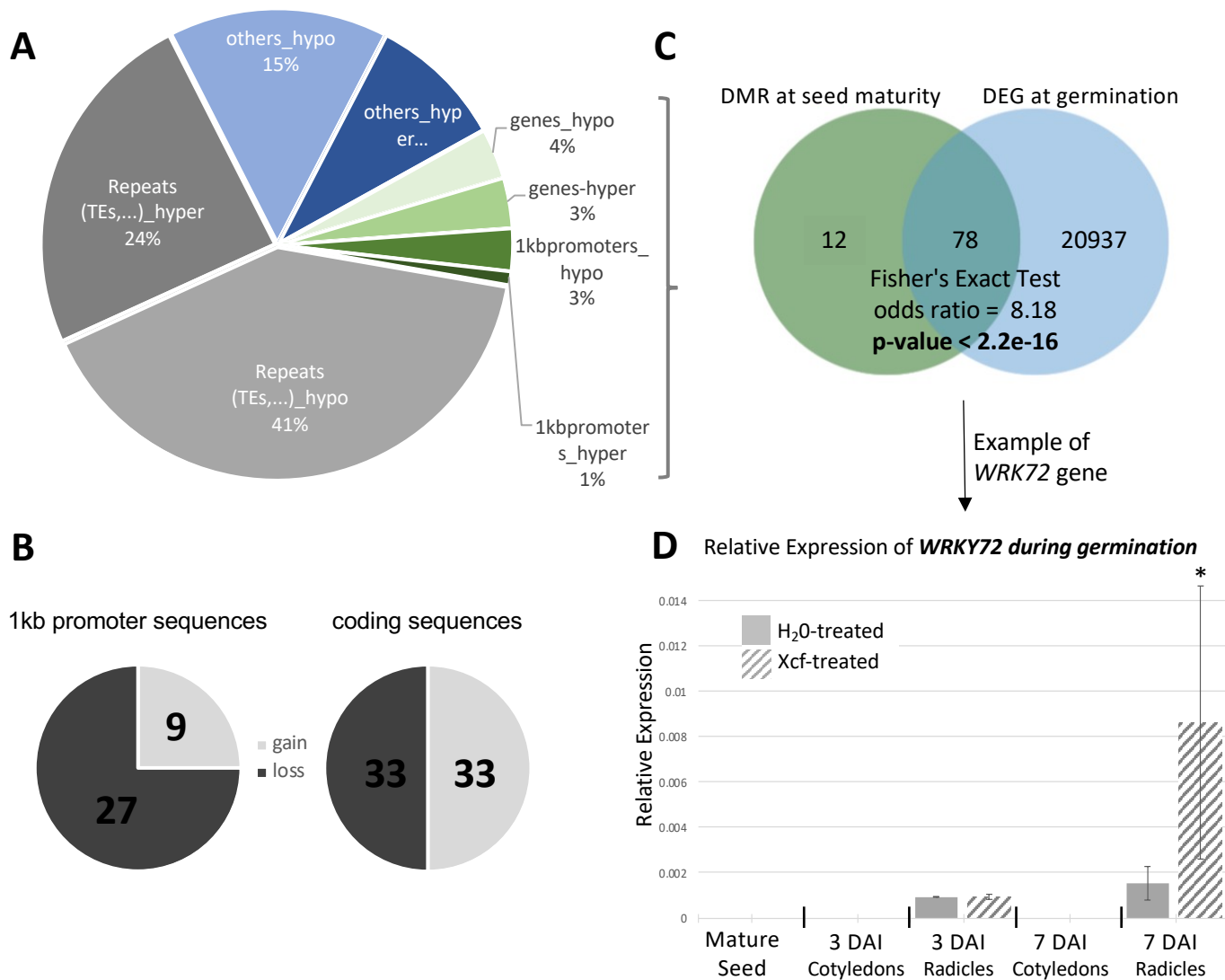


**Figure 1. Transmission of Xcf to bean seeds.** (A) Seed water content (B) Seed dry weight (gram) and (C) Xcf population size (log<sub>10</sub> CFU per gram of seed) at the different sampling stages (24DAP, 35DAP and 42DAP). Differences between the sampling stage and the treatment (H<sub>2</sub>O- or Xcf-inoculated) were assessed by Kruskal-Wallis test followed by post-hoc Dunn's test. The percentages of observed contaminated seeds at different seed developmental stages are indicated (expressed as averages with SD between brackets). P-values are indicated as \* <5%, \*\* <1% and \*\*\* <0.1%.

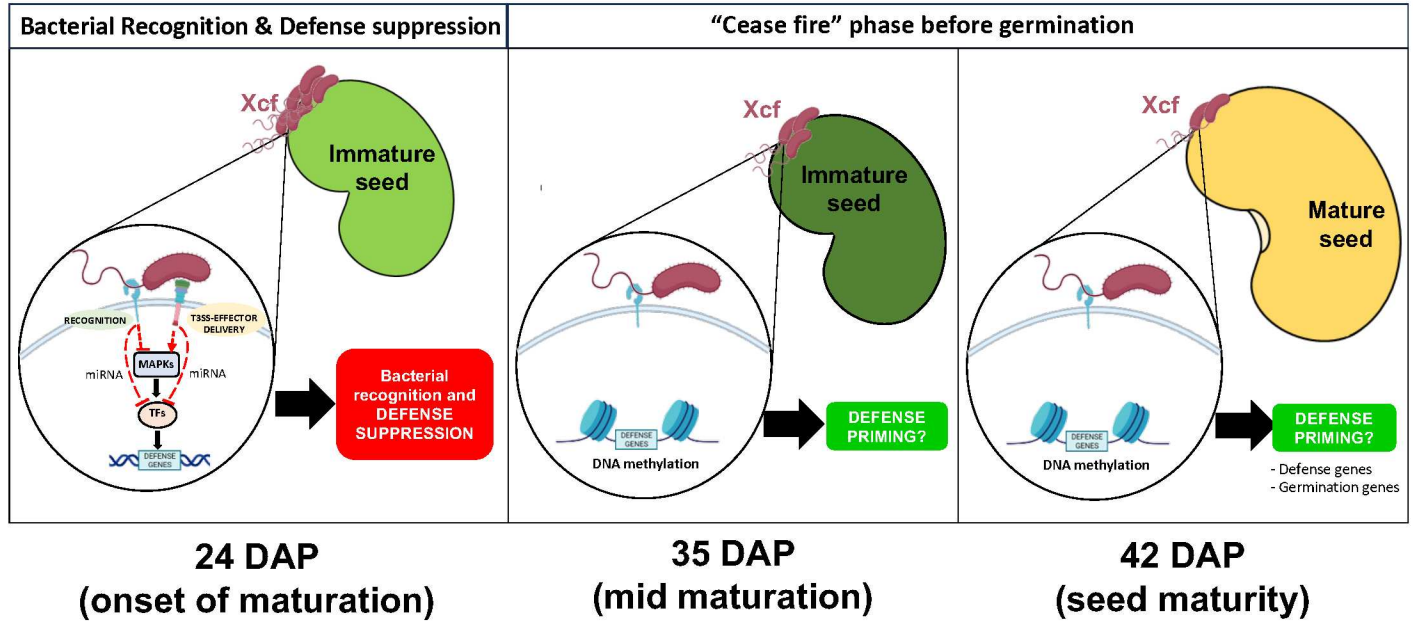


**Figure 2. Dual transcriptomic analysis of the *Xcf-P. vulgaris* seed interaction.**

(A)(C) Histograms summarizing the number of differentially expressed genes (DEGs) detected comparing datasets from different seed development stages from *Xcf* samples (A) and DEGs from different development stages from *P. vulgaris* samples (C). The number of DEGs is indicated on the bars. (B) (D) Dot plots showing category enrichment results obtained through gene ontology analysis of DEGs from *Xcf* (B) and *P. vulgaris* (D). Gene ontology analysis was performed with the ClusterProfiler package for R.



**Figure 3. Summary of methylome analysis data generated by comparing *Xcf*-colonized and uncolonized seeds at 42 DAP.** (A) Pie chart illustrating the repartition of differentially methylated regions (DMRs) following *Xcf* colonization on *P. vulgaris* genome at 42 DAP. (B) Pie charts illustrating the number of hypo-(loss) and hyper-(gain) methylated DMRs located in annotated genes (1kb promoter or coding sequences). (C) Venn diagram illustrating the overlap between gene sequences containing DMRs at 42 DAP and differentially expressed genes (DEGs) during germination (see details in text). (D) Relative expression of *WRKY72* during germination (at 3 and 7 Days after imbibition, DAI) in H<sub>2</sub>O- and *Xcf*-treated seeds.



**Figure 4. Schematic model of the *Xcf*-bean seed dialogue.** Left panel: at early seed development stages (24 DAP), *Xcf* is recognized by the host. Despite the bacterial recognition, defense transduction pathways based on MAP kinases cascades (MAPKs) and transcription factors (TFs) activation are suppressed in seeds, thus failing to induce a defense reaction. Red dotted lines with flat end indicate hypothetical inhibition. Middle Panel: at 35 DAP, both the bacterial pathogen and the host plant are still transcriptionally active. Bacterial populations continue to grow, but the T3SS is no longer active, suggesting that the bacteria lowered its weapons, keeping the seed alive and healthy. Right panel: at seed maturation (42 DAP), the dialogue between *Xcf* and seed is much less detectable in comparison to earlier stages but epigenetic mechanisms such as DNA methylation could be active, which was observed at seed maturity by the changes in the methylation status of genes identified as involved in both defense and germination processes. This change in DNA methylation could prime genes involved in defense/germination, ultimately preparing the host for the post-germination battle with the virulent *Xcf* (see text for more details).



Table 2. List of differentially methylated regions located in defense-associated genes in of *P. vulg*

<i>P. vulgaris</i> locus ID	Location	<i>P. vulgaris</i> annotation
Phvul.001G233000	gene	protein kinase (SD-1)
Phvul.002G125500	within 5kb	not annotated
Phvul.002G130300	within 5kb	not annotated
Phvul.002G130400	within 5kb	not annotated
Phvul.003G021700	1kbProm	transferase transferring phosphorus-containing group
Phvul.003G040300	1kbProm	6-deoxocastasterone 6-oxidase
Phvul.003G056900	within 5kb	systemic acquired resistance (SAR) regulator protein (SNI1)
Phvul.003G068700	gene	transcription factor (WRKY)
Phvul.003G068700	within 5kb	transcription factor (WRKY)
Phvul.003G175700	gene	DRB4-DRB7.1 regulator complex.component DRB7
Phvul.004G076100	within 5kb	not annotated
Phvul.004G105600	within 5kb	not annotated
Phvul.005G162000	1kbProm	transferase transferring phosphorus-containing group
Phvul.005G162000	within 5kb	transferase transferring phosphorus-containing group
Phvul.005G162100	within 5kb	transferase transferring phosphorus-containing group
Phvul.005G163000	gene	transferase transferring phosphorus-containing group
Phvul.005G163000	within 5kb	transferase transferring phosphorus-containing group
Phvul.006G006800	gene	TKL protein kinase superfamily.protein kinase (DUF26)
Phvul.006G033200	gene	not annotated
Phvul.007G187700	1kbProm	not annotated
Phvul.007G241200	gene	transcription factor (MYB-related)
Phvul.007G241200	within 5kb	transcription factor (MYB-related)
Phvul.007G241300	within 5kb	Ser/Thr protein kinase
Phvul.008G164500	within 5kb	transferase transferring phosphorus-containing group
Phvul.008G164600	gene	not annotated
Phvul.008G164600	within 5kb	not annotated
Phvul.008G228714	gene	S8-class protease (subtilisin) families.protease (SBT4)
Phvul.008G229400	gene	S8-class protease (subtilisin) families.protease (SBT4)
Phvul.010G026400	1kbProm	effector receptor (NLR)
Phvul.010G026400	within 5kb	effector receptor (NLR)
Phvul.010G027900	within 5kb	effector receptor (NLR)
Phvul.010G028000	within 5kb	effector receptor (NLR)
Phvul.010G062500	within 5kb	WRKY33-dependent plant immunity transcription factor
Phvul.011G064700	gene	U-Box E3 ligase activities.E3 ubiquitin ligase (PUB)
Phvul.011G108300	gene	transferase transferring phosphorus-containing group
Phvul.011G176100	gene	transferase transferring one-carbon group

3aris seeds following Xcf colonization at 42 DAP. DMRs were located in promoter or gene sequences:

<i>A. thaliana</i> putative ortholog	<i>A. thaliana</i> symbol	<i>A. thaliana</i> annotation
AT3G16030	CES101	lectin protein kinase family protein
AT5G08315		Defensin-like (DEFL) family protein
AT3G14470		NB-ARC domain-containing disease resistance protein
AT3G14470		NB-ARC domain-containing disease resistance protein
AT1G70740		Protein kinase superfamily protein
AT3G30180	BR6OX2	brassinosteroid-6-oxidase 2
AT4G18470	SNI1	negative regulator of systemic acquired resistance (SNI1)
AT5G15130	WRKY72	WRKY DNA-binding protein 72
AT5G15130	WRKY72	WRKY DNA-binding protein 72
AT5G20320	DCL4	dicer-like 4
AT3G14470		NB-ARC domain-containing disease resistance protein
AT2G34930		disease resistance family protein / LRR family protein
AT4G29990		Leucine-rich repeat transmembrane protein kinase protein
AT4G29990		Leucine-rich repeat transmembrane protein kinase protein
AT1G51800		Leucine-rich repeat protein kinase family protein
AT4G29990		Leucine-rich repeat transmembrane protein kinase protein
AT4G29990		Leucine-rich repeat transmembrane protein kinase protein
AT4G05200	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25
AT5G38280	PR5K	PR5-like receptor kinase
AT3G04720	PR4	pathogenesis-related 4
AT5G47390		myb-like transcription factor family protein
AT5G47390		myb-like transcription factor family protein
AT1G50240	FU	Protein kinase family protein with ARM repeat domain
AT3G21340		Leucine-rich repeat protein kinase family protein
AT1G05700		Leucine-rich repeat transmembrane protein kinase protein
AT1G05700		Leucine-rich repeat transmembrane protein kinase protein
AT3G46850		Subtilase family protein
AT5G59100		Subtilisin-like serine endopeptidase family protein
AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family
AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family
AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family
AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family
AT2G38470	WRKY33	WRKY DNA-binding protein 33
AT3G46510	PUB13	plant U-box 13
AT1G29730		Leucine-rich repeat transmembrane protein kinase
AT3G11480	BSMT1	S-adenosyl-L-methionine-dependent methyltransferases family protein



s, but also in transposable elements located within 5kb of genic regions. The *P. vulgaris* annotation column

Methylation FC (Xcf vs H2O)	Gain or loss of methylation in Xcf-treated seeds
0.52	loss
	loss
	gain
	gain
0.51	loss
2.98	gain
	loss
4.30	gain
	gain
0.37	loss
	loss
	loss
2.36	gain
	gain
	gain
0.38	loss
	loss
0.18	loss
0.52	loss
0.37	loss
3.25	gain
	gain
	gain
	loss
0.45	loss
	loss
4.29	gain
0.48	loss
0.35	loss
	loss
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	loss
4.06	gain
2.32	gain
2.56	gain

	loss	gain
Protein kinases	6	2
Resistance proteins	1	0
Transcription factors	0	1
Antimicrobial proteins	2	1
	loss	gain
Protein kinases	4	3
Resistance proteins	4	2
Transcription factors	1	1
Antimicrobial proteins	1	0

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rise to Xcf colonization at 42 DAP. FC, fold change of methylation between Xcf- versus H<sub>2</sub>O-treated se

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eds. FC ratios are not indicated for DMRs within 5kb of genic regions because they correspond to m

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Do not distribute

Seed developmental stages	DEseq2		
	Up- or down-regulation in <i>Xcf</i> -colonized seeds	mature miR	variants
24DAP	Up	<b>miR162</b>	a,b
	Up	<b>miR172</b>	a,c,d,e,f,g,h,i,l
	Up	<b>miR396</b>	a,b,c,d,e,i
	Up	<b>miR482</b>	3p, b-3p, d-3p
	Up	<b>miR6478</b>	-
	Up	<b>miR8175</b>	-
	Down	<b>let7</b>	a,c,d,f
	Down	<b>miR21</b>	a
	Down	<b>miR2111</b>	a,b,c,d,e,f,g,h,i,j,k,m,n,o
	Down	<b>miR482</b>	5p
42DAP	Up	<b>miR31</b>	-
	Down	<b>miR451</b>	a
	Down	<b>miR164</b>	a,b,c,d,e,f,g,h,i,j,k



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psRNA target combined with corresponding significant expression changes from RNAseq data
<b>putative targets using psRNA target (= miRNA potential target genes )</b>
Phvul.007G067800 (HSF), Phvul.008G055500 (TGD3), Phvul.006G176000 (tripleix DNA-binding), Phvul.008G114700 (Rab-GDP)
Phvul.009G014600 (cardiolipin deacylase), Phvul.001G212400 (RING-domain E3 ligase), Phvul.005G068800 (Probable E3 ubiquitin-protein ligase), Phvul.003G053000 (glycosyltransferase)
Phvul.009G246000 (SNF4-like), Phvul.001G229200 (pepsin-type protease), Phvul.002G026300 integrin-like protein), Phvul.003G154800 (HSP70)
Phvul.011G149100 Transducin/WD40 repeat-like), Phvul.008G055500 (ATPase component TGD3 of TGD), Phvul.003G295800 (ATG2-like), Phvul.011G082700 (P-loop NTPase), Phvul.010G141400 (DOF1-like TF), Phvul.002G261500 (RNA polymerase regulatory protein)
Phvul.003G155500 (component SR-alpha of SRP)
Phvul.002G059000 (Phosphoinpase A1), Phvul.002G274500 (PAD4-like), Phvul.010G082300 (UDP-D-glucuronic acid 4-epimerase), Phvul.005G035400 (mRNA-splicing factor 18), Phvul.001G240600 (Cal B domain)
Phvul.001G022700 (REIMORIN-LIKE), Phvul.003G119100 (calcium-dependent lipid-binding), Phvul.011G061600 (PTAC16 -like), Phvul.003G035400 (XYL1-like), Phvul.004G121666 (subunit of CF1 of ATP synthase), Phvul.008G163350 (cohesin cofactor (PDS5)), Phvul.011G050300 (protein kinase (PIKK) TOR-like ), Phvul.003G050600 (catalytic protein (CER2)), Phvul.007G069900, Phvul.011G001200 (SAC1-like), Phvul.002G185150 (sodium-proton antiporter (SOS1))
Phvul.010G157900 (MED15-like), Phvul.007G191600 (CHR8-like)
Phvul.001G269300 (MED13-like), Phvul.001G179300 (PGP1-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G168500 (Solute transport channels)
Phvul.004G170000 (STT3-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G244066, Phvul.002G189700 (LIP1-like)
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Phvul.009G100000 (UBP26-like)
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	Id	H24_1	H24_2	H24_3	X24_1	X24_2	
1							
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5	csi-miR482e-3p	492	0	0	0	1	0
6	ata-miR5168-3p	314	1	0	0	2	1
7	bdi-miR166h-3p	314	1	0	0	2	1
8	osa-miR166k-3p	314	1	0	0	2	1
9	osa-miR166l-3p	314	1	0	0	2	1
10	osa-miR166l-3p	314	1	0	0	2	1
11	sbi-miR166e	314	1	0	0	2	1
12	sbi-miR166g	314	1	0	0	2	1
13	sbi-miR166g	314	1	0	0	2	1
14	zma-miR166j-3p	314	1	0	0	2	1
15	zma-miR166k-3p	314	1	0	0	2	1
16	zma-miR166k-3p	314	1	0	0	2	1
17	zma-miR166n-3p	314	1	0	0	2	1
18	ami-let-7f-5p	53	36	153	153	10	39
19	ggo-let-7f	53	36	153	153	10	39
20	oar-let-7f	53	36	153	153	10	39
21	oar-let-7f	53	36	153	153	10	39
22	efu-let-7c	106	111	486	486	62	89
23	abu-let-7c	96	107	463	463	60	82
24	aca-let-7c-5p	96	107	463	463	60	82
25	aca-let-7c-5p	96	107	463	463	60	82
26	ami-let-7c-5p	96	107	463	463	60	82
27	bta-let-7c	96	107	463	463	60	82
28	cfa-let-7c	96	107	463	463	60	82
29	cfa-let-7c	96	107	463	463	60	82
30	chi-let-7c-5p	96	107	463	463	60	82
31	cja-let-7c	96	107	463	463	60	82
32	cli-let-7c-5p	96	107	463	463	60	82
33	cli-let-7c-5p	96	107	463	463	60	82
34	cpi-let-7c-5p	96	107	463	463	60	82
35	cpo-let-7c-5p	96	107	463	463	60	82
36	dma-let-7c	96	107	463	463	60	82
37	dma-let-7c	96	107	463	463	60	82
38	dno-let-7c-5p	96	107	463	463	60	82
39	dre-let-7c-5p	96	107	463	463	60	82
40	dre-let-7c-5p	96	107	463	463	60	82
41	eca-let-7c	96	107	463	463	60	82
42	gga-let-7c-5p	96	107	463	463	60	82
43	gmo-let-7c-5p	96	107	463	463	60	82
44	gmo-let-7c-5p	96	107	463	463	60	82
45	hhi-let-7c	96	107	463	463	60	82
46	hsa-let-7c-5p	96	107	463	463	60	82
47	ipu-let-7c	96	107	463	463	60	82
48	mml-let-7c-5p	96	107	463	463	60	82
49	mml-let-7c-5p	96	107	463	463	60	82
50	mmr-let-7c	96	107	463	463	60	82
51	mmu-let-7c-5p	96	107	463	463	60	82
52	mze-let-7c	96	107	463	463	60	82
53	mze-let-7c	96	107	463	463	60	82
54	nbr-let-7c	96	107	463	463	60	82
55	nle-let-7c	96	107	463	463	60	82
56	oan-let-7c-5p	96	107	463	463	60	82
57	oar-let-7c	96	107	463	463	60	82
58	oar-let-7c	96	107	463	463	60	82
59	ocu-let-7c-5p	96	107	463	463	60	82
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3	oga-let-7c	96	107	463	60	82
4	oha-let-7c-5p	96	107	463	60	82
5	oni-let-7c	96	107	463	60	82
6	pal-let-7c-5p	96	107	463	60	82
7	pbv-let-7c-5p	96	107	463	60	82
8	pha-let-7c	96	107	463	60	82
9	phv-let-7c	96	107	463	60	82
10	pon-let-7c	96	107	463	60	82
11	ppa-let-7c	96	107	463	60	82
12	ppy-let-7c	96	107	463	60	82
13	ptr-let-7c	96	107	463	60	82
14	rno-let-7c-5p	96	107	463	60	82
15	ssa-let-7c-5p	96	107	463	60	82
16	ssc-let-7c	96	107	463	60	82
17	tcf-let-7-5p	96	107	463	60	82
18	tgu-let-7c-5p	96	107	463	60	82
19	xla-let-7c-5p	96	107	463	60	82
20	xtr-let-7c	96	107	463	60	82
21	efu-let-7f	174	117	380	52	105
22	aca-let-7f-5p	172	115	379	52	105
23	bta-let-7f	172	115	379	52	105
24	cfa-let-7f	172	115	379	52	105
25	cgr-let-7f	172	115	379	52	105
26	chi-let-7f-5p	172	115	379	52	105
27	cja-let-7f	172	115	379	52	105
28	cli-let-7f-5p	172	115	379	52	105
29	cpi-let-7f-5p	172	115	379	52	105
30	cpo-let-7f-5p	172	115	379	52	105
31	dma-let-7f	172	115	379	52	105
32	dno-let-7f-5p	172	115	379	52	105
33	dre-let-7f	172	115	379	52	105
34	eca-let-7f	172	115	379	52	105
35	gga-let-7f-5p	172	115	379	52	105
36	gmo-let-7f-5p	172	115	379	52	105
37	hsa-let-7f-5p	172	115	379	52	105
38	ipu-let-7f	172	115	379	52	105
39	mdo-let-7f-5p	172	115	379	52	105
40	mml-let-7f-5p	172	115	379	52	105
41	mmr-let-7f	172	115	379	52	105
42	mmu-let-7f-5p	172	115	379	52	105
43	nle-let-7f	172	115	379	52	105
44	oan-let-7f-5p	172	115	379	52	105
45	ocu-let-7f-5p	172	115	379	52	105
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3	oga-let-7f	172	115	379	52	105
4	oha-let-7f-5p	172	115	379	52	105
5	oni-let-7f	172	115	379	52	105
6	pal-let-7f-5p	172	115	379	52	105
7	pbv-let-7f-5p	172	115	379	52	105
8	pha-let-7f	172	115	379	52	105
9	ppa-let-7f	172	115	379	52	105
10	ppy-let-7f	172	115	379	52	105
11	ptr-let-7f	172	115	379	52	105
12	rno-let-7f-5p	172	115	379	52	105
13	sbo-let-7f	172	115	379	52	105
14	ssc-let-7f-5p	172	115	379	52	105
15	tch-let-7f-5p	172	115	379	52	105
16	tgu-let-7f-5p	172	115	379	52	105
17	xla-let-7f-5p	172	115	379	52	105
18	xtr-let-7f	172	115	379	52	105
19	aly-miR2111a-5p	555	707	456	105	264
20	aly-miR2111b-5p	555	707	456	105	264
21	aly-miR2111c-5p	555	707	456	105	264
22	ath-miR2111a-5p	555	707	456	105	264
23	ath-miR2111b-5p	555	707	456	105	264
24	bna-miR2111a-5p	555	707	456	105	264
25	bna-miR2111b-5p	555	707	456	105	264
26	bna-miR2111d	555	707	456	105	264
27	bra-miR2111a-5p	555	707	456	105	264
28	bra-miR2111b-5p	555	707	456	105	264
29	cme-miR2111a	555	707	456	105	264
30	cme-miR2111b	555	707	456	105	264
31	gma-miR2111b	555	707	456	105	264
32	gma-miR2111c	555	707	456	105	264
33	gma-miR2111e	555	707	456	105	264
34	gma-miR2111f	555	707	456	105	264
35	lja-miR2111-5p	555	707	456	105	264
36	mdm-miR2111a	555	707	456	105	264
37	mdm-miR2111b	555	707	456	105	264
38	mes-miR2111a	555	707	456	105	264
39	mes-miR2111b	555	707	456	105	264
40	mtr-miR2111a-5p	555	707	456	105	264
41	mtr-miR2111b	555	707	456	105	264
42	mtr-miR2111c	555	707	456	105	264
43	mtr-miR2111d-5p	555	707	456	105	264
44	mtr-miR2111e-5p	555	707	456	105	264
45	mtr-miR2111f	555	707	456	105	264
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3	mtr-miR2111g-5p	555	707	456	105	264
4	mtr-miR2111h	555	707	456	105	264
5	mtr-miR2111i	555	707	456	105	264
6	mtr-miR2111j	555	707	456	105	264
7	mtr-miR2111k	555	707	456	105	264
8	mtr-miR2111m-5p	555	707	456	105	264
9	mtr-miR2111n	555	707	456	105	264
10	mtr-miR2111o	555	707	456	105	264
11	ppe-miR2111a	555	707	456	105	264
12	ppe-miR2111b	555	707	456	105	264
13	ppe-miR2111c	555	707	456	105	264
14	ppe-miR2111d	555	707	456	105	264
15	tcc-miR2111	555	707	456	105	264
16	csi-miR2111-5p	509	626	412	92	239
17	ptc-miR2111a	509	626	412	92	239
18	ptc-miR2111b	509	626	412	92	239
19	fve-miR2111a	509	626	411	92	239
20	fve-miR2111b-5p	509	626	411	92	239
21	fve-miR2111c	509	626	411	92	239
22	efu-let-7d	73	45	170	27	42
23	bta-let-7d	65	44	166	25	42
24	cgr-let-7d-5p	65	44	166	25	42
25	chi-let-7d-5p	65	44	166	25	42
26	cja-let-7d	65	44	166	25	42
27	cli-let-7d-5p	65	44	166	25	42
28	cpi-let-7d-5p	65	44	166	25	42
29	cpo-let-7d-5p	65	44	166	25	42
30	dno-let-7d-5p	65	44	166	25	42
31	eca-let-7d	65	44	166	25	42
32	hsa-let-7d-5p	65	44	166	25	42
33	mml-let-7d	65	44	166	25	42
34	mmu-let-7d-5p	65	44	166	25	42
35	oan-let-7d-5p	65	44	166	25	42
36	ocu-let-7d-5p	65	44	166	25	42
37	oha-let-7d-5p	65	44	166	25	42
38	pbv-let-7d-5p	65	44	166	25	42
39	ppy-let-7d	65	44	166	25	42
40	ptr-let-7d	65	44	166	25	42
41	rno-let-7d-5p	65	44	166	25	42
42	ssc-let-7d-5p	65	44	166	25	42
43	tgu-let-7d-5p	65	44	166	25	42
44	pvu-miR482-5p	395	278	197	141	106
45	bta-miR-21-5p	5527	1944	4924	1486	1872
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3	cpo-miR-21-5p	5527	1944	4924	1486	1872
4	dno-miR-21-5p	5527	1944	4924	1486	1872
5	ocu-miR-21-5p	5527	1944	4924	1486	1872
6	sha-miR-21	5527	1944	4924	1486	1872
7	ami-miR-21-5p	5489	1934	4893	1478	1859
8	chi-miR-21-5p	5489	1934	4893	1478	1859
9	dma-miR-21	5489	1934	4893	1478	1859
10	mmr-miR-21	5489	1934	4893	1478	1859
11	nle-miR-21	5489	1934	4893	1478	1859
12	oar-miR-21	5489	1934	4893	1478	1859
13	oga-miR-21	5489	1934	4893	1478	1859
14	pbv-miR-21-5p	5489	1934	4893	1478	1859
15	pha-miR-21	5489	1934	4893	1478	1859
16	sbo-miR-21	5489	1934	4893	1478	1859
17	aca-miR-21-5p	1292	407	432	239	354
18	age-miR-21	1292	407	432	239	354
19	cfa-miR-21	1292	407	432	239	354
20	cgr-miR-21-5p	1292	407	432	239	354
21	cja-miR-21	1292	407	432	239	354
22	cli-miR-21-5p	1292	407	432	239	354
23	cpi-miR-21-5p	1292	407	432	239	354
24	eca-miR-21	1292	407	432	239	354
25	gga-miR-21-5p	1292	407	432	239	354
26	ggo-miR-21	1292	407	432	239	354
27	hsa-miR-21-5p	1292	407	432	239	354
28	mdo-miR-21-5p	1292	407	432	239	354
29	mml-miR-21-5p	1292	407	432	239	354
30	mmu-miR-21a-5p	1292	407	432	239	354
31	mne-miR-21	1292	407	432	239	354
32	oan-miR-21-5p	1292	407	432	239	354
33	oha-miR-21-5p	1292	407	432	239	354
34	pal-miR-21-5p	1292	407	432	239	354
35	ppa-miR-21	1292	407	432	239	354
36	ppy-miR-21	1292	407	432	239	354
37	ptr-miR-21	1292	407	432	239	354
38	rno-miR-21-5p	1292	407	432	239	354
39	ssc-miR-21-5p	1292	407	432	239	354
40	tch-miR-21-5p	1292	407	432	239	354
41	tgu-miR-21-5p	1292	407	432	239	354
42	efu-miR-34a	175	95	221	65	86
43	ami-miR-34a-5p	174	95	220	65	86
44	cja-miR-34a	174	95	220	65	86
45	gga-miR-34a-5p	174	95	220	65	86
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3	mdo-miR-34a-5p	174	95	220	65	86
4	oha-miR-34a-5p	174	95	220	65	86
5	tch-miR-34a-5p	174	95	220	65	86
6	xtr-miR-34a	174	95	220	65	86
7						
8	ame-let-7-5p	80	75	204	53	63
9						
10	bdo-let-7	80	75	204	53	63
11	bmo-let-7-5p	80	75	204	53	63
12						
13	cte-let-7	80	75	204	53	63
14	dan-let-7	80	75	204	53	63
15	der-let-7	80	75	204	53	63
16	dgr-let-7	80	75	204	53	63
17						
18	dme-let-7-5p	80	75	204	53	63
19	dmo-let-7	80	75	204	53	63
20						
21	dpe-let-7	80	75	204	53	63
22	dps-let-7	80	75	204	53	63
23	dqu-let-7-5p	80	75	204	53	63
24	dse-let-7	80	75	204	53	63
25						
26	dsi-let-7	80	75	204	53	63
27	dvi-let-7	80	75	204	53	63
28	dwi-let-7	80	75	204	53	63
29						
30	dya-let-7	80	75	204	53	63
31	ggo-let-7a	80	75	204	53	63
32	isc-let-7	80	75	204	53	63
33						
34	ngi-let-7	80	75	204	53	63
35	nvi-let-7	80	75	204	53	63
36	ola-let-7a-5p	80	75	204	53	63
37						
38	sha-let-7a	80	75	204	53	63
39	hme-let-7	80	75	204	53	64
40	pca-let-7-5p	80	75	204	53	64
41						
42	abu-miR-34	134	76	189	56	75
43	age-miR-34a	134	76	189	56	75
44	bta-miR-34a	134	76	189	56	75
45	ccr-miR-34	134	76	189	56	75
46	cfa-miR-34a	134	76	189	56	75
47	cgr-miR-34a	134	76	189	56	75
48	chi-miR-34a	134	76	189	56	75
49						
50	cli-miR-34a-5p	134	76	189	56	75
51	cpi-miR-34a-5p	134	76	189	56	75
52	cpo-miR-34a-5p	134	76	189	56	75
53	dno-miR-34a-5p	134	76	189	56	75
54						
55	dre-miR-34a	134	76	189	56	75
56	eca-miR-34a	134	76	189	56	75
57	ega-miR-34a	134	76	189	56	75
58						
59	ggo-miR-34a	134	76	189	56	75
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3	gmo-miR-34-5p	134	76	189	56	75
4	hsa-miR-34a-5p	134	76	189	56	75
5	ipu-miR-34a	134	76	189	56	75
6	lla-miR-34a	134	76	189	56	75
7	lla-miR-34a	134	76	189	56	75
8	mml-miR-34a-5p	134	76	189	56	75
9	mml-miR-34a-5p	134	76	189	56	75
10	mmr-miR-34a	134	76	189	56	75
11	mmu-miR-34a-5p	134	76	189	56	75
12	mmu-miR-34a-5p	134	76	189	56	75
13	mne-miR-34a	134	76	189	56	75
14	mze-miR-34	134	76	189	56	75
15	nbr-miR-34	134	76	189	56	75
16	nle-miR-34a	134	76	189	56	75
17	nle-miR-34a	134	76	189	56	75
18	ocu-miR-34a-5p	134	76	189	56	75
19	oga-miR-34a	134	76	189	56	75
20	oni-miR-34	134	76	189	56	75
21	oni-miR-34	134	76	189	56	75
22	pal-miR-34a-5p	134	76	189	56	75
23	pbv-miR-34a-5p	134	76	189	56	75
24	pbv-miR-34a-5p	134	76	189	56	75
25	ppy-miR-34	134	76	189	56	75
26	ppa-miR-34a	134	76	189	56	75
27	ppy-miR-34a	134	76	189	56	75
28	ptr-miR-34a	134	76	189	56	75
29	ptr-miR-34a	134	76	189	56	75
30	rno-miR-34a-5p	134	76	189	56	75
31	sla-miR-34a	134	76	189	56	75
32	sla-miR-34a	134	76	189	56	75
33	ssc-miR-34a	134	76	189	56	75
34	tgu-miR-34a	134	76	189	56	75
35	prd-let-7-5p	283	201	540	169	186
36	abu-let-7a	276	195	528	165	184
37	abu-let-7a	276	195	528	165	184
38	aca-let-7a-5p	276	195	528	165	184
39	ami-let-7a-5p	276	195	528	165	184
40	asu-let-7-5p	276	195	528	165	184
41	asu-let-7-5p	276	195	528	165	184
42	bbe-let-7a-5p	276	195	528	165	184
43	bfl-let-7a-5p	276	195	528	165	184
44	bma-let-7	276	195	528	165	184
45	bta-let-7a-5p	276	195	528	165	184
46	bta-let-7a-5p	276	195	528	165	184
47	cbn-let-7	276	195	528	165	184
48	cbr-let-7	276	195	528	165	184
49	cbr-let-7	276	195	528	165	184
50	ccr-let-7a	276	195	528	165	184
51	cel-let-7-5p	276	195	528	165	184
52	cfa-let-7a	276	195	528	165	184
53	cfa-let-7a	276	195	528	165	184
54	cgr-let-7a	276	195	528	165	184
55	chi-let-7a-5p	276	195	528	165	184
56	cja-let-7a	276	195	528	165	184
57	cja-let-7a	276	195	528	165	184
58	cli-let-7a-5p	276	195	528	165	184
59	cpi-let-7a-5p	276	195	528	165	184
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3	cpo-let-7a-5p	276	195	528	165	184
4	crm-let-7	276	195	528	165	184
5	dma-let-7a	276	195	528	165	184
6	dno-let-7a-5p	276	195	528	165	184
7	dre-let-7a	276	195	528	165	184
8	eca-let-7a	276	195	528	165	184
9	fru-let-7a	276	195	528	165	184
10	gga-let-7a-5p	276	195	528	165	184
11	gga-let-7j-5p	276	195	528	165	184
12	gmo-let-7a-5p	276	195	528	165	184
13	hpo-let-7-5p	276	195	528	165	184
14	hsa-let-7a-5p	276	195	528	165	184
15	ipu-let-7a	276	195	528	165	184
16	lgi-let-7	276	195	528	165	184
17	mdo-let-7a-5p	276	195	528	165	184
18	mml-let-7a-5p	276	195	528	165	184
19	mmr-let-7a	276	195	528	165	184
20	mmu-let-7a-5p	276	195	528	165	184
21	mze-let-7a	276	195	528	165	184
22	nbr-let-7a	276	195	528	165	184
23	nle-let-7a	276	195	528	165	184
24	oar-let-7a	276	195	528	165	184
25	ocu-let-7a-5p	276	195	528	165	184
26	oga-let-7a	276	195	528	165	184
27	oha-let-7a	276	195	528	165	184
28	oha-let-7a-5p	276	195	528	165	184
29	ola-let-7a	276	195	528	165	184
30	oni-let-7a	276	195	528	165	184
31	pal-let-7a-5p	276	195	528	165	184
32	pbv-let-7a-5p	276	195	528	165	184
33	pha-let-7a	276	195	528	165	184
34	pma-let-7a	276	195	528	165	184
35	pny-let-7a	276	195	528	165	184
36	ppa-let-7a	276	195	528	165	184
37	ppc-let-7	276	195	528	165	184
38	ppy-let-7a	276	195	528	165	184
39	pte-let-7-5p	276	195	528	165	184
40	ptr-let-7a	276	195	528	165	184
41	rno-let-7a-5p	276	195	528	165	184
42	sbo-let-7a	276	195	528	165	184
43	sko-let-7	276	195	528	165	184
44	ssa-let-7a-5p	276	195	528	165	184
45	ssc-let-7a	276	195	528	165	184
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3	tgu-let-7a-5p	276	195	528	165	184
4	tni-let-7a	276	195	528	165	184
5	xla-let-7a-5p	276	195	528	165	184
6	xtr-let-7a	276	195	528	165	184
7						
8	abu-miR-429b	9	37	167	23	39
9	aca-miR-429-3p	9	37	167	23	39
10	bta-miR-429	9	37	167	23	39
11	cca-miR-429	9	37	167	23	39
12	ccr-miR-429	9	37	167	23	39
13	cfa-miR-429	9	37	167	23	39
14	cgr-miR-429	9	37	167	23	39
15	cli-miR-429-3p	9	37	167	23	39
16	cpi-miR-429-3p	9	37	167	23	39
17	cpo-miR-429-3p	9	37	167	23	39
18	dno-miR-429-3p	9	37	167	23	39
19	dre-miR-429a	9	37	167	23	39
20	efu-miR-429	9	37	167	23	39
21	fru-miR-429	9	37	167	23	39
22	gga-miR-429-3p	9	37	167	23	39
23	gmo-miR-429-3p	9	37	167	23	39
24	mmu-miR-429-3p	9	37	167	23	39
25	mze-miR-429b	9	37	167	23	39
26	nbr-miR-429b	9	37	167	23	39
27	oan-miR-429-3p	9	37	167	23	39
28	oha-miR-429-3p	9	37	167	23	39
29	oni-miR-429b	9	37	167	23	39
30	pal-miR-429-3p	9	37	167	23	39
31	pbv-miR-429-3p	9	37	167	23	39
32	ppy-miR-429b	9	37	167	23	39
33	rno-miR-429	9	37	167	23	39
34	ssc-miR-429	9	37	167	23	39
35	tni-miR-429	9	37	167	23	39
36	xla-miR-429-3p	9	37	167	23	39
37	xtr-miR-429	9	37	167	23	39
38						
39	aof-miR166c	101	1840	1341	461	530
40	ath-miR165a-3p	101	1840	1341	461	530
41	ath-miR165b	101	1840	1341	461	530
42	bna-miR166f	101	1840	1341	461	530
43	cas-miR165a	101	1840	1341	461	530
44	lus-miR166b	101	1840	1341	461	530
45						
46	cli-let-7i-5p	203	105	205	74	111
47	abu-let-7i	201	103	204	74	111
48	aca-let-7i-5p	201	103	204	74	111
49	bta-let-7i	201	103	204	74	111
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3	chi-let-7i-5p	201	103	204	74	111
4	cja-let-7i	201	103	204	74	111
5	cpi-let-7i-5p	201	103	204	74	111
6	cpo-let-7i-5p	201	103	204	74	111
7	dno-let-7i-5p	201	103	204	74	111
8	dre-let-7i	201	103	204	74	111
9	fru-let-7i	201	103	204	74	111
10	gmo-let-7i-5p	201	103	204	74	111
11	hsa-let-7i-5p	201	103	204	74	111
12	ipu-let-7i	201	103	204	74	111
13	mml-let-7i-5p	201	103	204	74	111
14	mmu-let-7i-5p	201	103	204	74	111
15	mze-let-7i	201	103	204	74	111
16	nbr-let-7i	201	103	204	74	111
17	nle-let-7i	201	103	204	74	111
18	oar-let-7i	201	103	204	74	111
19	ocu-let-7i-5p	201	103	204	74	111
20	oga-let-7i	201	103	204	74	111
21	oha-let-7i-5p	201	103	204	74	111
22	oni-let-7i	201	103	204	74	111
23	pal-let-7i-5p	201	103	204	74	111
24	pbv-let-7i-5p	201	103	204	74	111
25	pha-let-7i	201	103	204	74	111
26	ppy-let-7i	201	103	204	74	111
27	ppa-let-7i	201	103	204	74	111
28	ppp-let-7i	201	103	204	74	111
29	ptr-let-7i	201	103	204	74	111
30	rno-let-7i-5p	201	103	204	74	111
31	ssa-let-7i-5p	201	103	204	74	111
32	tch-let-7i-5p	201	103	204	74	111
33	tgu-let-7i-5p	201	103	204	74	111
34	tni-let-7i	201	103	204	74	111
35	ami-miR-30d-5p	75	82	136	31	60
36	bta-miR-30d	75	82	136	31	60
37	cfa-miR-30d	75	82	136	31	60
38	cli-miR-30d-5p	75	82	136	31	60
39	cpo-miR-30d-5p	75	82	136	31	60
40	dno-miR-30d-5p	75	82	136	31	60
41	gmo-miR-30a-5p	75	82	136	31	60
42	nle-miR-30d	75	82	136	31	60
43	ocu-miR-30d-5p	75	82	136	31	60
44	oga-miR-30d	75	82	136	31	60
45	oha-miR-30d-5p	75	82	136	31	60
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3	pal-miR-30d-5p	75	82	136	31	60
4	pbv-miR-30d-5p	75	82	136	31	60
5	pha-miR-30d	75	82	136	31	60
6	ssa-miR-30b-5p	75	82	136	31	60
7	ssa-miR-30d	75	82	136	31	60
8	ssc-miR-30d	75	82	136	31	60
9	tgu-miR-30d-5p	75	82	136	31	60
10	xla-miR-30d-5p	75	82	136	31	60
11	cgr-miR-29a-3p	88	63	108	32	67
12	chi-miR-29a-3p	88	63	108	32	67
13	oar-miR-29a	88	63	108	32	67
14	tch-miR-29a-3p	88	63	108	32	67
15	ssa-miR-23b-3p	101	31	58	21	45
16	ami-miR-23b-3p	98	30	57	21	45
17	bta-miR-10174-3p	98	30	57	21	45
18	bta-miR-23b-3p	98	30	57	21	45
19	cpo-miR-23b-3p	98	30	57	21	45
20	dno-miR-23b-3p	98	30	57	21	45
21	dre-miR-23b-3p	98	30	57	21	45
22	efu-miR-23b	98	30	57	21	45
23	hsa-miR-23b-3p	98	30	57	21	45
24	ocu-miR-23b-3p	98	30	57	21	45
25	oga-miR-23b	98	30	57	21	45
26	oha-miR-23b-3p	98	30	57	21	45
27	ola-miR-23b	98	30	57	21	45
28	pbv-miR-23b-3p	98	30	57	21	45
29	pma-miR-23b	98	30	57	21	45
30	ppa-miR-23b	98	30	57	21	45
31	ppy-miR-23b	98	30	57	21	45
32	ptr-miR-23b	98	30	57	21	45
33	tch-miR-23b-3p	98	30	57	21	45
34	cfa-miR-29a	117	82	137	45	82
35	cja-miR-29a	117	82	137	45	82
36	cpo-miR-29a-3p	117	82	137	45	82
37	dma-miR-29a	117	82	137	45	82
38	dno-miR-29a-3p	117	82	137	45	82
39	eca-miR-29a	117	82	137	45	82
40	hsa-miR-29a-3p	117	82	137	45	82
41	mmr-miR-29a	117	82	137	45	82
42	mmu-miR-29a-3p	117	82	137	45	82
43	nle-miR-29a	117	82	137	45	82
44	ocu-miR-29a-3p	117	82	137	45	82
45	oga-miR-29a	117	82	137	45	82
46	pal-miR-29a-3p	117	82	137	45	82
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3	pha-miR-29a	117	82	137	45	82
4	rno-miR-29a-3p	117	82	137	45	82
5	cli-miR-23b-3p	99	30	57	22	45
6	age-miR-29a	170	93	148	58	108
7	ggo-miR-29a	170	93	148	58	108
8	lla-miR-29a	170	93	148	58	108
9	mml-miR-29a-3p	170	93	148	58	108
10	mne-miR-29a	170	93	148	58	108
11	ppa-miR-29a	170	93	148	58	108
12	ppy-miR-29a	170	93	148	58	108
13	ptr-miR-29a	170	93	148	58	108
14	sbo-miR-29a	170	93	148	58	108
15	sla-miR-29a	170	93	148	58	108
16	gga-miR-126-3p	752	501	671	291	487
17	bta-miR-200c	2	59	226	29	53
18	cfa-miR-200c	2	59	226	29	53
19	cgr-miR-200c	2	59	226	29	53
20	chi-miR-200c	2	59	226	29	53
21	cja-miR-200c	2	59	226	29	53
22	cpo-miR-200c-3p	2	59	226	29	53
23	eca-miR-200c	2	59	226	29	53
24	efu-miR-200c	2	59	226	29	53
25	hsa-miR-200c-3p	2	59	226	29	53
26	mmu-miR-200c-3p	2	59	226	29	53
27	ocu-miR-200c-3p	2	59	226	29	53
28	pal-miR-200c-3p	2	59	226	29	53
29	ptr-miR-200c	2	59	226	29	53
30	tch-miR-200c-3p	2	59	226	29	53
31	aca-miR-126-3p	752	499	671	291	487
32	ami-miR-126-3p	752	499	671	291	487
33	cgr-miR-126a	752	499	671	291	487
34	cja-miR-126	752	499	671	291	487
35	cli-miR-126-3p	752	499	671	291	487
36	cpi-miR-126-3p	752	499	671	291	487
37	cpo-miR-126-3p	752	499	671	291	487
38	dno-miR-126-3p	752	499	671	291	487
39	eca-miR-126-3p	752	499	671	291	487
40	hsa-miR-126-3p	752	499	671	291	487
41	mdo-miR-126-3p	752	499	671	291	487
42	mml-miR-126	752	499	671	291	487
43	mmu-miR-126a-3p	752	499	671	291	487
44	oan-miR-126-3p	752	499	671	291	487
45	pbv-miR-126-3p	752	499	671	291	487
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3	ppy-miR-126	752	499	671	291	487
4	ptr-miR-126	752	499	671	291	487
5	rno-miR-126a-3p	752	499	671	291	487
6	ssc-miR-126-3p	752	499	671	291	487
7	ssc-miR-126-3p	752	499	671	291	487
8	tgu-miR-126-3p	752	499	671	291	487
9	tgu-miR-126-3p	752	499	671	291	487
10	ccr-miR-30d	46	49	94	18	34
11	cja-miR-30d	46	49	94	18	34
12	cpi-miR-30d-5p	46	49	94	18	34
13	cpi-miR-30d-5p	46	49	94	18	34
14	oan-miR-30d-5p	46	49	94	18	34
15	ola-miR-30d-5p	46	49	94	18	34
16	efu-miR-126	756	506	678	291	498
17	ccr-miR-100	126	30	25	38	32
18	cgr-miR-100-5p	126	30	25	38	32
19	cgr-miR-100-5p	126	30	25	38	32
20	chi-miR-100-5p	126	30	25	38	32
21	chi-miR-100-5p	126	30	25	38	32
22	cpi-miR-100-5p	126	30	25	38	32
23	cpi-miR-100-5p	126	30	25	38	32
24	dma-miR-100	126	30	25	38	32
25	mdo-miR-100-5p	126	30	25	38	32
26	pmi-miR-100-5p	126	30	25	38	32
27	sbo-miR-100	126	30	25	38	32
28	sha-miR-100	126	30	25	38	32
29	sha-miR-100	126	30	25	38	32
30	tgu-miR-100-5p	126	30	25	38	32
31	efu-miR-29a	207	117	182	73	128
32	gga-let-7g-5p	27	68	130	39	56
33	gga-let-7g-5p	27	68	130	39	56
34	ggo-let-7g	27	68	130	39	56
35	mdo-let-7g-5p	27	68	130	39	56
36	oar-let-7g	27	68	130	39	56
37	oar-let-7g	27	68	130	39	56
38	sha-let-7g	27	68	130	39	56
39	bta-miR-29a	200	114	179	73	124
40	ssc-miR-29a-3p	200	114	179	73	124
41	ssc-miR-29a-3p	200	114	179	73	124
42	cpo-miR-16b-5p	401	204	217	133	202
43	dno-miR-16b-5p	401	204	217	133	202
44	dno-miR-16b-5p	401	204	217	133	202
45	efu-miR-16	401	204	217	133	202
46	ocu-miR-16b-5p	401	204	217	133	202
47	bta-miR-375	12	470	1593	199	498
48	efu-miR-375	12	470	1593	199	498
49	efu-miR-375	12	470	1593	199	498
50	mdo-miR-375	12	470	1593	199	498
51	cfa-miR-375	12	464	1564	196	491
52	cpo-miR-375-3p	12	464	1564	196	491
53	dno-miR-375-3p	12	464	1564	196	491
54	dno-miR-375-3p	12	464	1564	196	491
55	ggo-miR-375	12	464	1564	196	491
56	hsa-miR-375-3p	12	464	1564	196	491
57	hsa-miR-375-3p	12	464	1564	196	491
58	mml-miR-375	12	464	1564	196	491
59	mmu-miR-375-3p	12	464	1564	196	491
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2						
3	ocu-miR-375-3p	12	464	1564	196	491
4	pal-miR-375-3p	12	464	1564	196	491
5	ppy-miR-375	12	464	1564	196	491
6	ptr-miR-375	12	464	1564	196	491
7	rno-miR-375-3p	12	464	1564	196	491
8	ssc-miR-375	12	464	1564	196	491
9	gma-miR390a-3p	6474	6483	8058	5160	4809
10	gma-miR390c	6474	6483	8058	5160	4809
11	mes-miR390	6474	6483	8058	5160	4809
12	nle-miR-148a	0	84	241	41	76
13	oga-miR-148a	0	84	241	41	76
14	pha-miR-148a	0	84	241	41	76
15	ppa-miR-148a	0	84	241	41	76
16	abu-miR-26a	519	374	526	243	334
17	aca-miR-26-3-5p	519	374	526	243	334
18	ami-miR-26-5p	519	374	526	243	334
19	bta-miR-26a	519	374	526	243	334
20	ccb-miR-26a	519	374	526	243	334
21	cfa-miR-26a	519	374	526	243	334
22	chi-miR-26a-5p	519	374	526	243	334
23	cja-miR-26a	519	374	526	243	334
24	cli-miR-26-5p	519	374	526	243	334
25	cpi-miR-26-5p	519	374	526	243	334
26	cpo-miR-26a-5p	519	374	526	243	334
27	dma-miR-26a	519	374	526	243	334
28	dno-miR-26a-5p	519	374	526	243	334
29	dre-miR-26a-5p	519	374	526	243	334
30	eca-miR-26a	519	374	526	243	334
31	fru-miR-26	519	374	526	243	334
32	gga-miR-26a-2-5p	519	374	526	243	334
33	ggo-miR-26a	519	374	526	243	334
34	gmo-miR-26a-5p	519	374	526	243	334
35	hsa-miR-26a-5p	519	374	526	243	334
36	ipu-miR-26a	519	374	526	243	334
37	lla-miR-26a	519	374	526	243	334
38	mml-miR-26a-5p	519	374	526	243	334
39	mmr-miR-26a	519	374	526	243	334
40	mmu-miR-26a-5p	519	374	526	243	334
41	mne-miR-26a	519	374	526	243	334
42	mze-miR-26a	519	374	526	243	334
43	nbr-miR-26a	519	374	526	243	334
44	nle-miR-26a	519	374	526	243	334
45	oan-miR-26-5p	519	374	526	243	334
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3	oar-miR-26a	519	374	526	243	334
4	ocu-miR-26a-5p	519	374	526	243	334
5	oga-miR-26a	519	374	526	243	334
6	oha-miR-26-5p	519	374	526	243	334
7	oni-miR-26a	519	374	526	243	334
8	oni-miR-26a	519	374	526	243	334
9	oni-miR-26a	519	374	526	243	334
10	pal-miR-26a-5p	519	374	526	243	334
11	pbv-miR-26-5p	519	374	526	243	334
12	pha-miR-26a	519	374	526	243	334
13	pha-miR-26a	519	374	526	243	334
14	pma-miR-26a-5p	519	374	526	243	334
15	ppy-miR-26a	519	374	526	243	334
16	ppa-miR-26a	519	374	526	243	334
17	ppa-miR-26a	519	374	526	243	334
18	ppy-miR-26a	519	374	526	243	334
19	ptr-miR-26a	519	374	526	243	334
20	ptr-miR-26a	519	374	526	243	334
21	rno-miR-26a-5p	519	374	526	243	334
22	sbo-miR-26a	519	374	526	243	334
23	ssa-miR-26a-5p	519	374	526	243	334
24	ssc-miR-26a	519	374	526	243	334
25	ssc-miR-26a	519	374	526	243	334
26	tch-miR-26a-5p	519	374	526	243	334
27	tgu-miR-26-5p	519	374	526	243	334
28	tni-miR-26	519	374	526	243	334
29	tni-miR-26	519	374	526	243	334
30	xla-miR-26-5p	519	374	526	243	334
31	efu-miR-26a	521	375	527	243	334
32	efu-miR-26c	521	375	527	243	334
33	efu-miR-26c	521	375	527	243	334
34	gma-miR391-5p	85	196	96	86	109
35	aca-let-7g	85	147	289	94	135
36	ami-let-7g-5p	85	147	289	94	135
37	ami-let-7g-5p	85	147	289	94	135
38	bta-let-7g	85	147	289	94	135
39	cfa-let-7g	85	147	289	94	135
40	cgr-let-7g-5p	85	147	289	94	135
41	cgr-let-7g-5p	85	147	289	94	135
42	chi-let-7g-5p	85	147	289	94	135
43	cja-let-7g	85	147	289	94	135
44	cli-let-7g-5p	85	147	289	94	135
45	cli-let-7g-5p	85	147	289	94	135
46	cpi-let-7g-5p	85	147	289	94	135
47	cpo-let-7g-5p	85	147	289	94	135
48	dma-let-7g	85	147	289	94	135
49	dma-let-7g	85	147	289	94	135
50	dno-let-7g-5p	85	147	289	94	135
51	eca-let-7g	85	147	289	94	135
52	hsa-let-7g-5p	85	147	289	94	135
53	hsa-let-7g-5p	85	147	289	94	135
54	mml-let-7g-5p	85	147	289	94	135
55	mmr-let-7g	85	147	289	94	135
56	mmu-let-7g-5p	85	147	289	94	135
57	mmu-let-7g-5p	85	147	289	94	135
58	nle-let-7g	85	147	289	94	135
59	oan-let-7g-5p	85	147	289	94	135
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3	ocu-let-7g-5p	85	147	289	94	135
4	oga-let-7g	85	147	289	94	135
5	oha-let-7g-5p	85	147	289	94	135
6	pal-let-7g-5p	85	147	289	94	135
7	pal-let-7g-5p	85	147	289	94	135
8	pbv-let-7g-5p	85	147	289	94	135
9	pbv-let-7g-5p	85	147	289	94	135
10	pha-let-7g	85	147	289	94	135
11	ppa-let-7g	85	147	289	94	135
12	ppy-let-7g	85	147	289	94	135
13	ppy-let-7g	85	147	289	94	135
14	ptr-let-7g	85	147	289	94	135
15	rno-let-7g-5p	85	147	289	94	135
16	ssc-let-7g	85	147	289	94	135
17	ssc-let-7g	85	147	289	94	135
18	tch-let-7g-5p	85	147	289	94	135
19	tgu-let-7g-5p	85	147	289	94	135
20	tgu-let-7g-5p	85	147	289	94	135
21	aly-miR390a-3p	7408	7479	8969	5907	5712
22	ath-miR390a-3p	7408	7479	8969	5907	5712
23	cas-miR390a-3p	7408	7479	8969	5907	5712
24	csi-miR390a-3p	7408	7479	8969	5907	5712
25	csi-miR390a-3p	7408	7479	8969	5907	5712
26	lja-miR390a-3p	7408	7479	8969	5907	5712
27	lja-miR390b-3p	7408	7479	8969	5907	5712
28	sly-miR390b-3p	7408	7479	8969	5907	5712
29	sly-miR390b-3p	7408	7479	8969	5907	5712
30	pal-miR-126-3p	144	117	122	63	112
31	xla-miR-126-3p	144	117	122	63	112
32	aof-miR166a	7981	8169	8133	5956	6604
33	aof-miR166a	7981	8169	8133	5956	6604
34	atr-miR166b	7981	8169	8133	5956	6604
35	bdi-miR166f	7981	8169	8133	5956	6604
36	csi-miR166b-3p	7981	8169	8133	5956	6604
37	csi-miR166b-3p	7981	8169	8133	5956	6604
38	csi-miR166d-3p	7981	8169	8133	5956	6604
39	csi-miR166g-3p	7981	8169	8133	5956	6604
40	gma-miR166h-3p	7981	8169	8133	5956	6604
41	gma-miR166h-3p	7981	8169	8133	5956	6604
42	gma-miR166k	7981	8169	8133	5956	6604
43	pab-miR166e	7981	8169	8133	5956	6604
44	abu-let-7b	225	214	386	156	214
45	abu-let-7b	225	214	386	156	214
46	ami-let-7b-5p	225	214	386	156	214
47	bta-let-7b	225	214	386	156	214
48	ccb-let-7b	225	214	386	156	214
49	ccb-let-7b	225	214	386	156	214
50	cfa-let-7b	225	214	386	156	214
51	cgr-let-7b	225	214	386	156	214
52	chi-let-7b-5p	225	214	386	156	214
53	chi-let-7b-5p	225	214	386	156	214
54	cja-let-7b	225	214	386	156	214
55	cpi-let-7b-5p	225	214	386	156	214
56	cpi-let-7b-5p	225	214	386	156	214
57	cpo-let-7b-5p	225	214	386	156	214
58	dma-let-7b	225	214	386	156	214
59	dno-let-7b-5p	225	214	386	156	214
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3	dre-let-7b	225	214	386	156	214
4	fru-let-7b	225	214	386	156	214
5	gga-let-7b	225	214	386	156	214
6	gga-let-7b	225	214	386	156	214
7	hsa-let-7b-5p	225	214	386	156	214
8	mdo-let-7b	225	214	386	156	214
9	mml-let-7b-5p	225	214	386	156	214
10	mml-let-7b-5p	225	214	386	156	214
11	mmr-let-7b	225	214	386	156	214
12	mmu-let-7b-5p	225	214	386	156	214
13	mmu-let-7b-5p	225	214	386	156	214
14	mze-let-7b	225	214	386	156	214
15	nbr-let-7b	225	214	386	156	214
16	oan-let-7b-5p	225	214	386	156	214
17	oan-let-7b-5p	225	214	386	156	214
18	ocu-let-7b-5p	225	214	386	156	214
19	oga-let-7b	225	214	386	156	214
20	oha-let-7b-5p	225	214	386	156	214
21	oha-let-7b-5p	225	214	386	156	214
22	oni-let-7b	225	214	386	156	214
23	pbv-let-7b-5p	225	214	386	156	214
24	pha-let-7b	225	214	386	156	214
25	pha-let-7b	225	214	386	156	214
26	pony-let-7b	225	214	386	156	214
27	pol-let-7b-5p	225	214	386	156	214
28	ppa-let-7b	225	214	386	156	214
29	ppa-let-7b	225	214	386	156	214
30	ppy-let-7b	225	214	386	156	214
31	ptr-let-7b	225	214	386	156	214
32	rno-let-7b-5p	225	214	386	156	214
33	rno-let-7b-5p	225	214	386	156	214
34	sbo-let-7b	225	214	386	156	214
35	ssa-let-7b-5p	225	214	386	156	214
36	tgu-let-7b-5p	225	214	386	156	214
37	tgu-let-7b-5p	225	214	386	156	214
38	tni-let-7b	225	214	386	156	214
39	bta-miR-126-3p	144	115	122	63	112
40	xla-miR-126-2-3p	144	115	122	63	112
41	xla-miR-126-2-3p	144	115	122	63	112
42	efu-miR-22	1415	908	1298	714	916
43	xla-miR-22-3p	1415	908	1298	714	916
44	ama-miR156	4349	4087	2522	2892	2048
45	aly-miR156a-5p	4346	4087	2521	2892	2048
46	aly-miR156a-5p	4346	4087	2521	2892	2048
47	aly-miR156b-5p	4346	4087	2521	2892	2048
48	aly-miR156c-5p	4346	4087	2521	2892	2048
49	aly-miR156c-5p	4346	4087	2521	2892	2048
50	aly-miR156d-5p	4346	4087	2521	2892	2048
51	aly-miR156e-5p	4346	4087	2521	2892	2048
52	aly-miR156f-5p	4346	4087	2521	2892	2048
53	aly-miR156f-5p	4346	4087	2521	2892	2048
54	aof-miR156a	4346	4087	2521	2892	2048
55	ata-miR156a-5p	4346	4087	2521	2892	2048
56	ata-miR156b-5p	4346	4087	2521	2892	2048
57	ata-miR156b-5p	4346	4087	2521	2892	2048
58	ata-miR156c-5p	4346	4087	2521	2892	2048
59	ata-miR156d-5p	4346	4087	2521	2892	2048
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3	ata-miR156e-5p	4346	4087	2521	2892	2048
4	ath-miR156a-5p	4346	4087	2521	2892	2048
5	ath-miR156b-5p	4346	4087	2521	2892	2048
6	ath-miR156c-5p	4346	4087	2521	2892	2048
7	ath-miR156d-5p	4346	4087	2521	2892	2048
8	ath-miR156e	4346	4087	2521	2892	2048
9	ath-miR156f-5p	4346	4087	2521	2892	2048
10	atr-miR156b	4346	4087	2521	2892	2048
11	atr-miR156d	4346	4087	2521	2892	2048
12	bdi-miR156b-5p	4346	4087	2521	2892	2048
13	bdi-miR156c	4346	4087	2521	2892	2048
14	bdi-miR156d-5p	4346	4087	2521	2892	2048
15	bdi-miR156e-5p	4346	4087	2521	2892	2048
16	bdi-miR156f-5p	4346	4087	2521	2892	2048
17	bdi-miR156g-5p	4346	4087	2521	2892	2048
18	bdi-miR156h-5p	4346	4087	2521	2892	2048
19	bdi-miR156i-5p	4346	4087	2521	2892	2048
20	bna-miR156d	4346	4087	2521	2892	2048
21	bna-miR156e	4346	4087	2521	2892	2048
22	bna-miR156f	4346	4087	2521	2892	2048
23	bra-miR156a-5p	4346	4087	2521	2892	2048
24	bra-miR156b-5p	4346	4087	2521	2892	2048
25	bra-miR156c-5p	4346	4087	2521	2892	2048
26	bra-miR156d-5p	4346	4087	2521	2892	2048
27	bra-miR156e-5p	4346	4087	2521	2892	2048
28	bra-miR156f-5p	4346	4087	2521	2892	2048
29	bra-miR156g-5p	4346	4087	2521	2892	2048
30	cas-miR156a	4346	4087	2521	2892	2048
31	cas-miR156b-5p	4346	4087	2521	2892	2048
32	cas-miR156c-5p	4346	4087	2521	2892	2048
33	cas-miR156d-5p	4346	4087	2521	2892	2048
34	cas-miR156e-5p	4346	4087	2521	2892	2048
35	cas-miR156f-5p	4346	4087	2521	2892	2048
36	cas-miR156k-5p	4346	4087	2521	2892	2048
37	cca-miR156a	4346	4087	2521	2892	2048
38	cme-miR156a	4346	4087	2521	2892	2048
39	cme-miR156c	4346	4087	2521	2892	2048
40	cme-miR156d	4346	4087	2521	2892	2048
41	cme-miR156i	4346	4087	2521	2892	2048
42	cpa-miR156a	4346	4087	2521	2892	2048
43	cpa-miR156b	4346	4087	2521	2892	2048
44	cpa-miR156c	4346	4087	2521	2892	2048
45	cpa-miR156d	4346	4087	2521	2892	2048
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3	csi-miR156a-5p	4346	4087	2521	2892	2048
4	csi-miR156b-5p	4346	4087	2521	2892	2048
5	csi-miR156c-5p	4346	4087	2521	2892	2048
6	csi-miR156c-5p	4346	4087	2521	2892	2048
7	ctr-miR156	4346	4087	2521	2892	2048
8	dpr-miR156b	4346	4087	2521	2892	2048
9	dpr-miR156b	4346	4087	2521	2892	2048
10	fve-miR156d	4346	4087	2521	2892	2048
11	ghr-miR156a	4346	4087	2521	2892	2048
12	ghr-miR156a	4346	4087	2521	2892	2048
13	ghr-miR156b	4346	4087	2521	2892	2048
14	ghr-miR156d	4346	4087	2521	2892	2048
15	gma-miR156a	4346	4087	2521	2892	2048
16	gma-miR156h	4346	4087	2521	2892	2048
17	gma-miR156h	4346	4087	2521	2892	2048
18	gma-miR156u	4346	4087	2521	2892	2048
19	gma-miR156v	4346	4087	2521	2892	2048
20	gma-miR156w	4346	4087	2521	2892	2048
21	gma-miR156w	4346	4087	2521	2892	2048
22	gma-miR156x	4346	4087	2521	2892	2048
23	gma-miR156y	4346	4087	2521	2892	2048
24	gma-miR156y	4346	4087	2521	2892	2048
25	han-miR156a	4346	4087	2521	2892	2048
26	han-miR156b	4346	4087	2521	2892	2048
27	har-miR156a	4346	4087	2521	2892	2048
28	htu-miR156a	4346	4087	2521	2892	2048
29	htu-miR156a	4346	4087	2521	2892	2048
30	lus-miR156a	4346	4087	2521	2892	2048
31	lus-miR156g	4346	4087	2521	2892	2048
32	mdm-miR156a	4346	4087	2521	2892	2048
33	mdm-miR156a	4346	4087	2521	2892	2048
34	mdm-miR156b	4346	4087	2521	2892	2048
35	mdm-miR156c	4346	4087	2521	2892	2048
36	mdm-miR156c	4346	4087	2521	2892	2048
37	mdm-miR156d	4346	4087	2521	2892	2048
38	mdm-miR156e	4346	4087	2521	2892	2048
39	mdm-miR156f	4346	4087	2521	2892	2048
40	mdm-miR156f	4346	4087	2521	2892	2048
41	mdm-miR156g	4346	4087	2521	2892	2048
42	mdm-miR156h	4346	4087	2521	2892	2048
43	mdm-miR156i	4346	4087	2521	2892	2048
44	mdm-miR156i	4346	4087	2521	2892	2048
45	mdm-miR156j	4346	4087	2521	2892	2048
46	mdm-miR156k	4346	4087	2521	2892	2048
47	mdm-miR156l	4346	4087	2521	2892	2048
48	mdm-miR156l	4346	4087	2521	2892	2048
49	mdm-miR156m	4346	4087	2521	2892	2048
50	mdm-miR156n	4346	4087	2521	2892	2048
51	mdm-miR156o	4346	4087	2521	2892	2048
52	mes-miR156a	4346	4087	2521	2892	2048
53	mes-miR156a	4346	4087	2521	2892	2048
54	mes-miR156b	4346	4087	2521	2892	2048
55	mes-miR156c	4346	4087	2521	2892	2048
56	mes-miR156d	4346	4087	2521	2892	2048
57	mes-miR156d	4346	4087	2521	2892	2048
58	mes-miR156e	4346	4087	2521	2892	2048
59	mes-miR156f	4346	4087	2521	2892	2048
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3	mes-miR156g	4346	4087	2521	2892	2048
4	mtr-miR156b-5p	4346	4087	2521	2892	2048
5	mtr-miR156c-5p	4346	4087	2521	2892	2048
6	mtr-miR156d-5p	4346	4087	2521	2892	2048
7	mtr-miR156i-5p	4346	4087	2521	2892	2048
8	nta-miR156a	4346	4087	2521	2892	2048
9	nta-miR156b	4346	4087	2521	2892	2048
10	nta-miR156c	4346	4087	2521	2892	2048
11	nta-miR156d	4346	4087	2521	2892	2048
12	nta-miR156e	4346	4087	2521	2892	2048
13	osa-miR156a	4346	4087	2521	2892	2048
14	osa-miR156b-5p	4346	4087	2521	2892	2048
15	osa-miR156c-5p	4346	4087	2521	2892	2048
16	osa-miR156d	4346	4087	2521	2892	2048
17	osa-miR156e	4346	4087	2521	2892	2048
18	osa-miR156f-5p	4346	4087	2521	2892	2048
19	osa-miR156g-5p	4346	4087	2521	2892	2048
20	osa-miR156h-5p	4346	4087	2521	2892	2048
21	osa-miR156i	4346	4087	2521	2892	2048
22	osa-miR156j-5p	4346	4087	2521	2892	2048
23	pab-miR156a	4346	4087	2521	2892	2048
24	pab-miR156l	4346	4087	2521	2892	2048
25	ppe-miR156c	4346	4087	2521	2892	2048
26	ppe-miR156d	4346	4087	2521	2892	2048
27	ppe-miR156e	4346	4087	2521	2892	2048
28	ppt-miR156a	4346	4087	2521	2892	2048
29	ppt-miR156b	4346	4087	2521	2892	2048
30	ppt-miR156c	4346	4087	2521	2892	2048
31	ptc-miR156a	4346	4087	2521	2892	2048
32	ptc-miR156b	4346	4087	2521	2892	2048
33	ptc-miR156c	4346	4087	2521	2892	2048
34	ptc-miR156d	4346	4087	2521	2892	2048
35	ptc-miR156e	4346	4087	2521	2892	2048
36	ptc-miR156f	4346	4087	2521	2892	2048
37	sbi-miR156a	4346	4087	2521	2892	2048
38	sbi-miR156b	4346	4087	2521	2892	2048
39	sbi-miR156c	4346	4087	2521	2892	2048
40	sbi-miR156f	4346	4087	2521	2892	2048
41	sbi-miR156g	4346	4087	2521	2892	2048
42	sbi-miR156h	4346	4087	2521	2892	2048
43	sbi-miR156i	4346	4087	2521	2892	2048
44	sly-miR156d-5p	4346	4087	2521	2892	2048
45	sof-miR156	4346	4087	2521	2892	2048
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3	stu-miR156e	4346	4087	2521	2892	2048
4	stu-miR156g-5p	4346	4087	2521	2892	2048
5	stu-miR156h-5p	4346	4087	2521	2892	2048
6	stu-miR156i-5p	4346	4087	2521	2892	2048
7	stu-miR156j-5p	4346	4087	2521	2892	2048
8	stu-miR156k-5p	4346	4087	2521	2892	2048
9	stu-miR156l-5p	4346	4087	2521	2892	2048
10	tcc-miR156b	4346	4087	2521	2892	2048
11	tcc-miR156c	4346	4087	2521	2892	2048
12	tcc-miR156d	4346	4087	2521	2892	2048
13	tcc-miR156g	4346	4087	2521	2892	2048
14	vca-miR156a-5p	4346	4087	2521	2892	2048
15	vun-miR156a	4346	4087	2521	2892	2048
16	vvi-miR156b	4346	4087	2521	2892	2048
17	vvi-miR156c	4346	4087	2521	2892	2048
18	vvi-miR156d	4346	4087	2521	2892	2048
19	zma-miR156a-5p	4346	4087	2521	2892	2048
20	zma-miR156b-5p	4346	4087	2521	2892	2048
21	zma-miR156c	4346	4087	2521	2892	2048
22	zma-miR156d-5p	4346	4087	2521	2892	2048
23	zma-miR156e-5p	4346	4087	2521	2892	2048
24	zma-miR156f-5p	4346	4087	2521	2892	2048
25	zma-miR156g-5p	4346	4087	2521	2892	2048
26	zma-miR156h-5p	4346	4087	2521	2892	2048
27	zma-miR156i-5p	4346	4087	2521	2892	2048
28	zma-miR156l-5p	4346	4087	2521	2892	2048
29	cme-miR156j	4473	4226	2603	2978	2127
30	fve-miR156a	4473	4226	2603	2978	2127
31	fve-miR156b	4473	4226	2603	2978	2127
32	fve-miR156c	4473	4226	2603	2978	2127
33	fve-miR156e	4473	4226	2603	2978	2127
34	gma-miR156k	4473	4226	2603	2978	2127
35	gma-miR156n	4473	4226	2603	2978	2127
36	gma-miR156o	4473	4226	2603	2978	2127
37	bna-miR156a	4370	4109	2532	2903	2073
38	hvu-miR156a	4370	4109	2532	2903	2073
39	hvu-miR156b	4370	4109	2532	2903	2073
40	rco-miR156a	4370	4109	2532	2903	2073
41	rco-miR156b	4370	4109	2532	2903	2073
42	rco-miR156c	4370	4109	2532	2903	2073
43	rco-miR156d	4370	4109	2532	2903	2073
44	ssl-miR156	4370	4109	2532	2903	2073
45	ssp-miR156	4370	4109	2532	2903	2073
46	tae-miR156	4370	4109	2532	2903	2073
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3	gma-miR156q	4361	4101	2529	2913	2052
4	gma-miR156s	4361	4101	2529	2913	2052
5	aca-miR-148a-3p	0	61	174	33	60
6	bta-miR-148a	0	61	174	33	60
7	cfa-miR-148a	0	61	174	33	60
8	cgr-miR-148a	0	61	174	33	60
9	chi-miR-148a-3p	0	61	174	33	60
10	cja-miR-148a	0	61	174	33	60
11	cli-miR-148a-3p	0	61	174	33	60
12	cpi-miR-148a-3p	0	61	174	33	60
13	cpo-miR-148a-3p	0	61	174	33	60
14	dno-miR-148a-3p	0	61	174	33	60
15	eca-miR-148a	0	61	174	33	60
16	gga-miR-148a-3p	0	61	174	33	60
17	hsa-miR-148a-3p	0	61	174	33	60
18	mdo-miR-148-3p	0	61	174	33	60
19	mml-miR-148a-3p	0	61	174	33	60
20	mmu-miR-148a-3p	0	61	174	33	60
21	oan-miR-148-3p	0	61	174	33	60
22	oar-miR-148a	0	61	174	33	60
23	ocu-miR-148a-3p	0	61	174	33	60
24	pal-miR-148a-3p	0	61	174	33	60
25	pbv-miR-148a-3p	0	61	174	33	60
26	ppy-miR-148a	0	61	174	33	60
27	ptr-miR-148a	0	61	174	33	60
28	sbo-miR-148a	0	61	174	33	60
29	ssc-miR-148a-3p	0	61	174	33	60
30	tch-miR-148a-3p	0	61	174	33	60
31	tgu-miR-148a-3p	0	61	174	33	60
32	xtr-miR-148a	0	61	174	33	60
33	age-miR-22	1379	886	1272	702	902
34	aja-miR-22	1379	886	1272	702	902
35	cfa-miR-22	1379	886	1272	702	902
36	cgr-miR-22-3p	1379	886	1272	702	902
37	cja-miR-22	1379	886	1272	702	902
38	cli-miR-22-3p	1379	886	1272	702	902
39	cpi-miR-22-3p	1379	886	1272	702	902
40	cpo-miR-22-3p	1379	886	1272	702	902
41	dma-miR-22	1379	886	1272	702	902
42	dno-miR-22-3p	1379	886	1272	702	902
43	eca-miR-22	1379	886	1272	702	902
44	gga-miR-22-3p	1379	886	1272	702	902
45	hsa-miR-22-3p	1379	886	1272	702	902
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3	lca-miR-22	1379	886	1272	702	902
4	lla-miR-22	1379	886	1272	702	902
5	mml-miR-22	1379	886	1272	702	902
6	mmr-miR-22	1379	886	1272	702	902
7	mmr-miR-22	1379	886	1272	702	902
8	mmu-miR-22-3p	1379	886	1272	702	902
9	mmu-miR-22-3p	1379	886	1272	702	902
10	mne-miR-22	1379	886	1272	702	902
11	nle-miR-22	1379	886	1272	702	902
12	nle-miR-22	1379	886	1272	702	902
13	oan-miR-22-3p	1379	886	1272	702	902
14	ocu-miR-22-3p	1379	886	1272	702	902
15	oga-miR-22	1379	886	1272	702	902
16	oha-miR-22a	1379	886	1272	702	902
17	oha-miR-22a	1379	886	1272	702	902
18	pal-miR-22-3p	1379	886	1272	702	902
19	pbv-miR-22-3p	1379	886	1272	702	902
20	pbv-miR-22-3p	1379	886	1272	702	902
21	pha-miR-22	1379	886	1272	702	902
22	ppa-miR-22	1379	886	1272	702	902
23	ppy-miR-22	1379	886	1272	702	902
24	ptr-miR-22	1379	886	1272	702	902
25	ptr-miR-22	1379	886	1272	702	902
26	rno-miR-22-3p	1379	886	1272	702	902
27	sbo-miR-22	1379	886	1272	702	902
28	sla-miR-22	1379	886	1272	702	902
29	sla-miR-22	1379	886	1272	702	902
30	ssc-miR-22-3p	1379	886	1272	702	902
31	tch-miR-22-3p	1379	886	1272	702	902
32	xtr-miR-22-3p	1379	886	1272	702	902
33	xtr-miR-22-3p	1379	886	1272	702	902
34	aly-miR170-5p	8021	6868	7105	4211	6540
35	aly-miR171a-5p	8021	6868	7105	4211	6540
36	ath-miR170-5p	8021	6868	7105	4211	6540
37	ath-miR170-5p	8021	6868	7105	4211	6540
38	ath-miR171a-5p	8021	6868	7105	4211	6540
39	cas-miR170	8021	6868	7105	4211	6540
40	cas-miR171a-5p	8021	6868	7105	4211	6540
41	cas-miR171a-5p	8021	6868	7105	4211	6540
42	csi-miR171f-5p	8021	6868	7105	4211	6540
43	gma-miR171j-5p	8021	6868	7105	4211	6540
44	sly-miR171f	8021	6868	7105	4211	6540
45	stu-miR171a-5p	8021	6868	7105	4211	6540
46	stu-miR171a-5p	8021	6868	7105	4211	6540
47	stu-miR171c-5p	8021	6868	7105	4211	6540
48	age-miR-16	266	163	163	103	156
49	cfa-miR-16	266	163	163	103	156
50	cfa-miR-16	266	163	163	103	156
51	cgr-miR-16-5p	266	163	163	103	156
52	cja-miR-16	266	163	163	103	156
53	cja-miR-16	266	163	163	103	156
54	cpi-miR-16a-5p	266	163	163	103	156
55	dma-miR-16	266	163	163	103	156
56	eca-miR-16	266	163	163	103	156
57	eca-miR-16	266	163	163	103	156
58	ggo-miR-16	266	163	163	103	156
59	hsa-miR-16-5p	266	163	163	103	156
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3	lla-miR-16	266	163	163	103	156
4	mdo-miR-16-5p	266	163	163	103	156
5	mml-miR-16-5p	266	163	163	103	156
6	mmu-miR-16-5p	266	163	163	103	156
7	mne-miR-16	266	163	163	103	156
8	mze-miR-16a	266	163	163	103	156
9	nle-miR-16	266	163	163	103	156
10	oan-miR-16a-5p	266	163	163	103	156
11	oga-miR-16	266	163	163	103	156
12	oni-miR-16a	266	163	163	103	156
13	pal-miR-16-5p	266	163	163	103	156
14	pha-miR-16	266	163	163	103	156
15	ppa-miR-16	266	163	163	103	156
16	ptr-miR-16	266	163	163	103	156
17	rno-miR-16-5p	266	163	163	103	156
18	sbo-miR-16	266	163	163	103	156
19	sla-miR-16	266	163	163	103	156
20	ssa-miR-16c-5p	266	163	163	103	156
21	ssc-miR-16	266	163	163	103	156
22	xla-miR-148a-3p	0	61	177	34	60
23	efu-miR-133-3p	331	233	127	128	219
24	chi-miR-133a-3p	324	223	125	127	212
25	cli-miR-133a-3p	324	223	125	127	212
26	cpi-miR-133a-3p	324	223	125	127	212
27	cpo-miR-133a-3p	324	223	125	127	212
28	dno-miR-133a-3p	324	223	125	127	212
29	ocu-miR-133a-3p	324	223	125	127	212
30	pbv-miR-133a-3p	324	223	125	127	212
31	aca-miR-200a-3p	2	58	166	41	61
32	ami-miR-200a-3p	2	58	166	41	61
33	dre-miR-200a-3p	2	58	166	41	61
34	eca-miR-200a	2	58	166	41	61
35	fru-miR-200a	2	58	166	41	61
36	gga-miR-200a-3p	2	58	166	41	61
37	ggo-miR-200a	2	58	166	41	61
38	gmo-miR-200a-3p	2	58	166	41	61
39	hsa-miR-200a-3p	2	58	166	41	61
40	mdo-miR-200a-3p	2	58	166	41	61
41	mml-miR-200a-3p	2	58	166	41	61
42	mmu-miR-200a-3p	2	58	166	41	61
43	ppy-miR-200a	2	58	166	41	61
44	ptr-miR-200a	2	58	166	41	61
45	rno-miR-200a-3p	2	58	166	41	61
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3	tni-miR-200a	2	58	166	41	61
4	xtr-miR-200a	2	58	166	41	61
5	osa-miR159f	1487	3915	3203	2104	1946
6	aof-miR171b	340	402	379	288	323
7	fve-miR171f-3p	340	402	379	288	323
8	gma-miR171k-3p	340	402	379	288	323
9	lja-miR171d-5p	340	402	379	288	323
10	mdm-miR171j	340	402	379	288	323
11	mdm-miR171k	340	402	379	288	323
12	mdm-miR171l	340	402	379	288	323
13	mes-miR171e	340	402	379	288	323
14	nta-miR171b	340	402	379	288	323
15	pab-miR171b	340	402	379	288	323
16	pab-miR171c	340	402	379	288	323
17	ppe-miR171b	340	402	379	288	323
18	ssl-miR171b	340	402	379	288	323
19	vvi-miR171f	340	402	379	288	323
20	abu-miR-200a	16	197	535	142	189
21	bta-miR-200a	16	197	535	142	189
22	cgr-miR-200a	16	197	535	142	189
23	cli-miR-200a-3p	16	197	535	142	189
24	cpi-miR-200a-3p	16	197	535	142	189
25	cpo-miR-200a-3p	16	197	535	142	189
26	efu-miR-200a	16	197	535	142	189
27	mze-miR-200a	16	197	535	142	189
28	nbr-miR-200a	16	197	535	142	189
29	oan-miR-200a-3p	16	197	535	142	189
30	oha-miR-200a	16	197	535	142	189
31	oni-miR-200a	16	197	535	142	189
32	pal-miR-200a-3p	16	197	535	142	189
33	pbv-miR-200a-3p	16	197	535	142	189
34	pony-miR-200a	16	197	535	142	189
35	ssa-miR-200b-3p	16	197	535	142	189
36	tch-miR-200a-3p	16	197	535	142	189
37	tgu-miR-200a-3p	16	197	535	142	189
38	xla-miR-200a-3p	16	197	535	142	189
39	aca-miR-181a	221	179	302	129	188
40	ami-miR-181a-5p	221	179	302	129	188
41	cgr-miR-181a-5p	221	179	302	129	188
42	cja-miR-181a	221	179	302	129	188
43	cpi-miR-181a-5p	221	179	302	129	188
44	dma-miR-181a	221	179	302	129	188
45	dre-miR-181a-5p	221	179	302	129	188
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3	eca-miR-181a	221	179	302	129	188
4	fru-miR-181a-5p	221	179	302	129	188
5	gga-miR-181a-5p	221	179	302	129	188
6	ggo-miR-181a-5p	221	179	302	129	188
7	gmo-miR-181a-5p	221	179	302	129	188
8	gmo-miR-181a-5p	221	179	302	129	188
9	gmo-miR-181a-5p	221	179	302	129	188
10	hsa-miR-181a-5p	221	179	302	129	188
11	lla-miR-181a-5p	221	179	302	129	188
12	mdo-miR-181a-5p	221	179	302	129	188
13	mml-miR-181a-5p	221	179	302	129	188
14	mml-miR-181a-5p	221	179	302	129	188
15	mmu-miR-181a-5p	221	179	302	129	188
16	mne-miR-181a-5p	221	179	302	129	188
17	mne-miR-181a-5p	221	179	302	129	188
18	nle-miR-181a	221	179	302	129	188
19	oan-miR-181a-5p	221	179	302	129	188
20	oar-miR-181a	221	179	302	129	188
21	oar-miR-181a	221	179	302	129	188
22	oga-miR-181a	221	179	302	129	188
23	oga-miR-181a	221	179	302	129	188
24	pha-miR-181a	221	179	302	129	188
25	pma-miR-181a-5p	221	179	302	129	188
26	ppa-miR-181a-5p	221	179	302	129	188
27	ppy-miR-181a-5p	221	179	302	129	188
28	ptr-miR-181a-5p	221	179	302	129	188
29	ptr-miR-181a-5p	221	179	302	129	188
30	rno-miR-181a-5p	221	179	302	129	188
31	sla-miR-181a	221	179	302	129	188
32	ssa-miR-181a-5p	221	179	302	129	188
33	ssa-miR-181a-5p	221	179	302	129	188
34	tch-miR-181a-5p	221	179	302	129	188
35	tgu-miR-181a-5p	221	179	302	129	188
36	tni-miR-181a-5p	221	179	302	129	188
37	tni-miR-181a-5p	221	179	302	129	188
38	xtr-miR-181a-5p	221	179	302	129	188
39	bta-miR-181a	264	202	337	151	211
40	cli-miR-181a-5p	264	202	337	151	211
41	cli-miR-181a-5p	264	202	337	151	211
42	cpo-miR-181a-5p	264	202	337	151	211
43	dno-miR-181a-5p	264	202	337	151	211
44	dno-miR-181a-5p	264	202	337	151	211
45	ocu-miR-181a-5p	264	202	337	151	211
46	oha-miR-181a-5p	264	202	337	151	211
47	pal-miR-181a-5p	264	202	337	151	211
48	pbv-miR-181a-5p	264	202	337	151	211
49	pbv-miR-181a-5p	264	202	337	151	211
50	ssc-miR-181a	264	202	337	151	211
51	abu-miR-221	90	49	41	42	43
52	ami-miR-221-3p	90	49	41	42	43
53	cgr-miR-221-3p	90	49	41	42	43
54	cgr-miR-221-3p	90	49	41	42	43
55	cpo-miR-221-3p	90	49	41	42	43
56	dma-miR-221	90	49	41	42	43
57	dno-miR-221-3p	90	49	41	42	43
58	dno-miR-221-3p	90	49	41	42	43
59	dre-miR-221-3p	90	49	41	42	43
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3	eca-miR-221	90	49	41	42	43
4	fru-miR-221	90	49	41	42	43
5	gga-miR-221-3p	90	49	41	42	43
6	ggo-miR-221	90	49	41	42	43
7	ggo-miR-221	90	49	41	42	43
8	hsa-miR-221-3p	90	49	41	42	43
9	mdo-miR-221-3p	90	49	41	42	43
10	mml-miR-221-3p	90	49	41	42	43
11	mml-miR-221-3p	90	49	41	42	43
12	mml-miR-221-3p	90	49	41	42	43
13	mmr-miR-221	90	49	41	42	43
14	mmu-miR-221-3p	90	49	41	42	43
15	mze-miR-221	90	49	41	42	43
16	nbr-miR-221	90	49	41	42	43
17	nbr-miR-221	90	49	41	42	43
18	nle-miR-221	90	49	41	42	43
19	ocu-miR-221-3p	90	49	41	42	43
20	oga-miR-221	90	49	41	42	43
21	oga-miR-221	90	49	41	42	43
22	oha-miR-221-3p	90	49	41	42	43
23	ola-miR-221	90	49	41	42	43
24	oni-miR-221	90	49	41	42	43
25	oni-miR-221	90	49	41	42	43
26	pha-miR-221	90	49	41	42	43
27	phn-miR-221	90	49	41	42	43
28	ppa-miR-221	90	49	41	42	43
29	ppa-miR-221	90	49	41	42	43
30	ppy-miR-221	90	49	41	42	43
31	ptr-miR-221	90	49	41	42	43
32	ptr-miR-221	90	49	41	42	43
33	rno-miR-221-3p	90	49	41	42	43
34	sbo-miR-221	90	49	41	42	43
35	tgu-miR-221-3p	90	49	41	42	43
36	tni-miR-221	90	49	41	42	43
37	tni-miR-221	90	49	41	42	43
38	xtr-miR-221	90	49	41	42	43
39	gma-miR159e-5p	2364	1927	1599	1667	1619
40	cli-miR-199-3p	191	104	103	82	111
41	cli-miR-199-3p	191	104	103	82	111
42	efu-miR-199	191	104	103	82	111
43	dre-miR-199-3p	182	97	95	75	108
44	oha-miR-199c-3p	182	97	95	75	108
45	oha-miR-199c-3p	182	97	95	75	108
46	ssc-miR-199b-3p	182	97	95	75	108
47	xtr-miR-199a-3p	182	97	95	75	108
48	aca-miR-23a-3p	177	117	122	81	117
49	age-miR-23a	177	117	122	81	117
50	age-miR-23a	177	117	122	81	117
51	ccr-miR-23a	177	117	122	81	117
52	cgr-miR-23a-3p	177	117	122	81	117
53	chi-miR-23a	177	117	122	81	117
54	chi-miR-23a	177	117	122	81	117
55	cpi-miR-23a-3p	177	117	122	81	117
56	eca-miR-23a	177	117	122	81	117
57	ggo-miR-23a	177	117	122	81	117
58	ggo-miR-23a	177	117	122	81	117
59	hsa-miR-23a-3p	177	117	122	81	117
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3	ipu-miR-23a	177	117	122	81	117
4	lca-miR-23a	177	117	122	81	117
5	mml-miR-23a-3p	177	117	122	81	117
6	mmu-miR-23a-3p	177	117	122	81	117
7	mne-miR-23a	177	117	122	81	117
8	pbv-miR-23a-3p	177	117	122	81	117
9	pha-miR-23a	177	117	122	81	117
10	phn-miR-23a	177	117	122	81	117
11	ppa-miR-23a	177	117	122	81	117
12	ppy-miR-23a	177	117	122	81	117
13	ptr-miR-23a	177	117	122	81	117
14	rno-miR-23a-3p	177	117	122	81	117
15	sla-miR-23a	177	117	122	81	117
16	ssa-miR-23a-3p	177	117	122	81	117
17	ssc-miR-23a	177	117	122	81	117
18	xla-miR-23a	177	117	122	81	117
19	xtr-miR-23a	177	117	122	81	117
20	aly-miR168a-5p	28942	22785	27536	20618	22487
21	aly-miR168b-5p	28942	22785	27536	20618	22487
22	aof-miR168a	28942	22785	27536	20618	22487
23	ath-miR168a-5p	28942	22785	27536	20618	22487
24	ath-miR168b-5p	28942	22785	27536	20618	22487
25	atr-miR168	28942	22785	27536	20618	22487
26	bna-miR168a	28942	22785	27536	20618	22487
27	bra-miR168a-5p	28942	22785	27536	20618	22487
28	cca-miR168a	28942	22785	27536	20618	22487
29	ccl-miR168	28942	22785	27536	20618	22487
30	crt-miR168	28942	22785	27536	20618	22487
31	csi-miR168-5p	28942	22785	27536	20618	22487
32	fve-miR168-5p	28942	22785	27536	20618	22487
33	gma-miR168a	28942	22785	27536	20618	22487
34	lus-miR168a	28942	22785	27536	20618	22487
35	lus-miR168b	28942	22785	27536	20618	22487
36	mdm-miR168a	28942	22785	27536	20618	22487
37	mdm-miR168b	28942	22785	27536	20618	22487
38	mes-miR168a	28942	22785	27536	20618	22487
39	mtr-miR168b	28942	22785	27536	20618	22487
40	mtr-miR168c-5p	28942	22785	27536	20618	22487
41	nta-miR168d	28942	22785	27536	20618	22487
42	nta-miR168e	28942	22785	27536	20618	22487
43	pab-miR168a	28942	22785	27536	20618	22487
44	ppe-miR168	28942	22785	27536	20618	22487
45	ptc-miR168a-5p	28942	22785	27536	20618	22487
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3	ptc-miR168b-5p	28942	22785	27536	20618	22487
4	rco-miR168	28942	22785	27536	20618	22487
5	tcc-miR168	28942	22785	27536	20618	22487
6	vca-miR168a-5p	28942	22785	27536	20618	22487
7	vca-miR168b-5p	28942	22785	27536	20618	22487
8	vun-miR168	28942	22785	27536	20618	22487
9	vvi-miR168	28942	22785	27536	20618	22487
10	lja-miR168-5p	29003	22843	27583	20701	22538
11	oha-miR-1a-3p	135	103	63	65	98
12	pma-miR-1c-3p	135	103	63	65	98
13	ami-miR-27b-3p	67	83	148	54	80
14	dma-miR-27b	67	83	148	54	80
15	gmo-miR-27b-3p	67	83	148	54	80
16	nle-miR-27b	67	83	148	54	80
17	oga-miR-27b	67	83	148	54	80
18	pha-miR-27b	67	83	148	54	80
19	csi-miR167c-3p	377	359	421	357	328
20	aae-miR-133	206	143	77	83	146
21	abu-miR-133a	206	143	77	83	146
22	aga-miR-133	206	143	77	83	146
23	age-miR-133a	206	143	77	83	146
24	ame-miR-133-3p	206	143	77	83	146
25	bbe-miR-133-5p	206	143	77	83	146
26	bmo-miR-133	206	143	77	83	146
27	ccr-miR-133a-3p	206	143	77	83	146
28	cfa-miR-133a	206	143	77	83	146
29	cja-miR-133a	206	143	77	83	146
30	cqu-miR-133	206	143	77	83	146
31	cte-miR-133	206	143	77	83	146
32	dan-miR-133	206	143	77	83	146
33	der-miR-133	206	143	77	83	146
34	dgr-miR-133	206	143	77	83	146
35	dme-miR-133-3p	206	143	77	83	146
36	dmo-miR-133	206	143	77	83	146
37	dpe-miR-133	206	143	77	83	146
38	dps-miR-133	206	143	77	83	146
39	dpu-miR-133	206	143	77	83	146
40	dqu-miR-133-3p	206	143	77	83	146
41	dse-miR-133	206	143	77	83	146
42	dsi-miR-133	206	143	77	83	146
43	dvi-miR-133-3p	206	143	77	83	146
44	dwi-miR-133	206	143	77	83	146
45	dya-miR-133	206	143	77	83	146
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3	gga-miR-133a-3p	206	143	77	83	146
4	ggo-miR-133a	206	143	77	83	146
5	gmo-miR-133a-3p	206	143	77	83	146
6	ipu-miR-133a	206	143	77	83	146
7	isc-miR-133	206	143	77	83	146
8	lgi-miR-133-3p	206	143	77	83	146
9	lla-miR-133a	206	143	77	83	146
10	mdo-miR-133a-3p	206	143	77	83	146
11	mne-miR-133a	206	143	77	83	146
12	mse-miR-133	206	143	77	83	146
13	mze-miR-133a	206	143	77	83	146
14	nbr-miR-133a	206	143	77	83	146
15	ngi-miR-133	206	143	77	83	146
16	nlo-miR-133	206	143	77	83	146
17	nvi-miR-133	206	143	77	83	146
18	oan-miR-133a-3p	206	143	77	83	146
19	oar-miR-133	206	143	77	83	146
20	oni-miR-133a	206	143	77	83	146
21	pal-miR-133a-3p	206	143	77	83	146
22	pca-miR-133-3p	206	143	77	83	146
23	ppa-miR-133a	206	143	77	83	146
24	sko-miR-133	206	143	77	83	146
25	sla-miR-133a	206	143	77	83	146
26	ssa-miR-133a-3p	206	143	77	83	146
27	tca-miR-133-3p	206	143	77	83	146
28	tcf-miR-133	206	143	77	83	146
29	tur-miR-133-3p	206	143	77	83	146
30	xla-miR-133a	206	143	77	83	146
31	xtr-miR-133a	206	143	77	83	146
32	ami-miR-199-3p	152	98	96	73	100
33	bta-miR-199a-3p	152	98	96	73	100
34	cpi-miR-199-3p	152	98	96	73	100
35	cpo-miR-199-3p	152	98	96	73	100
36	dno-miR-199-3p	152	98	96	73	100
37	eca-miR-199a-3p	152	98	96	73	100
38	eca-miR-199b-3p	152	98	96	73	100
39	gmo-miR-199-3p	152	98	96	73	100
40	hsa-miR-199a-3p	152	98	96	73	100
41	hsa-miR-199b-3p	152	98	96	73	100
42	mml-miR-199a-3p	152	98	96	73	100
43	mmu-miR-199a-3p	152	98	96	73	100
44	mmu-miR-199b-3p	152	98	96	73	100
45	ocu-miR-199a-3p	152	98	96	73	100
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3	oha-miR-199a-3p	152	98	96	73	100
4	ola-miR-199a-3p	152	98	96	73	100
5	pol-miR-199a-3p	152	98	96	73	100
6	ptr-miR-199a-3p	152	98	96	73	100
7	ptr-miR-199b	152	98	96	73	100
8	rno-miR-199a-3p	152	98	96	73	100
9	ssc-miR-199a-3p	152	98	96	73	100
10	xla-miR-199-3p	152	98	96	73	100
11	bdi-miR166e-3p	1001	1255	1211	1048	894
12	atr-miR319a	4040	3144	2272	2517	2469
13	atr-miR319c	4040	3144	2272	2517	2469
14	cme-miR319a	4040	3144	2272	2517	2469
15	cme-miR319b	4040	3144	2272	2517	2469
16	ctr-miR319	4040	3144	2272	2517	2469
17	gma-miR319a	4040	3144	2272	2517	2469
18	gma-miR319b	4040	3144	2272	2517	2469
19	gma-miR319e	4040	3144	2272	2517	2469
20	lus-miR319b	4040	3144	2272	2517	2469
21	mtr-miR319a-3p	4040	3144	2272	2517	2469
22	mtr-miR319b-3p	4040	3144	2272	2517	2469
23	pab-miR319a	4040	3144	2272	2517	2469
24	pab-miR319b	4040	3144	2272	2517	2469
25	pab-miR319c	4040	3144	2272	2517	2469
26	pab-miR319f	4040	3144	2272	2517	2469
27	pab-miR319g	4040	3144	2272	2517	2469
28	pab-miR319i	4040	3144	2272	2517	2469
29	pab-miR319k	4040	3144	2272	2517	2469
30	pab-miR319l	4040	3144	2272	2517	2469
31	pab-miR319m	4040	3144	2272	2517	2469
32	pab-miR319n	4040	3144	2272	2517	2469
33	ppe-miR319a	4040	3144	2272	2517	2469
34	ptc-miR319a	4040	3144	2272	2517	2469
35	ptc-miR319b	4040	3144	2272	2517	2469
36	ptc-miR319c	4040	3144	2272	2517	2469
37	ptc-miR319d	4040	3144	2272	2517	2469
38	mes-miR166i	65	161	139	108	79
39	csi-miR159c-3p	4060	3182	2307	2548	2498
40	ppt-miR319c	4060	3182	2307	2548	2498
41	ppt-miR319d-3p	4060	3182	2307	2548	2498
42	ppt-miR319e	4060	3182	2307	2548	2498
43	abu-miR-199-3p	144	91	88	66	97
44	ccr-miR-199-3p	144	91	88	66	97
45	cfa-miR-199	144	91	88	66	97
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3	cgr-miR-199a-3p	144	91	88	66	97
4	chi-miR-199a-3p	144	91	88	66	97
5	chi-miR-199b-3p	144	91	88	66	97
6	chi-miR-199c-3p	144	91	88	66	97
7	chi-miR-199c-3p	144	91	88	66	97
8	cja-miR-199	144	91	88	66	97
9	cja-miR-199	144	91	88	66	97
10	dma-miR-199	144	91	88	66	97
11	gmo-miR-199-4-3p	144	91	88	66	97
12	ipu-miR-199a-3p	144	91	88	66	97
13	ipu-miR-199a-3p	144	91	88	66	97
14	mdo-miR-199b-3p	144	91	88	66	97
15	mmr-miR-199	144	91	88	66	97
16	mze-miR-199	144	91	88	66	97
17	mze-miR-199	144	91	88	66	97
18	nbr-miR-199	144	91	88	66	97
19	nle-miR-199a	144	91	88	66	97
20	nle-miR-199b	144	91	88	66	97
21	nle-miR-199b	144	91	88	66	97
22	oan-miR-199-3p	144	91	88	66	97
23	oar-miR-199a-3p	144	91	88	66	97
24	oga-miR-199	144	91	88	66	97
25	oga-miR-199	144	91	88	66	97
26	oni-miR-199a	144	91	88	66	97
27	pal-miR-199-3p	144	91	88	66	97
28	pbv-miR-199-3p	144	91	88	66	97
29	pbv-miR-199-3p	144	91	88	66	97
30	pha-miR-199	144	91	88	66	97
31	phny-miR-199	144	91	88	66	97
32	ppa-miR-199b	144	91	88	66	97
33	ppa-miR-199b	144	91	88	66	97
34	sbo-miR-199	144	91	88	66	97
35	sha-miR-199a	144	91	88	66	97
36	ssa-miR-199a-3p	144	91	88	66	97
37	ssa-miR-199a-3p	144	91	88	66	97
38	tch-miR-199a-3p	144	91	88	66	97
39	tch-miR-199b-3p	144	91	88	66	97
40	tch-miR-199b-3p	144	91	88	66	97
41	tgu-miR-199-3p	144	91	88	66	97
42	mtr-miR319c-3p	4046	3147	2279	2525	2473
43	vvi-miR319g	4046	3147	2279	2525	2473
44	csi-miR396f-3p	870	702	698	707	569
45	csi-miR396f-3p	870	702	698	707	569
46	gma-miR396b-3p	870	702	698	707	569
47	gma-miR396k-3p	870	702	698	707	569
48	mtr-miR396a-3p	870	702	698	707	569
49	mtr-miR396a-3p	870	702	698	707	569
50	cpo-miR-23a-3p	264	180	170	131	175
51	dno-miR-23a-3p	264	180	170	131	175
52	efu-miR-23a	270	183	174	134	177
53	efu-miR-23a	270	183	174	134	177
54	abu-miR-92a	107	89	126	64	97
55	aca-miR-92a	107	89	126	64	97
56	age-miR-92	107	89	126	64	97
57	ami-miR-92a-3p	107	89	126	64	97
58	ami-miR-92a-3p	107	89	126	64	97
59	bta-miR-92a	107	89	126	64	97
60	bta-miR-92a	107	89	126	64	97

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3	ccr-miR-92a	107	89	126	64	97
4	cfa-miR-92a	107	89	126	64	97
5	cgr-miR-92a-3p	107	89	126	64	97
6	chi-miR-92a-3p	107	89	126	64	97
7	chi-miR-92b	107	89	126	64	97
8	cja-miR-92a	107	89	126	64	97
9	cli-miR-92-3p	107	89	126	64	97
10	cpo-miR-92a-3p	107	89	126	64	97
11	dma-miR-92a	107	89	126	64	97
12	dno-miR-92a-3p	107	89	126	64	97
13	dre-miR-92a-3p	107	89	126	64	97
14	eca-miR-92a	107	89	126	64	97
15	efu-miR-92a	107	89	126	64	97
16	fru-miR-92	107	89	126	64	97
17	ggo-miR-92	107	89	126	64	97
18	hsa-miR-92a-3p	107	89	126	64	97
19	ipu-miR-92a	107	89	126	64	97
20	lca-miR-92	107	89	126	64	97
21	lla-miR-92	107	89	126	64	97
22	mdo-miR-92a-3p	107	89	126	64	97
23	mml-miR-92a-3p	107	89	126	64	97
24	mmr-miR-92a	107	89	126	64	97
25	mmr-miR-92b	107	89	126	64	97
26	mne-miR-92	107	89	126	64	97
27	mze-miR-92a	107	89	126	64	97
28	nbr-miR-92a	107	89	126	64	97
29	nle-miR-92a	107	89	126	64	97
30	oan-miR-92a-3p	107	89	126	64	97
31	ocu-miR-92a-3p	107	89	126	64	97
32	oga-miR-92a	107	89	126	64	97
33	oha-miR-92a	107	89	126	64	97
34	oha-miR-92a-3p	107	89	126	64	97
35	oni-miR-92a	107	89	126	64	97
36	pal-miR-92a-3p	107	89	126	64	97
37	pbv-miR-92a-3p	107	89	126	64	97
38	pha-miR-92a	107	89	126	64	97
39	pony-miR-92	107	89	126	64	97
40	ppa-miR-92a	107	89	126	64	97
41	ppy-miR-92	107	89	126	64	97
42	ptr-miR-92	107	89	126	64	97
43	sbo-miR-92a	107	89	126	64	97
44	sla-miR-92	107	89	126	64	97
45	ssa-miR-92a-3p	107	89	126	64	97
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3	ssc-miR-92a	107	89	126	64	97
4	tch-miR-92a-3p	107	89	126	64	97
5	tgu-miR-92-3p	107	89	126	64	97
6	tni-miR-92	107	89	126	64	97
7	tni-miR-92	107	89	126	64	97
8	xla-miR-92a-3p	107	89	126	64	97
9	xla-miR-92a-3p	107	89	126	64	97
10	aaU-miR319	5644	4160	3002	3409	3391
11	aly-miR319a-3p	5644	4160	3002	3409	3391
12	aly-miR319b-3p	5644	4160	3002	3409	3391
13	aly-miR319b-3p	5644	4160	3002	3409	3391
14	amg-miR319	5644	4160	3002	3409	3391
15	aof-miR319a	5644	4160	3002	3409	3391
16	aqc-miR319	5644	4160	3002	3409	3391
17	aqc-miR319	5644	4160	3002	3409	3391
18	ath-miR319a	5644	4160	3002	3409	3391
19	ath-miR319b	5644	4160	3002	3409	3391
20	bra-miR319-3p	5644	4160	3002	3409	3391
21	bra-miR319-3p	5644	4160	3002	3409	3391
22	cca-miR319	5644	4160	3002	3409	3391
23	gma-miR319h	5644	4160	3002	3409	3391
24	gma-miR319j	5644	4160	3002	3409	3391
25	gma-miR319j	5644	4160	3002	3409	3391
26	gma-miR319k	5644	4160	3002	3409	3391
27	gma-miR319m	5644	4160	3002	3409	3391
28	gma-miR319m	5644	4160	3002	3409	3391
29	hbr-miR319	5644	4160	3002	3409	3391
30	lus-miR319a	5644	4160	3002	3409	3391
31	mdm-miR319a	5644	4160	3002	3409	3391
32	mdm-miR319b-3p	5644	4160	3002	3409	3391
33	mdm-miR319b-3p	5644	4160	3002	3409	3391
34	mes-miR319a	5644	4160	3002	3409	3391
35	mes-miR319b	5644	4160	3002	3409	3391
36	mes-miR319c	5644	4160	3002	3409	3391
37	mes-miR319c	5644	4160	3002	3409	3391
38	mes-miR319d	5644	4160	3002	3409	3391
39	mes-miR319e	5644	4160	3002	3409	3391
40	mes-miR319e	5644	4160	3002	3409	3391
41	mtr-miR319d-3p	5644	4160	3002	3409	3391
42	nta-miR319a	5644	4160	3002	3409	3391
43	nta-miR319b	5644	4160	3002	3409	3391
44	nta-miR319b	5644	4160	3002	3409	3391
45	rco-miR319a	5644	4160	3002	3409	3391
46	rco-miR319b	5644	4160	3002	3409	3391
47	rco-miR319c	5644	4160	3002	3409	3391
48	rco-miR319c	5644	4160	3002	3409	3391
49	sly-miR319b	5644	4160	3002	3409	3391
50	stu-miR319a-3p	5644	4160	3002	3409	3391
51	tae-miR319	5644	4160	3002	3409	3391
52	vun-miR319a	5644	4160	3002	3409	3391
53	vun-miR319a	5644	4160	3002	3409	3391
54	vvi-miR319b	5644	4160	3002	3409	3391
55	vvi-miR319c	5644	4160	3002	3409	3391
56	vvi-miR319f	5644	4160	3002	3409	3391
57	vvi-miR319f	5644	4160	3002	3409	3391
58	gma-miR5374-5p	200	176	217	147	170
59	abu-miR-23a	257	176	161	129	171
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3	ami-miR-23a-3p	257	176	161	129	171
4	bta-miR-23a	257	176	161	129	171
5	cja-miR-23a	257	176	161	129	171
6	dre-miR-23a-3p	257	176	161	129	171
7	fru-miR-23a	257	176	161	129	171
8	gmo-miR-23a-3p	257	176	161	129	171
9	hhi-miR-23a	257	176	161	129	171
10	mze-miR-23a	257	176	161	129	171
11	nbr-miR-23a	257	176	161	129	171
12	oan-miR-23a-3p	257	176	161	129	171
13	oar-miR-23a	257	176	161	129	171
14	oga-miR-23a	257	176	161	129	171
15	oha-miR-23a-3p	257	176	161	129	171
16	ola-miR-23a	257	176	161	129	171
17	oni-miR-23a	257	176	161	129	171
18	pal-miR-23a-3p	257	176	161	129	171
19	tni-miR-23a	257	176	161	129	171
20	xla-miR-23a-3p	257	176	161	129	171
21	aly-miR171b-3p	717	906	916	769	739
22	aly-miR171c-3p	717	906	916	769	739
23	ata-miR171c-3p	717	906	916	769	739
24	ath-miR171b-3p	717	906	916	769	739
25	ath-miR171c-3p	717	906	916	769	739
26	bna-miR171a	717	906	916	769	739
27	bna-miR171b	717	906	916	769	739
28	bna-miR171c	717	906	916	769	739
29	bna-miR171d	717	906	916	769	739
30	bna-miR171e	717	906	916	769	739
31	bol-miR171a	717	906	916	769	739
32	bra-miR171a	717	906	916	769	739
33	bra-miR171b	717	906	916	769	739
34	bra-miR171c	717	906	916	769	739
35	bra-miR171d	717	906	916	769	739
36	cas-miR171b	717	906	916	769	739
37	cas-miR171c-3p	717	906	916	769	739
38	cme-miR171b	717	906	916	769	739
39	cme-miR171d	717	906	916	769	739
40	gma-miR171i-3p	717	906	916	769	739
41	lus-miR171i	717	906	916	769	739
42	mdm-miR171f-3p	717	906	916	769	739
43	mes-miR171b	717	906	916	769	739
44	mes-miR171c	717	906	916	769	739
45	mtr-miR171f	717	906	916	769	739
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3	ptc-miR171a-3p	717	906	916	769	739
4	ptc-miR171b	717	906	916	769	739
5	rco-miR171a	717	906	916	769	739
6	rco-miR171b	717	906	916	769	739
7	sly-miR171b-3p	717	906	916	769	739
8	ssl-miR171a	717	906	916	769	739
9	stu-miR171d-3p	717	906	916	769	739
10	tae-miR171b	717	906	916	769	739
11	ptc-miR396e-3p	559	463	485	488	383
12	aly-miR390a-5p	4718	5643	4258	4695	3692
13	aly-miR390b-5p	4718	5643	4258	4695	3692
14	aof-miR390	4718	5643	4258	4695	3692
15	ata-miR390-5p	4718	5643	4258	4695	3692
16	ath-miR390a-5p	4718	5643	4258	4695	3692
17	ath-miR390b-5p	4718	5643	4258	4695	3692
18	atr-miR390.2	4718	5643	4258	4695	3692
19	bdi-miR390a-5p	4718	5643	4258	4695	3692
20	bna-miR390a	4718	5643	4258	4695	3692
21	bna-miR390b	4718	5643	4258	4695	3692
22	bna-miR390c	4718	5643	4258	4695	3692
23	bra-miR390-5p	4718	5643	4258	4695	3692
24	cas-miR390a-5p	4718	5643	4258	4695	3692
25	cas-miR390b	4718	5643	4258	4695	3692
26	cme-miR390a	4718	5643	4258	4695	3692
27	cme-miR390b	4718	5643	4258	4695	3692
28	cme-miR390c	4718	5643	4258	4695	3692
29	cme-miR390d	4718	5643	4258	4695	3692
30	cpa-miR390a	4718	5643	4258	4695	3692
31	cpa-miR390b	4718	5643	4258	4695	3692
32	csi-miR390a-5p	4718	5643	4258	4695	3692
33	fve-miR390a	4718	5643	4258	4695	3692
34	fve-miR390b	4718	5643	4258	4695	3692
35	ghr-miR390a	4718	5643	4258	4695	3692
36	ghr-miR390b	4718	5643	4258	4695	3692
37	ghr-miR390c	4718	5643	4258	4695	3692
38	gma-miR390a-5p	4718	5643	4258	4695	3692
39	gma-miR390f	4718	5643	4258	4695	3692
40	gma-miR390g	4718	5643	4258	4695	3692
41	hex-miR390a	4718	5643	4258	4695	3692
42	hex-miR390b	4718	5643	4258	4695	3692
43	lja-miR390a-5p	4718	5643	4258	4695	3692
44	lja-miR390b-5p	4718	5643	4258	4695	3692
45	lus-miR390a	4718	5643	4258	4695	3692
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3	lus-miR390b	4718	5643	4258	4695	3692
4	lus-miR390c	4718	5643	4258	4695	3692
5	lus-miR390d	4718	5643	4258	4695	3692
6	mdm-miR390a	4718	5643	4258	4695	3692
7	mdm-miR390b	4718	5643	4258	4695	3692
8	mdm-miR390c	4718	5643	4258	4695	3692
9	mdm-miR390d	4718	5643	4258	4695	3692
10	mdm-miR390e	4718	5643	4258	4695	3692
11	mdm-miR390f	4718	5643	4258	4695	3692
12	mes-miR390b	4718	5643	4258	4695	3692
13	mtr-miR390	4718	5643	4258	4695	3692
14	nta-miR390b	4718	5643	4258	4695	3692
15	nta-miR390c	4718	5643	4258	4695	3692
16	osa-miR390-5p	4718	5643	4258	4695	3692
17	pab-miR390a	4718	5643	4258	4695	3692
18	pab-miR390b	4718	5643	4258	4695	3692
19	ppe-miR390	4718	5643	4258	4695	3692
20	ppt-miR390a	4718	5643	4258	4695	3692
21	ppt-miR390b	4718	5643	4258	4695	3692
22	ptc-miR390a	4718	5643	4258	4695	3692
23	ptc-miR390b	4718	5643	4258	4695	3692
24	ptc-miR390c	4718	5643	4258	4695	3692
25	ptc-miR390d-5p	4718	5643	4258	4695	3692
26	rco-miR390a	4718	5643	4258	4695	3692
27	rco-miR390b	4718	5643	4258	4695	3692
28	sbi-miR390	4718	5643	4258	4695	3692
29	sly-miR390b-5p	4718	5643	4258	4695	3692
30	tcc-miR390a	4718	5643	4258	4695	3692
31	tcc-miR390b	4718	5643	4258	4695	3692
32	vvi-miR390	4718	5643	4258	4695	3692
33	zma-miR390a-5p	4718	5643	4258	4695	3692
34	zma-miR390b-5p	4718	5643	4258	4695	3692
35	aae-miR-125-5p	89	54	61	42	55
36	abu-miR-125b	89	54	61	42	55
37	aca-miR-125b	89	54	61	42	55
38	aga-miR-125	89	54	61	42	55
39	age-miR-125b	89	54	61	42	55
40	ami-miR-125b-5p	89	54	61	42	55
41	bbe-miR-125a-5p	89	54	61	42	55
42	bdo-miR-125	89	54	61	42	55
43	bfl-miR-125a-5p	89	54	61	42	55
44	bta-miR-125b	89	54	61	42	55
45	ccr-miR-125b	89	54	61	42	55
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3	cfa-miR-125b	89	54	61	42	55
4	cgr-miR-125b-5p	89	54	61	42	55
5	cja-miR-125	89	54	61	42	55
6	cja-miR-125b	89	54	61	42	55
7	cli-miR-125-5p	89	54	61	42	55
8	cpi-miR-125b-5p	89	54	61	42	55
9	cpo-miR-125b-5p	89	54	61	42	55
10	cqu-miR-125-5p	89	54	61	42	55
11	cte-miR-125	89	54	61	42	55
12	dan-miR-125	89	54	61	42	55
13	der-miR-125	89	54	61	42	55
14	dgr-miR-125	89	54	61	42	55
15	dma-miR-125b	89	54	61	42	55
16	dme-miR-125-5p	89	54	61	42	55
17	dmo-miR-125	89	54	61	42	55
18	dno-miR-125b-5p	89	54	61	42	55
19	dpe-miR-125	89	54	61	42	55
20	dps-miR-125	89	54	61	42	55
21	dqu-miR-125-5p	89	54	61	42	55
22	dre-miR-125b-5p	89	54	61	42	55
23	dse-miR-125	89	54	61	42	55
24	dsi-miR-125	89	54	61	42	55
25	dwi-miR-125	89	54	61	42	55
26	dya-miR-125	89	54	61	42	55
27	eca-miR-125b-5p	89	54	61	42	55
28	efu-miR-125b	89	54	61	42	55
29	fru-miR-125b	89	54	61	42	55
30	gga-miR-125b-5p	89	54	61	42	55
31	ggo-miR-125b	89	54	61	42	55
32	gmo-miR-125b-5p	89	54	61	42	55
33	hsa-miR-125b-5p	89	54	61	42	55
34	ipu-miR-125b	89	54	61	42	55
35	lca-miR-125b	89	54	61	42	55
36	lla-miR-125b	89	54	61	42	55
37	lva-miR-125-5p	89	54	61	42	55
38	mdo-miR-125b-5p	89	54	61	42	55
39	mml-miR-125b-5p	89	54	61	42	55
40	mmr-miR-125a	89	54	61	42	55
41	mmu-miR-125b-5p	89	54	61	42	55
42	mne-miR-125b	89	54	61	42	55
43	mze-miR-125b	89	54	61	42	55
44	nbr-miR-125b	89	54	61	42	55
45	nle-miR-125b	89	54	61	42	55
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3	nlo-miR-125	89	54	61	42	55
4	nvi-miR-125	89	54	61	42	55
5	oan-miR-125-5p	89	54	61	42	55
6	ocu-miR-125b-5p	89	54	61	42	55
7	oga-miR-125b	89	54	61	42	55
8	oha-miR-125b-5p	89	54	61	42	55
9	ola-miR-125b	89	54	61	42	55
10	ola-miR-125c	89	54	61	42	55
11	oni-miR-125b	89	54	61	42	55
12	pal-miR-125b-5p	89	54	61	42	55
13	pbv-miR-125b-5p	89	54	61	42	55
14	pha-miR-125b	89	54	61	42	55
15	pma-miR-125-5p	89	54	61	42	55
16	pmi-miR-125-5p	89	54	61	42	55
17	ppy-miR-125b	89	54	61	42	55
18	ppa-miR-125b	89	54	61	42	55
19	ppp-miR-125b	89	54	61	42	55
20	ptr-miR-125b	89	54	61	42	55
21	rno-miR-125b-5p	89	54	61	42	55
22	sha-miR-125a	89	54	61	42	55
23	sko-miR-125a	89	54	61	42	55
24	sla-miR-125b	89	54	61	42	55
25	spu-miR-125-5p	89	54	61	42	55
26	ssa-miR-125a-5p	89	54	61	42	55
27	ssc-miR-125b	89	54	61	42	55
28	tca-miR-125-5p	89	54	61	42	55
29	tcf-miR-125	89	54	61	42	55
30	tch-miR-125b-5p	89	54	61	42	55
31	tgu-miR-125-5p	89	54	61	42	55
32	tni-miR-125b	89	54	61	42	55
33	xla-miR-125b-5p	89	54	61	42	55
34	xtr-miR-125b	89	54	61	42	55
35	cpa-miR166d	9876	9912	11328	9107	9264
36	gma-miR166j-3p	9876	9912	11328	9107	9264
37	crt-miR166a	9887	9917	11339	9118	9271
38	mes-miR166h	9887	9917	11339	9118	9271
39	atr-miR171b	613	340	332	360	408
40	gma-miR171c-3p	613	340	332	360	408
41	gma-miR171o-3p	613	340	332	360	408
42	gma-miR171q	613	340	332	360	408
43	mdm-miR171m	613	340	332	360	408
44	mdm-miR171n	613	340	332	360	408
45	zma-miR171f-3p	613	340	332	360	408
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3	gma-miR169e	561	651	624	465	600
4	mtr-miR169e-5p	565	652	625	467	602
5	vvi-miR169m	565	652	625	467	602
6	vvi-miR169n	565	652	625	467	602
7	vvi-miR169p	565	652	625	467	602
8	vvi-miR169q	565	652	625	467	602
9	ata-miR169h-5p	566	657	625	469	603
10	bdi-miR169b	566	657	625	469	603
11	mes-miR169f	566	657	625	469	603
12	osa-miR169e	566	657	625	469	603
13	sbi-miR169e	566	657	625	469	603
14	sbi-miR169j	566	657	625	469	603
15	ssp-miR169	566	657	625	469	603
16	zma-miR169p-5p	566	657	625	469	603
17	cme-miR168	953	1082	894	850	845
18	bra-miR168b-5p	965	1101	912	870	854
19	bra-miR168c-5p	965	1101	912	870	854
20	nta-miR168a	965	1101	912	870	854
21	nta-miR168b	965	1101	912	870	854
22	nta-miR168c	965	1101	912	870	854
23	sly-miR168a-5p	965	1101	912	870	854
24	sly-miR168b-5p	965	1101	912	870	854
25	aof-miR167b	10888	9933	10539	8743	9558
26	ata-miR167b-5p	10888	9933	10539	8743	9558
27	ata-miR167d-5p	10888	9933	10539	8743	9558
28	bdi-miR167c-5p	10888	9933	10539	8743	9558
29	bdi-miR167d-5p	10888	9933	10539	8743	9558
30	bdi-miR167e-5p	10888	9933	10539	8743	9558
31	bdi-miR167g	10888	9933	10539	8743	9558
32	ccl-miR167a	10888	9933	10539	8743	9558
33	ccl-miR167b	10888	9933	10539	8743	9558
34	cpa-miR167d	10888	9933	10539	8743	9558
35	ctr-miR167	10888	9933	10539	8743	9558
36	eun-miR167a-5p	10888	9933	10539	8743	9558
37	gma-miR167g	10888	9933	10539	8743	9558
38	mes-miR167d	10888	9933	10539	8743	9558
39	mes-miR167e	10888	9933	10539	8743	9558
40	mes-miR167f	10888	9933	10539	8743	9558
41	ppe-miR167c	10888	9933	10539	8743	9558
42	vca-miR167a-5p	10888	9933	10539	8743	9558
43	vca-miR167b-5p	10888	9933	10539	8743	9558
44	aof-miR167c	10502	9647	10322	8511	9280
45	atr-miR167	10502	9647	10322	8511	9280
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3	cme-miR167d	10502	9647	10322	8511	9280
4	cme-miR167f	10502	9647	10322	8511	9280
5	csi-miR167a-5p	10502	9647	10322	8511	9280
6	csi-miR167c-5p	10502	9647	10322	8511	9280
7	dpr-miR167c	10502	9647	10322	8511	9280
8	gma-miR167c	10502	9647	10322	8511	9280
9	gma-miR167j	10502	9647	10322	8511	9280
10	gso-miR167a	10502	9647	10322	8511	9280
11	lja-miR167	10502	9647	10322	8511	9280
12	lus-miR167f	10502	9647	10322	8511	9280
13	lus-miR167g	10502	9647	10322	8511	9280
14	lus-miR167i	10502	9647	10322	8511	9280
15	mes-miR167a	10502	9647	10322	8511	9280
16	mtr-miR167b-5p	10502	9647	10322	8511	9280
17	osa-miR167d-5p	10502	9647	10322	8511	9280
18	osa-miR167e-5p	10502	9647	10322	8511	9280
19	osa-miR167f	10502	9647	10322	8511	9280
20	osa-miR167g	10502	9647	10322	8511	9280
21	osa-miR167h-5p	10502	9647	10322	8511	9280
22	osa-miR167i-5p	10502	9647	10322	8511	9280
23	osa-miR167j	10502	9647	10322	8511	9280
24	ptc-miR167e	10502	9647	10322	8511	9280
25	sbi-miR167c	10502	9647	10322	8511	9280
26	sbi-miR167d	10502	9647	10322	8511	9280
27	sbi-miR167e	10502	9647	10322	8511	9280
28	sbi-miR167f	10502	9647	10322	8511	9280
29	sbi-miR167g	10502	9647	10322	8511	9280
30	sbi-miR167h	10502	9647	10322	8511	9280
31	sof-miR167a	10502	9647	10322	8511	9280
32	sof-miR167b	10502	9647	10322	8511	9280
33	ssp-miR167b	10502	9647	10322	8511	9280
34	vvi-miR167a	10502	9647	10322	8511	9280
35	zma-miR167e-5p	10502	9647	10322	8511	9280
36	zma-miR167f-5p	10502	9647	10322	8511	9280
37	zma-miR167g-5p	10502	9647	10322	8511	9280
38	zma-miR167h-5p	10502	9647	10322	8511	9280
39	zma-miR167i-5p	10502	9647	10322	8511	9280
40	zma-miR167j-5p	10502	9647	10322	8511	9280
41	aca-let-7b-5p	28	71	150	47	82
42	ggo-let-7b	28	71	150	47	82
43	ipu-let-7b	28	71	150	47	82
44	oar-let-7b	28	71	150	47	82
45	ola-let-7b	28	71	150	47	82
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3	ata-miR167f-5p	10504	9649	10324	8514	9284
4	tae-miR167c-5p	10504	9649	10324	8514	9284
5	ppt-miR390c-5p	278	325	186	285	168
6	efu-miR-99a	203	319	406	196	297
7	aof-miR166b	356	315	387	316	314
8	csi-miR390b-5p	275	324	186	285	167
9	gma-miR390e	275	324	186	285	167
10	abu-miR-27b	109	114	188	89	124
11	bta-miR-27b	109	114	188	89	124
12	cfa-miR-27b	109	114	188	89	124
13	cgr-miR-27b-3p	109	114	188	89	124
14	chi-miR-27b-3p	109	114	188	89	124
15	cja-miR-27b	109	114	188	89	124
16	cli-miR-27b-3p	109	114	188	89	124
17	cpi-miR-27b-3p	109	114	188	89	124
18	cpo-miR-27b-3p	109	114	188	89	124
19	dno-miR-27b-3p	109	114	188	89	124
20	eca-miR-27b	109	114	188	89	124
21	gga-miR-27b-3p	109	114	188	89	124
22	ggo-miR-27b	109	114	188	89	124
23	hsa-miR-27b-3p	109	114	188	89	124
24	ipu-miR-27b	109	114	188	89	124
25	mdo-miR-27b-3p	109	114	188	89	124
26	mml-miR-27b-3p	109	114	188	89	124
27	mmr-miR-27b	109	114	188	89	124
28	mmu-miR-27b-3p	109	114	188	89	124
29	mze-miR-27b	109	114	188	89	124
30	nbr-miR-27b	109	114	188	89	124
31	oan-miR-27b-3p	109	114	188	89	124
32	ocu-miR-27b-3p	109	114	188	89	124
33	oni-miR-27b	109	114	188	89	124
34	pal-miR-27b-3p	109	114	188	89	124
35	pbv-miR-27b-3p	109	114	188	89	124
36	pma-miR-27b-3p	109	114	188	89	124
37	pony-miR-27b	109	114	188	89	124
38	ppa-miR-27b	109	114	188	89	124
39	ppy-miR-27b	109	114	188	89	124
40	ptr-miR-27b	109	114	188	89	124
41	rno-miR-27b-3p	109	114	188	89	124
42	sbo-miR-27b	109	114	188	89	124
43	sha-miR-27b	109	114	188	89	124
44	ssa-miR-27b-3p	109	114	188	89	124
45	ssc-miR-27b-3p	109	114	188	89	124
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3	tch-miR-27b-3p	109	114	188	89	124
4	tgu-miR-27-3p	109	114	188	89	124
5	xtr-miR-27b	109	114	188	89	124
6	aca-miR-27b-3p	116	124	192	94	134
7	aca-miR-27b-3p	116	124	192	94	134
8	aca-miR-27b-3p	116	124	192	94	134
9	aca-miR-27b-3p	116	124	192	94	134
10	aca-miR-27b-3p	116	124	192	94	134
11	aca-miR-27b-3p	116	124	192	94	134
12	aca-miR-27b-3p	116	124	192	94	134
13	aca-miR-27b-3p	116	124	192	94	134
14	aca-miR-27b-3p	116	124	192	94	134
15	efu-miR-378	167	180	151	115	162
16	ggo-miR-378a	166	180	151	115	162
17	ggo-miR-378a	166	180	151	115	162
18	gma-miR169n-5p	387	611	589	332	607
19	mtr-miR169c	387	611	589	332	607
20	aca-miR-99a-5p	201	311	402	194	294
21	ami-miR-99a-5p	201	311	402	194	294
22	ami-miR-99a-5p	201	311	402	194	294
23	cli-miR-99-5p	201	311	402	194	294
24	cpi-miR-99a-5p	201	311	402	194	294
25	cpi-miR-99a-5p	201	311	402	194	294
26	cpo-miR-99a-5p	201	311	402	194	294
27	dno-miR-99a-5p	201	311	402	194	294
28	dre-miR-99	201	311	402	194	294
29	dre-miR-99	201	311	402	194	294
30	eca-miR-99a	201	311	402	194	294
31	gga-miR-99a-5p	201	311	402	194	294
32	ggo-miR-99a	201	311	402	194	294
33	ggo-miR-99a	201	311	402	194	294
34	gmo-miR-99-5p	201	311	402	194	294
35	hsa-miR-99a-5p	201	311	402	194	294
36	ipu-miR-99a	201	311	402	194	294
37	ipu-miR-99a	201	311	402	194	294
38	lla-miR-99a	201	311	402	194	294
39	mml-miR-99a-5p	201	311	402	194	294
40	mmr-miR-99a	201	311	402	194	294
41	mmr-miR-99a	201	311	402	194	294
42	mmu-miR-99a-5p	201	311	402	194	294
43	mne-miR-99a	201	311	402	194	294
44	mze-miR-99b	201	311	402	194	294
45	mze-miR-99b	201	311	402	194	294
46	nbr-miR-99b	201	311	402	194	294
47	ocu-miR-99a-5p	201	311	402	194	294
48	oga-miR-99a	201	311	402	194	294
49	oga-miR-99a	201	311	402	194	294
50	oha-miR-99a-5p	201	311	402	194	294
51	oni-miR-99b	201	311	402	194	294
52	pbv-miR-99a-5p	201	311	402	194	294
53	pha-miR-99a	201	311	402	194	294
54	pha-miR-99a	201	311	402	194	294
55	ppy-miR-99b	201	311	402	194	294
56	ppa-miR-99a	201	311	402	194	294
57	ppy-miR-99a	201	311	402	194	294
58	ppy-miR-99a	201	311	402	194	294
59	ptr-miR-99a	201	311	402	194	294
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3	rno-miR-99a-5p	201	311	402	194	294
4	ssa-miR-99-5p	201	311	402	194	294
5	ssc-miR-99a-5p	201	311	402	194	294
6	tch-miR-99a-5p	201	311	402	194	294
7	xtr-miR-99	201	311	402	194	294
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9	bnm-miR167d	7576	6868	7151	6109	6451
10	fve-miR167a	7576	6868	7151	6109	6451
11	fve-miR167b	7576	6868	7151	6109	6451
12	fve-miR167c	7576	6868	7151	6109	6451
13	gma-miR167l	7576	6868	7151	6109	6451
14	lja-miR167a	7576	6868	7151	6109	6451
15	lja-miR167b	7576	6868	7151	6109	6451
16	lja-miR167c	7576	6868	7151	6109	6451
17	mes-miR167b	7576	6868	7151	6109	6451
18	lus-miR167a	7648	6940	7218	6183	6514
19	vvi-miR167c	7648	6940	7218	6183	6514
20	fve-miR167d	7696	6976	7256	6211	6559
21	aca-miR-191-5p	250	146	156	119	176
22	bta-miR-191	250	146	156	119	176
23	cgr-miR-191-5p	250	146	156	119	176
24	cja-miR-191	250	146	156	119	176
25	cpo-miR-191-5p	250	146	156	119	176
26	dma-miR-191	250	146	156	119	176
27	dno-miR-191-5p	250	146	156	119	176
28	eca-miR-191a	250	146	156	119	176
29	gga-miR-191-5p	250	146	156	119	176
30	hsa-miR-191-5p	250	146	156	119	176
31	mml-miR-191-5p	250	146	156	119	176
32	mmr-miR-191	250	146	156	119	176
33	mmu-miR-191-5p	250	146	156	119	176
34	nle-miR-191	250	146	156	119	176
35	ocu-miR-191-5p	250	146	156	119	176
36	oga-miR-191	250	146	156	119	176
37	oha-miR-191-5p	250	146	156	119	176
38	pbv-miR-191-5p	250	146	156	119	176
39	pha-miR-191	250	146	156	119	176
40	ppa-miR-191	250	146	156	119	176
41	ppy-miR-191	250	146	156	119	176
42	ptr-miR-191	250	146	156	119	176
43	rno-miR-191a-5p	250	146	156	119	176
44	sbo-miR-191	250	146	156	119	176
45	ssc-miR-191	250	146	156	119	176
46	bta-miR-378	166	179	151	115	162
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3	cfa-miR-378	166	179	151	115	162
4	cgr-miR-378-3p	166	179	151	115	162
5	chi-miR-378-3p	166	179	151	115	162
6	chi-miR-378-3p	166	179	151	115	162
7	cja-miR-378	166	179	151	115	162
8	cja-miR-378	166	179	151	115	162
9	cpo-miR-378-3p	166	179	151	115	162
10	dno-miR-378-3p	166	179	151	115	162
11	hsa-miR-378a-3p	166	179	151	115	162
12	hsa-miR-378a-3p	166	179	151	115	162
13	nle-miR-378a	166	179	151	115	162
14	ocu-miR-378-3p	166	179	151	115	162
15	oga-miR-378	166	179	151	115	162
16	oga-miR-378	166	179	151	115	162
17	pal-miR-378-3p	166	179	151	115	162
18	pha-miR-378	166	179	151	115	162
19	ppa-miR-378a	166	179	151	115	162
20	ppa-miR-378a	166	179	151	115	162
21	ssc-miR-378	166	179	151	115	162
22	tch-miR-378a-3p	166	179	151	115	162
23	ipu-miR-99b	220	333	441	213	320
24	abu-miR-99b	90	189	250	100	172
25	abu-miR-99b	90	189	250	100	172
26	bta-miR-99a-5p	90	189	250	100	172
27	ccr-miR-99	90	189	250	100	172
28	cfa-miR-99a	90	189	250	100	172
29	cfa-miR-99a	90	189	250	100	172
30	cgr-miR-99a-5p	90	189	250	100	172
31	chi-miR-99a-5p	90	189	250	100	172
32	chi-miR-99a-5p	90	189	250	100	172
33	cja-miR-99	90	189	250	100	172
34	nle-miR-99a	90	189	250	100	172
35	oan-miR-99-5p	90	189	250	100	172
36	pal-miR-99a-5p	90	189	250	100	172
37	pal-miR-99a-5p	90	189	250	100	172
38	sbo-miR-99a	90	189	250	100	172
39	tgu-miR-99-5p	90	189	250	100	172
40	xla-miR-99-5p	90	189	250	100	172
41	xla-miR-99-5p	90	189	250	100	172
42	abu-miR-30d	42	53	90	31	65
43	aca-miR-30b-5p	42	53	90	31	65
44	ami-miR-30b-5p	42	53	90	31	65
45	ami-miR-30b-5p	42	53	90	31	65
46	bta-miR-30b-5p	42	53	90	31	65
47	ccr-miR-30b	42	53	90	31	65
48	cfa-miR-30b	42	53	90	31	65
49	cfa-miR-30b	42	53	90	31	65
50	cgr-miR-30b-5p	42	53	90	31	65
51	chi-miR-30b-5p	42	53	90	31	65
52	chi-miR-30b-5p	42	53	90	31	65
53	cja-miR-30b	42	53	90	31	65
54	cpi-miR-30b-5p	42	53	90	31	65
55	cpo-miR-30b-5p	42	53	90	31	65
56	dno-miR-30b-5p	42	53	90	31	65
57	dno-miR-30b-5p	42	53	90	31	65
58	dre-miR-30b	42	53	90	31	65
59	eca-miR-30b	42	53	90	31	65
60	eca-miR-30b	42	53	90	31	65

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3	fru-miR-30b	42	53	90	31	65
4	gga-miR-30b-5p	42	53	90	31	65
5	gmo-miR-30c-5p	42	53	90	31	65
6	gmo-miR-30c-5p	42	53	90	31	65
7	hsa-miR-30b-5p	42	53	90	31	65
8	ipu-miR-30b	42	53	90	31	65
9	ipu-miR-30b	42	53	90	31	65
10	mdo-miR-30b-5p	42	53	90	31	65
11	mmu-miR-30b-5p	42	53	90	31	65
12	mmu-miR-30b-5p	42	53	90	31	65
13	mze-miR-30d	42	53	90	31	65
14	nbr-miR-30d	42	53	90	31	65
15	nle-miR-30b	42	53	90	31	65
16	oan-miR-30b-5p	42	53	90	31	65
17	oan-miR-30b-5p	42	53	90	31	65
18	ocu-miR-30b-5p	42	53	90	31	65
19	oga-miR-30b	42	53	90	31	65
20	oha-miR-30b-5p	42	53	90	31	65
21	oha-miR-30b-5p	42	53	90	31	65
22	oni-miR-30d	42	53	90	31	65
23	pal-miR-30b-5p	42	53	90	31	65
24	pbv-miR-30b-5p	42	53	90	31	65
25	pbv-miR-30b-5p	42	53	90	31	65
26	ppy-miR-30d	42	53	90	31	65
27	ppy-miR-30b	42	53	90	31	65
28	rno-miR-30b-5p	42	53	90	31	65
29	rno-miR-30b-5p	42	53	90	31	65
30	ssa-miR-30e-5p	42	53	90	31	65
31	ssc-miR-30b-5p	42	53	90	31	65
32	tch-miR-30b-5p	42	53	90	31	65
33	tch-miR-30b-5p	42	53	90	31	65
34	tgu-miR-30e	42	53	90	31	65
35	tni-miR-30b	42	53	90	31	65
36	xla-miR-30b-5p	42	53	90	31	65
37	xla-miR-30b-5p	42	53	90	31	65
38	xtr-miR-30b	42	53	90	31	65
39	mdo-miR-22-3p	55	48	121	42	82
40	crt-miR166b	1477	1442	1546	1462	1248
41	crt-miR166b	1477	1442	1546	1462	1248
42	cas-miR166e	1471	1437	1540	1457	1243
43	csi-miR166f-3p	1471	1437	1540	1457	1243
44	osa-miR166m	1471	1437	1540	1457	1243
45	osa-miR166m	1471	1437	1540	1457	1243
46	aly-miR166a-5p	5486	4533	6616	5391	4363
47	aly-miR166c-5p	5486	4533	6616	5391	4363
48	aly-miR166d-5p	5486	4533	6616	5391	4363
49	aly-miR166d-5p	5486	4533	6616	5391	4363
50	bdi-miR166e-5p	5486	4533	6616	5391	4363
51	cas-miR166a	5486	4533	6616	5391	4363
52	csi-miR166a-5p	5486	4533	6616	5391	4363
53	csi-miR166a-5p	5486	4533	6616	5391	4363
54	csi-miR166e-5p	5486	4533	6616	5391	4363
55	eun-miR166-5p	5486	4533	6616	5391	4363
56	gma-miR166a-5p	5486	4533	6616	5391	4363
57	gma-miR166c-5p	5486	4533	6616	5391	4363
58	gma-miR166c-5p	5486	4533	6616	5391	4363
59	gma-miR166l	5486	4533	6616	5391	4363
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3	mtr-miR166g-5p	5486	4533	6616	5391	4363
4	osa-miR166d-5p	5486	4533	6616	5391	4363
5	stu-miR166a-5p	5486	4533	6616	5391	4363
6	vca-miR166b-5p	5486	4533	6616	5391	4363
7	vca-miR166b-5p	5486	4533	6616	5391	4363
8	zma-miR166c-5p	5486	4533	6616	5391	4363
9	zma-miR166c-5p	5486	4533	6616	5391	4363
10	gma-miR169d	678	740	699	522	697
11	aly-miR167d-5p	14528	13834	15655	12374	13711
12	aly-miR167d-5p	14528	13834	15655	12374	13711
13	ath-miR167d	14528	13834	15655	12374	13711
14	cca-miR167	14528	13834	15655	12374	13711
15	eun-miR167b-5p	14528	13834	15655	12374	13711
16	nta-miR167a	14528	13834	15655	12374	13711
17	nta-miR167a	14528	13834	15655	12374	13711
18	nta-miR167b	14528	13834	15655	12374	13711
19	nta-miR167c	14528	13834	15655	12374	13711
20	pab-miR167b	14528	13834	15655	12374	13711
21	pab-miR167b	14528	13834	15655	12374	13711
22	rco-miR167c	14528	13834	15655	12374	13711
23	mes-miR394c	20373	13190	6876	10560	9404
24	vvi-miR394a	20373	13190	6876	10560	9404
25	vvi-miR394a	20373	13190	6876	10560	9404
26	vvi-miR394c	20373	13190	6876	10560	9404
27	ahy-miR394	20361	13174	6869	10551	9394
28	aly-miR394a-5p	20361	13174	6869	10551	9394
29	aly-miR394a-5p	20361	13174	6869	10551	9394
30	aly-miR394b-5p	20361	13174	6869	10551	9394
31	aof-miR394	20361	13174	6869	10551	9394
32	ata-miR394-5p	20361	13174	6869	10551	9394
33	ata-miR394-5p	20361	13174	6869	10551	9394
34	ath-miR394a	20361	13174	6869	10551	9394
35	ath-miR394b-5p	20361	13174	6869	10551	9394
36	atr-miR394	20361	13174	6869	10551	9394
37	atr-miR394	20361	13174	6869	10551	9394
38	bdi-miR394	20361	13174	6869	10551	9394
39	bna-miR394a	20361	13174	6869	10551	9394
40	bna-miR394a	20361	13174	6869	10551	9394
41	bna-miR394b	20361	13174	6869	10551	9394
42	cca-miR394	20361	13174	6869	10551	9394
43	cme-miR394a	20361	13174	6869	10551	9394
44	cme-miR394a	20361	13174	6869	10551	9394
45	cme-miR394b	20361	13174	6869	10551	9394
46	cpa-miR394a	20361	13174	6869	10551	9394
47	cpa-miR394a	20361	13174	6869	10551	9394
48	cpa-miR394b	20361	13174	6869	10551	9394
49	csi-miR394a	20361	13174	6869	10551	9394
50	csi-miR394a	20361	13174	6869	10551	9394
51	csi-miR394b-5p	20361	13174	6869	10551	9394
52	fve-miR394	20361	13174	6869	10551	9394
53	ghr-miR394	20361	13174	6869	10551	9394
54	ghr-miR394a	20361	13174	6869	10551	9394
55	ghr-miR394b	20361	13174	6869	10551	9394
56	gma-miR394a-5p	20361	13174	6869	10551	9394
57	gma-miR394a-5p	20361	13174	6869	10551	9394
58	gma-miR394b-5p	20361	13174	6869	10551	9394
59	gma-miR394c-5p	20361	13174	6869	10551	9394
60	gma-miR394d	20361	13174	6869	10551	9394

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3	gma-miR394e	20361	13174	6869	10551	9394
4	gma-miR394f	20361	13174	6869	10551	9394
5	gma-miR394g	20361	13174	6869	10551	9394
6	lus-miR394a	20361	13174	6869	10551	9394
7	lus-miR394b	20361	13174	6869	10551	9394
8	mdm-miR394a	20361	13174	6869	10551	9394
9	mdm-miR394b	20361	13174	6869	10551	9394
10	mes-miR394a	20361	13174	6869	10551	9394
11	mes-miR394b	20361	13174	6869	10551	9394
12	nta-miR394	20361	13174	6869	10551	9394
13	osa-miR394	20361	13174	6869	10551	9394
14	pab-miR394c	20361	13174	6869	10551	9394
15	ppe-miR394a	20361	13174	6869	10551	9394
16	ppe-miR394b	20361	13174	6869	10551	9394
17	ptc-miR394a-5p	20361	13174	6869	10551	9394
18	ptc-miR394b-5p	20361	13174	6869	10551	9394
19	sbi-miR394a	20361	13174	6869	10551	9394
20	sbi-miR394b	20361	13174	6869	10551	9394
21	sly-miR394-5p	20361	13174	6869	10551	9394
22	ssl-miR394	20361	13174	6869	10551	9394
23	stu-miR384-5p	20361	13174	6869	10551	9394
24	tcc-miR394a	20361	13174	6869	10551	9394
25	tcc-miR394b	20361	13174	6869	10551	9394
26	vvi-miR394b	20361	13174	6869	10551	9394
27	zma-miR394a-5p	20361	13174	6869	10551	9394
28	zma-miR394b-5p	20361	13174	6869	10551	9394
29	aly-miR396a-3p	248	215	161	180	207
30	ath-miR396a-3p	248	215	161	180	207
31	csi-miR396b-3p	248	215	161	180	207
32	eun-miR396a-3p	248	215	161	180	207
33	fve-miR396a-3p	248	215	161	180	207
34	fve-miR396c-3p	248	215	161	180	207
35	gma-miR396i-3p	248	215	161	180	207
36	mtr-miR396b-3p	248	215	161	180	207
37	sly-miR396a-3p	248	215	161	180	207
38	cas-miR394	20411	13198	6897	10582	9441
39	bnm-miR167a	13781	13587	11418	10576	12688
40	bnm-miR167b	13781	13587	11418	10576	12688
41	aly-miR167a-5p	13768	13581	11415	10571	12683
42	aly-miR167b-5p	13768	13581	11415	10571	12683
43	aof-miR167a	13768	13581	11415	10571	12683
44	ata-miR167a-5p	13768	13581	11415	10571	12683
45	ata-miR167c-5p	13768	13581	11415	10571	12683
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3	ata-miR167e-5p	13768	13581	11415	10571	12683
4	ath-miR167a-5p	13768	13581	11415	10571	12683
5	ath-miR167b	13768	13581	11415	10571	12683
6	ath-miR167b	13768	13581	11415	10571	12683
7	bdi-miR167a	13768	13581	11415	10571	12683
8	bdi-miR167b	13768	13581	11415	10571	12683
9	bdi-miR167b	13768	13581	11415	10571	12683
10	bdi-miR167f	13768	13581	11415	10571	12683
11	bna-miR167c	13768	13581	11415	10571	12683
12	bra-miR167a	13768	13581	11415	10571	12683
13	bra-miR167a	13768	13581	11415	10571	12683
14	bra-miR167b	13768	13581	11415	10571	12683
15	bra-miR167c	13768	13581	11415	10571	12683
16	bra-miR167c	13768	13581	11415	10571	12683
17	bra-miR167d	13768	13581	11415	10571	12683
18	cme-miR167a	13768	13581	11415	10571	12683
19	cme-miR167b	13768	13581	11415	10571	12683
20	cpa-miR167a	13768	13581	11415	10571	12683
21	cpa-miR167a	13768	13581	11415	10571	12683
22	cpa-miR167b	13768	13581	11415	10571	12683
23	csi-miR167d-5p	13768	13581	11415	10571	12683
24	csi-miR167e-5p	13768	13581	11415	10571	12683
25	csi-miR167e-5p	13768	13581	11415	10571	12683
26	dpr-miR167a	13768	13581	11415	10571	12683
27	dpr-miR167b	13768	13581	11415	10571	12683
28	dpr-miR167b	13768	13581	11415	10571	12683
29	ghr-miR167a	13768	13581	11415	10571	12683
30	ghr-miR167b	13768	13581	11415	10571	12683
31	ghr-miR167b	13768	13581	11415	10571	12683
32	gma-miR167a	13768	13581	11415	10571	12683
33	gma-miR167b	13768	13581	11415	10571	12683
34	gma-miR167d	13768	13581	11415	10571	12683
35	lus-miR167c	13768	13581	11415	10571	12683
36	lus-miR167d	13768	13581	11415	10571	12683
37	lus-miR167d	13768	13581	11415	10571	12683
38	lus-miR167e	13768	13581	11415	10571	12683
39	lus-miR167h	13768	13581	11415	10571	12683
40	mdm-miR167b	13768	13581	11415	10571	12683
41	mdm-miR167b	13768	13581	11415	10571	12683
42	mdm-miR167c	13768	13581	11415	10571	12683
43	mdm-miR167d	13768	13581	11415	10571	12683
44	mdm-miR167d	13768	13581	11415	10571	12683
45	mdm-miR167e	13768	13581	11415	10571	12683
46	mdm-miR167f	13768	13581	11415	10571	12683
47	mdm-miR167g	13768	13581	11415	10571	12683
48	mdm-miR167g	13768	13581	11415	10571	12683
49	mes-miR167c	13768	13581	11415	10571	12683
50	mtr-miR167a	13768	13581	11415	10571	12683
51	nta-miR167d	13768	13581	11415	10571	12683
52	nta-miR167d	13768	13581	11415	10571	12683
53	nta-miR167e	13768	13581	11415	10571	12683
54	osa-miR167a-5p	13768	13581	11415	10571	12683
55	osa-miR167b	13768	13581	11415	10571	12683
56	osa-miR167c-5p	13768	13581	11415	10571	12683
57	osa-miR167c-5p	13768	13581	11415	10571	12683
58	ppe-miR167a	13768	13581	11415	10571	12683
59	ppe-miR167b	13768	13581	11415	10571	12683
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4	ptc-miR167b	13768	13581	11415	10571	12683
5	ptc-miR167c	13768	13581	11415	10571	12683
6	ptc-miR167d	13768	13581	11415	10571	12683
7	ptc-miR167d	13768	13581	11415	10571	12683
8	rco-miR167a	13768	13581	11415	10571	12683
9	rco-miR167b	13768	13581	11415	10571	12683
10	rco-miR167b	13768	13581	11415	10571	12683
11	sbi-miR167a	13768	13581	11415	10571	12683
12	sbi-miR167b	13768	13581	11415	10571	12683
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14	sbi-miR167i	13768	13581	11415	10571	12683
15	sly-miR167a	13768	13581	11415	10571	12683
16	stu-miR167a-5p	13768	13581	11415	10571	12683
17	stu-miR167a-5p	13768	13581	11415	10571	12683
18	stu-miR167b-5p	13768	13581	11415	10571	12683
19	stu-miR167c-5p	13768	13581	11415	10571	12683
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21	stu-miR167d-5p	13768	13581	11415	10571	12683
22	tae-miR167a	13768	13581	11415	10571	12683
23	tcc-miR167a	13768	13581	11415	10571	12683
24	tcc-miR167b	13768	13581	11415	10571	12683
25	tcc-miR167b	13768	13581	11415	10571	12683
26	vvi-miR167b	13768	13581	11415	10571	12683
27	vvi-miR167d	13768	13581	11415	10571	12683
28	vvi-miR167e	13768	13581	11415	10571	12683
29	vvi-miR167e	13768	13581	11415	10571	12683
30	zma-miR167a-5p	13768	13581	11415	10571	12683
31	zma-miR167b-5p	13768	13581	11415	10571	12683
32	zma-miR167c-5p	13768	13581	11415	10571	12683
33	zma-miR167c-5p	13768	13581	11415	10571	12683
34	zma-miR167d-5p	13768	13581	11415	10571	12683
35	efu-miR-27b	118	125	193	96	138
36	gma-miR166u	276	242	308	248	245
37	gma-miR166u	276	242	308	248	245
38	ami-miR-191-5p	140	88	106	70	105
39	cfa-miR-191	140	88	106	70	105
40	chi-miR-191-5p	140	88	106	70	105
41	chi-miR-191-5p	140	88	106	70	105
42	cpi-miR-191-5p	140	88	106	70	105
43	mdo-miR-191-5p	140	88	106	70	105
44	oan-miR-191-5p	140	88	106	70	105
45	oan-miR-191-5p	140	88	106	70	105
46	oar-miR-191	140	88	106	70	105
47	pal-miR-191-5p	140	88	106	70	105
48	tch-miR-191-5p	140	88	106	70	105
49	tch-miR-191-5p	140	88	106	70	105
50	xla-miR-191-5p	140	88	106	70	105
51	xtr-miR-191	140	88	106	70	105
52	aly-miR166a-3p	117790	98898	110407	105198	91820
53	aly-miR166b-3p	117790	98898	110407	105198	91820
54	aly-miR166b-3p	117790	98898	110407	105198	91820
55	aly-miR166c-3p	117790	98898	110407	105198	91820
56	aly-miR166d-3p	117790	98898	110407	105198	91820
57	aly-miR166d-3p	117790	98898	110407	105198	91820
58	aly-miR166e-3p	117790	98898	110407	105198	91820
59	aly-miR166f-3p	117790	98898	110407	105198	91820
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3	aly-miR166g-3p	117790	98898	110407	105198	91820
4	aly-miR166h-3p	117790	98898	110407	105198	91820
5	aof-miR166d	117790	98898	110407	105198	91820
6	aqc-miR166b	117790	98898	110407	105198	91820
7	aqc-miR166e	117790	98898	110407	105198	91820
8	ata-miR166a-3p	117790	98898	110407	105198	91820
9	ata-miR166b-3p	117790	98898	110407	105198	91820
10	ata-miR166d-3p	117790	98898	110407	105198	91820
11	ata-miR166e-3p	117790	98898	110407	105198	91820
12	ath-miR166a-3p	117790	98898	110407	105198	91820
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16	ath-miR166e-3p	117790	98898	110407	105198	91820
17	ath-miR166f	117790	98898	110407	105198	91820
18	ath-miR166g	117790	98898	110407	105198	91820
19	atr-miR166a	117790	98898	110407	105198	91820
20	atr-miR166c	117790	98898	110407	105198	91820
21	gma-miR166i-3p	117790	98898	110407	105198	91820
22	hpa-miR166a	117790	98898	110407	105198	91820
23	hpe-miR166a	117790	98898	110407	105198	91820
24	hvu-miR166a	117790	98898	110407	105198	91820
25	hvu-miR166b	117790	98898	110407	105198	91820
26	hvu-miR166c	117790	98898	110407	105198	91820
27	lus-miR166a	117790	98898	110407	105198	91820
28	lus-miR166c	117790	98898	110407	105198	91820
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31	lus-miR166h	117790	98898	110407	105198	91820
32	lus-miR166j	117790	98898	110407	105198	91820
33	mdm-miR166a	117790	98898	110407	105198	91820
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35	mdm-miR166c	117790	98898	110407	105198	91820
36	mdm-miR166d	117790	98898	110407	105198	91820
37	mdm-miR166e	117790	98898	110407	105198	91820
38	mdm-miR166f	117790	98898	110407	105198	91820
39	mdm-miR166h	117790	98898	110407	105198	91820
40	mdm-miR166i	117790	98898	110407	105198	91820
41	mdm-miR166j	117790	98898	110407	105198	91820
42	mes-miR166a	117790	98898	110407	105198	91820
43	mes-miR166b	117790	98898	110407	105198	91820
44	mtr-miR166g-3p	117790	98898	110407	105198	91820
45	nta-miR166a	117790	98898	110407	105198	91820
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4	osa-miR166b-3p	117790	98898	110407	105198	91820
5	osa-miR166c-3p	117790	98898	110407	105198	91820
6	osa-miR166c-3p	117790	98898	110407	105198	91820
7	rco-miR166c	117790	98898	110407	105198	91820
8	atr-miR166d	117790	98898	110407	105198	91820
9	atr-miR166d	117790	98898	110407	105198	91820
10	bdi-miR166a-3p	117790	98898	110407	105198	91820
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23	bna-miR166e	117790	98898	110407	105198	91820
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30	cme-miR166h	117790	98898	110407	105198	91820
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34	cpa-miR166c	117790	98898	110407	105198	91820
35	csi-miR166e-3p	117790	98898	110407	105198	91820
36	dpr-miR166b	117790	98898	110407	105198	91820
37	dpr-miR166b	117790	98898	110407	105198	91820
38	eun-miR166-3p	117790	98898	110407	105198	91820
39	fve-miR166a	117790	98898	110407	105198	91820
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44	fve-miR166d-3p	117790	98898	110407	105198	91820
45	fve-miR166e	117790	98898	110407	105198	91820
46	fve-miR166e	117790	98898	110407	105198	91820
47	fve-miR166f	117790	98898	110407	105198	91820
48	ghr-miR166b	117790	98898	110407	105198	91820
49	gma-miR166b	117790	98898	110407	105198	91820
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59	gma-miR166g	117790	98898	110407	105198	91820
60	gma-miR166n	117790	98898	110407	105198	91820
	gma-miR166o	117790	98898	110407	105198	91820

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7	mes-miR166f	117790	98898	110407	105198	91820
8	mes-miR166g	117790	98898	110407	105198	91820
9	mtr-miR166a	117790	98898	110407	105198	91820
10	mtr-miR166e-3p	117790	98898	110407	105198	91820
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45	ptc-miR166e	117790	98898	110407	105198	91820
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3	ptc-miR166f	117790	98898	110407	105198	91820
4	ptc-miR166g	117790	98898	110407	105198	91820
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6	ptc-miR166i	117790	98898	110407	105198	91820
7	ptc-miR166j	117790	98898	110407	105198	91820
8	ptc-miR166k	117790	98898	110407	105198	91820
9	ptc-miR166l	117790	98898	110407	105198	91820
10	ptc-miR166m	117790	98898	110407	105198	91820
11	pvu-miR166a	117790	98898	110407	105198	91820
12	rco-miR166a	117790	98898	110407	105198	91820
13	rco-miR166b	117790	98898	110407	105198	91820
14	rco-miR166d	117790	98898	110407	105198	91820
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16	sly-miR166a	117790	98898	110407	105198	91820
17	sly-miR166b	117790	98898	110407	105198	91820
18	smo-miR166a	117790	98898	110407	105198	91820
19	smo-miR166b	117790	98898	110407	105198	91820
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21	ssl-miR166b	117790	98898	110407	105198	91820
22	ssp-miR166	117790	98898	110407	105198	91820
23	stu-miR166a-3p	117790	98898	110407	105198	91820
24	stu-miR166c-3p	117790	98898	110407	105198	91820
25	stu-miR166d-3p	117790	98898	110407	105198	91820
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28	vca-miR166a-3p	117790	98898	110407	105198	91820
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31	vvi-miR166c	117790	98898	110407	105198	91820
32	vvi-miR166d	117790	98898	110407	105198	91820
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35	vvi-miR166g	117790	98898	110407	105198	91820
36	vvi-miR166h	117790	98898	110407	105198	91820
37	zma-miR166a-3p	117790	98898	110407	105198	91820
38	csi-miR166a-3p	117813	98934	110449	105238	91846
39	ctr-miR166	117813	98934	110449	105238	91846
40	hbr-miR166b	117813	98934	110449	105238	91846
41	lus-miR166i	117813	98934	110449	105238	91846
42	lus-miR166k	117813	98934	110449	105238	91846
43	cas-miR166c-3p	118539	99568	111102	105947	92546
44	cas-miR166d	118539	99568	111102	105947	92546
45	cas-miR166f-3p	118539	99568	111102	105947	92546
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3	lja-miR166-3p	122067	102434	113916	109193	95425
4	bta-miR-22-3p	51	45	113	42	74
5	ggo-miR-22	51	45	113	42	74
6	oar-miR-22-3p	51	45	113	42	74
7	abu-miR-499	79	68	58	44	65
8	aca-miR-499-5p	79	68	58	44	65
9	cca-miR-499	79	68	58	44	65
10	ccr-miR-499	79	68	58	44	65
11	cgr-miR-499-5p	79	68	58	44	65
12	cpi-miR-499-5p	79	68	58	44	65
13	cpo-miR-499-5p	79	68	58	44	65
14	dno-miR-499-5p	79	68	58	44	65
15	dre-miR-499-5p	79	68	58	44	65
16	gmo-miR-499-5p	79	68	58	44	65
17	mze-miR-499	79	68	58	44	65
18	nbr-miR-499	79	68	58	44	65
19	ocu-miR-499-5p	79	68	58	44	65
20	oha-miR-499-5p	79	68	58	44	65
21	oni-miR-499	79	68	58	44	65
22	pbv-miR-499-5p	79	68	58	44	65
23	ppy-miR-499	79	68	58	44	65
24	ssa-miR-499b-5p	79	68	58	44	65
25	xla-miR-499-5p	79	68	58	44	65
26	xtr-miR-499	79	68	58	44	65
27	cme-miR166g	954	916	1017	975	810
28	csi-miR166c-3p	954	916	1017	975	810
29	gma-miR166p	954	916	1017	975	810
30	gma-miR166q	954	916	1017	975	810
31	gma-miR166r	954	916	1017	975	810
32	gma-miR166s	954	916	1017	975	810
33	gma-miR166t	954	916	1017	975	810
34	sbi-miR166a	954	916	1017	975	810
35	sbi-miR166b	954	916	1017	975	810
36	sbi-miR166c	954	916	1017	975	810
37	sbi-miR166d	954	916	1017	975	810
38	sbi-miR166h	954	916	1017	975	810
39	sbi-miR166i	954	916	1017	975	810
40	sbi-miR166j	954	916	1017	975	810
41	tcc-miR166b	954	916	1017	975	810
42	zma-miR166b-3p	954	916	1017	975	810
43	zma-miR166c-3p	954	916	1017	975	810
44	zma-miR166d-3p	954	916	1017	975	810
45	zma-miR166e	954	916	1017	975	810
46	zma-miR166f	954	916	1017	975	810
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3	zma-miR166g-3p	954	916	1017	975	810
4	zma-miR166h-3p	954	916	1017	975	810
5	zma-miR166i-3p	954	916	1017	975	810
6	zma-miR166i-3p	954	916	1017	975	810
7	ahy-miR156b-5p	494	477	394	447	305
8	aly-miR157a-5p	494	477	394	447	305
9	aly-miR157a-5p	494	477	394	447	305
10	aly-miR157b-5p	494	477	394	447	305
11	aly-miR157c-5p	494	477	394	447	305
12	aly-miR157c-5p	494	477	394	447	305
13	aof-miR156b	494	477	394	447	305
14	ath-miR157a-5p	494	477	394	447	305
15	ath-miR157b-5p	494	477	394	447	305
16	ath-miR157b-5p	494	477	394	447	305
17	ath-miR157c-5p	494	477	394	447	305
18	atr-miR156a	494	477	394	447	305
19	atr-miR156a	494	477	394	447	305
20	atr-miR156c	494	477	394	447	305
21	atr-miR156c	494	477	394	447	305
22	atr-miR156c	494	477	394	447	305
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24	atr-miR156c	494	477	394	447	305
25	atr-miR156c	494	477	394	447	305
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28	atr-miR156c	494	477	394	447	305
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34	atr-miR156c	494	477	394	447	305
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46	atr-miR156c	494	477	394	447	305
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51	atr-miR156c	494	477	394	447	305
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53	atr-miR156c	494	477	394	447	305
54	atr-miR156c	494	477	394	447	305
55	atr-miR156c	494	477	394	447	305
56	atr-miR156c	494	477	394	447	305
57	atr-miR156c	494	477	394	447	305
58	atr-miR156c	494	477	394	447	305
59	atr-miR156c	494	477	394	447	305
60	atr-miR156c	494	477	394	447	305

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3	mes-miR156j	494	477	394	447	305
4	mtr-miR156e	494	477	394	447	305
5	mtr-miR156f	494	477	394	447	305
6	mtr-miR156h-5p	494	477	394	447	305
7	ppe-miR156g	494	477	394	447	305
8	ppe-miR156h	494	477	394	447	305
9	ppe-miR156i	494	477	394	447	305
10	ptc-miR156g	494	477	394	447	305
11	ptc-miR156h	494	477	394	447	305
12	ptc-miR156i	494	477	394	447	305
13	ptc-miR156j	494	477	394	447	305
14	rco-miR156f	494	477	394	447	305
15	rco-miR156g	494	477	394	447	305
16	rco-miR156h	494	477	394	447	305
17	sly-miR156a	494	477	394	447	305
18	sly-miR156b	494	477	394	447	305
19	sly-miR156c	494	477	394	447	305
20	stu-miR156a	494	477	394	447	305
21	stu-miR156b	494	477	394	447	305
22	stu-miR156c	494	477	394	447	305
23	stu-miR156d-5p	494	477	394	447	305
24	tcc-miR156e	494	477	394	447	305
25	tcc-miR156f	494	477	394	447	305
26	vca-miR156b-5p	494	477	394	447	305
27	vun-miR156b	494	477	394	447	305
28	vvi-miR156f	494	477	394	447	305
29	vvi-miR156g	494	477	394	447	305
30	vvi-miR156i	494	477	394	447	305
31	gma-miR169s-5p	678	780	744	545	782
32	mtr-miR169d-5p	678	780	744	545	782
33	pab-miR166j	569	1967	1318	1082	984
34	asu-miR-100a-5p	531	277	204	309	269
35	prd-miR-100-5p	531	277	204	309	269
36	bcy-miR156	494	477	394	447	305
37	bgg-miR156	494	477	394	447	305
38	bfl-miR-100-5p	531	266	185	305	259
39	dpu-miR-100	531	266	185	305	259
40	hpo-miR-100-5p	531	266	185	305	259
41	isc-miR-100	531	266	185	305	259
42	efu-miR-499	80	69	58	45	68
43	aof-miR171a	9653	12047	12181	10431	10297
44	aqc-miR171a	9653	12047	12181	10431	10297
45	aqc-miR171b	9653	12047	12181	10431	10297
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3	aqc-miR171d	9653	12047	12181	10431	10297
4	ata-miR171b-3p	9653	12047	12181	10431	10297
5	ata-miR171d-3p	9653	12047	12181	10431	10297
6	ata-miR171d-3p	9653	12047	12181	10431	10297
7	bdi-miR171b	9653	12047	12181	10431	10297
8	bdi-miR171c-3p	9653	12047	12181	10431	10297
9	bdi-miR171c-3p	9653	12047	12181	10431	10297
10	bdi-miR171d-3p	9653	12047	12181	10431	10297
11	bdi-miR171e	9653	12047	12181	10431	10297
12	cme-miR171c	9653	12047	12181	10431	10297
13	cme-miR171c	9653	12047	12181	10431	10297
14	cme-miR171f	9653	12047	12181	10431	10297
15	cpa-miR171a	9653	12047	12181	10431	10297
16	cpa-miR171b	9653	12047	12181	10431	10297
17	cpa-miR171b	9653	12047	12181	10431	10297
18	cpa-miR171c	9653	12047	12181	10431	10297
19	cpa-miR171d	9653	12047	12181	10431	10297
20	crt-miR171	9653	12047	12181	10431	10297
21	crt-miR171	9653	12047	12181	10431	10297
22	csi-miR171c-3p	9653	12047	12181	10431	10297
23	csi-miR171d-3p	9653	12047	12181	10431	10297
24	csi-miR171d-3p	9653	12047	12181	10431	10297
25	csi-miR171f-3p	9653	12047	12181	10431	10297
26	csi-miR171h-3p	9653	12047	12181	10431	10297
27	csi-miR171i-3p	9653	12047	12181	10431	10297
28	far-miR171	9653	12047	12181	10431	10297
29	far-miR171	9653	12047	12181	10431	10297
30	fve-miR171a	9653	12047	12181	10431	10297
31	fve-miR171c-3p	9653	12047	12181	10431	10297
32	fve-miR171d	9653	12047	12181	10431	10297
33	fve-miR171d	9653	12047	12181	10431	10297
34	fve-miR171e	9653	12047	12181	10431	10297
35	fve-miR171g	9653	12047	12181	10431	10297
36	fve-miR171g	9653	12047	12181	10431	10297
37	gma-miR171e	9653	12047	12181	10431	10297
38	gma-miR171f	9653	12047	12181	10431	10297
39	gma-miR171g	9653	12047	12181	10431	10297
40	gma-miR171j-3p	9653	12047	12181	10431	10297
41	gma-miR171j-3p	9653	12047	12181	10431	10297
42	gma-miR171u	9653	12047	12181	10431	10297
43	hpa-miR171a	9653	12047	12181	10431	10297
44	htu-miR171b	9653	12047	12181	10431	10297
45	htu-miR171b	9653	12047	12181	10431	10297
46	htu-miR171c	9653	12047	12181	10431	10297
47	hvu-miR171-3p	9653	12047	12181	10431	10297
48	hvu-miR171-3p	9653	12047	12181	10431	10297
49	lja-miR171a	9653	12047	12181	10431	10297
50	lus-miR171b	9653	12047	12181	10431	10297
51	lus-miR171c	9653	12047	12181	10431	10297
52	lus-miR171e	9653	12047	12181	10431	10297
53	mdm-miR171g	9653	12047	12181	10431	10297
54	mdm-miR171g	9653	12047	12181	10431	10297
55	mdm-miR171h	9653	12047	12181	10431	10297
56	mes-miR171g	9653	12047	12181	10431	10297
57	mes-miR171h	9653	12047	12181	10431	10297
58	mes-miR171h	9653	12047	12181	10431	10297
59	mes-miR171i	9653	12047	12181	10431	10297
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3	mes-miR171j	9653	12047	12181	10431	10297
4	mes-miR171k	9653	12047	12181	10431	10297
5	mtr-miR171d	9653	12047	12181	10431	10297
6	nta-miR171c	9653	12047	12181	10431	10297
7	nta-miR171c	9653	12047	12181	10431	10297
8	osa-miR171b	9653	12047	12181	10431	10297
9	osa-miR171b	9653	12047	12181	10431	10297
10	osa-miR171c-3p	9653	12047	12181	10431	10297
11	osa-miR171d-3p	9653	12047	12181	10431	10297
12	osa-miR171e-3p	9653	12047	12181	10431	10297
13	osa-miR171e-3p	9653	12047	12181	10431	10297
14	osa-miR171f-3p	9653	12047	12181	10431	10297
15	pde-miR171	9653	12047	12181	10431	10297
16	ppe-miR171a	9653	12047	12181	10431	10297
17	ppe-miR171a	9653	12047	12181	10431	10297
18	ppe-miR171c	9653	12047	12181	10431	10297
19	ppe-miR171f	9653	12047	12181	10431	10297
20	ppe-miR171f	9653	12047	12181	10431	10297
21	ppe-miR171g	9653	12047	12181	10431	10297
22	ptc-miR171e	9653	12047	12181	10431	10297
23	ptc-miR171f	9653	12047	12181	10431	10297
24	ptc-miR171g-3p	9653	12047	12181	10431	10297
25	ptc-miR171g-3p	9653	12047	12181	10431	10297
26	ptc-miR171h-3p	9653	12047	12181	10431	10297
27	ptc-miR171i	9653	12047	12181	10431	10297
28	rco-miR171c	9653	12047	12181	10431	10297
29	rco-miR171c	9653	12047	12181	10431	10297
30	rco-miR171d	9653	12047	12181	10431	10297
31	rco-miR171e	9653	12047	12181	10431	10297
32	rco-miR171e	9653	12047	12181	10431	10297
33	rco-miR171f	9653	12047	12181	10431	10297
34	sbi-miR171a	9653	12047	12181	10431	10297
35	sbi-miR171b	9653	12047	12181	10431	10297
36	sbi-miR171b	9653	12047	12181	10431	10297
37	sbi-miR171d	9653	12047	12181	10431	10297
38	sbi-miR171i	9653	12047	12181	10431	10297
39	sbi-miR171i	9653	12047	12181	10431	10297
40	sbi-miR171k	9653	12047	12181	10431	10297
41	sly-miR171a	9653	12047	12181	10431	10297
42	stu-miR171a-3p	9653	12047	12181	10431	10297
43	stu-miR171e	9653	12047	12181	10431	10297
44	tae-miR171a	9653	12047	12181	10431	10297
45	tae-miR171a	9653	12047	12181	10431	10297
46	tcc-miR171d	9653	12047	12181	10431	10297
47	tcc-miR171e	9653	12047	12181	10431	10297
48	tcc-miR171e	9653	12047	12181	10431	10297
49	tcc-miR171f	9653	12047	12181	10431	10297
50	tcc-miR171g	9653	12047	12181	10431	10297
51	tcc-miR171h	9653	12047	12181	10431	10297
52	vvi-miR171a	9653	12047	12181	10431	10297
53	vvi-miR171a	9653	12047	12181	10431	10297
54	vvi-miR171c	9653	12047	12181	10431	10297
55	vvi-miR171d	9653	12047	12181	10431	10297
56	vvi-miR171i	9653	12047	12181	10431	10297
57	vvi-miR171i	9653	12047	12181	10431	10297
58	vvi-miR171j	9653	12047	12181	10431	10297
59	zma-miR171d-3p	9653	12047	12181	10431	10297
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3	zma-miR171e-3p	9653	12047	12181	10431	10297
4	zma-miR171i-3p	9653	12047	12181	10431	10297
5	zma-miR171j-3p	9653	12047	12181	10431	10297
6	zma-miR171j-3p	9653	12047	12181	10431	10297
7	gma-miR166m	458	1911	1254	1011	935
8	mdm-miR167h	332445	328666	280552	259175	328814
9	mdm-miR167i	332445	328666	280552	259175	328814
10	mdm-miR167i	332445	328666	280552	259175	328814
11	mdm-miR167j	332445	328666	280552	259175	328814
12	ppe-miR167d	332445	328666	280552	259175	328814
13	ppe-miR167d	332445	328666	280552	259175	328814
14	ahy-miR159	124202	95587	114081	103220	93839
15	aly-miR159a-3p	124202	95587	114081	103220	93839
16	aof-miR159	124202	95587	114081	103220	93839
17	aof-miR159	124202	95587	114081	103220	93839
18	ath-miR159a	124202	95587	114081	103220	93839
19	atr-miR159	124202	95587	114081	103220	93839
20	atr-miR159	124202	95587	114081	103220	93839
21	atp-miR159	124202	95587	114081	103220	93839
22	bra-miR159a	124202	95587	114081	103220	93839
23	bra-miR159a	124202	95587	114081	103220	93839
24	cme-miR159a	124202	95587	114081	103220	93839
25	cpa-miR159a	124202	95587	114081	103220	93839
26	csi-miR159a-3p	124202	95587	114081	103220	93839
27	fve-miR159a-3p	124202	95587	114081	103220	93839
28	gma-miR159a-3p	124202	95587	114081	103220	93839
29	gma-miR159a-3p	124202	95587	114081	103220	93839
30	gma-miR159e-3p	124202	95587	114081	103220	93839
31	hbr-miR159a	124202	95587	114081	103220	93839
32	htu-miR159a	124202	95587	114081	103220	93839
33	htu-miR159a	124202	95587	114081	103220	93839
34	mdm-miR159d	124202	95587	114081	103220	93839
35	mdm-miR159e	124202	95587	114081	103220	93839
36	mdm-miR159f	124202	95587	114081	103220	93839
37	mdm-miR159f	124202	95587	114081	103220	93839
38	mes-miR159a-3p	124202	95587	114081	103220	93839
39	mes-miR159b	124202	95587	114081	103220	93839
40	mes-miR159b	124202	95587	114081	103220	93839
41	mtr-miR159a	124202	95587	114081	103220	93839
42	nta-miR159	124202	95587	114081	103220	93839
43	nta-miR159	124202	95587	114081	103220	93839
44	ppe-miR159	124202	95587	114081	103220	93839
45	ptc-miR159a	124202	95587	114081	103220	93839
46	ptc-miR159b	124202	95587	114081	103220	93839
47	pvu-miR159a.1	124202	95587	114081	103220	93839
48	rco-miR159	124202	95587	114081	103220	93839
49	rco-miR159	124202	95587	114081	103220	93839
50	sly-miR159	124202	95587	114081	103220	93839
51	vca-miR159-3p	124202	95587	114081	103220	93839
52	vvi-miR159c	124202	95587	114081	103220	93839
53	vvi-miR159c	124202	95587	114081	103220	93839
54	tca-miR-100-5p	477	244	170	288	241
55	oha-miR-100-5p	479	244	170	287	242
56	csi-miR393b-5p	200	229	175	202	173
57	gma-miR393h	200	229	175	202	173
58	gma-miR393h	200	229	175	202	173
59	gma-miR393i	200	229	175	202	173
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3	gma-miR393j	200	229	175	202	173
4	gma-miR393k	200	229	175	202	173
5	aae-miR-100	476	244	170	287	241
6	abu-miR-100	476	244	170	287	241
7	aca-miR-100	476	244	170	287	241
8	aga-miR-100	476	244	170	287	241
9	age-miR-100	476	244	170	287	241
10	ame-miR-100-5p	476	244	170	287	241
11	ami-miR-100-5p	476	244	170	287	241
12	bbe-miR-100-5p	476	244	170	287	241
13	bma-miR-100b	476	244	170	287	241
14	bmo-miR-100	476	244	170	287	241
15	bta-miR-100	476	244	170	287	241
16	cja-miR-100	476	244	170	287	241
17	cli-miR-100-5p	476	244	170	287	241
18	cpo-miR-100-5p	476	244	170	287	241
19	cqu-miR-100-5p	476	244	170	287	241
20	dno-miR-100-5p	476	244	170	287	241
21	dre-miR-100-5p	476	244	170	287	241
22	eca-miR-100	476	244	170	287	241
23	fru-miR-100	476	244	170	287	241
24	gga-miR-100-5p	476	244	170	287	241
25	ggo-miR-100	476	244	170	287	241
26	gmo-miR-100a-5p	476	244	170	287	241
27	hsa-miR-100-5p	476	244	170	287	241
28	ipu-miR-100	476	244	170	287	241
29	lgi-miR-100	476	244	170	287	241
30	lla-miR-100	476	244	170	287	241
31	mml-miR-100-5p	476	244	170	287	241
32	mmr-miR-100	476	244	170	287	241
33	mmu-miR-100-5p	476	244	170	287	241
34	mse-miR-100	476	244	170	287	241
35	mze-miR-100	476	244	170	287	241
36	nbr-miR-100	476	244	170	287	241
37	nle-miR-100	476	244	170	287	241
38	nvi-miR-100	476	244	170	287	241
39	oan-miR-100-5p	476	244	170	287	241
40	ocu-miR-100-5p	476	244	170	287	241
41	oga-miR-100	476	244	170	287	241
42	oni-miR-100	476	244	170	287	241
43	pal-miR-100-5p	476	244	170	287	241
44	pbv-miR-100-5p	476	244	170	287	241
45	pha-miR-100	476	244	170	287	241
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3	pma-miR-100a-5p	476	244	170	287	241
4	ppy-miR-100	476	244	170	287	241
5	ppa-miR-100	476	244	170	287	241
6	ppa-miR-100	476	244	170	287	241
7	ppp-miR-100	476	244	170	287	241
8	pte-miR-100b-5p	476	244	170	287	241
9	ptr-miR-100	476	244	170	287	241
10	ptr-miR-100	476	244	170	287	241
11	rno-miR-100-5p	476	244	170	287	241
12	sko-miR-100	476	244	170	287	241
13	sko-miR-100	476	244	170	287	241
14	sla-miR-100	476	244	170	287	241
15	ssa-miR-100a-5p	476	244	170	287	241
16	ssc-miR-100	476	244	170	287	241
17	ssc-miR-100	476	244	170	287	241
18	tcf-miR-100	476	244	170	287	241
19	tch-miR-100-5p	476	244	170	287	241
20	tni-miR-100	476	244	170	287	241
21	tni-miR-100	476	244	170	287	241
22	xla-miR-100-5p	476	244	170	287	241
23	xtr-miR-100	476	244	170	287	241
24	xtr-miR-100	476	244	170	287	241
25	ahy-miR167-5p	125567	123159	109633	103163	121638
26	cme-miR167c	125567	123159	109633	103163	121638
27	cpa-miR167c	125567	123159	109633	103163	121638
28	csi-miR167b-5p	125567	123159	109633	103163	121638
29	csi-miR167b-5p	125567	123159	109633	103163	121638
30	gma-miR167e	125567	123159	109633	103163	121638
31	gma-miR167f	125567	123159	109633	103163	121638
32	lus-miR167b	125567	123159	109633	103163	121638
33	lus-miR167b	125567	123159	109633	103163	121638
34	mes-miR167g	125567	123159	109633	103163	121638
35	mes-miR167h	125567	123159	109633	103163	121638
36	ptc-miR167f-5p	125567	123159	109633	103163	121638
37	ptc-miR167f-5p	125567	123159	109633	103163	121638
38	ptc-miR167g-5p	125567	123159	109633	103163	121638
39	tcc-miR167c	125567	123159	109633	103163	121638
40	gma-miR171n	127	110	106	97	124
41	gma-miR171n	127	110	106	97	124
42	gma-miR171p	127	110	106	97	124
43	aly-miR169b-5p	6230	7972	6743	5589	7610
44	aly-miR169c-5p	6230	7972	6743	5589	7610
45	aly-miR169c-5p	6230	7972	6743	5589	7610
46	aqc-miR169c	6230	7972	6743	5589	7610
47	ata-miR169d-5p	6230	7972	6743	5589	7610
48	ath-miR169b-5p	6230	7972	6743	5589	7610
49	ath-miR169c	6230	7972	6743	5589	7610
50	ath-miR169c	6230	7972	6743	5589	7610
51	bdi-miR169c-5p	6230	7972	6743	5589	7610
52	bdi-miR169f	6230	7972	6743	5589	7610
53	bdi-miR169f	6230	7972	6743	5589	7610
54	bna-miR169n	6230	7972	6743	5589	7610
55	cas-miR169b	6230	7972	6743	5589	7610
56	cme-miR169f	6230	7972	6743	5589	7610
57	cme-miR169h	6230	7972	6743	5589	7610
58	cme-miR169h	6230	7972	6743	5589	7610
59	csi-miR169g-5p	6230	7972	6743	5589	7610
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3	csi-miR169k-5p	6230	7972	6743	5589	7610
4	csi-miR169m-5p	6230	7972	6743	5589	7610
5	csi-miR169n-5p	6230	7972	6743	5589	7610
6	csi-miR169o-5p	6230	7972	6743	5589	7610
7	csi-miR169p-5p	6230	7972	6743	5589	7610
8	csi-miR169r-5p	6230	7972	6743	5589	7610
9	gma-miR169a	6230	7972	6743	5589	7610
10	gma-miR169f	6230	7972	6743	5589	7610
11	gma-miR169g	6230	7972	6743	5589	7610
12	gma-miR169m	6230	7972	6743	5589	7610
13	lus-miR169f	6230	7972	6743	5589	7610
14	lus-miR169h	6230	7972	6743	5589	7610
15	lus-miR169j	6230	7972	6743	5589	7610
16	mdm-miR169a	6230	7972	6743	5589	7610
17	mdm-miR169g	6230	7972	6743	5589	7610
18	mdm-miR169h	6230	7972	6743	5589	7610
19	mdm-miR169i	6230	7972	6743	5589	7610
20	mdm-miR169j	6230	7972	6743	5589	7610
21	mes-miR169a	6230	7972	6743	5589	7610
22	mes-miR169b	6230	7972	6743	5589	7610
23	mes-miR169c	6230	7972	6743	5589	7610
24	mes-miR169d	6230	7972	6743	5589	7610
25	mes-miR169e	6230	7972	6743	5589	7610
26	mtr-miR169b	6230	7972	6743	5589	7610
27	mtr-miR169g	6230	7972	6743	5589	7610
28	mtr-miR169l-5p	6230	7972	6743	5589	7610
29	nta-miR169q	6230	7972	6743	5589	7610
30	nta-miR169r	6230	7972	6743	5589	7610
31	nta-miR169s	6230	7972	6743	5589	7610
32	osa-miR169b	6230	7972	6743	5589	7610
33	osa-miR169c	6230	7972	6743	5589	7610
34	ppe-miR169a	6230	7972	6743	5589	7610
35	ppe-miR169b	6230	7972	6743	5589	7610
36	ppe-miR169c	6230	7972	6743	5589	7610
37	ptc-miR169d	6230	7972	6743	5589	7610
38	ptc-miR169e	6230	7972	6743	5589	7610
39	ptc-miR169f	6230	7972	6743	5589	7610
40	ptc-miR169g	6230	7972	6743	5589	7610
41	ptc-miR169h	6230	7972	6743	5589	7610
42	ptc-miR169p	6230	7972	6743	5589	7610
43	rco-miR169a	6230	7972	6743	5589	7610
44	rco-miR169b	6230	7972	6743	5589	7610
45	sbi-miR169b	6230	7972	6743	5589	7610
46	sbi-miR169k	6230	7972	6743	5589	7610
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3	sly-miR169a	6230	7972	6743	5589	7610
4	tcc-miR169b	6230	7972	6743	5589	7610
5	tcc-miR169k	6230	7972	6743	5589	7610
6	tcc-miR169l	6230	7972	6743	5589	7610
7	vun-miR169	6230	7972	6743	5589	7610
8	vvi-miR169a	6230	7972	6743	5589	7610
9	vvi-miR169c	6230	7972	6743	5589	7610
10	vvi-miR169j	6230	7972	6743	5589	7610
11	vvi-miR169k	6230	7972	6743	5589	7610
12	vvi-miR169s	6230	7972	6743	5589	7610
13	vvi-miR169w	6230	7972	6743	5589	7610
14	zma-miR169c-5p	6230	7972	6743	5589	7610
15	zma-miR169r-5p	6230	7972	6743	5589	7610
16	gma-miR156f	2621	2691	2018	2315	1867
17	aly-miR164a-5p	7094	4921	2155	4855	3374
18	aly-miR164b-5p	7094	4921	2155	4855	3374
19	aof-miR164	7094	4921	2155	4855	3374
20	ata-miR164b-5p	7094	4921	2155	4855	3374
21	ata-miR164c-5p	7094	4921	2155	4855	3374
22	ath-miR164a	7094	4921	2155	4855	3374
23	ath-miR164b-5p	7094	4921	2155	4855	3374
24	atr-miR164a	7094	4921	2155	4855	3374
25	atr-miR164b	7094	4921	2155	4855	3374
26	bdi-miR164a-5p	7094	4921	2155	4855	3374
27	bdi-miR164b	7094	4921	2155	4855	3374
28	bdi-miR164e	7094	4921	2155	4855	3374
29	bna-miR164a	7094	4921	2155	4855	3374
30	bra-miR164a	7094	4921	2155	4855	3374
31	cas-miR164	7094	4921	2155	4855	3374
32	cme-miR164c	7094	4921	2155	4855	3374
33	cme-miR164d	7094	4921	2155	4855	3374
34	cpa-miR164a	7094	4921	2155	4855	3374
35	cpa-miR164b	7094	4921	2155	4855	3374
36	cpa-miR164c	7094	4921	2155	4855	3374
37	csi-miR164a-5p	7094	4921	2155	4855	3374
38	csi-miR164b-5p	7094	4921	2155	4855	3374
39	csi-miR164c-5p	7094	4921	2155	4855	3374
40	csi-miR164d-5p	7094	4921	2155	4855	3374
41	ctr-miR164	7094	4921	2155	4855	3374
42	fve-miR164a-5p	7094	4921	2155	4855	3374
43	fve-miR164b	7094	4921	2155	4855	3374
44	ghr-miR164	7094	4921	2155	4855	3374
45	gma-miR164a	7094	4921	2155	4855	3374
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3	gma-miR164e	7094	4921	2155	4855	3374
4	gma-miR164f	7094	4921	2155	4855	3374
5	gma-miR164g	7094	4921	2155	4855	3374
6	gma-miR164h	7094	4921	2155	4855	3374
7	gma-miR164i	7094	4921	2155	4855	3374
8	gma-miR164j	7094	4921	2155	4855	3374
9	gma-miR164k	7094	4921	2155	4855	3374
10	lus-miR164a	7094	4921	2155	4855	3374
11	lus-miR164b	7094	4921	2155	4855	3374
12	lus-miR164c	7094	4921	2155	4855	3374
13	lus-miR164d	7094	4921	2155	4855	3374
14	lus-miR164e	7094	4921	2155	4855	3374
15	mdm-miR164b	7094	4921	2155	4855	3374
16	mdm-miR164c	7094	4921	2155	4855	3374
17	mdm-miR164d	7094	4921	2155	4855	3374
18	mdm-miR164e	7094	4921	2155	4855	3374
19	mdm-miR164f	7094	4921	2155	4855	3374
20	mes-miR164a	7094	4921	2155	4855	3374
21	mes-miR164b	7094	4921	2155	4855	3374
22	mes-miR164c	7094	4921	2155	4855	3374
23	mtr-miR164a	7094	4921	2155	4855	3374
24	mtr-miR164b	7094	4921	2155	4855	3374
25	mtr-miR164c	7094	4921	2155	4855	3374
26	nta-miR164a	7094	4921	2155	4855	3374
27	nta-miR164b	7094	4921	2155	4855	3374
28	osa-miR164a	7094	4921	2155	4855	3374
29	osa-miR164b	7094	4921	2155	4855	3374
30	osa-miR164f	7094	4921	2155	4855	3374
31	ppe-miR164a	7094	4921	2155	4855	3374
32	ppe-miR164b	7094	4921	2155	4855	3374
33	ppe-miR164c	7094	4921	2155	4855	3374
34	ptc-miR164a	7094	4921	2155	4855	3374
35	ptc-miR164b	7094	4921	2155	4855	3374
36	ptc-miR164c	7094	4921	2155	4855	3374
37	ptc-miR164d	7094	4921	2155	4855	3374
38	ptc-miR164e	7094	4921	2155	4855	3374
39	rco-miR164a	7094	4921	2155	4855	3374
40	rco-miR164b	7094	4921	2155	4855	3374
41	rco-miR164c	7094	4921	2155	4855	3374
42	sbi-miR164a	7094	4921	2155	4855	3374
43	sbi-miR164d	7094	4921	2155	4855	3374
44	sbi-miR164e	7094	4921	2155	4855	3374
45	sly-miR164a-5p	7094	4921	2155	4855	3374
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3	sly-miR164b-5p	7094	4921	2155	4855	3374
4	ssl-miR164a	7094	4921	2155	4855	3374
5	ssl-miR164b	7094	4921	2155	4855	3374
6	tae-miR164	7094	4921	2155	4855	3374
7	tcc-miR164a	7094	4921	2155	4855	3374
8	tcc-miR164b	7094	4921	2155	4855	3374
9	vvi-miR164a	7094	4921	2155	4855	3374
10	vvi-miR164c	7094	4921	2155	4855	3374
11	vvi-miR164d	7094	4921	2155	4855	3374
12	zma-miR164a-5p	7094	4921	2155	4855	3374
13	zma-miR164b-5p	7094	4921	2155	4855	3374
14	zma-miR164c-5p	7094	4921	2155	4855	3374
15	zma-miR164d-5p	7094	4921	2155	4855	3374
16	zma-miR164g-5p	7094	4921	2155	4855	3374
17	bra-miR164e-5p	7101	4935	2160	4861	3386
18	ahy-miR156c	2606	2676	2010	2308	1861
19	far-miR156b	2606	2676	2010	2308	1861
20	mdm-miR156t	2606	2676	2010	2308	1861
21	mdm-miR156u	2606	2676	2010	2308	1861
22	mdm-miR156v	2606	2676	2010	2308	1861
23	mdm-miR156w	2606	2676	2010	2308	1861
24	mes-miR156k	2606	2676	2010	2308	1861
25	aly-miR166g-5p	364	304	383	343	358
26	cas-miR166f-5p	364	304	383	343	358
27	csi-miR166b-5p	364	304	383	343	358
28	gma-miR166h-5p	364	304	383	343	358
29	gma-miR166j-5p	364	304	383	343	358
30	stu-miR166c-5p	364	304	383	343	358
31	gma-miR159d	1575	1537	1275	1561	1314
32	aof-miR398	8721	10351	12418	9258	10489
33	aqc-miR398b	8721	10351	12418	9258	10489
34	bdi-miR398a	8721	10351	12418	9258	10489
35	cca-miR398	8721	10351	12418	9258	10489
36	cme-miR398a	8721	10351	12418	9258	10489
37	csi-miR398b-3p	8721	10351	12418	9258	10489
38	gma-miR398c	8721	10351	12418	9258	10489
39	gma-miR398d	8721	10351	12418	9258	10489
40	lus-miR398a	8721	10351	12418	9258	10489
41	mdm-miR398b	8721	10351	12418	9258	10489
42	mdm-miR398c	8721	10351	12418	9258	10489
43	mes-miR398	8721	10351	12418	9258	10489
44	mtr-miR398b	8721	10351	12418	9258	10489
45	mtr-miR398c	8721	10351	12418	9258	10489
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3	nta-miR398	8721	10351	12418	9258	10489
4	osa-miR398b	8721	10351	12418	9258	10489
5	ppe-miR398a-3p	8721	10351	12418	9258	10489
6	ptc-miR398b	8721	10351	12418	9258	10489
7	ptc-miR398c-3p	8721	10351	12418	9258	10489
8	rco-miR398b	8721	10351	12418	9258	10489
9	tcc-miR398a	8721	10351	12418	9258	10489
10	vvi-miR398b	8721	10351	12418	9258	10489
11	vvi-miR398c	8721	10351	12418	9258	10489
12	abu-miR-222	350	182	148	265	177
13	age-miR-222	350	182	148	265	177
14	ami-miR-222a-3p	350	182	148	265	177
15	cgr-miR-222-3p	350	182	148	265	177
16	chi-miR-222-3p	350	182	148	265	177
17	cli-miR-222a-3p	350	182	148	265	177
18	cpo-miR-222-3p	350	182	148	265	177
19	dma-miR-222	350	182	148	265	177
20	dno-miR-222-3p	350	182	148	265	177
21	dre-miR-222a-3p	350	182	148	265	177
22	fru-miR-222	350	182	148	265	177
23	gga-miR-222a	350	182	148	265	177
24	mdo-miR-222a	350	182	148	265	177
25	mmr-miR-222	350	182	148	265	177
26	mze-miR-222	350	182	148	265	177
27	nbr-miR-222	350	182	148	265	177
28	nle-miR-222	350	182	148	265	177
29	ocu-miR-222-3p	350	182	148	265	177
30	oga-miR-222	350	182	148	265	177
31	oha-miR-222a-3p	350	182	148	265	177
32	oni-miR-222	350	182	148	265	177
33	pbv-miR-222a-3p	350	182	148	265	177
34	pha-miR-222	350	182	148	265	177
35	ppy-miR-222	350	182	148	265	177
36	ppa-miR-222	350	182	148	265	177
37	ssa-miR-222a-3p	350	182	148	265	177
38	ssc-miR-222	350	182	148	265	177
39	tgu-miR-222-3p	350	182	148	265	177
40	tni-miR-222	350	182	148	265	177
41	xtr-miR-222	350	182	148	265	177
42	lja-miR1511-3p	49605	43469	45736	42592	43044
43	aly-miR170-3p	1478	1986	1879	1793	1706
44	ath-miR170-3p	1478	1986	1879	1793	1706
45	stu-miR171c-3p	1478	1986	1879	1793	1706
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3	gma-miR159a-5p	3882	3147	2995	3451	3205
4	gma-miR319f	134	171	91	133	95
5	ahy-miR167-3p	1040	1379	1214	1227	1117
6	ptc-miR167f-3p	1040	1379	1214	1227	1117
7	ptc-miR167g-3p	1040	1379	1214	1227	1117
8	ptc-miR167h-3p	1040	1379	1214	1227	1117
9	aja-miR-143	282	344	295	207	331
10	bta-miR-143	282	344	295	207	331
11	chi-miR-143-3p	282	344	295	207	331
12	gga-miR-143-3p	282	344	295	207	331
13	mdo-miR-143-3p	282	344	295	207	331
14	tch-miR-143-3p	282	344	295	207	331
15	xtr-miR-143	282	344	295	207	331
16	eca-miR-378	96	126	95	78	112
17	mml-miR-378a	96	126	95	78	112
18	mmu-miR-378a-3p	96	126	95	78	112
19	ptr-miR-378a	96	126	95	78	112
20	rno-miR-378a-3p	96	126	95	78	112
21	efu-miR-143	283	345	298	208	334
22	abu-miR-143	281	342	295	207	331
23	aca-miR-143-3p	281	342	295	207	331
24	ami-miR-143-3p	281	342	295	207	331
25	cfa-miR-143	281	342	295	207	331
26	cgr-miR-143	281	342	295	207	331
27	cli-miR-143-3p	281	342	295	207	331
28	cpi-miR-143-3p	281	342	295	207	331
29	cpo-miR-143-3p	281	342	295	207	331
30	dno-miR-143-3p	281	342	295	207	331
31	dre-miR-143	281	342	295	207	331
32	eca-miR-143	281	342	295	207	331
33	hsa-miR-143-3p	281	342	295	207	331
34	ipu-miR-143	281	342	295	207	331
35	mml-miR-143-3p	281	342	295	207	331
36	mmu-miR-143-3p	281	342	295	207	331
37	nle-miR-143	281	342	295	207	331
38	oan-miR-143-3p	281	342	295	207	331
39	oar-miR-143	281	342	295	207	331
40	ocu-miR-143-3p	281	342	295	207	331
41	oga-miR-143	281	342	295	207	331
42	oni-miR-143	281	342	295	207	331
43	pal-miR-143-3p	281	342	295	207	331
44	pbv-miR-143-3p	281	342	295	207	331
45	pha-miR-143	281	342	295	207	331
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3	ssa-miR-143-3p	281	342	295	207	331
4	ssc-miR-143-3p	281	342	295	207	331
5	xla-miR-143-3p	281	342	295	207	331
6						
7	gma-miR171m	53026	54481	53808	50160	52786
8	gma-miR171t	53026	54481	53808	50160	52786
9						
10	dma-miR-143	294	397	330	230	360
11	ggo-miR-143	294	397	330	230	360
12	lla-miR-143	294	397	330	230	360
13	oha-miR-143-3p	294	397	330	230	360
14	ppa-miR-143	294	397	330	230	360
15	ppy-miR-143	294	397	330	230	360
16	ptr-miR-143	294	397	330	230	360
17	rno-miR-143-3p	294	397	330	230	360
18						
19	bta-miR-99b	96	69	60	61	73
20	cfa-miR-99b	96	69	60	61	73
21	chi-miR-99b-5p	96	69	60	61	73
22	cpo-miR-99b-5p	96	69	60	61	73
23	eca-miR-99b	96	69	60	61	73
24	efu-miR-99b	96	69	60	61	73
25	hsa-miR-99b-5p	96	69	60	61	73
26	mml-miR-99b-5p	96	69	60	61	73
27	mmu-miR-99b-5p	96	69	60	61	73
28	oga-miR-99b	96	69	60	61	73
29	pal-miR-99b-5p	96	69	60	61	73
30	ptr-miR-99b	96	69	60	61	73
31	rno-miR-99b-5p	96	69	60	61	73
32	ssc-miR-99b	96	69	60	61	73
33	tch-miR-99b-5p	96	69	60	61	73
34						
35	bbe-miR-216-5p	0	53	196	23	82
36	bfl-miR-216-5p	0	53	196	23	82
37	cpo-miR-216a-5p	0	53	196	23	82
38	dno-miR-216a-5p	0	53	196	23	82
39	ocu-miR-216a-5p	0	53	196	23	82
40	oha-miR-216-5p	0	53	196	23	82
41	ssc-miR-216	0	53	196	23	82
42	xla-miR-216-5p	0	53	196	23	82
43	aca-miR-216a	0	52	194	22	82
44	bta-miR-216a	0	52	194	22	82
45	cja-miR-216a	0	52	194	22	82
46	cli-miR-216a-5p	0	52	194	22	82
47	cpi-miR-216a-5p	0	52	194	22	82
48	dre-miR-216a	0	52	194	22	82
49	eca-miR-216a	0	52	194	22	82
50						
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3	hsa-miR-216a-5p	0	52	194	22	82
4	ipu-miR-216a	0	52	194	22	82
5	mml-miR-216a-5p	0	52	194	22	82
6	mmu-miR-216a-5p	0	52	194	22	82
7	oan-miR-216a-5p	0	52	194	22	82
8	pbv-miR-216a-5p	0	52	194	22	82
9	rno-miR-216a-5p	0	52	194	22	82
10	ssa-miR-216b-5p	0	52	194	22	82
11	tgu-miR-216a-5p	0	52	194	22	82
12	ppt-miR160b	140	221	113	163	136
13	ppt-miR160i	140	221	113	163	136
14	gma-miR169k	6868	8249	7252	5755	8943
15	gma-miR169l-5p	6868	8249	7252	5755	8943
16	mes-miR169l	6868	8249	7252	5755	8943
17	mes-miR169m	6868	8249	7252	5755	8943
18	eun-miR167b-3p	57	82	78	57	90
19	aly-miR168a-3p	11285	8749	11690	11552	9913
20	ath-miR168a-3p	11285	8749	11690	11552	9913
21	bra-miR168b-3p	11285	8749	11690	11552	9913
22	bra-miR168c-3p	11285	8749	11690	11552	9913
23	cas-miR168	11285	8749	11690	11552	9913
24	csi-miR168-3p	11285	8749	11690	11552	9913
25	fve-miR168-3p	11285	8749	11690	11552	9913
26	mtr-miR168c-3p	11285	8749	11690	11552	9913
27	ptc-miR168a-3p	11285	8749	11690	11552	9913
28	ptc-miR168b-3p	11285	8749	11690	11552	9913
29	sly-miR168b-3p	11285	8749	11690	11552	9913
30	lja-miR168-3p	11316	8762	11718	11574	9938
31	bdi-miR159b-3p.1	7101	5451	6272	6828	5467
32	far-miR159	7101	5451	6272	6828	5467
33	hvu-miR159a	7101	5451	6272	6828	5467
34	hvu-miR159b	7101	5451	6272	6828	5467
35	osa-miR159a.1	7101	5451	6272	6828	5467
36	osa-miR159b	7101	5451	6272	6828	5467
37	sbi-miR159a	7101	5451	6272	6828	5467
38	sof-miR159a	7101	5451	6272	6828	5467
39	sof-miR159b	7101	5451	6272	6828	5467
40	sof-miR159d	7101	5451	6272	6828	5467
41	ssp-miR159a	7101	5451	6272	6828	5467
42	tae-miR159a	7101	5451	6272	6828	5467
43	tae-miR159b	7101	5451	6272	6828	5467
44	zma-miR159a-3p	7101	5451	6272	6828	5467
45	zma-miR159b-3p	7101	5451	6272	6828	5467
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3	zma-miR159f-3p	7101	5451	6272	6828	5467
4	zma-miR159j-3p	7101	5451	6272	6828	5467
5	zma-miR159k-3p	7101	5451	6272	6828	5467
6	zma-miR159k-3p	7101	5451	6272	6828	5467
7	cfa-miR-24	315	341	375	296	362
8	cgr-miR-24-3p	315	341	375	296	362
9	ipu-miR-24	315	341	375	296	362
10	ipu-miR-24	315	341	375	296	362
11	oga-miR-24	315	341	375	296	362
12	oga-miR-24	315	341	375	296	362
13	oha-miR-24-3p	315	341	375	296	362
14	cpo-miR-27a-3p	240	305	307	171	360
15	tch-miR-27a-3p	240	305	307	171	360
16	abu-miR-24b-3p	314	340	374	296	362
17	abu-miR-24b-3p	314	340	374	296	362
18	aca-miR-24-3p	314	340	374	296	362
19	ami-miR-24-3p	314	340	374	296	362
20	ami-miR-24-3p	314	340	374	296	362
21	bta-miR-24-3p	314	340	374	296	362
22	ccb-miR-24	314	340	374	296	362
23	cja-miR-24	314	340	374	296	362
24	cja-miR-24	314	340	374	296	362
25	cpo-miR-24-3p	314	340	374	296	362
26	dno-miR-24a-3p	314	340	374	296	362
27	dre-miR-24	314	340	374	296	362
28	eca-miR-24	314	340	374	296	362
29	eca-miR-24	314	340	374	296	362
30	fru-miR-24-3p	314	340	374	296	362
31	gga-miR-24-3p	314	340	374	296	362
32	ggo-miR-24	314	340	374	296	362
33	ggo-miR-24	314	340	374	296	362
34	hsa-miR-24-3p	314	340	374	296	362
35	mml-miR-24-3p	314	340	374	296	362
36	mmu-miR-24-3p	314	340	374	296	362
37	mmu-miR-24-3p	314	340	374	296	362
38	mne-miR-24-3p	314	340	374	296	362
39	nbr-miR-24a	314	340	374	296	362
40	oan-miR-24-3p	314	340	374	296	362
41	oan-miR-24-3p	314	340	374	296	362
42	ocu-miR-24-3p	314	340	374	296	362
43	ola-miR-24a	314	340	374	296	362
44	oni-miR-24a	314	340	374	296	362
45	oni-miR-24a	314	340	374	296	362
46	pbv-miR-24-3p	314	340	374	296	362
47	pma-miR-24	314	340	374	296	362
48	pony-miR-24a	314	340	374	296	362
49	pony-miR-24a	314	340	374	296	362
50	ppa-miR-24-3p	314	340	374	296	362
51	ppy-miR-24-3p	314	340	374	296	362
52	ptr-miR-24	314	340	374	296	362
53	ptr-miR-24	314	340	374	296	362
54	rno-miR-24-3p	314	340	374	296	362
55	ssc-miR-24-3p	314	340	374	296	362
56	tgu-miR-24-3p	314	340	374	296	362
57	tgu-miR-24-3p	314	340	374	296	362
58	tni-miR-24	314	340	374	296	362
59	xla-miR-24a-3p	314	340	374	296	362
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3	xtr-miR-24a-3p	314	340	374	296	362
4	dre-miR-27a-3p	371	363	323	231	421
5	ipu-miR-27a	371	363	323	231	421
6	ssa-miR-27a-3p	371	363	323	231	421
7	ssa-miR-27a-3p	371	363	323	231	421
8	gma-miR169u	194	322	243	235	264
9	gma-miR169u	194	322	243	235	264
10	aly-miR159b-3p	7112	5791	6708	7202	5808
11	ath-miR159b-3p	7112	5791	6708	7202	5808
12	ath-miR159b-3p	7112	5791	6708	7202	5808
13	cas-miR159b-3p	7112	5791	6708	7202	5808
14	cas-miR159c-3p	7112	5791	6708	7202	5808
15	lus-miR159c	7112	5791	6708	7202	5808
16	lus-miR159b	6733	5459	6276	6835	5464
17	lus-miR159b	6733	5459	6276	6835	5464
18	age-miR-27a	322	338	307	213	395
19	ggo-miR-27a	322	338	307	213	395
20	ggo-miR-27a	322	338	307	213	395
21	lca-miR-27a	322	338	307	213	395
22	mml-miR-27a-3p	322	338	307	213	395
23	mne-miR-27a	322	338	307	213	395
24	oha-miR-27a-3p	322	338	307	213	395
25	oha-miR-27a-3p	322	338	307	213	395
26	ppa-miR-27a	322	338	307	213	395
27	ppy-miR-27a	322	338	307	213	395
28	ptr-miR-27a	322	338	307	213	395
29	ptr-miR-27a	322	338	307	213	395
30	sla-miR-27a	322	338	307	213	395
31	gma-miR1515a	8322	9086	9113	9201	9449
32	gma-miR1515b	8322	9086	9113	9201	9449
33	gma-miR1515b	8322	9086	9113	9201	9449
34	abu-miR-27a	321	336	307	212	395
35	aca-miR-27a-3p	321	336	307	212	395
36	ami-miR-27a-3p	321	336	307	212	395
37	ami-miR-27a-3p	321	336	307	212	395
38	ccr-miR-27a	321	336	307	212	395
39	cgr-miR-27a-3p	321	336	307	212	395
40	cja-miR-27a	321	336	307	212	395
41	cja-miR-27a	321	336	307	212	395
42	cpi-miR-27a-3p	321	336	307	212	395
43	dno-miR-27a-3p	321	336	307	212	395
44	eca-miR-27a	321	336	307	212	395
45	eca-miR-27a	321	336	307	212	395
46	hsa-miR-27a-3p	321	336	307	212	395
47	mdo-miR-27a-3p	321	336	307	212	395
48	mdu-miR-27a-3p	321	336	307	212	395
49	mmu-miR-27a-3p	321	336	307	212	395
50	mze-miR-27a	321	336	307	212	395
51	nbr-miR-27a	321	336	307	212	395
52	oan-miR-27a-3p	321	336	307	212	395
53	oar-miR-27a	321	336	307	212	395
54	oar-miR-27a	321	336	307	212	395
55	oni-miR-27a	321	336	307	212	395
56	pbv-miR-27a-3p	321	336	307	212	395
57	pony-miR-27a	321	336	307	212	395
58	pony-miR-27a	321	336	307	212	395
59	rno-miR-27a-3p	321	336	307	212	395
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3	sbo-miR-27a	321	336	307	212	395
4	ssc-miR-27a	321	336	307	212	395
5	xtr-miR-27a	321	336	307	212	395
6	mtr-miR171c	68	35	65	57	56
7	csi-miR160a-5p	143	213	110	176	127
8	htu-miR171a	66	32	63	54	54
9	bta-miR-27a-3p	186	259	253	146	314
10	cfa-miR-27a	186	259	253	146	314
11	chi-miR-27a-3p	186	259	253	146	314
12	gmo-miR-27d-3p	186	259	253	146	314
13	oga-miR-27a	186	259	253	146	314
14	ola-miR-27a	186	259	253	146	314
15	pal-miR-27a-3p	186	259	253	146	314
16	xla-miR-27a-3p	186	259	253	146	314
17	ppe-miR398b	90	204	173	190	132
18	pvu-miR1514a	6440	5014	5169	5730	6269
19	lja-miR398-3p	244	215	201	208	250
20	stu-miR398b-3p	244	215	201	208	250
21	aof-miR171c	558	594	556	633	559
22	csi-miR171e-3p	558	594	556	633	559
23	csi-miR171g-3p	558	594	556	633	559
24	ctr-miR171	558	594	556	633	559
25	fve-miR171h	558	594	556	633	559
26	mdm-miR171a	558	594	556	633	559
27	mdm-miR171b	558	594	556	633	559
28	mdm-miR171p	558	594	556	633	559
29	mes-miR171a	558	594	556	633	559
30	ppe-miR171h	558	594	556	633	559
31	gma-miR319p	782	300	384	525	514
32	cpi-miR-24-3p	113	167	178	134	178
33	sbo-miR-24	113	167	178	134	178
34	sly-miR171e	650	620	638	712	643
35	stu-miR171b-3p	650	620	638	712	643
36	gma-miR169l-3p	188	237	210	201	252
37	bta-miR-451	2138	3477	2414	2108	3233
38	cja-miR-451	2138	3477	2414	2108	3233
39	cpo-miR-451-5p	2138	3477	2414	2108	3233
40	dno-miR-451-5p	2138	3477	2414	2108	3233
41	gga-miR-451	2138	3477	2414	2108	3233
42	oan-miR-451	2138	3477	2414	2108	3233
43	ocu-miR-451-5p	2138	3477	2414	2108	3233
44	oha-miR-451-??	2138	3477	2414	2108	3233
45	tgu-miR-451	2138	3477	2414	2108	3233
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3	aly-miR169a-5p	156	232	193	178	222
4	ata-miR169e-5p	156	232	193	178	222
5	ata-miR169f-5p	156	232	193	178	222
6	ata-miR169g-5p	156	232	193	178	222
7	ata-miR169g-5p	156	232	193	178	222
8	ath-miR169a-5p	156	232	193	178	222
9	ath-miR169a-5p	156	232	193	178	222
10	bdi-miR169a-5p	156	232	193	178	222
11	bna-miR169a	156	232	193	178	222
12	bna-miR169b	156	232	193	178	222
13	bna-miR169b	156	232	193	178	222
14	cas-miR169a	156	232	193	178	222
15	gma-miR169b	156	232	193	178	222
16	lus-miR169g	156	232	193	178	222
17	lus-miR169g	156	232	193	178	222
18	lus-miR169l	156	232	193	178	222
19	mes-miR169g	156	232	193	178	222
20	mtr-miR169a	156	232	193	178	222
21	mtr-miR169a	156	232	193	178	222
22	nta-miR169a	156	232	193	178	222
23	nta-miR169b	156	232	193	178	222
24	nta-miR169b	156	232	193	178	222
25	nta-miR169c	156	232	193	178	222
26	nta-miR169d	156	232	193	178	222
27	nta-miR169e	156	232	193	178	222
28	nta-miR169e	156	232	193	178	222
29	nta-miR169f	156	232	193	178	222
30	nta-miR169g	156	232	193	178	222
31	nta-miR169g	156	232	193	178	222
32	nta-miR169h	156	232	193	178	222
33	nta-miR169i	156	232	193	178	222
34	nta-miR169j	156	232	193	178	222
35	nta-miR169k	156	232	193	178	222
36	nta-miR169l	156	232	193	178	222
37	nta-miR169l	156	232	193	178	222
38	nta-miR169m	156	232	193	178	222
39	nta-miR169o	156	232	193	178	222
40	nta-miR169p	156	232	193	178	222
41	nta-miR169p	156	232	193	178	222
42	osa-miR169a	156	232	193	178	222
43	ptc-miR169a	156	232	193	178	222
44	ptc-miR169b-5p	156	232	193	178	222
45	ptc-miR169b-5p	156	232	193	178	222
46	ptc-miR169c	156	232	193	178	222
47	sbi-miR169a	156	232	193	178	222
48	sly-miR169c	156	232	193	178	222
49	tcc-miR169a	156	232	193	178	222
50	tcc-miR169a	156	232	193	178	222
51	tcc-miR169c	156	232	193	178	222
52	tcc-miR169c	156	232	193	178	222
53	tcc-miR169e	156	232	193	178	222
54	vvi-miR169f	156	232	193	178	222
55	vvi-miR169g	156	232	193	178	222
56	zma-miR169a-5p	156	232	193	178	222
57	zma-miR169b-5p	156	232	193	178	222
58	zma-miR169b-5p	156	232	193	178	222
59	lus-miR398f	83	201	178	192	134
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3	sly-miR156e-3p	3491	2619	3494	3738	3412
4	stu-miR156g-3p	3491	2619	3494	3738	3412
5	cas-miR156k-3p	3496	2620	3499	3743	3418
6	mtr-miR156c-3p	3496	2620	3499	3743	3418
7	ptc-miR169s	152	230	188	178	217
8						
9	gma-miR2118a-3p	4554	3424	4675	5118	4056
10	gma-miR2118b-3p	4554	3424	4675	5118	4056
11						
12	cme-miR169t	55	85	57	55	76
13	cme-miR169r	55	85	56	55	74
14	mes-miR169i	55	85	56	55	74
15	mes-miR169j	55	85	56	55	74
16	mes-miR169k	55	85	56	55	74
17	ptc-miR169t	55	85	56	55	74
18	smo-miR171a	90	75	72	101	88
19						
20	gso-miR2218	208359	92323	117761	205633	84468
21	pvu-miR2118	208359	92323	117761	205633	84468
22	vun-miR2118	208359	92323	117761	205633	84468
23						
24	aly-miR164c-5p	162	120	47	149	74
25	ath-miR164c-5p	162	120	47	149	74
26	bnm-miR164b	162	120	47	149	74
27	bnm-miR164c	162	120	47	149	74
28	bnm-miR164d	162	120	47	149	74
29	bra-miR164b-5p	162	120	47	149	74
30	bra-miR164c-5p	162	120	47	149	74
31	bra-miR164d-5p	162	120	47	149	74
32	cln-miR164	162	120	47	149	74
33						
34	gma-miR403a	7423	9152	8806	11066	9104
35	gma-miR403b	7423	9152	8806	11066	9104
36	mes-miR319h	246	211	206	260	191
37	vun-miR319b	246	211	206	260	191
38	aly-miR319c-3p	249	223	210	269	192
39	aly-miR319d-3p	249	223	210	269	192
40	ath-miR319c	249	223	210	269	192
41	mes-miR319g	249	223	210	269	192
42	pvu-miR319c	249	223	210	269	192
43	rco-miR319d	249	223	210	269	192
44	sly-miR319c-3p	249	223	210	269	192
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46	csi-miR858-3p	197	158	133	206	178
47	ppe-miR858	197	158	133	206	178
48	csi-miR171a	87	72	70	98	87
49	zma-miR171b-3p	87	72	70	98	87
50						
51	cme-miR319c	236	200	198	246	186
52	cme-miR319d	236	200	198	246	186
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3	gma-miR319c	236	200	198	246	186
4	ptc-miR319e	236	200	198	246	186
5	ptc-miR319f	236	200	198	246	186
6	ptc-miR319g	236	200	198	246	186
7	ptc-miR319h	236	200	198	246	186
8	stu-miR319b	236	200	198	246	186
9	gma-miR164b	161	118	44	147	74
10	gma-miR164c	161	118	44	147	74
11	gma-miR164d	161	118	44	147	74
12	aca-miR-451-5p	1022	2047	1417	1272	1853
13	cfa-miR-451	1022	2047	1417	1272	1853
14	cgr-miR-451a	1022	2047	1417	1272	1853
15	dre-miR-451	1022	2047	1417	1272	1853
16	hsa-miR-451a	1022	2047	1417	1272	1853
17	mml-miR-451	1022	2047	1417	1272	1853
18	mmu-miR-451a	1022	2047	1417	1272	1853
19	ppy-miR-451	1022	2047	1417	1272	1853
20	ptr-miR-451	1022	2047	1417	1272	1853
21	rno-miR-451-5p	1022	2047	1417	1272	1853
22	ssc-miR-451	1022	2047	1417	1272	1853
23	xtr-miR-451	1022	2047	1417	1272	1853
24	bta-miR-146b	10	54	85	44	70
25	chi-miR-146b-5p	10	54	85	44	70
26	cja-miR-146b	10	54	85	44	70
27	dno-miR-146b-5p	10	54	85	44	70
28	ggo-miR-146b	10	54	85	44	70
29	mmr-miR-146b	10	54	85	44	70
30	nle-miR-146b	10	54	85	44	70
31	pal-miR-146b-5p	10	54	85	44	70
32	pha-miR-146b	10	54	85	44	70
33	ppa-miR-146b	10	54	85	44	70
34	rno-miR-146b-5p	10	54	85	44	70
35	sbo-miR-146b	10	54	85	44	70
36	aqc-miR166a	53	98	104	113	82
37	aqc-miR166d	53	98	104	113	82
38	cme-miR166e	53	98	104	113	82
39	dpr-miR166a	53	98	104	113	82
40	lus-miR166e	53	98	104	113	82
41	mtr-miR166c	53	98	104	113	82
42	mtr-miR166f	53	98	104	113	82
43	osa-miR166g-3p	53	98	104	113	82
44	osa-miR166h-3p	53	98	104	113	82
45	pab-miR166a	53	98	104	113	82
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3	sbi-miR166f	53	98	104	113	82
4	sly-miR166c-3p	53	98	104	113	82
5	ssl-miR166a	53	98	104	113	82
6	ssl-miR166a	53	98	104	113	82
7	stu-miR166b	53	98	104	113	82
8	tcc-miR166c	53	98	104	113	82
9	tcc-miR166c	53	98	104	113	82
10	zma-miR166l-3p	53	98	104	113	82
11	zma-miR166m-3p	53	98	104	113	82
12	zma-miR166m-3p	53	98	104	113	82
13	cfa-miR-181a	37	83	114	49	106
14	ipu-miR-181a	37	83	114	49	106
15	mmr-miR-181a	37	83	114	49	106
16	oni-miR-181c	37	83	114	49	106
17	oni-miR-181c	37	83	114	49	106
18	sbo-miR-181a	37	83	114	49	106
19	gma-miR169j-5p	52	92	58	58	81
20	ata-miR164a-5p	176	122	48	165	80
21	ata-miR164a-5p	176	122	48	165	80
22	bdi-miR164c-5p	176	122	48	165	80
23	cme-miR164a	176	122	48	165	80
24	osa-miR164d	176	122	48	165	80
25	osa-miR164d	176	122	48	165	80
26	sbi-miR164b	176	122	48	165	80
27	zma-miR164f-5p	176	122	48	165	80
28	gma-miR319i	236	227	265	341	247
29	gma-miR319i	236	227	265	341	247
30	aof-miR319b	4672	2814	3138	4518	3420
31	atr-miR319b	4672	2814	3138	4518	3420
32	atr-miR319d	4672	2814	3138	4518	3420
33	atr-miR319d	4672	2814	3138	4518	3420
34	atr-miR319e	4672	2814	3138	4518	3420
35	cas-miR319c	4672	2814	3138	4518	3420
36	csi-miR159d	4672	2814	3138	4518	3420
37	csi-miR159d	4672	2814	3138	4518	3420
38	fve-miR319	4672	2814	3138	4518	3420
39	tcc-miR319	4672	2814	3138	4518	3420
40	vvi-miR319e	4672	2814	3138	4518	3420
41	vvi-miR319e	4672	2814	3138	4518	3420
42	gma-miR319d	227	215	254	333	240
43	gma-miR319o	227	215	254	333	240
44	efu-miR-93	47	76	69	48	88
45	ccr-miR-181a	16	73	83	36	79
46	ccr-miR-181a	16	73	83	36	79
47	xla-miR-181a-5p	16	73	83	36	79
48	eun-miR160-3p	61	100	57	105	75
49	gma-miR160a-3p	61	100	57	105	75
50	gma-miR160a-3p	61	100	57	105	75
51	stu-miR160a-3p	61	100	57	105	75
52	gma-miR1511	7940	9451	8131	9671	9157
53	ami-miR-93-5p	43	75	65	46	87
54	ami-miR-93-5p	43	75	65	46	87
55	cfa-miR-93	43	75	65	46	87
56	cgr-miR-93-5p	43	75	65	46	87
57	chi-miR-93-5p	43	75	65	46	87
58	chi-miR-93-5p	43	75	65	46	87
59	cja-miR-93	43	75	65	46	87
60	cja-miR-93	43	75	65	46	87

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3	cpo-miR-93-5p	43	75	65	46	87
4	dma-miR-93	43	75	65	46	87
5	dno-miR-93-5p	43	75	65	46	87
6	eca-miR-93	43	75	65	46	87
7	eca-miR-93	43	75	65	46	87
8	hsa-miR-93-5p	43	75	65	46	87
9	hsa-miR-93-5p	43	75	65	46	87
10	mmu-miR-93-5p	43	75	65	46	87
11	nle-miR-93	43	75	65	46	87
12	nle-miR-93	43	75	65	46	87
13	ocu-miR-93-5p	43	75	65	46	87
14	oga-miR-93	43	75	65	46	87
15	pal-miR-93-5p	43	75	65	46	87
16	pha-miR-93	43	75	65	46	87
17	pha-miR-93	43	75	65	46	87
18	rno-miR-93-5p	43	75	65	46	87
19	tch-miR-93-5p	43	75	65	46	87
20	tch-miR-93-5p	43	75	65	46	87
21	xla-miR-93-5p	43	75	65	46	87
22	aau-miR162	7770	6558	7618	8453	10462
23	aly-miR162a-3p	7770	6558	7618	8453	10462
24	aly-miR162b-3p	7770	6558	7618	8453	10462
25	aly-miR162b-3p	7770	6558	7618	8453	10462
26	ath-miR162a-3p	7770	6558	7618	8453	10462
27	ath-miR162b-3p	7770	6558	7618	8453	10462
28	ath-miR162b-3p	7770	6558	7618	8453	10462
29	bra-miR162-3p	7770	6558	7618	8453	10462
30	cme-miR162	7770	6558	7618	8453	10462
31	cpa-miR162a	7770	6558	7618	8453	10462
32	csi-miR162-3p	7770	6558	7618	8453	10462
33	csi-miR162-3p	7770	6558	7618	8453	10462
34	eun-miR162-3p	7770	6558	7618	8453	10462
35	fve-miR162-3p	7770	6558	7618	8453	10462
36	ghr-miR162a	7770	6558	7618	8453	10462
37	ghr-miR162a	7770	6558	7618	8453	10462
38	gma-miR162b	7770	6558	7618	8453	10462
39	gma-miR162c	7770	6558	7618	8453	10462
40	gma-miR162c	7770	6558	7618	8453	10462
41	hpe-miR162a	7770	6558	7618	8453	10462
42	htu-miR162a	7770	6558	7618	8453	10462
43	lus-miR162a	7770	6558	7618	8453	10462
44	lus-miR162a	7770	6558	7618	8453	10462
45	lus-miR162b	7770	6558	7618	8453	10462
46	mdm-miR162a	7770	6558	7618	8453	10462
47	mdm-miR162b	7770	6558	7618	8453	10462
48	mdm-miR162b	7770	6558	7618	8453	10462
49	mes-miR162	7770	6558	7618	8453	10462
50	mtr-miR162	7770	6558	7618	8453	10462
51	nta-miR162a	7770	6558	7618	8453	10462
52	nta-miR162b	7770	6558	7618	8453	10462
53	nta-miR162b	7770	6558	7618	8453	10462
54	osa-miR162a	7770	6558	7618	8453	10462
55	pde-miR162	7770	6558	7618	8453	10462
56	ppe-miR162	7770	6558	7618	8453	10462
57	ppe-miR162	7770	6558	7618	8453	10462
58	ptc-miR162a	7770	6558	7618	8453	10462
59	ptc-miR162b	7770	6558	7618	8453	10462
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3	rco-miR162	7770	6558	7618	8453	10462
4	sbi-miR162	7770	6558	7618	8453	10462
5	sly-miR162	7770	6558	7618	8453	10462
6	stu-miR162a-3p	7770	6558	7618	8453	10462
7	stu-miR162b-3p	7770	6558	7618	8453	10462
8	tcc-miR162	7770	6558	7618	8453	10462
9	vun-miR162	7770	6558	7618	8453	10462
10	vvi-miR162	7770	6558	7618	8453	10462
11	aly-miR396b-5p	9275	5516	6221	9477	8412
12	ama-miR396-5p	9275	5516	6221	9477	8412
13	aqc-miR396b	9275	5516	6221	9477	8412
14	ata-miR396c-5p	9275	5516	6221	9477	8412
15	ath-miR396b-5p	9275	5516	6221	9477	8412
16	atr-miR396b	9275	5516	6221	9477	8412
17	atr-miR396c	9275	5516	6221	9477	8412
18	atr-miR396e	9275	5516	6221	9477	8412
19	bcy-miR396b	9275	5516	6221	9477	8412
20	bdi-miR396e-5p	9275	5516	6221	9477	8412
21	bgy-miR396b	9275	5516	6221	9477	8412
22	bna-miR396a	9275	5516	6221	9477	8412
23	bra-miR396-5p	9275	5516	6221	9477	8412
24	cas-miR396b	9275	5516	6221	9477	8412
25	cca-miR396a-5p	9275	5516	6221	9477	8412
26	ccl-miR396	9275	5516	6221	9477	8412
27	cme-miR396a	9275	5516	6221	9477	8412
28	cme-miR396c	9275	5516	6221	9477	8412
29	cme-miR396d	9275	5516	6221	9477	8412
30	csi-miR396f-5p	9275	5516	6221	9477	8412
31	fve-miR396b-5p	9275	5516	6221	9477	8412
32	gma-miR396b-5p	9275	5516	6221	9477	8412
33	gma-miR396c	9275	5516	6221	9477	8412
34	gma-miR396k-5p	9275	5516	6221	9477	8412
35	lus-miR396b	9275	5516	6221	9477	8412
36	lus-miR396e	9275	5516	6221	9477	8412
37	mdm-miR396c	9275	5516	6221	9477	8412
38	mdm-miR396d	9275	5516	6221	9477	8412
39	mdm-miR396e	9275	5516	6221	9477	8412
40	mes-miR396c	9275	5516	6221	9477	8412
41	mes-miR396d	9275	5516	6221	9477	8412
42	mes-miR396e	9275	5516	6221	9477	8412
43	mes-miR396f	9275	5516	6221	9477	8412
44	mtr-miR396a-5p	9275	5516	6221	9477	8412
45	nta-miR396b	9275	5516	6221	9477	8412
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3	nta-miR396c	9275	5516	6221	9477	8412
4	osa-miR396c-5p	9275	5516	6221	9477	8412
5	pab-miR396g	9275	5516	6221	9477	8412
6	pab-miR396h	9275	5516	6221	9477	8412
7	ppe-miR396b	9275	5516	6221	9477	8412
8	pta-miR396	9275	5516	6221	9477	8412
9	ptc-miR396c	9275	5516	6221	9477	8412
10	ptc-miR396d	9275	5516	6221	9477	8412
11	ptc-miR396e-5p	9275	5516	6221	9477	8412
12	rco-miR396	9275	5516	6221	9477	8412
13	sbi-miR396c	9275	5516	6221	9477	8412
14	sly-miR396b	9275	5516	6221	9477	8412
15	stu-miR396-5p	9275	5516	6221	9477	8412
16	tcc-miR396c	9275	5516	6221	9477	8412
17	tcc-miR396e	9275	5516	6221	9477	8412
18	zma-miR396e-5p	9275	5516	6221	9477	8412
19	zma-miR396f-5p	9275	5516	6221	9477	8412
20	mes-miR160g	11771	13787	9505	15781	13869
21	mtr-miR160b	11715	13747	9463	15716	13825
22	mtr-miR160d	11715	13747	9463	15716	13825
23	mtr-miR160e	11715	13747	9463	15716	13825
24	nta-miR160a	11715	13747	9463	15716	13825
25	nta-miR160b	11715	13747	9463	15716	13825
26	nta-miR160c	11715	13747	9463	15716	13825
27	osa-miR160a-5p	11715	13747	9463	15716	13825
28	osa-miR160b-5p	11715	13747	9463	15716	13825
29	osa-miR160c-5p	11715	13747	9463	15716	13825
30	osa-miR160d-5p	11715	13747	9463	15716	13825
31	pab-miR160a	11715	13747	9463	15716	13825
32	pab-miR160b	11715	13747	9463	15716	13825
33	pab-miR160d	11715	13747	9463	15716	13825
34	ppe-miR160a	11715	13747	9463	15716	13825
35	ppe-miR160b	11715	13747	9463	15716	13825
36	ppt-miR160a	11715	13747	9463	15716	13825
37	ppt-miR160e	11715	13747	9463	15716	13825
38	ppt-miR160f	11715	13747	9463	15716	13825
39	ptc-miR160a	11715	13747	9463	15716	13825
40	ptc-miR160b-5p	11715	13747	9463	15716	13825
41	ptc-miR160c-5p	11715	13747	9463	15716	13825
42	ptc-miR160d	11715	13747	9463	15716	13825
43	rco-miR160a	11715	13747	9463	15716	13825
44	rco-miR160b	11715	13747	9463	15716	13825
45	sbi-miR160a	11715	13747	9463	15716	13825
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4	sbi-miR160c	11715	13747	9463	15716	13825
5	sbi-miR160d	11715	13747	9463	15716	13825
6	sbi-miR160e	11715	13747	9463	15716	13825
7	sly-miR160a	11715	13747	9463	15716	13825
8	sly-miR160a	11715	13747	9463	15716	13825
9	sly-miR160a	11715	13747	9463	15716	13825
10	smo-miR160a	11715	13747	9463	15716	13825
11	smo-miR160b	11715	13747	9463	15716	13825
12	smo-miR160b	11715	13747	9463	15716	13825
13	stu-miR160a-5p	11715	13747	9463	15716	13825
14	stu-miR160b	11715	13747	9463	15716	13825
15	tae-miR160	11715	13747	9463	15716	13825
16	tcc-miR160b	11715	13747	9463	15716	13825
17	tcc-miR160b	11715	13747	9463	15716	13825
18	ttu-miR160	11715	13747	9463	15716	13825
19	vun-miR160	11715	13747	9463	15716	13825
20	vun-miR160	11715	13747	9463	15716	13825
21	vvi-miR160c	11715	13747	9463	15716	13825
22	vvi-miR160d	11715	13747	9463	15716	13825
23	vvi-miR160e	11715	13747	9463	15716	13825
24	vvi-miR160e	11715	13747	9463	15716	13825
25	zma-miR160a-5p	11715	13747	9463	15716	13825
26	zma-miR160b-5p	11715	13747	9463	15716	13825
27	zma-miR160c-5p	11715	13747	9463	15716	13825
28	zma-miR160d-5p	11715	13747	9463	15716	13825
29	zma-miR160d-5p	11715	13747	9463	15716	13825
30	zma-miR160e	11715	13747	9463	15716	13825
31	zma-miR160g-5p	11715	13747	9463	15716	13825
32	zma-miR160g-5p	11715	13747	9463	15716	13825
33	aly-miR160a-5p	11715	13747	9463	15716	13825
34	aly-miR160b-5p	11715	13747	9463	15716	13825
35	aly-miR160c-5p	11715	13747	9463	15716	13825
36	aof-miR160c	11715	13747	9463	15716	13825
37	aof-miR160c	11715	13747	9463	15716	13825
38	aqc-miR160b	11715	13747	9463	15716	13825
39	ata-miR160a-5p	11715	13747	9463	15716	13825
40	ata-miR160b-5p	11715	13747	9463	15716	13825
41	ata-miR160b-5p	11715	13747	9463	15716	13825
42	ata-miR160c-5p	11715	13747	9463	15716	13825
43	ath-miR160a-5p	11715	13747	9463	15716	13825
44	ath-miR160a-5p	11715	13747	9463	15716	13825
45	ath-miR160b	11715	13747	9463	15716	13825
46	ath-miR160c-5p	11715	13747	9463	15716	13825
47	atr-miR160	11715	13747	9463	15716	13825
48	atr-miR160	11715	13747	9463	15716	13825
49	bdi-miR160a-5p	11715	13747	9463	15716	13825
50	bdi-miR160b-5p	11715	13747	9463	15716	13825
51	bdi-miR160c-5p	11715	13747	9463	15716	13825
52	bdi-miR160d-5p	11715	13747	9463	15716	13825
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54	bna-miR160a	11715	13747	9463	15716	13825
55	bna-miR160b	11715	13747	9463	15716	13825
56	bna-miR160c	11715	13747	9463	15716	13825
57	bna-miR160c	11715	13747	9463	15716	13825
58	bna-miR160d	11715	13747	9463	15716	13825
59	bra-miR160a-5p	11715	13747	9463	15716	13825
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3	cca-miR160b	11715	13747	9463	15716	13825
4	cme-miR160a	11715	13747	9463	15716	13825
5	cme-miR160b	11715	13747	9463	15716	13825
6	cme-miR160c	11715	13747	9463	15716	13825
7	cme-miR160c	11715	13747	9463	15716	13825
8	cpa-miR160a	11715	13747	9463	15716	13825
9	cpa-miR160b	11715	13747	9463	15716	13825
10	cpa-miR160b	11715	13747	9463	15716	13825
11	cpa-miR160c-5p	11715	13747	9463	15716	13825
12	cpa-miR160e	11715	13747	9463	15716	13825
13	cpa-miR160e	11715	13747	9463	15716	13825
14	cpa-miR160f-5p	11715	13747	9463	15716	13825
15	eun-miR160-5p	11715	13747	9463	15716	13825
16	far-miR160	11715	13747	9463	15716	13825
17	far-miR160	11715	13747	9463	15716	13825
18	fve-miR160a	11715	13747	9463	15716	13825
19	fve-miR160b	11715	13747	9463	15716	13825
20	fve-miR160b	11715	13747	9463	15716	13825
21	gma-miR160a-5p	11715	13747	9463	15716	13825
22	gma-miR160f	11715	13747	9463	15716	13825
23	gma-miR160f	11715	13747	9463	15716	13825
24	lus-miR160a	11715	13747	9463	15716	13825
25	lus-miR160b	11715	13747	9463	15716	13825
26	lus-miR160d	11715	13747	9463	15716	13825
27	lus-miR160e	11715	13747	9463	15716	13825
28	lus-miR160f	11715	13747	9463	15716	13825
29	lus-miR160f	11715	13747	9463	15716	13825
30	lus-miR160h	11715	13747	9463	15716	13825
31	lus-miR160i	11715	13747	9463	15716	13825
32	lus-miR160i	11715	13747	9463	15716	13825
33	lus-miR160j	11715	13747	9463	15716	13825
34	mdm-miR160a	11715	13747	9463	15716	13825
35	mdm-miR160b	11715	13747	9463	15716	13825
36	mdm-miR160c	11715	13747	9463	15716	13825
37	mdm-miR160c	11715	13747	9463	15716	13825
38	mdm-miR160d	11715	13747	9463	15716	13825
39	mdm-miR160e	11715	13747	9463	15716	13825
40	mdm-miR160e	11715	13747	9463	15716	13825
41	mes-miR160a	11715	13747	9463	15716	13825
42	mes-miR160b	11715	13747	9463	15716	13825
43	mes-miR160d	11715	13747	9463	15716	13825
44	mes-miR160d	11715	13747	9463	15716	13825
45	mtr-miR160a	11715	13747	9463	15716	13825
46	mes-miR160h	11832	13835	9531	15859	13897
47	mtr-miR166e-5p	339	293	315	457	332
48	osa-miR166h-5p	339	293	315	457	332
49	osa-miR166h-5p	339	293	315	457	332
50	zma-miR166m-5p	339	293	315	457	332
51	abu-miR-19b	19	71	82	57	84
52	ami-miR-19b-3p	19	71	82	57	84
53	ami-miR-19b-3p	19	71	82	57	84
54	cfa-miR-19b	19	71	82	57	84
55	cpi-miR-19b-3p	19	71	82	57	84
56	dma-miR-19b	19	71	82	57	84
57	dma-miR-19b	19	71	82	57	84
58	mmr-miR-19b	19	71	82	57	84
59	mze-miR-19b	19	71	82	57	84
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3	nbr-miR-19b	19	71	82	57	84
4	nle-miR-19b	19	71	82	57	84
5	oga-miR-19b	19	71	82	57	84
6	oni-miR-19b	19	71	82	57	84
7	oni-miR-19b	19	71	82	57	84
8	pbv-miR-19b-3p	19	71	82	57	84
9	pha-miR-19b	19	71	82	57	84
10	pha-miR-19b	19	71	82	57	84
11	pony-miR-19b	19	71	82	57	84
12	ssa-miR-19c-3p	19	71	82	57	84
13	ssa-miR-19c-3p	19	71	82	57	84
14	bta-miR-93	32	63	53	40	75
15	gmo-miR-451-5p	273	833	548	505	753
16	cpa-miR169	110	134	151	133	168
17	cli-miR-451-5p	47	54	35	45	64
18	cli-miR-451-5p	47	54	35	45	64
19	gma-miR319g	3386	2896	2088	3830	3074
20	gma-miR319l	3386	2896	2088	3830	3074
21	gma-miR319l	3386	2896	2088	3830	3074
22	cpi-miR-93-5p	30	58	53	38	72
23	sha-miR-93	30	58	53	38	72
24	sha-miR-93	30	58	53	38	72
25	gma-miR319q	3108	2667	1865	3525	2844
26	csi-miR160b-5p	213	172	140	262	200
27	mes-miR160c	213	172	140	262	200
28	osa-miR160e-5p	213	172	140	262	200
29	osa-miR160e-5p	213	172	140	262	200
30	zma-miR160f-5p	213	172	140	262	200
31	zma-miR160f-5p	213	172	140	262	200
32	gma-miR482c-3p	526	292	405	598	453
33	gma-miR482a-3p	41395	12714	21203	36812	21935
34	vun-miR482	41395	12714	21203	36812	21935
35	age-miR-19b	22	77	92	65	95
36	bta-miR-19b	22	77	92	65	95
37	bta-miR-19b	22	77	92	65	95
38	cgr-miR-19b-3p	22	77	92	65	95
39	chi-miR-19b-3p	22	77	92	65	95
40	chi-miR-19b-3p	22	77	92	65	95
41	cja-miR-19b	22	77	92	65	95
42	cli-miR-19b-3p	22	77	92	65	95
43	cpo-miR-19b-3p	22	77	92	65	95
44	dno-miR-19b-3p	22	77	92	65	95
45	dno-miR-19b-3p	22	77	92	65	95
46	dre-miR-19b-3p	22	77	92	65	95
47	eca-miR-19b	22	77	92	65	95
48	efu-miR-19	22	77	92	65	95
49	efu-miR-19	22	77	92	65	95
50	fru-miR-19b	22	77	92	65	95
51	gga-miR-19b-3p	22	77	92	65	95
52	ggo-miR-19b	22	77	92	65	95
53	ggo-miR-19b	22	77	92	65	95
54	gmo-miR-19b-3p	22	77	92	65	95
55	hsa-miR-19b-3p	22	77	92	65	95
56	lca-miR-19b	22	77	92	65	95
57	lla-miR-19b	22	77	92	65	95
58	lla-miR-19b	22	77	92	65	95
59	mdo-miR-19b-3p	22	77	92	65	95
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3	mml-miR-19b	22	77	92	65	95
4	mmu-miR-19b-3p	22	77	92	65	95
5	mne-miR-19b	22	77	92	65	95
6	oan-miR-19b-3p	22	77	92	65	95
7	oar-miR-19b	22	77	92	65	95
8	ocu-miR-19b-3p	22	77	92	65	95
9	oha-miR-19b-3p	22	77	92	65	95
10	pal-miR-19-3p	22	77	92	65	95
11	pma-miR-19b-3p	22	77	92	65	95
12	ppa-miR-19b	22	77	92	65	95
13	ppy-miR-19b	22	77	92	65	95
14	ptr-miR-19b	22	77	92	65	95
15	rno-miR-19b-3p	22	77	92	65	95
16	sha-miR-19b	22	77	92	65	95
17	sla-miR-19b	22	77	92	65	95
18	ssc-miR-19b	22	77	92	65	95
19	tch-miR-19b-3p	22	77	92	65	95
20	tgu-miR-19b-3p	22	77	92	65	95
21	tni-miR-19b	22	77	92	65	95
22	xla-miR-19b	22	77	92	65	95
23	xla-miR-19b-3p	22	77	92	65	95
24	xtr-miR-19b	22	77	92	65	95
25	dno-miR-146a-5p	100	162	130	106	197
26	vca-miR396-5p	391	229	265	455	360
27	vvi-miR396b	391	229	265	455	360
28	pab-miR396a-5p	398	229	275	467	366
29	vvi-miR396a	398	229	275	467	366
30	pvu-miR159a.2	134	136	90	158	147
31	bdi-miR160f	187	170	138	259	194
32	cas-miR160a	187	170	138	259	194
33	cas-miR160b-5p	187	170	138	259	194
34	gma-miR160b	187	170	138	259	194
35	gma-miR160c	187	170	138	259	194
36	gma-miR160d	187	170	138	259	194
37	gma-miR160e	187	170	138	259	194
38	htu-miR160a	187	170	138	259	194
39	pab-miR160c	187	170	138	259	194
40	pab-miR160e	187	170	138	259	194
41	pab-miR160f	187	170	138	259	194
42	ahy-miR408-3p	67	57	51	88	75
43	aly-miR408-3p	67	57	51	88	75
44	ath-miR408-3p	67	57	51	88	75
45	cas-miR408	67	57	51	88	75
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3	cme-miR408	67	57	51	88	75
4	csi-miR408-3p	67	57	51	88	75
5	gma-miR408a-3p	67	57	51	88	75
6	gma-miR408b-3p	67	57	51	88	75
7	gma-miR408c-3p	67	57	51	88	75
8	lus-miR408a	67	57	51	88	75
9	mdm-miR408a	67	57	51	88	75
10	mes-miR408	67	57	51	88	75
11	mtr-miR408-3p	67	57	51	88	75
12	pta-miR408	67	57	51	88	75
13	ptc-miR408-3p	67	57	51	88	75
14	vun-miR408	67	57	51	88	75
15	vvi-miR408	67	57	51	88	75
16	ahy-miR160-5p	46	54	41	76	49
17	aof-miR160a	46	54	41	76	49
18	bdi-miR160e-5p	46	54	41	76	49
19	cme-miR160d	46	54	41	76	49
20	cpa-miR160d	46	54	41	76	49
21	mes-miR160e	46	54	41	76	49
22	mes-miR160f	46	54	41	76	49
23	mtr-miR160c	46	54	41	76	49
24	osa-miR160f-5p	46	54	41	76	49
25	ptc-miR160e-5p	46	54	41	76	49
26	ptc-miR160f	46	54	41	76	49
27	rco-miR160c	46	54	41	76	49
28	sbi-miR160f	46	54	41	76	49
29	tcc-miR160a	46	54	41	76	49
30	vca-miR160-5p	46	54	41	76	49
31	vvi-miR160a	46	54	41	76	49
32	vvi-miR160b	46	54	41	76	49
33	gma-miR396e	964	595	612	1072	1081
34	aaU-miR396	963	594	611	1071	1079
35	aly-miR396a-5p	963	594	611	1071	1079
36	amg-miR396	963	594	611	1071	1079
37	aof-miR396b	963	594	611	1071	1079
38	aqc-miR396a	963	594	611	1071	1079
39	ata-miR396e-5p	963	594	611	1071	1079
40	ath-miR396a-5p	963	594	611	1071	1079
41	bcy-miR396a	963	594	611	1071	1079
42	bdi-miR396c-5p	963	594	611	1071	1079
43	bdi-miR396d-5p	963	594	611	1071	1079
44	bgy-miR396a	963	594	611	1071	1079
45	cas-miR396a	963	594	611	1071	1079
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3	cme-miR396b	963	594	611	1071	1079
4	cpa-miR396	963	594	611	1071	1079
5	csi-miR396a-5p	963	594	611	1071	1079
6	csi-miR396b-5p	963	594	611	1071	1079
7	dpr-miR396	963	594	611	1071	1079
8	eun-miR396b-5p	963	594	611	1071	1079
9	fve-miR396a-5p	963	594	611	1071	1079
10	fve-miR396c-5p	963	594	611	1071	1079
11	fve-miR396d	963	594	611	1071	1079
12	ghr-miR396a	963	594	611	1071	1079
13	ghr-miR396b	963	594	611	1071	1079
14	gma-miR396a-5p	963	594	611	1071	1079
15	gma-miR396i-5p	963	594	611	1071	1079
16	hbr-miR396b	963	594	611	1071	1079
17	lja-miR396	963	594	611	1071	1079
18	lus-miR396a	963	594	611	1071	1079
19	lus-miR396c	963	594	611	1071	1079
20	mdm-miR396b	963	594	611	1071	1079
21	mes-miR396a	963	594	611	1071	1079
22	mes-miR396b	963	594	611	1071	1079
23	mtr-miR396b-5p	963	594	611	1071	1079
24	nta-miR396a	963	594	611	1071	1079
25	osa-miR396a-5p	963	594	611	1071	1079
26	osa-miR396b-5p	963	594	611	1071	1079
27	ptc-miR396a	963	594	611	1071	1079
28	ptc-miR396b	963	594	611	1071	1079
29	sbi-miR396a	963	594	611	1071	1079
30	sbi-miR396b	963	594	611	1071	1079
31	sly-miR396a-5p	963	594	611	1071	1079
32	sof-miR396	963	594	611	1071	1079
33	ssl-miR396	963	594	611	1071	1079
34	ssp-miR396	963	594	611	1071	1079
35	tcc-miR396a	963	594	611	1071	1079
36	tcc-miR396b	963	594	611	1071	1079
37	vvi-miR396c	963	594	611	1071	1079
38	vvi-miR396d	963	594	611	1071	1079
39	zma-miR396a-5p	963	594	611	1071	1079
40	zma-miR396b-5p	963	594	611	1071	1079
41	cli-miR-146a-5p	57	144	112	93	177
42	cpo-miR-146a-5p	57	144	112	93	177
43	ocu-miR-146a-5p	57	144	112	93	177
44	cfa-miR-146a	57	142	110	93	175
45	cgr-miR-146a	57	142	110	93	175
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3	cja-miR-146a	57	142	110	93	175
4	eca-miR-146a	57	142	110	93	175
5	gga-miR-146a-5p	57	142	110	93	175
6	hsa-miR-146a-5p	57	142	110	93	175
7	mdo-miR-146a-5p	57	142	110	93	175
8	mml-miR-146a-5p	57	142	110	93	175
9	mmr-miR-146a	57	142	110	93	175
10	mmu-miR-146a-5p	57	142	110	93	175
11	nle-miR-146a	57	142	110	93	175
12	pal-miR-146a-5p	57	142	110	93	175
13	pha-miR-146a	57	142	110	93	175
14	ppy-miR-146a	57	142	110	93	175
15	ptr-miR-146a	57	142	110	93	175
16	rno-miR-146a-5p	57	142	110	93	175
17	ssc-miR-146a-5p	57	142	110	93	175
18	tch-miR-146a-5p	57	142	110	93	175
19	tgu-miR-146c	57	142	110	93	175
20	pvu-miR482-3p	324	179	265	440	347
21	gma-miR482b-3p	702	430	337	987	535
22	gma-miR482d-3p	702	430	337	987	535
23	cme-miR172a	183	184	189	324	359
24	gma-miR172c	183	184	189	324	359
25	lus-miR172e	183	184	189	324	359
26	lus-miR172i	183	184	189	324	359
27	mdm-miR172l	183	184	189	324	359
28	mes-miR172e	183	184	189	324	359
29	mes-miR172f	183	184	189	324	359
30	ppe-miR172d	183	184	189	324	359
31	ptc-miR172g-3p	183	184	189	324	359
32	ptc-miR172h-3p	183	184	189	324	359
33	rco-miR172	183	184	189	324	359
34	sly-miR172d	183	184	189	324	359
35	stu-miR172d-3p	183	184	189	324	359
36	vvi-miR172c	183	184	189	324	359
37	csi-miR172c-3p	183	184	189	324	360
38	gma-miR172d	187	185	189	328	359
39	gma-miR172e	187	185	189	328	359
40	ath-miR162a-5p	82	49	39	95	127
41	ath-miR162b-5p	82	49	39	95	127
42	csi-miR162-5p	82	49	39	95	127
43	ptc-miR6478	19612	41570	19446	47793	34975
44	ath-miR8175	64	22	33	60	95
45	csi-miR482d-3p	1692	0	0	1	0
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3	ata-miR168-5p	1231	1	1	1	0
4	bdi-miR168-5p	1231	1	1	1	0
5	hvu-miR168-5p	1231	1	1	1	0
6	osa-miR168a-5p	1231	1	1	1	0
7	osa-miR168a-5p	1231	1	1	1	0
8	sbi-miR168	1231	1	1	1	0
9	sbi-miR168	1231	1	1	1	0
10	sof-miR168a	1231	1	1	1	0
11	ssp-miR168a	1231	1	1	1	0
12	ssp-miR168a	1231	1	1	1	0
13	zma-miR168a-5p	1231	1	1	1	0
14	zma-miR168b-5p	1231	1	1	1	0
15	csi-miR482a-3p	370	0	0	0	0
16	csi-miR482g-3p	370	0	0	0	0
17	csi-miR482g-3p	370	0	0	0	0
18	osa-miR444b.1	359	0	0	0	0
19	osa-miR444c.1	359	0	0	0	0
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Do not distribute



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3	125	83	106	427	72	86	115
4	125	83	106	427	72	86	115
5	125	83	106	427	72	86	115
6	125	83	106	427	72	86	115
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3	125	149	114	350	62	110	115
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35	68	40	53	38	91	51	62
36	68	40	53	38	91	51	62
37	68	40	53	38	91	51	62
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40	68	40	53	38	91	51	62
41	68	40	53	38	91	51	62
42	68	40	53	38	91	51	62
43	840	836	588	565	1288	1129	770
44	840	835	587	564	1287	1127	770
45	840	835	587	564	1287	1127	770
46	840	835	587	564	1287	1127	770
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53	199	49	142	103	112	185	182
54	199	49	142	103	112	185	182
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56	199	49	142	103	112	185	182
57	198	49	140	102	112	183	181
58	198	49	140	102	112	183	181
59	198	49	140	102	112	183	181
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23	198	49	140	102	112	183	181
24	198	49	140	102	112	183	181
25	198	49	140	102	112	183	181
26	331	281	177	245	529	362	303
27	711	609	425	311	1186	559	652
28	711	609	425	311	1186	559	652
29	222	159	182	174	389	375	203
30	222	159	182	174	389	375	203
31	222	159	182	174	389	375	203
32	222	159	182	174	389	375	203
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46	222	159	182	174	389	375	203
47	222	159	182	174	389	375	203
48	222	159	182	174	389	376	203
49	226	162	183	174	394	375	207
50	226	162	183	174	394	375	207
51	53	71	48	36	114	133	49
52	53	71	48	36	114	133	49
53	53	71	48	36	114	133	49
54	53	71	48	36	114	133	49
55	61152	17008	41078	17947	57410	36531	56050
56	82	56	22	30	72	99	75
57	0	1467	0	0	1	0	0
58							
59							
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3	0	1068	1	1	1	0	0	
4	0	1068	1	1	1	0	0	
5	0	1068	1	1	1	0	0	
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15	0	321	0	0	0	0	0	
16	0	321	0	0	0	0	0	
17	0	311	0	0	0	0	0	
18	0	311	0	0	0	0	0	
19	0	311	0	0	0	0	0	
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Do not distribute





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3	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
4	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
5	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
6	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
7	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
8	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
9	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
10	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
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12	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
13	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
14	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
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16	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
17	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
18	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
19	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
20	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
21	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
22	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
23	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
24	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
25	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
26	148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
27	150.81	206	96	0.998	-1.101538	-2.472	0.01344867
28	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
29	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
30	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
31	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
32	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
33	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
34	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
35	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
36	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
37	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
38	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
39	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
40	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
41	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
42	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
43	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
44	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
45	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
46	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
47	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
48	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
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52	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
53	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
54	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
55	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
56	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
57	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
58	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
59	149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
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3	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
4	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
5	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
6	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
7	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
8	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
9	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
10	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
11	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
12	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
13	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
14	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
15	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
16	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
17	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
18	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
19	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
20	393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
21	355.67	480	232	0.997	-1.0489096	-2.704	0.00684464
22	355.67	480	232	0.997	-1.0489096	-2.704	0.00684464
23	355.67	480	232	0.997	-1.0489096	-2.704	0.00684464
24	355.52	480	232	0.997	-1.0489096	-2.701	0.00691441
25	355.52	480	232	0.997	-1.0489096	-2.701	0.00691441
26	355.52	480	232	0.997	-1.0489096	-2.701	0.00691441
27	355.52	480	232	0.997	-1.0489096	-2.701	0.00691441
28	65.54	88	43	0.998	-1.0331669	-2.034	0.04198944
29	63.05	84	42	0.999	-1	-1.935	0.05293459
30	63.05	84	42	0.999	-1	-1.935	0.05293459
31	63.05	84	42	0.999	-1	-1.935	0.05293459
32	63.05	84	42	0.999	-1	-1.935	0.05293459
33	63.05	84	42	0.999	-1	-1.935	0.05293459
34	63.05	84	42	0.999	-1	-1.935	0.05293459
35	63.05	84	42	0.999	-1	-1.935	0.05293459
36	63.05	84	42	0.999	-1	-1.935	0.05293459
37	63.05	84	42	0.999	-1	-1.935	0.05293459
38	63.05	84	42	0.999	-1	-1.935	0.05293459
39	63.05	84	42	0.999	-1	-1.935	0.05293459
40	63.05	84	42	0.999	-1	-1.935	0.05293459
41	63.05	84	42	0.999	-1	-1.935	0.05293459
42	63.05	84	42	0.999	-1	-1.935	0.05293459
43	63.05	84	42	0.999	-1	-1.935	0.05293459
44	63.05	84	42	0.999	-1	-1.935	0.05293459
45	63.05	84	42	0.999	-1	-1.935	0.05293459
46	63.05	84	42	0.999	-1	-1.935	0.05293459
47	63.05	84	42	0.999	-1	-1.935	0.05293459
48	63.05	84	42	0.999	-1	-1.935	0.05293459
49	63.05	84	42	0.999	-1	-1.935	0.05293459
50	63.05	84	42	0.999	-1	-1.935	0.05293459
51	63.05	84	42	0.999	-1	-1.935	0.05293459
52	63.05	84	42	0.999	-1	-1.935	0.05293459
53	63.05	84	42	0.999	-1	-1.935	0.05293459
54	63.05	84	42	0.999	-1	-1.935	0.05293459
55	63.05	84	42	0.999	-1	-1.935	0.05293459
56	63.05	84	42	0.999	-1	-1.935	0.05293459
57	201.09	267	136	0.997	-0.9732331	-2.801	0.00508989
58	2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
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3	2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
4	2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
5	2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
6	2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
7	2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
8	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
9	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
10	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
11	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
12	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
13	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
14	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
15	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
16	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
17	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
18	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
19	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
20	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
21	2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
22	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
23	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
24	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
25	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
26	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
27	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
28	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
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32	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
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37	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
38	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
39	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
40	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
41	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
42	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
43	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
44	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
45	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
46	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
47	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
48	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
49	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
50	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
51	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
52	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
53	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
54	495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
55	120.03	150	90	0.998	-0.7369656	-1.922	0.05465553
56	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
57	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
58	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
59	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
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3	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
4	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
5	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
6	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
7	119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
8	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
9	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
10	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
11	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
12	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
13	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
14	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
15	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
16	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
17	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
18	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
19	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
20	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
21	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
22	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
23	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
24	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
25	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
26	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
27	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
28	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
29	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
30	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
31	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
32	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
33	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
34	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
35	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
36	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
37	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
38	89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
39	89.42	110	68	0.999	-0.6938969	-1.546	0.1220541
40	89.42	110	68	0.999	-0.6938969	-1.546	0.1220541
41	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
42	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
43	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
44	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
45	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
46	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
47	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
48	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
49	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
50	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
51	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
52	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
53	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
54	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
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56	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
57	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
58	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
59	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
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3	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
4	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
5	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
6	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
7	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
8	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
9	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
10	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
11	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
12	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
13	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
14	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
15	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
16	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
17	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
18	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
19	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
20	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
21	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
22	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
23	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
24	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
25	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
26	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
27	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
28	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
29	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
30	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
31	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
32	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
33	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
34	99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
35	257.5	314	201	0.998	-0.6435691	-1.744	0.08120503
36	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
37	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
38	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
39	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
40	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
41	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
42	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
43	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
44	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
45	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
46	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
47	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
48	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
49	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
50	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
51	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
52	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
53	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
54	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
55	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
56	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
57	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
58	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
59	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
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3	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
4	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
5	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
6	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
7	251.74	306	197	0.998	-0.635336	-1.715	0.08641366
8							
9	54.25	66	43	1	-0.6181294	-0.883	0.37716247
10	54.25	66	43	1	-0.6181294	-0.883	0.37716247
11	54.25	66	43	1	-0.6181294	-0.883	0.37716247
12	54.25	66	43	1	-0.6181294	-0.883	0.37716247
13	54.25	66	43	1	-0.6181294	-0.883	0.37716247
14	54.25	66	43	1	-0.6181294	-0.883	0.37716247
15	54.25	66	43	1	-0.6181294	-0.883	0.37716247
16	54.25	66	43	1	-0.6181294	-0.883	0.37716247
17	54.25	66	43	1	-0.6181294	-0.883	0.37716247
18	54.25	66	43	1	-0.6181294	-0.883	0.37716247
19	54.25	66	43	1	-0.6181294	-0.883	0.37716247
20	54.25	66	43	1	-0.6181294	-0.883	0.37716247
21	54.25	66	43	1	-0.6181294	-0.883	0.37716247
22	54.25	66	43	1	-0.6181294	-0.883	0.37716247
23	54.25	66	43	1	-0.6181294	-0.883	0.37716247
24	54.25	66	43	1	-0.6181294	-0.883	0.37716247
25	54.25	66	43	1	-0.6181294	-0.883	0.37716247
26	54.25	66	43	1	-0.6181294	-0.883	0.37716247
27	54.25	66	43	1	-0.6181294	-0.883	0.37716247
28	54.25	66	43	1	-0.6181294	-0.883	0.37716247
29	54.25	66	43	1	-0.6181294	-0.883	0.37716247
30	54.25	66	43	1	-0.6181294	-0.883	0.37716247
31	54.25	66	43	1	-0.6181294	-0.883	0.37716247
32	54.25	66	43	1	-0.6181294	-0.883	0.37716247
33	54.25	66	43	1	-0.6181294	-0.883	0.37716247
34	54.25	66	43	1	-0.6181294	-0.883	0.37716247
35	54.25	66	43	1	-0.6181294	-0.883	0.37716247
36	54.25	66	43	1	-0.6181294	-0.883	0.37716247
37	54.25	66	43	1	-0.6181294	-0.883	0.37716247
38	54.25	66	43	1	-0.6181294	-0.883	0.37716247
39	54.25	66	43	1	-0.6181294	-0.883	0.37716247
40	54.25	66	43	1	-0.6181294	-0.883	0.37716247
41	54.25	66	43	1	-0.6181294	-0.883	0.37716247
42	54.25	66	43	1	-0.6181294	-0.883	0.37716247
43	54.25	66	43	1	-0.6181294	-0.883	0.37716247
44	54.25	66	43	1	-0.6181294	-0.883	0.37716247
45	54.25	66	43	1	-0.6181294	-0.883	0.37716247
46	54.25	66	43	1	-0.6181294	-0.883	0.37716247
47	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
48	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
49	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
50	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
51	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
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53	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
54	866.11	1048	685	1	-0.6134628	-0.588	0.5562651
55	133.23	156	110	0.999	-0.5040425	-1.394	0.16338548
56	132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
57	132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
58	132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
59	132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
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3	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
4	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
5	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
6	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
7	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
8	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
9	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
10	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
11	77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
12	68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
13	68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
14	68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
15	68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
16	68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
17	68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
18	49.52	58	42	0.999	-0.4656636	-0.875	0.38167002
19	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
20	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
21	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
22	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
23	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
24	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
25	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
26	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
27	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
28	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
29	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
30	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
31	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
32	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
33	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
34	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
35	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
36	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
37	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
38	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
39	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
40	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
41	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
42	48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
43	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
44	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
45	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
46	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
47	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
48	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
49	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
50	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
51	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
52	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
53	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
54	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
55	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
56	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
57	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
58	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
59	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
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3	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
4	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
5	89.9	103	77	0.999	-0.419714	-1.087	0.27699077
6	48.96	56	42	0.999	-0.4150375	-0.812	0.41681107
7	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
8	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
9	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
10	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
11	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
12	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
13	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
14	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
15	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
16	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
17	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
18	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
19	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
20	109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
21	516.58	589	445	0.998	-0.4044623	-1.436	0.15106432
22	78.59	90	68	1	-0.4043903	-0.284	0.77668962
23	78.59	90	68	1	-0.4043903	-0.284	0.77668962
24	78.59	90	68	1	-0.4043903	-0.284	0.77668962
25	78.59	90	68	1	-0.4043903	-0.284	0.77668962
26	78.59	90	68	1	-0.4043903	-0.284	0.77668962
27	78.59	90	68	1	-0.4043903	-0.284	0.77668962
28	78.59	90	68	1	-0.4043903	-0.284	0.77668962
29	78.59	90	68	1	-0.4043903	-0.284	0.77668962
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32	78.59	90	68	1	-0.4043903	-0.284	0.77668962
33	78.59	90	68	1	-0.4043903	-0.284	0.77668962
34	78.59	90	68	1	-0.4043903	-0.284	0.77668962
35	78.59	90	68	1	-0.4043903	-0.284	0.77668962
36	78.59	90	68	1	-0.4043903	-0.284	0.77668962
37	78.59	90	68	1	-0.4043903	-0.284	0.77668962
38	78.59	90	68	1	-0.4043903	-0.284	0.77668962
39	78.59	90	68	1	-0.4043903	-0.284	0.77668962
40	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
41	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
42	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
43	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
44	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
45	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
46	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
47	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
48	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
49	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
50	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
51	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
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59	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
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3	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
4	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
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6	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
7	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
8	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
9	516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
10	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
11	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
12	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
13	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
14	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
15	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
16	50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
17	522.35	594	451	0.998	-0.3973355	-1.395	0.16306794
18	47.66	54	41	1	-0.3973355	-0.662	0.50787169
19	47.66	54	41	1	-0.3973355	-0.662	0.50787169
20	47.66	54	41	1	-0.3973355	-0.662	0.50787169
21	47.66	54	41	1	-0.3973355	-0.662	0.50787169
22	47.66	54	41	1	-0.3973355	-0.662	0.50787169
23	47.66	54	41	1	-0.3973355	-0.662	0.50787169
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25	47.66	54	41	1	-0.3973355	-0.662	0.50787169
26	47.66	54	41	1	-0.3973355	-0.662	0.50787169
27	47.66	54	41	1	-0.3973355	-0.662	0.50787169
28	47.66	54	41	1	-0.3973355	-0.662	0.50787169
29	47.66	54	41	1	-0.3973355	-0.662	0.50787169
30	47.66	54	41	1	-0.3973355	-0.662	0.50787169
31	135.93	155	118	0.999	-0.3934814	-1.118	0.26368155
32	62.13	70	54	1	-0.3743955	-0.704	0.48146024
33	62.13	70	54	1	-0.3743955	-0.704	0.48146024
34	62.13	70	54	1	-0.3743955	-0.704	0.48146024
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36	62.13	70	54	1	-0.3743955	-0.704	0.48146024
37	62.13	70	54	1	-0.3743955	-0.704	0.48146024
38	62.13	70	54	1	-0.3743955	-0.704	0.48146024
39	133.11	150	116	0.999	-0.3708377	-1.073	0.2832042
40	133.11	150	116	0.999	-0.3708377	-1.073	0.2832042
41	222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
42	222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
43	222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
44	222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
45	222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
46	222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
47	579.63	648	511	1	-0.3426705	-0.238	0.8116487
48	579.63	648	511	1	-0.3426705	-0.238	0.8116487
49	579.63	648	511	1	-0.3426705	-0.238	0.8116487
50	579.63	648	511	1	-0.3426705	-0.238	0.8116487
51	570.69	637	504	1	-0.3378696	-0.236	0.813742
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60	570.69	637	504	1	-0.3378696	-0.236	0.813742

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3	570.69	637	504	1	-0.3378696	-0.236	0.813742
4	570.69	637	504	1	-0.3378696	-0.236	0.813742
5	570.69	637	504	1	-0.3378696	-0.236	0.813742
6	570.69	637	504	1	-0.3378696	-0.236	0.813742
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9	570.69	637	504	1	-0.3378696	-0.236	0.813742
10	570.69	637	504	1	-0.3378696	-0.236	0.813742
11	5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
12	5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
13	5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
14	5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
15	92.35	102	83	1	-0.2973859	-0.164	0.86953914
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17	92.35	102	83	1	-0.2973859	-0.164	0.86953914
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19	92.35	102	83	1	-0.2973859	-0.164	0.86953914
20	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
21	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
22	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
23	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
24	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
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26	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
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35	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
36	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
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29	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
30	394.28	435	354	0.999	-0.297266	-1.046	0.29548296
31	395.34	436	355	0.999	-0.2965091	-1.045	0.29591636
32	395.34	436	355	0.999	-0.2965091	-1.045	0.29591636
33	108.97	119	99	1	-0.2654611	-0.603	0.5464287
34	148.63	162	135	1	-0.2630344	-0.591	0.55445819
35	148.63	162	135	1	-0.2630344	-0.591	0.55445819
36	148.63	162	135	1	-0.2630344	-0.591	0.55445819
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44	148.63	162	135	1	-0.2630344	-0.591	0.55445819
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47	148.63	162	135	1	-0.2630344	-0.591	0.55445819
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17	148.63	162	135	1	-0.2630344	-0.591	0.55445819	
18	148.63	162	135	1	-0.2630344	-0.591	0.55445819	
19	148.63	162	135	1	-0.2630344	-0.591	0.55445819	
20	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
21	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
22	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
23	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
24	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
25	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
26	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
27	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
28	6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539	
29	108.07	118	99	0.999	-0.2532864	-0.74	0.45937141	
30	108.07	118	99	0.999	-0.2532864	-0.74	0.45937141	
31	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
32	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
33	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
34	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
35	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
36	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
37	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
38	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
39	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
40	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
41	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
42	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
43	6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102	
44	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415	
45	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415	
46	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415	
47	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415	
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8	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
9	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
10	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
11	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
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37	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
38	234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
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27	168.39	181	156	0.999	-0.2144437	-0.63	0.52868577
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29							
30	197	211	183	0.999	-0.2053994	-0.563	0.57337155
31	192.15	205	179	1	-0.1956643	-0.536	0.59161889
32	192.15	205	179	1	-0.1956643	-0.536	0.59161889
33	192.15	205	179	1	-0.1956643	-0.536	0.59161889
34	192.15	205	179	1	-0.1956643	-0.536	0.59161889
35	192.15	205	179	1	-0.1956643	-0.536	0.59161889
36	192.15	205	179	1	-0.1956643	-0.536	0.59161889
37	192.15	205	179	1	-0.1956643	-0.536	0.59161889
38	192.15	205	179	1	-0.1956643	-0.536	0.59161889
39	192.15	205	179	1	-0.1956643	-0.536	0.59161889
40	66.42	71	62	1	-0.1955508	-0.144	0.88527875
41	66.42	71	62	1	-0.1955508	-0.144	0.88527875
42	66.42	71	62	1	-0.1955508	-0.144	0.88527875
43	66.42	71	62	1	-0.1955508	-0.144	0.88527875
44	66.42	71	62	1	-0.1955508	-0.144	0.88527875
45	66.42	71	62	1	-0.1955508	-0.144	0.88527875
46	66.42	71	62	1	-0.1955508	-0.144	0.88527875
47	66.42	71	62	1	-0.1955508	-0.144	0.88527875
48	66.42	71	62	1	-0.1955508	-0.144	0.88527875
49	66.42	71	62	1	-0.1955508	-0.144	0.88527875
50	66.42	71	62	1	-0.1955508	-0.144	0.88527875
51	66.42	71	62	1	-0.1955508	-0.144	0.88527875
52	66.42	71	62	1	-0.1955508	-0.144	0.88527875
53	66.42	71	62	1	-0.1955508	-0.144	0.88527875
54	66.42	71	62	1	-0.1955508	-0.144	0.88527875
55	66.42	71	62	1	-0.1955508	-0.144	0.88527875
56	66.42	71	62	1	-0.1955508	-0.144	0.88527875
57	66.42	71	62	1	-0.1955508	-0.144	0.88527875
58	66.42	71	62	1	-0.1955508	-0.144	0.88527875
59	66.42	71	62	1	-0.1955508	-0.144	0.88527875
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3	66.42	71	62	1	-0.1955508	-0.144	0.88527875	
4	66.42	71	62	1	-0.1955508	-0.144	0.88527875	
5	66.42	71	62	1	-0.1955508	-0.144	0.88527875	
6	2539.04	2705	2373	0.999	-0.1889165	-0.524	0.60007218	
7	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
8	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
9	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
10	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
11	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
12	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
13	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
14	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
15	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
16	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
17	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
18	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
19	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
20	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
21	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
22	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
23	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
24	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
25	326.79	347	306	0.999	-0.181404	-0.613	0.53988147	
26	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
27	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
28	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
29	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
30	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
31	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
32	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
33	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
34	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
35	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
36	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
37	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
38	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
39	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
40	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
41	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
42	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
43	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
44	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
45	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
46	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
47	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
48	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
49	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
50	220.39	234	207	1	-0.1768778	-0.157	0.87513213	
51	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
52	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
53	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
54	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
55	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
56	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
57	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
58	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
59	204.01	216	192	0.999	-0.169925	-0.504	0.61408312	
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3	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
4	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
5	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
6	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
7	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
8	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
9	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
10	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
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12	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
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14	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
15	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
16	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
17	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
18	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
19	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
20	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
21	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
22	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
23	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
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25	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
26	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
27	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
28	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
29	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
30	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
31	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
32	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
33	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
34	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
35	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
36	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
37	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
38	204.01	216	192	0.999	-0.169925	-0.504	0.61408312
39	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
40	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
41	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
42	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
43	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
44	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
45	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
46	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
47	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
48	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
49	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
50	233.46	247	220	0.999	-0.1670075	-0.507	0.61220945
51	51.83	55	49	1	-0.1666499	-0.368	0.71321265
52	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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56	51.83	55	49	1	-0.1666499	-0.368	0.71321265
57	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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59	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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3	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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5	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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7	51.83	55	49	1	-0.1666499	-0.368	0.71321265
8	51.83	55	49	1	-0.1666499	-0.368	0.71321265
9	51.83	55	49	1	-0.1666499	-0.368	0.71321265
10	51.83	55	49	1	-0.1666499	-0.368	0.71321265
11	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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13	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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17	51.83	55	49	1	-0.1666499	-0.368	0.71321265
18	51.83	55	49	1	-0.1666499	-0.368	0.71321265
19	51.83	55	49	1	-0.1666499	-0.368	0.71321265
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26	51.83	55	49	1	-0.1666499	-0.368	0.71321265
27	51.83	55	49	1	-0.1666499	-0.368	0.71321265
28	51.83	55	49	1	-0.1666499	-0.368	0.71321265
29	51.83	55	49	1	-0.1666499	-0.368	0.71321265
30	51.83	55	49	1	-0.1666499	-0.368	0.71321265
31	51.83	55	49	1	-0.1666499	-0.368	0.71321265
32	51.83	55	49	1	-0.1666499	-0.368	0.71321265
33	51.83	55	49	1	-0.1666499	-0.368	0.71321265
34	51.83	55	49	1	-0.1666499	-0.368	0.71321265
35	51.83	55	49	1	-0.1666499	-0.368	0.71321265
36	51.83	55	49	1	-0.1666499	-0.368	0.71321265
37	51.83	55	49	1	-0.1666499	-0.368	0.71321265
38	51.83	55	49	1	-0.1666499	-0.368	0.71321265
39	1733.99	1810	1658	0.999	-0.1265457	-0.455	0.64893761
40	116.02	121	111	1	-0.1244474	-0.354	0.72348885
41	116.02	121	111	1	-0.1244474	-0.354	0.72348885
42	116.02	121	111	1	-0.1244474	-0.354	0.72348885
43	109.35	114	105	1	-0.1186445	-0.316	0.75199545
44	109.35	114	105	1	-0.1186445	-0.316	0.75199545
45	109.35	114	105	1	-0.1186445	-0.316	0.75199545
46	109.35	114	105	1	-0.1186445	-0.316	0.75199545
47	109.35	114	105	1	-0.1186445	-0.316	0.75199545
48	122.05	127	117	1	-0.11832	-0.359	0.71963611
49	122.05	127	117	1	-0.11832	-0.359	0.71963611
50	122.05	127	117	1	-0.11832	-0.359	0.71963611
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57	122.05	127	117	1	-0.11832	-0.359	0.71963611
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59	122.05	127	117	1	-0.11832	-0.359	0.71963611
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3	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
4	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
5	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
6	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
7	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
8	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
9	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
10	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
11	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
12	23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
13	23443.87	24394	22494	0.999	-0.1169861	-0.485	0.62792869
14	88.92	92	85	1	-0.114171	-0.28	0.77917697
15	88.92	92	85	1	-0.114171	-0.28	0.77917697
16	88.73	92	85	1	-0.114171	-0.261	0.79421214
17	88.73	92	85	1	-0.114171	-0.261	0.79421214
18	88.73	92	85	1	-0.114171	-0.261	0.79421214
19	88.73	92	85	1	-0.114171	-0.261	0.79421214
20	88.73	92	85	1	-0.114171	-0.261	0.79421214
21	88.73	92	85	1	-0.114171	-0.261	0.79421214
22	88.73	92	85	1	-0.114171	-0.261	0.79421214
23	88.73	92	85	1	-0.114171	-0.261	0.79421214
24	88.73	92	85	1	-0.114171	-0.261	0.79421214
25	343.45	357	330	1	-0.113458	-0.357	0.72111184
26	125.84	130	121	1	-0.1035046	-0.256	0.79780294
27	125.84	130	121	1	-0.1035046	-0.256	0.79780294
28	125.84	130	121	1	-0.1035046	-0.256	0.79780294
29	125.84	130	121	1	-0.1035046	-0.256	0.79780294
30	125.84	130	121	1	-0.1035046	-0.256	0.79780294
31	125.84	130	121	1	-0.1035046	-0.256	0.79780294
32	125.84	130	121	1	-0.1035046	-0.256	0.79780294
33	125.84	130	121	1	-0.1035046	-0.256	0.79780294
34	125.84	130	121	1	-0.1035046	-0.256	0.79780294
35	125.84	130	121	1	-0.1035046	-0.256	0.79780294
36	125.84	130	121	1	-0.1035046	-0.256	0.79780294
37	125.84	130	121	1	-0.1035046	-0.256	0.79780294
38	125.84	130	121	1	-0.1035046	-0.256	0.79780294
39	125.84	130	121	1	-0.1035046	-0.256	0.79780294
40	125.84	130	121	1	-0.1035046	-0.256	0.79780294
41	125.84	130	121	1	-0.1035046	-0.256	0.79780294
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49	110.69	114	107	1	-0.091423	-0.237	0.81250559
50	2842.26	2931	2753	1	-0.0903884	-0.33	0.74155968
51	2842.26	2931	2753	1	-0.0903884	-0.33	0.74155968
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57	95.93	99	93	1	-0.0901978	-0.225	0.82178739
58	95.93	99	93	1	-0.0901978	-0.225	0.82178739
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42	2819.23	2907	2731	1	-0.0901018	-0.327	0.7435407
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44	676.25	697	655	1	-0.0896637	-0.322	0.74747518
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49	182.57	188	177	1	-0.0869833	-0.269	0.78810939
50	182.57	188	177	1	-0.0869833	-0.269	0.78810939
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52	186.56	192	181	1	-0.0851166	-0.261	0.79376626
53	96.62	99	94	1	-0.0747678	-0.195	0.84528898
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9	96.62	99	94	1	-0.0747678	-0.195	0.84528898
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56	3830.32	3926	3735	1	-0.0719519	-0.256	0.79827963
57	177.95	182	174	1	-0.0648511	-0.255	0.79889255
58	177.65	182	174	1	-0.0648511	-0.212	0.83202546
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3	771.21	787	755	1	-0.059887	-0.209	0.83434281
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12	771.21	787	755	1	-0.059887	-0.209	0.83434281
13	771.21	787	755	1	-0.059887	-0.209	0.83434281
14	454.99	464	447	1	-0.05385	-0.185	0.8529207
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46	9468.94	9605	9333	1	-0.0414447	-0.16	0.87272051
47	9468.94	9605	9333	1	-0.0414447	-0.16	0.87272051
48	9477.23	9613	9341	1	-0.0414097	-0.16	0.8729265
49	9477.23	9613	9341	1	-0.0414097	-0.16	0.8729265
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51	387.8	391	384	1	-0.0260623	-0.086	0.9317648
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4	565.2	570	560	1	-0.0255351	-0.098	0.92160242
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11	567.35	572	562	1	-0.025445	-0.094	0.92520655
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21	567.35	572	562	1	-0.025445	-0.094	0.92520655
22	899.51	907	892	1	-0.0240588	-0.091	0.92787414
23	914.7	922	907	1	-0.0236642	-0.09	0.92849191
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57	9327.76	9389	9267	1	-0.0188691	-0.079	0.93684212
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5	9330.28	9391	9270	1	-0.0187095	-0.078	0.93755891
6	243.3	245	242	1	-0.0177747	-0.047	0.96233375
7	287.67	289	286	1	-0.0150543	-0.025	0.98000584
8	324.32	326	323	1	-0.0133378	-0.048	0.96155246
9	324.32	326	323	1	-0.0133378	-0.048	0.96155246
10	242.53	243	241	1	-0.0119232	-0.033	0.97335829
11	242.53	243	241	1	-0.0119232	-0.033	0.97335829
12	126.22	127	126	1	-0.0114048	-0.037	0.97014762
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36	126.22	127	126	1	-0.0114048	-0.037	0.97014762
37	126.22	127	126	1	-0.0114048	-0.037	0.97014762
38	126.22	127	126	1	-0.0114048	-0.037	0.97014762
39	126.22	127	126	1	-0.0114048	-0.037	0.97014762
40	126.22	127	126	1	-0.0114048	-0.037	0.97014762
41	126.22	127	126	1	-0.0114048	-0.037	0.97014762
42	126.22	127	126	1	-0.0114048	-0.037	0.97014762
43	126.22	127	126	1	-0.0114048	-0.037	0.97014762
44	126.22	127	126	1	-0.0114048	-0.037	0.97014762
45	126.22	127	126	1	-0.0114048	-0.037	0.97014762
46	126.22	127	126	1	-0.0114048	-0.037	0.97014762
47	126.22	127	126	1	-0.0114048	-0.037	0.97014762
48	126.22	127	126	1	-0.0114048	-0.037	0.97014762
49	126.22	127	126	1	-0.0114048	-0.037	0.97014762
50	126.22	127	126	1	-0.0114048	-0.037	0.97014762
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5	126.22	127	126	1	-0.0114048	-0.037	0.97014762	
6	126.22	127	126	1	-0.0114048	-0.037	0.97014762	
7	133.31	134	133	1	-0.0108068	-0.003	0.99758817	
8	133.31	134	133	1	-0.0108068	-0.003	0.99758817	
9	133.31	134	133	1	-0.0108068	-0.003	0.99758817	
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12	133.31	134	133	1	-0.0108068	-0.003	0.99758817	
13	133.31	134	133	1	-0.0108068	-0.003	0.99758817	
14	133.31	134	133	1	-0.0108068	-0.003	0.99758817	
15	153.44	154	153	1	-0.0093987	-0.031	0.97526153	
16	153.29	154	153	1	-0.0093987	-0.022	0.98223593	
17	493.69	495	493	1	-0.0058409	-0.009	0.99246682	
18	493.69	495	493	1	-0.0058409	-0.009	0.99246682	
19	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
20	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
21	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
22	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
23	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
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29	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
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32	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
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39	283.61	284	283	1	-0.0050889	-0.014	0.98870936	
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8	283.61	284	283	1	-0.0050889	-0.014	0.98870936
9	283.61	284	283	1	-0.0050889	-0.014	0.98870936
10	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
11	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
12	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
13	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
14	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
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19	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
20	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
21	6646.44	6652	6641	1	-0.0023877	-0.011	0.99140382
22	6714.73	6717	6712	1	-0.0010743	-0.005	0.99606538
23	6714.73	6717	6712	1	-0.0010743	-0.005	0.99606538
24	6754.36	6755	6754	1	-0.0002136	-0.001	0.99929018
25	167.97	168	168	1	0	-0.02	0.98434459
26	167.97	168	168	1	0	-0.02	0.98434459
27	167.97	168	168	1	0	-0.02	0.98434459
28	167.97	168	168	1	0	-0.02	0.98434459
29	167.97	168	168	1	0	-0.02	0.98434459
30	167.97	168	168	1	0	-0.02	0.98434459
31	167.97	168	168	1	0	-0.02	0.98434459
32	167.97	168	168	1	0	-0.02	0.98434459
33	167.97	168	168	1	0	-0.02	0.98434459
34	167.97	168	168	1	0	-0.02	0.98434459
35	167.97	168	168	1	0	-0.02	0.98434459
36	167.97	168	168	1	0	-0.02	0.98434459
37	167.97	168	168	1	0	-0.02	0.98434459
38	167.97	168	168	1	0	-0.02	0.98434459
39	167.97	168	168	1	0	-0.02	0.98434459
40	167.97	168	168	1	0	-0.02	0.98434459
41	167.97	168	168	1	0	-0.02	0.98434459
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59	153.13	153	153	1	0	-0.012	0.99009238
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3	153.13	153	153	1	0	-0.012	0.99009238
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19	153.13	153	153	1	0	-0.012	0.99009238
20	153.13	153	153	1	0	-0.012	0.99009238
21	153.13	153	153	1	0	-0.012	0.99009238
22	153.13	153	153	1	0	-0.012	0.99009238
23	309.19	309	309	1	0	0.01	0.99177196
24	164.94	165	165	1	0	-0.004	0.99654392
25	164.94	165	165	1	0	-0.004	0.99654392
26	164.94	165	165	1	0	-0.004	0.99654392
27	164.94	165	165	1	0	-0.004	0.99654392
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31	164.94	165	165	1	0	-0.004	0.99654392
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34	164.94	165	165	1	0	-0.004	0.99654392
35	164.94	165	165	1	0	-0.004	0.99654392
36	164.94	165	165	1	0	-0.004	0.99654392
37	164.94	165	165	1	0	-0.004	0.99654392
38	164.94	165	165	1	0	-0.004	0.99654392
39	164.94	165	165	1	0	-0.004	0.99654392
40	164.94	165	165	1	0	-0.004	0.99654392
41	57.16	57	57	1	0	-0.003	0.99743997
42	57.16	57	57	1	0	-0.003	0.99743997
43	57.16	57	57	1	0	-0.003	0.99743997
44	57.16	57	57	1	0	-0.003	0.99743997
45	57.16	57	57	1	0	-0.003	0.99743997
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22	57.16	57	57	1	0	-0.003	0.99743997	
23	57.16	57	57	1	0	-0.003	0.99743997	
24	57.16	57	57	1	0	-0.003	0.99743997	
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35	57.16	57	57	1	0	-0.003	0.99743997	
36	57.16	57	57	1	0	-0.003	0.99743997	
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38	57.16	57	57	1	0	-0.003	0.99743997	
39	68.91	69	69	1	0	0.002	0.99831271	
40	1377.91	1378	1378	1	0	0.001	0.99896527	
41	1372.67	1372	1373	1	0.00105114	0.001	0.99909475	
42	1372.67	1372	1373	1	0.00105114	0.001	0.99909475	
43	1372.67	1372	1373	1	0.00105114	0.001	0.99909475	
44	1372.67	1372	1373	1	0.00105114	0.001	0.99909475	
45	5121.43	5114	5129	1	0.00422541	0.014	0.98860733	
46	5121.43	5114	5129	1	0.00422541	0.014	0.98860733	
47	5121.43	5114	5129	1	0.00422541	0.014	0.98860733	
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10	655.89	655	657	1	0.00439846	0.02	0.98425623
11	13597.03	13572	13622	1	0.0053052	0.022	0.98275741
12	13597.03	13572	13622	1	0.0053052	0.022	0.98275741
13	13597.03	13572	13622	1	0.0053052	0.022	0.98275741
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21	13597.03	13572	13622	1	0.0053052	0.022	0.98275741
22	13597.03	13572	13622	1	0.0053052	0.022	0.98275741
23	12378.44	12349	12408	1	0.00687637	0.019	0.9846047
24	12378.44	12349	12408	1	0.00687637	0.019	0.9846047
25	12378.44	12349	12408	1	0.00687637	0.019	0.9846047
26	12378.44	12349	12408	1	0.00687637	0.019	0.9846047
27	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
28	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
29	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
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42	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
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44	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
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46	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
47	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
48	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
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15	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
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36	12368.38	12338	12398	1	0.00699886	0.02	0.98415557
37							
38	192.38	192	193	1	0.00749454	0.011	0.99145863
39	192.38	192	193	1	0.00749454	0.011	0.99145863
40	192.38	192	193	1	0.00749454	0.011	0.99145863
41	192.38	192	193	1	0.00749454	0.011	0.99145863
42	192.38	192	193	1	0.00749454	0.011	0.99145863
43	192.38	192	193	1	0.00749454	0.011	0.99145863
44	192.38	192	193	1	0.00749454	0.011	0.99145863
45	192.38	192	193	1	0.00749454	0.011	0.99145863
46	192.38	192	193	1	0.00749454	0.011	0.99145863
47	192.38	192	193	1	0.00749454	0.011	0.99145863
48	192.38	192	193	1	0.00749454	0.011	0.99145863
49							
50	12403.15	12369	12437	1	0.00790966	0.022	0.98218512
51	12006.09	11972	12040	1	0.00817121	0.033	0.97360442
52	12006.09	11972	12040	1	0.00817121	0.033	0.97360442
53							
54	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
55	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
56	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
57	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
58	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
59	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
60							



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2							
3	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
4	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
5	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
6	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
7	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
8	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
9	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
10	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
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12	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
13	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
14	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
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18	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
19	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
20	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
21	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
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23	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
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31	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
32	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
33	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
34	11999.97	11965	12035	1	0.00841574	0.034	0.97317471
35	135.32	135	136	1	0.01064724	0.045	0.96378541
36	255.17	254	256	1	0.01131531	0.031	0.97536035
37	102.42	102	103	1	0.01407519	0.032	0.97472456
38	102.42	102	103	1	0.01407519	0.032	0.97472456
39	102.42	102	103	1	0.01407519	0.032	0.97472456
40	102.42	102	103	1	0.01407519	0.032	0.97472456
41	102.42	102	103	1	0.01407519	0.032	0.97472456
42	102.42	102	103	1	0.01407519	0.032	0.97472456
43	102.42	102	103	1	0.01407519	0.032	0.97472456
44	102.42	102	103	1	0.01407519	0.032	0.97472456
45	102.42	102	103	1	0.01407519	0.032	0.97472456
46	102.42	102	103	1	0.01407519	0.032	0.97472456
47	102.42	102	103	1	0.01407519	0.032	0.97472456
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49	102.42	102	103	1	0.01407519	0.032	0.97472456
50	102.42	102	103	1	0.01407519	0.032	0.97472456
51	102.42	102	103	1	0.01407519	0.032	0.97472456
52	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
53	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
54	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
55	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
56	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
57	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
58	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
59	101102.75	100591	101614	1	0.01459795	0.057	0.95461652
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3	104791.64	104071	105512	1	0.01983898	0.077	0.93839807
4	64.76	64	65	1	0.02236781	0.045	0.96402514
5	64.76	64	65	1	0.02236781	0.045	0.96402514
6	64.76	64	65	1	0.02236781	0.045	0.96402514
7	64.76	64	65	1	0.02236781	0.045	0.96402514
8	63.43	63	64	1	0.02272008	0.047	0.9626818
9	63.43	63	64	1	0.02272008	0.047	0.9626818
10	63.43	63	64	1	0.02272008	0.047	0.9626818
11	63.43	63	64	1	0.02272008	0.047	0.9626818
12	63.43	63	64	1	0.02272008	0.047	0.9626818
13	63.43	63	64	1	0.02272008	0.047	0.9626818
14	63.43	63	64	1	0.02272008	0.047	0.9626818
15	63.43	63	64	1	0.02272008	0.047	0.9626818
16	63.43	63	64	1	0.02272008	0.047	0.9626818
17	63.43	63	64	1	0.02272008	0.047	0.9626818
18	63.43	63	64	1	0.02272008	0.047	0.9626818
19	63.43	63	64	1	0.02272008	0.047	0.9626818
20	63.43	63	64	1	0.02272008	0.047	0.9626818
21	63.43	63	64	1	0.02272008	0.047	0.9626818
22	63.43	63	64	1	0.02272008	0.047	0.9626818
23	63.43	63	64	1	0.02272008	0.047	0.9626818
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28	63.43	63	64	1	0.02272008	0.047	0.9626818
29	63.43	63	64	1	0.02272008	0.047	0.9626818
30	63.43	63	64	1	0.02272008	0.047	0.9626818
31	63.43	63	64	1	0.02272008	0.047	0.9626818
32	63.43	63	64	1	0.02272008	0.047	0.9626818
33	63.43	63	64	1	0.02272008	0.047	0.9626818
34	898.71	890	907	1	0.02729721	0.093	0.92575378
35	898.71	890	907	1	0.02729721	0.093	0.92575378
36	898.71	890	907	1	0.02729721	0.093	0.92575378
37	898.71	890	907	1	0.02729721	0.093	0.92575378
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39	898.71	890	907	1	0.02729721	0.093	0.92575378
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43	898.71	890	907	1	0.02729721	0.093	0.92575378
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45	898.71	890	907	1	0.02729721	0.093	0.92575378
46	898.71	890	907	1	0.02729721	0.093	0.92575378
47	898.71	890	907	1	0.02729721	0.093	0.92575378
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56	898.71	890	907	1	0.02729721	0.093	0.92575378
57	898.71	890	907	1	0.02729721	0.093	0.92575378
58	898.71	890	907	1	0.02729721	0.093	0.92575378
59	898.71	890	907	1	0.02729721	0.093	0.92575378
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3	426.17	421	431	1	0.03386764	0.113	0.91022944
4	426.17	421	431	1	0.03386764	0.113	0.91022944
5	426.17	421	431	1	0.03386764	0.113	0.91022944
6	426.17	421	431	1	0.03386764	0.113	0.91022944
7	426.17	421	431	1	0.03386764	0.113	0.91022944
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9	426.17	421	431	1	0.03386764	0.113	0.91022944
10	426.17	421	431	1	0.03386764	0.113	0.91022944
11	426.17	421	431	1	0.03386764	0.113	0.91022944
12	426.17	421	431	1	0.03386764	0.113	0.91022944
13	426.17	421	431	1	0.03386764	0.113	0.91022944
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28	426.17	421	431	1	0.03386764	0.113	0.91022944
29	426.17	421	431	1	0.03386764	0.113	0.91022944
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31	426.17	421	431	1	0.03386764	0.113	0.91022944
32	426.17	421	431	1	0.03386764	0.113	0.91022944
33	426.17	421	431	1	0.03386764	0.113	0.91022944
34	426.17	421	431	1	0.03386764	0.113	0.91022944
35	426.17	421	431	1	0.03386764	0.113	0.91022944
36	426.17	421	431	1	0.03386764	0.113	0.91022944
37	426.17	421	431	1	0.03386764	0.113	0.91022944
38	426.17	421	431	1	0.03386764	0.113	0.91022944
39	426.17	421	431	1	0.03386764	0.113	0.91022944
40	690.48	682	699	1	0.03552072	0.137	0.89139279
41	690.48	682	699	1	0.03552072	0.137	0.89139279
42	690.48	682	699	1	0.03552072	0.137	0.89139279
43	1233.17	1218	1249	1	0.03625934	0.09	0.92820804
44	311.48	307	315	1	0.03711317	0.1	0.92051986
45	311.48	307	315	1	0.03711317	0.1	0.92051986
46	311.48	307	315	1	0.03711317	0.1	0.92051986
47	426.32	421	432	1	0.03721108	0.116	0.90750036
48	426.32	421	432	1	0.03721108	0.116	0.90750036
49	301.91	298	306	1	0.03821932	0.096	0.92346825
50	301.91	298	306	1	0.03821932	0.096	0.92346825
51	301.91	298	306	1	0.03821932	0.096	0.92346825
52	301.91	298	306	1	0.03821932	0.096	0.92346825
53	301.91	298	306	1	0.03821932	0.096	0.92346825
54	301.91	298	306	1	0.03821932	0.096	0.92346825
55	64.76	64	66	1	0.04439412	0.127	0.89859678
56	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
57	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
58	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
59	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
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3	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
4	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
5	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
6	10687.68	10506	10869	1	0.04900572	0.187	0.85154364
7	1169.81	1147	1192	1	0.05551884	0.129	0.89740317
8							
9	297059.98	290668	303452	1	0.06209608	0.25	0.80278167
10	297059.98	290668	303452	1	0.06209608	0.25	0.80278167
11	297059.98	290668	303452	1	0.06209608	0.25	0.80278167
12	297059.98	290668	303452	1	0.06209608	0.25	0.80278167
13							
14	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
15	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
16	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
17	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
18	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
19	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
20	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
21	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
22	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
23	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
24	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
25	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
26	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
27	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
28	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
29	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
30	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
31	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
32	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
33	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
34	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
35	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
36	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
37	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
38	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
39	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
40	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
41	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
42	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
43	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
44	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
45	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
46	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
47	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
48	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
49	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
50	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
51	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
52	104941.8	102484	107399	1	0.06758187	0.282	0.77831564
53							
54	277.05	271	284	1	0.06759808	0.177	0.85928993
55	277.32	271	284	1	0.06759808	0.168	0.86640625
56	191.44	187	196	1	0.06781538	0.201	0.8407443
57	191.44	187	196	1	0.06781538	0.201	0.8407443
58	191.44	187	196	1	0.06781538	0.201	0.8407443
59	191.44	187	196	1	0.06781538	0.201	0.8407443
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2							
3	276.71	270	283	1	0.06784265	0.176	0.86013823
4	276.71	270	283	1	0.06784265	0.176	0.86013823
5	276.71	270	283	1	0.06784265	0.176	0.86013823
6	276.71	270	283	1	0.06784265	0.176	0.86013823
7	276.71	270	283	1	0.06784265	0.176	0.86013823
8	276.71	270	283	1	0.06784265	0.176	0.86013823
9	276.71	270	283	1	0.06784265	0.176	0.86013823
10	276.71	270	283	1	0.06784265	0.176	0.86013823
11	276.71	270	283	1	0.06784265	0.176	0.86013823
12	276.71	270	283	1	0.06784265	0.176	0.86013823
13	276.71	270	283	1	0.06784265	0.176	0.86013823
14	276.71	270	283	1	0.06784265	0.176	0.86013823
15	276.71	270	283	1	0.06784265	0.176	0.86013823
16	276.71	270	283	1	0.06784265	0.176	0.86013823
17	276.71	270	283	1	0.06784265	0.176	0.86013823
18	276.71	270	283	1	0.06784265	0.176	0.86013823
19	276.71	270	283	1	0.06784265	0.176	0.86013823
20	276.71	270	283	1	0.06784265	0.176	0.86013823
21	276.71	270	283	1	0.06784265	0.176	0.86013823
22	276.71	270	283	1	0.06784265	0.176	0.86013823
23	276.71	270	283	1	0.06784265	0.176	0.86013823
24	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
25	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
26	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
27	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
28	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
29	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
30	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
31	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
32	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
33	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
34	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
35	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
36	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
37	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
38	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
39	113431.6	110592	116271	1	0.07224428	0.295	0.76780776
40	108.6	106	112	1	0.07943447	0.232	0.81671774
41	108.6	106	112	1	0.07943447	0.232	0.81671774
42	108.6	106	112	1	0.07943447	0.232	0.81671774
43	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
44	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
45	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
46	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
47	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
48	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
49	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
50	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
51	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
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55	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
56	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
57	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
58	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
59	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
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3	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
4	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
5	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
6	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
7	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
8	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
9	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
10	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
11	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
12	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
13	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
14	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
15	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
16	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
17	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
18	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
19	6704.36	6501	6907	1	0.08739757	0.333	0.73887466
20	2339.63	2265	2414	1	0.09191463	0.342	0.73253296
21	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
22	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
23	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
24	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
25	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
26	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
27	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
28	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
29	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
30	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
31	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
32	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
33	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
34	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
35	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
36	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
37	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
38	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
39	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
40	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
41	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
42	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
43	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
44	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
45	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
46	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
47	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
48	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
49	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
50	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
51	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
52	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
53	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
54	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
55	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
56	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
57	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
58	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
59	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
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3	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
4	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
5	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
6	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
7	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
8	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
9	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
10	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
11	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
12	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
13	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
14	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
15	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
16	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
17	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
18	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
19	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
20	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
21	4477.91	4335	4621	1	0.0921731	0.246	0.80583733
22	4486.82	4343	4631	1	0.0926318	0.247	0.8051075
23	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
24	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
25	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
26	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
27	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
28	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
29	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
30	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
31	2329.79	2253	2406	1	0.09478933	0.352	0.72478177
32	334.44	323	346	1	0.09923787	0.32	0.7490803
33	334.44	323	346	1	0.09923787	0.32	0.7490803
34	334.44	323	346	1	0.09923787	0.32	0.7490803
35	334.44	323	346	1	0.09923787	0.32	0.7490803
36	334.44	323	346	1	0.09923787	0.32	0.7490803
37	334.44	323	346	1	0.09923787	0.32	0.7490803
38	334.44	323	346	1	0.09923787	0.32	0.7490803
39	334.44	323	346	1	0.09923787	0.32	0.7490803
40	1403.77	1354	1454	1	0.10279953	0.361	0.71802608
41	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
42	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
43	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
44	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
45	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
46	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
47	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
48	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
49	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
50	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
51	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
52	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
53	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
54	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
55	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
56	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
57	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
58	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
59	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
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3	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
4	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
5	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
6	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
7	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
8	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
9	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
11	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
12	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
13	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
14	10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
15	214.69	207	223	1	0.10741294	0.271	0.78662955
16	214.69	207	223	1	0.10741294	0.271	0.78662955
17	214.69	207	223	1	0.10741294	0.271	0.78662955
18	214.69	207	223	1	0.10741294	0.271	0.78662955
19	214.69	207	223	1	0.10741294	0.271	0.78662955
20	214.69	207	223	1	0.10741294	0.271	0.78662955
21	214.69	207	223	1	0.10741294	0.271	0.78662955
22	214.69	207	223	1	0.10741294	0.271	0.78662955
23	214.69	207	223	1	0.10741294	0.271	0.78662955
24	214.69	207	223	1	0.10741294	0.271	0.78662955
25	214.69	207	223	1	0.10741294	0.271	0.78662955
26	214.69	207	223	1	0.10741294	0.271	0.78662955
27	214.69	207	223	1	0.10741294	0.271	0.78662955
28	214.69	207	223	1	0.10741294	0.271	0.78662955
29	214.69	207	223	1	0.10741294	0.271	0.78662955
30	214.69	207	223	1	0.10741294	0.271	0.78662955
31	214.69	207	223	1	0.10741294	0.271	0.78662955
32	214.69	207	223	1	0.10741294	0.271	0.78662955
33	214.69	207	223	1	0.10741294	0.271	0.78662955
34	214.69	207	223	1	0.10741294	0.271	0.78662955
35	214.69	207	223	1	0.10741294	0.271	0.78662955
36	214.69	207	223	1	0.10741294	0.271	0.78662955
37	214.69	207	223	1	0.10741294	0.271	0.78662955
38	214.69	207	223	1	0.10741294	0.271	0.78662955
39	214.69	207	223	1	0.10741294	0.271	0.78662955
40	214.69	207	223	1	0.10741294	0.271	0.78662955
41	214.69	207	223	1	0.10741294	0.271	0.78662955
42	214.69	207	223	1	0.10741294	0.271	0.78662955
43	214.69	207	223	1	0.10741294	0.271	0.78662955
44	214.69	207	223	1	0.10741294	0.271	0.78662955
45	214.69	207	223	1	0.10741294	0.271	0.78662955
46	214.69	207	223	1	0.10741294	0.271	0.78662955
47	214.69	207	223	1	0.10741294	0.271	0.78662955
48	214.69	207	223	1	0.10741294	0.271	0.78662955
49	214.69	207	223	1	0.10741294	0.271	0.78662955
50	214.69	207	223	1	0.10741294	0.271	0.78662955
51	214.69	207	223	1	0.10741294	0.271	0.78662955
52	214.69	207	223	1	0.10741294	0.271	0.78662955
53	214.69	207	223	1	0.10741294	0.271	0.78662955
54	214.69	207	223	1	0.10741294	0.271	0.78662955
55	44428.58	42728	46130	1.001	0.1105235	0.478	0.63249088
56	1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204
57	1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204
58	1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204
59	1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204
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3	3216.18	3080	3352	1.001	0.1220918	0.451	0.65179224
4	128.52	123	134	1	0.12357469	0.325	0.74501213
5	1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
6	1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
7	1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
8	1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
9	1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
10	1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
11	298.83	286	312	1	0.12553088	0.435	0.66325801
12	298.83	286	312	1	0.12553088	0.435	0.66325801
13	298.83	286	312	1	0.12553088	0.435	0.66325801
14	298.83	286	312	1	0.12553088	0.435	0.66325801
15	298.83	286	312	1	0.12553088	0.435	0.66325801
16	298.83	286	312	1	0.12553088	0.435	0.66325801
17	298.83	286	312	1	0.12553088	0.435	0.66325801
18	298.83	286	312	1	0.12553088	0.435	0.66325801
19	298.83	286	312	1	0.12553088	0.435	0.66325801
20	102.99	99	108	1	0.12553088	0.364	0.71579102
21	102.99	99	108	1	0.12553088	0.364	0.71579102
22	102.99	99	108	1	0.12553088	0.364	0.71579102
23	102.99	99	108	1	0.12553088	0.364	0.71579102
24	102.99	99	108	1	0.12553088	0.364	0.71579102
25	102.99	99	108	1	0.12553088	0.364	0.71579102
26	102.99	99	108	1	0.12553088	0.364	0.71579102
27	300.48	287	314	1.001	0.12971382	0.437	0.662293
28	298.21	285	312	1.001	0.13058411	0.447	0.65469903
29	298.21	285	312	1.001	0.13058411	0.447	0.65469903
30	298.21	285	312	1.001	0.13058411	0.447	0.65469903
31	298.21	285	312	1.001	0.13058411	0.447	0.65469903
32	298.21	285	312	1.001	0.13058411	0.447	0.65469903
33	298.21	285	312	1.001	0.13058411	0.447	0.65469903
34	298.21	285	312	1.001	0.13058411	0.447	0.65469903
35	298.21	285	312	1.001	0.13058411	0.447	0.65469903
36	298.21	285	312	1.001	0.13058411	0.447	0.65469903
37	298.21	285	312	1.001	0.13058411	0.447	0.65469903
38	298.21	285	312	1.001	0.13058411	0.447	0.65469903
39	298.21	285	312	1.001	0.13058411	0.447	0.65469903
40	298.21	285	312	1.001	0.13058411	0.447	0.65469903
41	298.21	285	312	1.001	0.13058411	0.447	0.65469903
42	298.21	285	312	1.001	0.13058411	0.447	0.65469903
43	298.21	285	312	1.001	0.13058411	0.447	0.65469903
44	298.21	285	312	1.001	0.13058411	0.447	0.65469903
45	298.21	285	312	1.001	0.13058411	0.447	0.65469903
46	298.21	285	312	1.001	0.13058411	0.447	0.65469903
47	298.21	285	312	1.001	0.13058411	0.447	0.65469903
48	298.21	285	312	1.001	0.13058411	0.447	0.65469903
49	298.21	285	312	1.001	0.13058411	0.447	0.65469903
50	298.21	285	312	1.001	0.13058411	0.447	0.65469903
51	298.21	285	312	1.001	0.13058411	0.447	0.65469903
52	298.21	285	312	1.001	0.13058411	0.447	0.65469903
53	298.21	285	312	1.001	0.13058411	0.447	0.65469903
54	298.21	285	312	1.001	0.13058411	0.447	0.65469903
55	298.21	285	312	1.001	0.13058411	0.447	0.65469903
56	298.21	285	312	1.001	0.13058411	0.447	0.65469903
57	298.21	285	312	1.001	0.13058411	0.447	0.65469903
58	298.21	285	312	1.001	0.13058411	0.447	0.65469903
59	298.21	285	312	1.001	0.13058411	0.447	0.65469903
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3	298.21	285	312	1.001	0.13058411	0.447	0.65469903
4	298.21	285	312	1.001	0.13058411	0.447	0.65469903
5	298.21	285	312	1.001	0.13058411	0.447	0.65469903
6	298.21	285	312	1.001	0.13058411	0.447	0.65469903
7	52297.91	49827	54769	1.001	0.13643182	0.577	0.56423435
8	52297.91	49827	54769	1.001	0.13643182	0.577	0.56423435
9							
10	333.04	317	349	1.001	0.1387442	0.455	0.649012
11	333.04	317	349	1.001	0.1387442	0.455	0.649012
12	333.04	317	349	1.001	0.1387442	0.455	0.649012
13	333.04	317	349	1.001	0.1387442	0.455	0.649012
14	333.04	317	349	1.001	0.1387442	0.455	0.649012
15	333.04	317	349	1.001	0.1387442	0.455	0.649012
16	333.04	317	349	1.001	0.1387442	0.455	0.649012
17	333.04	317	349	1.001	0.1387442	0.455	0.649012
18	333.04	317	349	1.001	0.1387442	0.455	0.649012
19	333.04	317	349	1.001	0.1387442	0.455	0.649012
20							
21	72.37	69	76	1	0.13940306	0.36	0.71890701
22	72.37	69	76	1	0.13940306	0.36	0.71890701
23	72.37	69	76	1	0.13940306	0.36	0.71890701
24	72.37	69	76	1	0.13940306	0.36	0.71890701
25	72.37	69	76	1	0.13940306	0.36	0.71890701
26	72.37	69	76	1	0.13940306	0.36	0.71890701
27	72.37	69	76	1	0.13940306	0.36	0.71890701
28	72.37	69	76	1	0.13940306	0.36	0.71890701
29	72.37	69	76	1	0.13940306	0.36	0.71890701
30	72.37	69	76	1	0.13940306	0.36	0.71890701
31	72.37	69	76	1	0.13940306	0.36	0.71890701
32	72.37	69	76	1	0.13940306	0.36	0.71890701
33	72.37	69	76	1	0.13940306	0.36	0.71890701
34	72.37	69	76	1	0.13940306	0.36	0.71890701
35	72.37	69	76	1	0.13940306	0.36	0.71890701
36	72.37	69	76	1	0.13940306	0.36	0.71890701
37	72.37	69	76	1	0.13940306	0.36	0.71890701
38	72.37	69	76	1	0.13940306	0.36	0.71890701
39	72.37	69	76	1	0.13940306	0.36	0.71890701
40							
41	81.89	78	86	1	0.14086254	0.079	0.93685001
42	81.89	78	86	1	0.14086254	0.079	0.93685001
43	81.89	78	86	1	0.14086254	0.079	0.93685001
44	81.89	78	86	1	0.14086254	0.079	0.93685001
45	81.89	78	86	1	0.14086254	0.079	0.93685001
46	81.89	78	86	1	0.14086254	0.079	0.93685001
47	81.89	78	86	1	0.14086254	0.079	0.93685001
48	81.89	78	86	1	0.14086254	0.079	0.93685001
49	81.89	78	86	1	0.14086254	0.079	0.93685001
50	81.89	78	86	1	0.14086254	0.079	0.93685001
51	81.07	77	85	1	0.1426044	0.082	0.93448171
52	81.07	77	85	1	0.1426044	0.082	0.93448171
53	81.07	77	85	1	0.1426044	0.082	0.93448171
54	81.07	77	85	1	0.1426044	0.082	0.93448171
55	81.07	77	85	1	0.1426044	0.082	0.93448171
56	81.07	77	85	1	0.1426044	0.082	0.93448171
57	81.07	77	85	1	0.1426044	0.082	0.93448171
58	81.07	77	85	1	0.1426044	0.082	0.93448171
59	81.07	77	85	1	0.1426044	0.082	0.93448171
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3	81.07	77	85	1	0.1426044	0.082	0.93448171
4	81.07	77	85	1	0.1426044	0.082	0.93448171
5	81.07	77	85	1	0.1426044	0.082	0.93448171
6	81.07	77	85	1	0.1426044	0.082	0.93448171
7	81.07	77	85	1	0.1426044	0.082	0.93448171
8	81.07	77	85	1	0.1426044	0.082	0.93448171
9	81.07	77	85	1	0.1426044	0.082	0.93448171
10	81.07	77	85	1	0.1426044	0.082	0.93448171
11	81.07	77	85	1	0.1426044	0.082	0.93448171
12	81.07	77	85	1	0.1426044	0.082	0.93448171
13	81.07	77	85	1	0.1426044	0.082	0.93448171
14	81.07	77	85	1	0.1426044	0.082	0.93448171
15	156.14	148	164	1	0.14809864	0.406	0.68495341
16	156.14	148	164	1	0.14809864	0.406	0.68495341
17							
18	7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
19	7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
20	7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
21	7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
22	7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
23	71.21	67	75	1	0.1627295	0.377	0.70593412
24							
25	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
26	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
27	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
28	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
29	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
30	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
31	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
32	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
33	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
34	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
35	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
36	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
37	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
38	10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
39	10349.39	9762	10937	1.001	0.16396841	0.604	0.54602043
40							
41	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
42	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
43	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
44	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
45	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
46	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
47	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
48	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
49	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
50	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
51	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
52	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
53	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
54	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
55	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
56	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
57	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
58	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
59	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
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3	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
4	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
5	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
6	6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
7	339.39	319	360	1.001	0.17444048	0.649	0.51662146
8	339.39	319	360	1.001	0.17444048	0.649	0.51662146
9	339.39	319	360	1.001	0.17444048	0.649	0.51662146
10	339.39	319	360	1.001	0.17444048	0.649	0.51662146
11	339.39	319	360	1.001	0.17444048	0.649	0.51662146
12	339.39	319	360	1.001	0.17444048	0.649	0.51662146
13	339.39	319	360	1.001	0.17444048	0.649	0.51662146
14	281.14	264	298	1.001	0.1747744	0.534	0.59319238
15	281.14	264	298	1.001	0.1747744	0.534	0.59319238
16	338.78	318	360	1.001	0.17897014	0.659	0.50981709
17	338.78	318	360	1.001	0.17897014	0.659	0.50981709
18	338.78	318	360	1.001	0.17897014	0.659	0.50981709
19	338.78	318	360	1.001	0.17897014	0.659	0.50981709
20	338.78	318	360	1.001	0.17897014	0.659	0.50981709
21	338.78	318	360	1.001	0.17897014	0.659	0.50981709
22	338.78	318	360	1.001	0.17897014	0.659	0.50981709
23	338.78	318	360	1.001	0.17897014	0.659	0.50981709
24	338.78	318	360	1.001	0.17897014	0.659	0.50981709
25	338.78	318	360	1.001	0.17897014	0.659	0.50981709
26	338.78	318	360	1.001	0.17897014	0.659	0.50981709
27	338.78	318	360	1.001	0.17897014	0.659	0.50981709
28	338.78	318	360	1.001	0.17897014	0.659	0.50981709
29	338.78	318	360	1.001	0.17897014	0.659	0.50981709
30	338.78	318	360	1.001	0.17897014	0.659	0.50981709
31	338.78	318	360	1.001	0.17897014	0.659	0.50981709
32	338.78	318	360	1.001	0.17897014	0.659	0.50981709
33	338.78	318	360	1.001	0.17897014	0.659	0.50981709
34	338.78	318	360	1.001	0.17897014	0.659	0.50981709
35	338.78	318	360	1.001	0.17897014	0.659	0.50981709
36	338.78	318	360	1.001	0.17897014	0.659	0.50981709
37	338.78	318	360	1.001	0.17897014	0.659	0.50981709
38	338.78	318	360	1.001	0.17897014	0.659	0.50981709
39	338.78	318	360	1.001	0.17897014	0.659	0.50981709
40	338.78	318	360	1.001	0.17897014	0.659	0.50981709
41	338.78	318	360	1.001	0.17897014	0.659	0.50981709
42	338.78	318	360	1.001	0.17897014	0.659	0.50981709
43	338.78	318	360	1.001	0.17897014	0.659	0.50981709
44	338.78	318	360	1.001	0.17897014	0.659	0.50981709
45	338.78	318	360	1.001	0.17897014	0.659	0.50981709
46	338.78	318	360	1.001	0.17897014	0.659	0.50981709
47	338.78	318	360	1.001	0.17897014	0.659	0.50981709
48	338.78	318	360	1.001	0.17897014	0.659	0.50981709
49	338.78	318	360	1.001	0.17897014	0.659	0.50981709
50	338.78	318	360	1.001	0.17897014	0.659	0.50981709
51	338.78	318	360	1.001	0.17897014	0.659	0.50981709
52	338.78	318	360	1.001	0.17897014	0.659	0.50981709
53	338.78	318	360	1.001	0.17897014	0.659	0.50981709
54	338.78	318	360	1.001	0.17897014	0.659	0.50981709
55	338.78	318	360	1.001	0.17897014	0.659	0.50981709
56	338.78	318	360	1.001	0.17897014	0.659	0.50981709
57	338.78	318	360	1.001	0.17897014	0.659	0.50981709
58	338.78	318	360	1.001	0.17897014	0.659	0.50981709
59	338.78	318	360	1.001	0.17897014	0.659	0.50981709
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3	338.78	318	360	1.001	0.17897014	0.659	0.50981709
4	348.16	326	370	1.001	0.18265331	0.625	0.53224409
5	348.16	326	370	1.001	0.18265331	0.625	0.53224409
6	348.16	326	370	1.001	0.18265331	0.625	0.53224409
7	348.16	326	370	1.001	0.18265331	0.625	0.53224409
8	253.77	237	271	1.001	0.19340579	0.6	0.54872062
9	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
10	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
11	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
12	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
13	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
14	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
15	6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
16	6097.27	5675	6519	1.001	0.20003028	0.772	0.43985612
17	321.48	299	344	1.001	0.20226308	0.686	0.49279709
18	321.48	299	344	1.001	0.20226308	0.686	0.49279709
19	321.48	299	344	1.001	0.20226308	0.686	0.49279709
20	321.48	299	344	1.001	0.20226308	0.686	0.49279709
21	321.48	299	344	1.001	0.20226308	0.686	0.49279709
22	321.48	299	344	1.001	0.20226308	0.686	0.49279709
23	321.48	299	344	1.001	0.20226308	0.686	0.49279709
24	321.48	299	344	1.001	0.20226308	0.686	0.49279709
25	321.48	299	344	1.001	0.20226308	0.686	0.49279709
26	321.48	299	344	1.001	0.20226308	0.686	0.49279709
27	321.48	299	344	1.001	0.20226308	0.686	0.49279709
28	321.48	299	344	1.001	0.20226308	0.686	0.49279709
29	321.48	299	344	1.001	0.20226308	0.686	0.49279709
30	321.48	299	344	1.001	0.20226308	0.686	0.49279709
31	8828.39	8202	9455	1.001	0.20510171	0.788	0.43096626
32	8828.39	8202	9455	1.001	0.20510171	0.788	0.43096626
33	320.81	298	344	1.001	0.20709623	0.695	0.48723533
34	320.81	298	344	1.001	0.20709623	0.695	0.48723533
35	320.81	298	344	1.001	0.20709623	0.695	0.48723533
36	320.81	298	344	1.001	0.20709623	0.695	0.48723533
37	320.81	298	344	1.001	0.20709623	0.695	0.48723533
38	320.81	298	344	1.001	0.20709623	0.695	0.48723533
39	320.81	298	344	1.001	0.20709623	0.695	0.48723533
40	320.81	298	344	1.001	0.20709623	0.695	0.48723533
41	320.81	298	344	1.001	0.20709623	0.695	0.48723533
42	320.81	298	344	1.001	0.20709623	0.695	0.48723533
43	320.81	298	344	1.001	0.20709623	0.695	0.48723533
44	320.81	298	344	1.001	0.20709623	0.695	0.48723533
45	320.81	298	344	1.001	0.20709623	0.695	0.48723533
46	320.81	298	344	1.001	0.20709623	0.695	0.48723533
47	320.81	298	344	1.001	0.20709623	0.695	0.48723533
48	320.81	298	344	1.001	0.20709623	0.695	0.48723533
49	320.81	298	344	1.001	0.20709623	0.695	0.48723533
50	320.81	298	344	1.001	0.20709623	0.695	0.48723533
51	320.81	298	344	1.001	0.20709623	0.695	0.48723533
52	320.81	298	344	1.001	0.20709623	0.695	0.48723533
53	320.81	298	344	1.001	0.20709623	0.695	0.48723533
54	320.81	298	344	1.001	0.20709623	0.695	0.48723533
55	320.81	298	344	1.001	0.20709623	0.695	0.48723533
56	320.81	298	344	1.001	0.20709623	0.695	0.48723533
57	320.81	298	344	1.001	0.20709623	0.695	0.48723533
58	320.81	298	344	1.001	0.20709623	0.695	0.48723533
59	320.81	298	344	1.001	0.20709623	0.695	0.48723533
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3	320.81	298	344	1.001	0.20709623	0.695	0.48723533
4	320.81	298	344	1.001	0.20709623	0.695	0.48723533
5	320.81	298	344	1.001	0.20709623	0.695	0.48723533
6	320.81	298	344	1.001	0.20709623	0.695	0.48723533
7	55.15	51	59	1	0.21021771	0.471	0.63787349
8	156.59	145	168	1.001	0.21240833	0.554	0.57976616
9	52.81	49	57	1	0.21818017	0.461	0.64493481
10	236.49	217	256	1.001	0.23844877	0.706	0.48005851
11	236.49	217	256	1.001	0.23844877	0.706	0.48005851
12	236.49	217	256	1.001	0.23844877	0.706	0.48005851
13	236.49	217	256	1.001	0.23844877	0.706	0.48005851
14	236.49	217	256	1.001	0.23844877	0.706	0.48005851
15	236.49	217	256	1.001	0.23844877	0.706	0.48005851
16	236.49	217	256	1.001	0.23844877	0.706	0.48005851
17	236.49	217	256	1.001	0.23844877	0.706	0.48005851
18	236.49	217	256	1.001	0.23844877	0.706	0.48005851
19	236.49	217	256	1.001	0.23844877	0.706	0.48005851
20	236.49	217	256	1.001	0.23844877	0.706	0.48005851
21	236.49	217	256	1.001	0.23844877	0.706	0.48005851
22	160.2	147	174	1.001	0.24327115	0.623	0.53310376
23	5602.86	5103	6102	1.001	0.25793654	1.016	0.30978276
24	223.27	203	243	1.001	0.25947659	0.91	0.36304605
25	223.27	203	243	1.001	0.25947659	0.91	0.36304605
26	223.27	203	243	1.001	0.25947659	0.91	0.36304605
27	581.23	528	634	1.001	0.26394491	0.982	0.32633394
28	581.23	528	634	1.001	0.26394491	0.982	0.32633394
29	581.23	528	634	1.001	0.26394491	0.982	0.32633394
30	581.23	528	634	1.001	0.26394491	0.982	0.32633394
31	581.23	528	634	1.001	0.26394491	0.982	0.32633394
32	581.23	528	634	1.001	0.26394491	0.982	0.32633394
33	581.23	528	634	1.001	0.26394491	0.982	0.32633394
34	581.23	528	634	1.001	0.26394491	0.982	0.32633394
35	581.23	528	634	1.001	0.26394491	0.982	0.32633394
36	581.23	528	634	1.001	0.26394491	0.982	0.32633394
37	581.23	528	634	1.001	0.26394491	0.982	0.32633394
38	581.23	528	634	1.001	0.26394491	0.982	0.32633394
39	581.23	528	634	1.001	0.26394491	0.982	0.32633394
40	487.58	443	532	1.001	0.26411955	0.75	0.45334014
41	157.14	142	172	1.001	0.27651764	0.81	0.41797895
42	157.14	142	172	1.001	0.27651764	0.81	0.41797895
43	157.14	142	172	1.001	0.27651764	0.81	0.41797895
44	651.94	589	716	1.001	0.28169195	1.071	0.28425623
45	651.94	589	716	1.001	0.28169195	1.071	0.28425623
46	651.94	589	716	1.001	0.28169195	1.071	0.28425623
47	218.97	197	241	1.001	0.29083752	0.969	0.33245343
48	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
49	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
50	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
51	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
52	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
53	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
54	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
55	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
56	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
57	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
58	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
59	2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
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3	3282.22	2947	3618	1.001	0.29594535	1.093	0.27458295
4	3282.22	2947	3618	1.001	0.29594535	1.093	0.27458295
5	3282.22	2947	3618	1.001	0.29594535	1.093	0.27458295
6	3286.22	2950	3622	1.001	0.29607159	1.093	0.27441971
7	3286.22	2950	3622	1.001	0.29607159	1.093	0.27441971
8	3286.22	2950	3622	1.001	0.29607159	1.093	0.27441971
9	198.08	178	219	1.001	0.29905363	0.946	0.34430522
10	4349.45	3882	4816	1.001	0.31103527	1.15	0.25017723
11	4349.45	3882	4816	1.001	0.31103527	1.15	0.25017723
12	69.16	62	77	1.001	0.31259023	0.807	0.41980832
13	68.66	61	76	1.001	0.31719018	0.79	0.42972192
14	68.66	61	76	1.001	0.31719018	0.79	0.42972192
15	68.66	61	76	1.001	0.31719018	0.79	0.42972192
16	68.66	61	76	1.001	0.31719018	0.79	0.42972192
17	68.66	61	76	1.001	0.31719018	0.79	0.42972192
18	68.66	61	76	1.001	0.31719018	0.79	0.42972192
19	68.66	61	76	1.001	0.31719018	0.79	0.42972192
20	68.66	61	76	1.001	0.31719018	0.79	0.42972192
21	81.9	73	91	1.001	0.31797008	0.794	0.42711485
22	142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
23	142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
24	142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
25	142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
26	114.05	101	127	1.001	0.3304732	0.717	0.47345655
27	114.05	101	127	1.001	0.3304732	0.717	0.47345655
28	114.05	101	127	1.001	0.3304732	0.717	0.47345655
29	114.05	101	127	1.001	0.3304732	0.717	0.47345655
30	114.05	101	127	1.001	0.3304732	0.717	0.47345655
31	114.05	101	127	1.001	0.3304732	0.717	0.47345655
32	114.05	101	127	1.001	0.3304732	0.717	0.47345655
33	114.05	101	127	1.001	0.3304732	0.717	0.47345655
34	114.05	101	127	1.001	0.3304732	0.717	0.47345655
35	114.05	101	127	1.001	0.3304732	0.717	0.47345655
36	114.05	101	127	1.001	0.3304732	0.717	0.47345655
37	114.05	101	127	1.001	0.3304732	0.717	0.47345655
38	8886.21	7869	9903	1.001	0.33168533	1.106	0.26867058
39	8886.21	7869	9903	1.001	0.33168533	1.106	0.26867058
40	230.53	204	257	1.001	0.33319921	1.097	0.27269201
41	230.53	204	257	1.001	0.33319921	1.097	0.27269201
42	230.53	204	257	1.001	0.33319921	1.097	0.27269201
43	237.82	210	266	1.001	0.34103692	1.105	0.26908289
44	237.82	210	266	1.001	0.34103692	1.105	0.26908289
45	237.82	210	266	1.001	0.34103692	1.105	0.26908289
46	237.82	210	266	1.001	0.34103692	1.105	0.26908289
47	237.82	210	266	1.001	0.34103692	1.105	0.26908289
48	237.82	210	266	1.001	0.34103692	1.105	0.26908289
49	237.82	210	266	1.001	0.34103692	1.105	0.26908289
50	237.82	210	266	1.001	0.34103692	1.105	0.26908289
51	237.82	210	266	1.001	0.34103692	1.105	0.26908289
52	169.94	150	190	1.001	0.34103692	0.99	0.32201644
53	169.94	150	190	1.001	0.34103692	0.99	0.32201644
54	169.94	150	190	1.001	0.34103692	0.99	0.32201644
55	79.74	70	89	1.001	0.34645041	0.843	0.39933402
56	79.74	70	89	1.001	0.34645041	0.843	0.39933402
57	221.45	195	248	1.001	0.346866	1.142	0.25331815
58	221.45	195	248	1.001	0.346866	1.142	0.25331815
59	221.45	195	248	1.001	0.346866	1.142	0.25331815
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3	221.45	195	248	1.001	0.346866	1.142	0.25331815
4	221.45	195	248	1.001	0.346866	1.142	0.25331815
5	221.45	195	248	1.001	0.346866	1.142	0.25331815
6	221.45	195	248	1.001	0.346866	1.142	0.25331815
7	221.45	195	248	1.001	0.346866	1.142	0.25331815
8	221.45	195	248	1.001	0.346866	1.142	0.25331815
9	221.45	195	248	1.001	0.346866	1.142	0.25331815
10	221.45	195	248	1.001	0.346866	1.142	0.25331815
11	112.25	99	126	1.001	0.3479233	0.723	0.46958971
12	112.25	99	126	1.001	0.3479233	0.723	0.46958971
13	112.25	99	126	1.001	0.3479233	0.723	0.46958971
14	112.25	99	126	1.001	0.3479233	0.723	0.46958971
15	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
16	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
17	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
18	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
19	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
20	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
21	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
22	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
23	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
24	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
25	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
26	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
27	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
28	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
29	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
30	1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
31	54.03	47	61	1	0.37614849	0.647	0.51791658
32	54.03	47	61	1	0.37614849	0.647	0.51791658
33	54.03	47	61	1	0.37614849	0.647	0.51791658
34	54.03	47	61	1	0.37614849	0.647	0.51791658
35	54.03	47	61	1	0.37614849	0.647	0.51791658
36	54.03	47	61	1	0.37614849	0.647	0.51791658
37	54.03	47	61	1	0.37614849	0.647	0.51791658
38	54.03	47	61	1	0.37614849	0.647	0.51791658
39	54.03	47	61	1	0.37614849	0.647	0.51791658
40	54.03	47	61	1	0.37614849	0.647	0.51791658
41	54.03	47	61	1	0.37614849	0.647	0.51791658
42	54.03	47	61	1	0.37614849	0.647	0.51791658
43	54.03	47	61	1	0.37614849	0.647	0.51791658
44	54.03	47	61	1	0.37614849	0.647	0.51791658
45	54.03	47	61	1	0.37614849	0.647	0.51791658
46	54.03	47	61	1	0.37614849	0.647	0.51791658
47	91.51	80	104	1.001	0.37851162	0.908	0.36403319
48	91.51	80	104	1.001	0.37851162	0.908	0.36403319
49	91.51	80	104	1.001	0.37851162	0.908	0.36403319
50	91.51	80	104	1.001	0.37851162	0.908	0.36403319
51	91.51	80	104	1.001	0.37851162	0.908	0.36403319
52	91.51	80	104	1.001	0.37851162	0.908	0.36403319
53	91.51	80	104	1.001	0.37851162	0.908	0.36403319
54	91.51	80	104	1.001	0.37851162	0.908	0.36403319
55	91.51	80	104	1.001	0.37851162	0.908	0.36403319
56	91.51	80	104	1.001	0.37851162	0.908	0.36403319
57	91.51	80	104	1.001	0.37851162	0.908	0.36403319
58	91.51	80	104	1.001	0.37851162	0.908	0.36403319
59	91.51	80	104	1.001	0.37851162	0.908	0.36403319
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3	91.51	80	104	1.001	0.37851162	0.908	0.36403319
4	91.51	80	104	1.001	0.37851162	0.908	0.36403319
5	91.51	80	104	1.001	0.37851162	0.908	0.36403319
6	91.51	80	104	1.001	0.37851162	0.908	0.36403319
7	91.51	80	104	1.001	0.37851162	0.908	0.36403319
8	91.51	80	104	1.001	0.37851162	0.908	0.36403319
9	91.51	80	104	1.001	0.37851162	0.908	0.36403319
10	91.51	80	104	1.001	0.37851162	0.908	0.36403319
11	91.51	80	104	1.001	0.37851162	0.908	0.36403319
12	91.51	80	104	1.001	0.37851162	0.908	0.36403319
13	83.91	73	95	1.001	0.38003105	0.793	0.42769265
14	83.91	73	95	1.001	0.38003105	0.793	0.42769265
15	83.91	73	95	1.001	0.38003105	0.793	0.42769265
16	83.91	73	95	1.001	0.38003105	0.793	0.42769265
17	83.91	73	95	1.001	0.38003105	0.793	0.42769265
18	83.91	73	95	1.001	0.38003105	0.793	0.42769265
19	72.27	63	82	1.001	0.38027208	0.89	0.37337613
20	122.03	106	138	1.001	0.380604	0.815	0.41490049
21	122.03	106	138	1.001	0.380604	0.815	0.41490049
22	122.03	106	138	1.001	0.380604	0.815	0.41490049
23	122.03	106	138	1.001	0.380604	0.815	0.41490049
24	122.03	106	138	1.001	0.380604	0.815	0.41490049
25	122.03	106	138	1.001	0.380604	0.815	0.41490049
26	122.03	106	138	1.001	0.380604	0.815	0.41490049
27	122.03	106	138	1.001	0.380604	0.815	0.41490049
28	259.73	225	295	1.001	0.39078995	1.2	0.23033198
29	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
30	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
31	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
32	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
33	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
34	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
35	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
36	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
37	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
38	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
39	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
40	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
41	3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
42	249.5	214	285	1.001	0.41335112	1.215	0.22435046
43	249.5	214	285	1.001	0.41335112	1.215	0.22435046
44	69.98	60	80	1.001	0.4150375	1.015	0.30994321
45	63.49	54	73	1	0.43493706	0.76	0.44723325
46	63.49	54	73	1	0.43493706	0.76	0.44723325
47	63.49	54	73	1	0.43493706	0.76	0.44723325
48	79.89	68	92	1.001	0.43609911	0.997	0.31868972
49	79.89	68	92	1.001	0.43609911	0.997	0.31868972
50	79.89	68	92	1.001	0.43609911	0.997	0.31868972
51	79.89	68	92	1.001	0.43609911	0.997	0.31868972
52	9348.17	7910	10787	1.002	0.44754409	1.79	0.07352049
53	67.43	57	78	1.001	0.4525122	1.045	0.29613926
54	67.43	57	78	1.001	0.4525122	1.045	0.29613926
55	67.43	57	78	1.001	0.4525122	1.045	0.29613926
56	67.43	57	78	1.001	0.4525122	1.045	0.29613926
57	67.43	57	78	1.001	0.4525122	1.045	0.29613926
58	67.43	57	78	1.001	0.4525122	1.045	0.29613926
59	67.43	57	78	1.001	0.4525122	1.045	0.29613926
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3	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
4	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
5	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
6	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
7	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
8	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
9	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
10	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
11	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
12	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
13	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
14	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
15	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
16	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
17	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
18	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
19	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
20	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
21	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
22	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
23	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
24	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
25	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
26	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
27	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
28	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
29	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
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31	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
32	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
33	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
34	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
35	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
36	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
37	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
38	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
39	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
40	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
41	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
42	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
43	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
44	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
45	12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
46	12991.21	10909	15073	1.002	0.46644773	1.612	0.1068821
47	347.85	292	404	1.002	0.46838692	1.537	0.12436711
48	347.85	292	404	1.002	0.46838692	1.537	0.12436711
49	347.85	292	404	1.002	0.46838692	1.537	0.12436711
50	347.85	292	404	1.002	0.46838692	1.537	0.12436711
51	65	54	76	1.001	0.49304001	0.947	0.34369062
52	65	54	76	1.001	0.49304001	0.947	0.34369062
53	65	54	76	1.001	0.49304001	0.947	0.34369062
54	65	54	76	1.001	0.49304001	0.947	0.34369062
55	65	54	76	1.001	0.49304001	0.947	0.34369062
56	65	54	76	1.001	0.49304001	0.947	0.34369062
57	65	54	76	1.001	0.49304001	0.947	0.34369062
58	65	54	76	1.001	0.49304001	0.947	0.34369062
59	65	54	76	1.001	0.49304001	0.947	0.34369062
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3	65	54	76	1.001	0.49304001	0.947	0.34369062
4	65	54	76	1.001	0.49304001	0.947	0.34369062
5	65	54	76	1.001	0.49304001	0.947	0.34369062
6	65	54	76	1.001	0.49304001	0.947	0.34369062
7	65	54	76	1.001	0.49304001	0.947	0.34369062
8	65	54	76	1.001	0.49304001	0.947	0.34369062
9	65	54	76	1.001	0.49304001	0.947	0.34369062
10	65	54	76	1.001	0.49304001	0.947	0.34369062
11	65	54	76	1.001	0.49304001	0.947	0.34369062
12	65	54	76	1.001	0.49304001	0.947	0.34369062
13	65	54	76	1.001	0.49304001	0.947	0.34369062
14	55.67	46	65	1.001	0.49880586	1.08	0.28008841
15	631.99	522	742	1.001	0.50736938	1.305	0.19192189
16	148.38	122	174	1.002	0.51220616	1.588	0.11236333
17	51.3	42	60	1.001	0.51457317	1.215	0.22453308
18	3130.67	2575	3686	1.002	0.51748364	1.818	0.06903456
19	3130.67	2575	3686	1.002	0.51748364	1.818	0.06903456
20	53.33	44	63	1.001	0.5178483	1.101	0.27100359
21	53.33	44	63	1.001	0.5178483	1.101	0.27100359
22	2865.44	2350	3380	1.002	0.52436249	1.813	0.06981196
23	197.1	161	233	1.002	0.53326927	1.552	0.12064702
24	197.1	161	233	1.002	0.53326927	1.552	0.12064702
25	197.1	161	233	1.002	0.53326927	1.552	0.12064702
26	197.1	161	233	1.002	0.53326927	1.552	0.12064702
27	197.1	161	233	1.002	0.53326927	1.552	0.12064702
28	458.01	373	543	1.002	0.54177657	1.723	0.08487894
29	27927.58	22677	33178	1.001	0.54899713	1.459	0.14448767
30	27927.58	22677	33178	1.001	0.54899713	1.459	0.14448767
31	73.92	60	88	1.001	0.55254102	1.099	0.27171185
32	73.92	60	88	1.001	0.55254102	1.099	0.27171185
33	73.92	60	88	1.001	0.55254102	1.099	0.27171185
34	73.92	60	88	1.001	0.55254102	1.099	0.27171185
35	73.92	60	88	1.001	0.55254102	1.099	0.27171185
36	73.92	60	88	1.001	0.55254102	1.099	0.27171185
37	73.92	60	88	1.001	0.55254102	1.099	0.27171185
38	73.92	60	88	1.001	0.55254102	1.099	0.27171185
39	73.92	60	88	1.001	0.55254102	1.099	0.27171185
40	73.92	60	88	1.001	0.55254102	1.099	0.27171185
41	73.92	60	88	1.001	0.55254102	1.099	0.27171185
42	73.92	60	88	1.001	0.55254102	1.099	0.27171185
43	73.92	60	88	1.001	0.55254102	1.099	0.27171185
44	73.92	60	88	1.001	0.55254102	1.099	0.27171185
45	73.92	60	88	1.001	0.55254102	1.099	0.27171185
46	73.92	60	88	1.001	0.55254102	1.099	0.27171185
47	73.92	60	88	1.001	0.55254102	1.099	0.27171185
48	73.92	60	88	1.001	0.55254102	1.099	0.27171185
49	73.92	60	88	1.001	0.55254102	1.099	0.27171185
50	73.92	60	88	1.001	0.55254102	1.099	0.27171185
51	73.92	60	88	1.001	0.55254102	1.099	0.27171185
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54	73.92	60	88	1.001	0.55254102	1.099	0.27171185
55	73.92	60	88	1.001	0.55254102	1.099	0.27171185
56	73.92	60	88	1.001	0.55254102	1.099	0.27171185
57	73.92	60	88	1.001	0.55254102	1.099	0.27171185
58	73.92	60	88	1.001	0.55254102	1.099	0.27171185
59	73.92	60	88	1.001	0.55254102	1.099	0.27171185
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3	73.92	60	88	1.001	0.55254102	1.099	0.27171185
4	73.92	60	88	1.001	0.55254102	1.099	0.27171185
5	73.92	60	88	1.001	0.55254102	1.099	0.27171185
6	73.92	60	88	1.001	0.55254102	1.099	0.27171185
7	73.92	60	88	1.001	0.55254102	1.099	0.27171185
8	73.92	60	88	1.001	0.55254102	1.099	0.27171185
9	73.92	60	88	1.001	0.55254102	1.099	0.27171185
10	73.92	60	88	1.001	0.55254102	1.099	0.27171185
11	73.92	60	88	1.001	0.55254102	1.099	0.27171185
12	73.92	60	88	1.001	0.55254102	1.099	0.27171185
13	73.92	60	88	1.001	0.55254102	1.099	0.27171185
14	73.92	60	88	1.001	0.55254102	1.099	0.27171185
15	73.92	60	88	1.001	0.55254102	1.099	0.27171185
16	73.92	60	88	1.001	0.55254102	1.099	0.27171185
17	73.92	60	88	1.001	0.55254102	1.099	0.27171185
18	73.92	60	88	1.001	0.55254102	1.099	0.27171185
19	73.92	60	88	1.001	0.55254102	1.099	0.27171185
20	73.92	60	88	1.001	0.55254102	1.099	0.27171185
21	73.92	60	88	1.001	0.55254102	1.099	0.27171185
22	73.92	60	88	1.001	0.55254102	1.099	0.27171185
23	73.92	60	88	1.001	0.55254102	1.099	0.27171185
24	73.92	60	88	1.001	0.55254102	1.099	0.27171185
25	73.92	60	88	1.001	0.55254102	1.099	0.27171185
26	73.92	60	88	1.001	0.55254102	1.099	0.27171185
27	73.92	60	88	1.001	0.55254102	1.099	0.27171185
28	73.92	60	88	1.001	0.55254102	1.099	0.27171185
29	73.92	60	88	1.001	0.55254102	1.099	0.27171185
30	73.92	60	88	1.001	0.55254102	1.099	0.27171185
31	73.92	60	88	1.001	0.55254102	1.099	0.27171185
32	151.17	122	180	1.001	0.56111576	1.54	0.12348132
33	336.41	270	403	1.002	0.57782043	1.731	0.08345349
34	336.41	270	403	1.002	0.57782043	1.731	0.08345349
35	336.41	270	403	1.002	0.57782043	1.731	0.08345349
36	343.18	275	411	1.002	0.57970678	1.735	0.08276887
37	343.18	275	411	1.002	0.57970678	1.735	0.08276887
38	343.18	275	411	1.002	0.57970678	1.735	0.08276887
39	138.5	111	166	1.002	0.58062356	1.705	0.08827572
40	190.44	152	228	1.002	0.5849625	1.712	0.08682214
41	190.44	152	228	1.002	0.5849625	1.712	0.08682214
42	190.44	152	228	1.002	0.5849625	1.712	0.08682214
43	190.44	152	228	1.002	0.5849625	1.712	0.08682214
44	190.44	152	228	1.002	0.5849625	1.712	0.08682214
45	190.44	152	228	1.002	0.5849625	1.712	0.08682214
46	190.44	152	228	1.002	0.5849625	1.712	0.08682214
47	190.44	152	228	1.002	0.5849625	1.712	0.08682214
48	190.44	152	228	1.002	0.5849625	1.712	0.08682214
49	190.44	152	228	1.002	0.5849625	1.712	0.08682214
50	190.44	152	228	1.002	0.5849625	1.712	0.08682214
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52	190.44	152	228	1.002	0.5849625	1.712	0.08682214
53	190.44	152	228	1.002	0.5849625	1.712	0.08682214
54	190.44	152	228	1.002	0.5849625	1.712	0.08682214
55	67.67	54	81	1.001	0.5849625	1.471	0.14133417
56	67.67	54	81	1.001	0.5849625	1.471	0.14133417
57	67.67	54	81	1.001	0.5849625	1.471	0.14133417
58	67.67	54	81	1.001	0.5849625	1.471	0.14133417
59	67.67	54	81	1.001	0.5849625	1.471	0.14133417
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2							
3	67.67	54	81	1.001	0.5849625	1.471	0.14133417
4	67.67	54	81	1.001	0.5849625	1.471	0.14133417
5	67.67	54	81	1.001	0.5849625	1.471	0.14133417
6	67.67	54	81	1.001	0.5849625	1.471	0.14133417
7	67.67	54	81	1.001	0.5849625	1.471	0.14133417
8	67.67	54	81	1.001	0.5849625	1.471	0.14133417
9	67.67	54	81	1.001	0.5849625	1.471	0.14133417
10	67.67	54	81	1.001	0.5849625	1.471	0.14133417
11	67.67	54	81	1.001	0.5849625	1.471	0.14133417
12	67.67	54	81	1.001	0.5849625	1.471	0.14133417
13	67.67	54	81	1.001	0.5849625	1.471	0.14133417
14	67.67	54	81	1.001	0.5849625	1.471	0.14133417
15	67.67	54	81	1.001	0.5849625	1.471	0.14133417
16	67.67	54	81	1.001	0.5849625	1.471	0.14133417
17	67.67	54	81	1.001	0.5849625	1.471	0.14133417
18	67.67	54	81	1.001	0.5849625	1.471	0.14133417
19	67.67	54	81	1.001	0.5849625	1.471	0.14133417
20	55.98	44	68	1.001	0.62803122	1.476	0.14006696
21	55.98	44	68	1.001	0.62803122	1.476	0.14006696
22	55.98	44	68	1.001	0.62803122	1.476	0.14006696
23	55.98	44	68	1.001	0.62803122	1.476	0.14006696
24	55.98	44	68	1.001	0.62803122	1.476	0.14006696
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30	55.98	44	68	1.001	0.62803122	1.476	0.14006696
31	55.98	44	68	1.001	0.62803122	1.476	0.14006696
32	55.98	44	68	1.001	0.62803122	1.476	0.14006696
33	55.98	44	68	1.001	0.62803122	1.476	0.14006696
34	55.98	44	68	1.001	0.62803122	1.476	0.14006696
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41	55.98	44	68	1.001	0.62803122	1.476	0.14006696
42	55.98	44	68	1.001	0.62803122	1.476	0.14006696
43	862.58	663	1062	1.003	0.67970299	2.254	0.02421726
44	861.57	662	1061	1.003	0.68052153	2.256	0.02408365
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53	129.01	98	160	1.001	0.70721825	1.667	0.09559944
54	129.01	98	160	1.001	0.70721825	1.667	0.09559944
55	129.01	98	160	1.001	0.70721825	1.667	0.09559944
56	129.01	98	160	1.001	0.70721825	1.667	0.09559944
57	127.88	97	159	1.001	0.71297011	1.697	0.08968646
58	127.88	97	159	1.001	0.71297011	1.697	0.08968646
59	127.88	97	159	1.001	0.71297011	1.697	0.08968646
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3	127.88	97	159	1.001	0.71297011	1.697	0.08968646
4	127.88	97	159	1.001	0.71297011	1.697	0.08968646
5	127.88	97	159	1.001	0.71297011	1.697	0.08968646
6	127.88	97	159	1.001	0.71297011	1.697	0.08968646
7	127.88	97	159	1.001	0.71297011	1.697	0.08968646
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24	127.88	97	159	1.001	0.71297011	1.697	0.08968646
25	127.88	97	159	1.001	0.71297011	1.697	0.08968646
26	316.13	234	398	1.003	0.7662599	2.333	0.01962831
27	623.47	448	799	1.002	0.83469677	2.31	0.02089101
28	623.47	448	799	1.002	0.83469677	2.31	0.02089101
29	247.1	172	322	1.003	0.90465212	2.733	0.0062736
30	247.1	172	322	1.003	0.90465212	2.733	0.0062736
31	247.1	172	322	1.003	0.90465212	2.733	0.0062736
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46	247.1	172	322	1.003	0.90465212	2.733	0.0062736
47	247.1	172	322	1.003	0.90465212	2.733	0.0062736
48	247.27	172	323	1.003	0.9091256	2.737	0.00620793
49	249.25	173	325	1.003	0.90966768	2.752	0.00592535
50	249.25	173	325	1.003	0.90966768	2.752	0.00592535
51	249.25	173	325	1.003	0.90966768	2.752	0.00592535
52	75.15	52	99	1.002	0.9289169	1.963	0.04960358
53	75.15	52	99	1.002	0.9289169	1.963	0.04960358
54	75.15	52	99	1.002	0.9289169	1.963	0.04960358
55	75.15	52	99	1.002	0.9289169	1.963	0.04960358
56	37670.73	25344	49997	1.003	0.98019729	2.724	0.00644433
57	59.03	36	82	1.002	1.187627	2.575	0.0100373
58	244.76	489	0	0.958	#NUM!	-2.636	NA
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178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
178.44	357	0	0.873	#NUM!	-3.119 NA
53.48	107	0	0	#NUM!	-5.87 NA
53.48	107	0	0	#NUM!	-5.87 NA
51.89	104	0	0	#NUM!	-5.91 NA
51.89	104	0	0	#NUM!	-5.91 NA

Do not distribute







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3	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
4	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
5	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
6	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
7	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
8	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
9	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
10	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
11	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
12	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
13	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
14	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
15	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
16	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
17	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
18	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
19	0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
20	0.99796172	0.1661	0.0774	0.1056	0.1056	TRUE	0.8728
21	0.99796172	0.1661	0.0774	0.1056	0.1056	TRUE	0.8728
22	0.99796172	0.1661	0.0774	0.1056	0.1056	TRUE	0.8728
23	0.99796172	0.1661	0.0774	0.1056	0.1056	TRUE	0.8728
24	0.99796172	0.1663	0.0774	0.1057	0.1057	TRUE	0.8721
25	0.99796172	0.1663	0.0774	0.1057	0.1057	TRUE	0.8721
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27	0.99796172	0.1663	0.0774	0.1057	0.1057	TRUE	0.8721
28	0.99796172	0.2291	0.142	0.1705	0.1705	TRUE	1.3856
29	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
30	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
31	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
32	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
33	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
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44	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
45	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
46	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
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54	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
55	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
56	0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
57	0.99796172	0.0681	0.0886	0.0815	0.0815	TRUE	0.164
58	0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
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3	0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
4	0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
5	0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
6	0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
7	0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
8	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
9	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
10	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
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14	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
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17	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
18	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
19	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
20	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
21	0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
22	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
23	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
24	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
25	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
26	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
27	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
28	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
29	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
30	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
31	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
32	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
33	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
34	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
35	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
36	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
37	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
38	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
39	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
40	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
41	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
42	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
43	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
44	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
45	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
46	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
47	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
48	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
49	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
50	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
51	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
52	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
53	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
54	0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
55	0.99796172	0.0756	0.106	0.0955	0.0955	TRUE	0.1354
56	0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
57	0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
58	0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
59	0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
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3	0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
4	0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
5	0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
6	0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
7	0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
8	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
9	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
10	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
11	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
12	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
13	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
14	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
15	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
16	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
17	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
18	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
19	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
20	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
21	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
22	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
23	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
24	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
25	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
26	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
27	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
28	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
29	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
30	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
31	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
32	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
33	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
34	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
35	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
36	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
37	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
38	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
39	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
40	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
41	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
42	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
43	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
44	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
45	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
46	0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
47	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
48	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
49	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
50	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
51	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
52	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
53	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
54	0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
55	0.99796172	0.058	0.1018	0.0866	0.0866	TRUE	0.9103
56	0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
57	0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
58	0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
59	0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
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3	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
4	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
5	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
6	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
7	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
8	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
9	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
10	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
11	0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
12	0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
13	0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
14	0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
15	0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
16	0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
17	0.99796172	0.1779	0.1676	0.1709	0.1709	TRUE	0.2444
18	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
19	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
20	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
21	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
22	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
23	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
24	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
25	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
26	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
27	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
28	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
29	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
30	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
31	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
32	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
33	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
34	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
35	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
36	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
37	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
38	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
39	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
40	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
41	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
42	0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
43	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
44	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
45	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
46	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
47	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
48	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
49	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
50	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
51	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
52	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
53	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
54	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
55	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
56	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
57	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
58	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
59	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
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3	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
4	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
5	0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
6	0.99796172	0.1709	0.1688	0.1695	0.1695	TRUE	0.2394
7	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
8	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
9	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
10	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
11	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
12	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
13	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
14	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
15	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
16	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
17	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
18	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
19	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
20	0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
21	0.99796172	0.0268	0.0729	0.0556	0.0556	TRUE	0.3966
22	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
23	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
24	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
25	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
26	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
27	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
28	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
29	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
30	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
31	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
32	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
33	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
34	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
35	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
36	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
37	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
38	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
39	0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
40	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
41	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
42	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
43	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
44	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
45	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
46	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
47	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
48	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
49	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
50	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
51	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
52	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
53	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
54	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
55	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
56	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
57	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
58	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
59	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
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3	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
4	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
5	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
6	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
7	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
8	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
9	0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
10	0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
11	0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
12	0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
13	0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
14	0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
15	0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
16	0.99796172	0.0288	0.0728	0.0563	0.0563	TRUE	0.4409
17	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
18	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
19	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
20	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
21	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
22	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
23	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
24	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
25	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
26	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
27	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
28	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
29	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
30	0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
31	0.99796172	0.0442	0.101	0.0813	0.0813	TRUE	0.5065
32	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
33	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
34	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
35	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
36	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
37	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
38	0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
39	0.99796172	0.0416	0.1018	0.0809	0.0809	TRUE	0.5051
40	0.99796172	0.0416	0.1018	0.0809	0.0809	TRUE	0.5051
41	0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
42	0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
43	0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
44	0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
45	0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
46	0.99796172	1.4958	0.0718	0.4403	1.4958	TRUE	0.4815
47	0.99796172	1.4958	0.0718	0.4403	1.4958	TRUE	0.4815
48	0.99796172	1.4958	0.0718	0.4403	1.4958	TRUE	0.4815
49	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
50	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
51	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
52	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
53	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
54	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
55	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
56	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
57	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
58	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
59	0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
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2							
3	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
4	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
5	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
6	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
7	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
8	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
9	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
10	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
11	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
12	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
13	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
14	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
15	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
16	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
17	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
18	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
19	0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
20	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
21	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
22	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
23	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
24	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
25	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
26	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
27	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
28	0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
29	0.99796172	0.0113	0.1108	0.0768	0.0768	TRUE	0.3753
30	0.99796172	0.0113	0.1108	0.0768	0.0768	TRUE	0.3753
31	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
32	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
33	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
34	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
35	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
36	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
37	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
38	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
39	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
40	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
41	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
42	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
43	0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
44	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
45	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
46	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
47	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
48	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
49	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
50	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
51	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
52	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
53	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
54	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
55	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
56	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
57	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
58	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
59	0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
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3	0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
4	0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
5	0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
6	0.99796172	0.1493	0.0649	0.0928	0.0928	TRUE	0.3897
7	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
8	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
9	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
10	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
11	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
12	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
13	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
14	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
15	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
16	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
17	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
18	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
19	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
20	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
21	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
22	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
23	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
24	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
25	0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
26	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
27	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
28	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
29	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
30	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
31	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
32	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
33	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
34	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
35	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
36	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
37	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
38	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
39	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
40	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
41	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
42	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
43	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
44	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
45	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
46	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
47	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
48	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
49	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
50	0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
51	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
52	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
53	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
54	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
55	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
56	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
57	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
58	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
59	0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
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2							
3	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
4	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
5	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
6	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
7	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
8	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
9	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
10	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
11	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
12	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
13	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
14	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
15	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
16	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
17	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
18	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
19	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
20	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
21	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
22	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
23	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
24	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
25	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
26	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
27	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
28	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
29	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
30	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
31	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
32	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
33	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
34	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
35	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
36	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
37	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
38	0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
39	0.99796172	0.0384	0.0658	0.0554	0.0554	TRUE	0.296
40	0.99796172	0.0454	0.1075	0.0855	0.0855	TRUE	1.0762
41	0.99796172	0.0454	0.1075	0.0855	0.0855	TRUE	1.0762
42	0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
43	0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
44	0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
45	0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
46	0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
47	0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
48	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
49	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
50	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
51	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
52	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
53	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
54	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
55	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
56	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
57	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
58	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
59	0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
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2							
3	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
4	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
5	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
6	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
7	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
8	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
9	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
10	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
11	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
12	0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
13	0.99796172	0.0105	0.0631	0.042	0.042	TRUE	0.2164
14	0.99796172	0.066	0.1212	0.1023	0.1023	TRUE	0.8714
15	0.99796172	0.066	0.1212	0.1023	0.1023	TRUE	0.8714
16	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
17	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
18	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
19	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
20	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
21	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
22	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
23	0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
24	0.99796172	0.0554	0.0779	0.0699	0.0699	TRUE	0.3326
25	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
26	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
27	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
28	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
29	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
30	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
31	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
32	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
33	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
34	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
35	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
36	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
37	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
38	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
39	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
40	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
41	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
42	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
43	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
44	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
45	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
46	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
47	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
48	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
49	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
50	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
51	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
52	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
53	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
54	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
55	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
56	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
57	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
58	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
59	0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
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3	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
4	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
5	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
6	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
7	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
8	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
9	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
10	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
11	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
12	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
13	0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
14	0.99796172	0.0389	0.0678	0.0569	0.0569	TRUE	0.57
15	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
16	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
17	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
18	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
19	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
20	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
21	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
22	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
23	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
24	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
25	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
26	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
27	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
28	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
29	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
30	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
31	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
32	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
33	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
34	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
35	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
36	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
37	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
38	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
39	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
40	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
41	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
42	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
43	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
44	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
45	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
46	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
47	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
48	0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
49	0.99796172	0.1448	0.1097	0.1212	0.1212	TRUE	0.6215
50	0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
51	0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
52	0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
53	0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
54	0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
55	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
56	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
57	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
58	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
59	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
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3	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
4	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
5	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
6	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
7	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
8	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
9	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
10	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
11	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
12	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
13	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
14	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
15	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
16	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
17	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
18	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
19	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
20	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
21	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
22	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
23	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
24	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
25	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
26	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
27	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
28	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
29	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
30	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
31	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
32	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
33	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
34	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
35	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
36	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
37	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
38	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
39	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
40	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
41	0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
42	0.99796172	0.0379	0.0647	0.0545	0.0545	TRUE	0.7025
43	0.99796172	0.0379	0.0647	0.0545	0.0545	TRUE	0.7025
44	0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
45	0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
46	0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
47	0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
48	0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
49	0.99796172	0.0193	0.0912	0.0647	0.0647	TRUE	0.4029
50	0.99796172	0.0193	0.0912	0.0647	0.0647	TRUE	0.4029
51	0.99796172	0.0193	0.0912	0.0647	0.0647	TRUE	0.4029
52	0.99796172	0.0199	0.0906	0.0645	0.0645	TRUE	0.4112
53	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
54	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
55	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
56	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
57	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
58	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
59	0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
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3	0.99796172	0.0156	0.072	0.05	0.05	TRUE	0.1884
4	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
5	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
6	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
7	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
8	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
9	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
10	0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
11	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
12	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
13	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
14	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
15	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
16	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
17	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
18	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
19	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
20	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
21	0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
22	0.99796172	0.0199	0.0686	0.0496	0.0496	TRUE	0.2919
23	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
24	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
25	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
26	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
27	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
28	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
29	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
30	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
31	0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
32	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
33	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
34	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
35	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
36	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
37	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
38	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
39	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
40	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
41	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
42	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
43	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
44	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
45	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
46	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
47	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
48	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
49	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
50	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
51	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
52	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
53	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
54	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
55	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
56	0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
57	0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
58	0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
59	0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
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2							
3	0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2087
4	0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2087
5	0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2087
6	0.99796172	0.1038	0.0842	0.0908	0.0908	TRUE	0.3848
7	0.99796172	0.0806	0.0809	0.0808	0.0808	TRUE	0.6606
8	0.99796172	0.0175	0.0788	0.0556	0.0556	TRUE	0.268
9	0.99796172	0.1042	0.0842	0.091	0.091	TRUE	0.4166
10	0.99796172	0.1042	0.0842	0.091	0.091	TRUE	0.4166
11	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
12	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
13	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
14	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
15	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
16	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
17	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
18	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
19	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
20	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
21	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
22	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
23	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
24	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
25	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
26	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
27	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
28	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
29	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
30	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
31	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
32	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
33	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
34	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
35	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
36	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
37	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
38	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
39	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
40	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
41	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
42	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
43	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
44	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
45	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
46	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
47	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
48	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
49	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
50	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
51	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
52	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
53	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
54	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
55	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
56	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
57	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
58	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
59	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
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3	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
4	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
5	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
6	0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
7	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
8	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
9	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
10	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
11	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
12	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
13	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
14	0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
15	0.99796172	0.0074	0.0966	0.0638	0.0638	TRUE	0.1927
16	0.99796172	0.0076	0.0967	0.0639	0.0639	TRUE	0.1981
17	0.99803669	0.0729	0.0733	0.0731	0.0731	TRUE	0.9276
18	0.99803669	0.0729	0.0733	0.0731	0.0731	TRUE	0.9276
19	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
20	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
21	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
22	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
23	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
24	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
25	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
26	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
27	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
28	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
29	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
30	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
31	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
32	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
33	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
34	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
35	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
36	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
37	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
38	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
39	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
40	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
41	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
42	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
43	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
44	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
45	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
46	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
47	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
48	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
49	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
50	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
51	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
52	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
53	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
54	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
55	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
56	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
57	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
58	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
59	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
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3	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
4	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
5	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
6	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
7	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
8	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
9	0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
10	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
11	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
12	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
13	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
14	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
15	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
16	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
17	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
18	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
19	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
20	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
21	0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
22	0.99803669	0.0066	0.0636	0.0399	0.0399	TRUE	0.135
23	0.99803669	0.0066	0.0636	0.0399	0.0399	TRUE	0.135
24	0.99929018	0.0064	0.0636	0.0398	0.0398	TRUE	0.1323
25	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
26	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
27	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
28	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
29	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
30	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
31	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
32	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
33	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
34	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
35	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
36	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
37	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
38	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
39	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
40	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
41	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
42	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
43	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
44	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
45	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
46	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
47	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
48	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
49	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
50	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
51	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
52	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
53	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
54	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
55	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
56	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
57	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
58	0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
59	0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
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3	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
4	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
5	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
6	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
7	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
8	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
9	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
10	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
11	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
12	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
13	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
14	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
15	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
16	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
17	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
18	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
19	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
20	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
21	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
22	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
23	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
24	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
25	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
26	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
27	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
28	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
29	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
30	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
31	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
32	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
33	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
34	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
35	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
36	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
37	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
38	0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
39	0.99868672	0.1466	0.1381	0.1409	0.1409	TRUE	1.4945
40	0.99916959	0.0318	0.0666	0.0533	0.0533	TRUE	0.5013
41	0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
42	0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
43	0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
44	0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
45	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
46	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
47	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
48	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
49	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
50	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
51	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
52	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
53	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
54	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
55	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
56	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
57	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
58	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
59	0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
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2							
3	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
4	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
5	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
6	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
7	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
8	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
9	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
10	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
11	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
12	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
13	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
14	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
15	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
16	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
17	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
18	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
19	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
20	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
21	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
22	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
23	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
24	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
25	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
26	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
27	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
28	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
29	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
30	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
31	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
32	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
33	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
34	0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
35	0.99796172	0.0429	0.1012	0.0805	0.0805	TRUE	0.7913
36	0.99796172	0.0144	0.0832	0.0573	0.0573	TRUE	0.1868
37	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
38	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
39	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
40	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
41	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
42	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
43	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
44	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
45	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
46	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
47	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
48	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
49	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
50	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
51	0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
52	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
53	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
54	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
55	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
56	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
57	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
58	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
59	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
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2							
3	0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5541
4	0.99796172	0.1357	0.1429	0.1405	0.1405	TRUE	2.663
5	0.99796172	0.1357	0.1429	0.1405	0.1405	TRUE	2.663
6	0.99796172	0.1357	0.1429	0.1405	0.1405	TRUE	2.663
7	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
8	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
9	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
10	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
11	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
12	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
13	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
14	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
15	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
16	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
17	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
18	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
19	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
20	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
21	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
22	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
23	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
24	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
25	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
26	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
27	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
28	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
29	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
30	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
31	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
32	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
33	0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
34	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
35	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
36	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
37	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
38	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
39	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
40	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
41	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
42	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
43	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
44	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
45	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
46	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
47	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
48	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
49	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
50	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
51	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
52	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
53	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
54	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
55	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
56	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
57	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
58	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
59	0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
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2							
3	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
4	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
5	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
6	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
7	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
8	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
9	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
10	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
11	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
12	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
13	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
14	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
15	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
16	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
17	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
18	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
19	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
20	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
21	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
22	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
23	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
24	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
25	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
26	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
27	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
28	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
29	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
30	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
31	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
32	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
33	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
34	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
35	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
36	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
37	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
38	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
39	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
40	0.99796172	0.0181	0.0704	0.0499	0.0499	TRUE	0.256
41	0.99796172	0.0181	0.0704	0.0499	0.0499	TRUE	0.256
42	0.99796172	0.0181	0.0704	0.0499	0.0499	TRUE	0.256
43	0.99796172	0.2192	0.067	0.115	0.115	TRUE	0.19
44	0.99796172	0.1072	0.0795	0.0889	0.0889	TRUE	0.6072
45	0.99796172	0.1072	0.0795	0.0889	0.0889	TRUE	0.6072
46	0.99796172	0.1072	0.0795	0.0889	0.0889	TRUE	0.6072
47	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2382
48	0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2382
49	0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
50	0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
51	0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
52	0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
53	0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
54	0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
55	0.99796172	0	0.1429	0.0963	0.0963	TRUE	0.2014
56	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
57	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
58	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
59	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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2							
3	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
4	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
5	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
6	0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
7	0.99796172	0.2731	0.0673	0.1304	0.1304	TRUE	0.2014
8	0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
9	0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
10	0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
11	0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
12	0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
13	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
14	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
15	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
16	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
17	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
18	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
19	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
20	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
21	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
22	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
23	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
24	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
25	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
26	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
27	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
28	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
29	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
30	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
31	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
32	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
33	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
34	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
35	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
36	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
37	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
38	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
39	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
40	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
41	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
42	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
43	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
44	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
45	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
46	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
47	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
48	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
49	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
50	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
51	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
52	0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
53	0.99796172	0.1275	0.0816	0.0969	0.0969	TRUE	0.5587
54	0.99796172	0.128	0.0815	0.0971	0.0971	TRUE	0.5664
55	0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
56	0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
57	0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
58	0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
59	0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
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2							
3	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
4	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
5	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
6	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
7	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
8	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
9	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
10	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
11	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
12	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
13	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
14	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
15	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
16	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
17	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
18	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
19	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
20	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
21	0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
22	0.99796172	0.1797	0.064	0.1013	0.1013	TRUE	0.6595
23	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
24	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
25	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
26	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
27	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
28	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
29	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
30	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
31	0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
32	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
33	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
34	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
35	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
36	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
37	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
38	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
39	0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
40	0.99796172	0.0417	0.0665	0.0572	0.0572	TRUE	0.4532
41	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
42	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
43	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
44	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
45	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
46	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
47	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
48	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
49	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
50	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
51	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
52	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
53	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
54	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
55	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
56	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
57	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
58	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
59	0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
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3	0.99796172	0.0296	0.0645	0.0523	0.0523	TRUE	0.1731
4	0.99796172	0.0809	0.1032	0.0956	0.0956	TRUE	0.4046
5	0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
6	0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
7	0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
8	0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
9	0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
10	0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
11	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
12	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
13	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
14	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
15	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
16	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
17	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
18	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
19	0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
20	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
21	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
22	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
23	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
24	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
25	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
26	0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
27	0.99796172	0.0272	0.0801	0.0605	0.0605	TRUE	0.3524
28	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
29	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
30	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
31	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
32	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
33	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
34	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
35	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
36	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
37	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
38	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
39	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
40	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
41	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
42	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
43	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
44	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
45	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
46	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
47	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
48	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
49	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
50	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
51	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
52	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
53	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
54	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
55	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
56	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
57	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
58	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
59	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
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3	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
4	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
5	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
6	0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
7	0.99796172	0.0085	0.0629	0.0403	0.0403	TRUE	0.1069
8	0.99796172	0.0085	0.0629	0.0403	0.0403	TRUE	0.1069
9	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
10	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
11	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
12	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
13	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
14	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
15	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
16	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
17	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
18	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
19	0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
20	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
21	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
22	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
23	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
24	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
25	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
26	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
27	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
28	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
29	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
30	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
31	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
32	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
33	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
34	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
35	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
36	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
37	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
38	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
39	0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
40	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
41	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
42	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
43	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
44	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
45	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
46	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
47	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
48	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
49	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
50	0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
51	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
52	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
53	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
54	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
55	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
56	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
57	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
58	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
59	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
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3	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
4	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
5	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
6	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
7	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
8	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
9	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
10	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
11	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
12	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
13	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
14	0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
15	0.99796172	0.0857	0.0961	0.0925	0.0925	TRUE	1.8099
16	0.99796172	0.0857	0.0961	0.0925	0.0925	TRUE	1.8099
17	0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
18	0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
19	0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
20	0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
21	0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
22	0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
23	0.99796172	0.0419	0.1357	0.1036	0.1036	TRUE	0.5118
24	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
25	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
26	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
27	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
28	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
29	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
30	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
31	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
32	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
33	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
34	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
35	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
36	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
37	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
38	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
39	0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4216
40	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
41	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
42	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
43	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
44	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
45	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
46	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
47	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
48	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
49	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
50	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
51	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
52	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
53	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
54	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
55	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
56	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
57	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
58	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
59	0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
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3	0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
4	0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
5	0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
6	0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
7	0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
8	0.99796172	0.048	0.0833	0.0706	0.0706	TRUE	0.4425
9	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
10	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
11	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
12	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
13	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
14	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
15	0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
16	0.99796172	0.0259	0.0637	0.0481	0.0481	TRUE	0.6277
17	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
18	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
19	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
20	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
21	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
22	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
23	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
24	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
25	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
26	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
27	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
28	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
29	0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
30	0.99796172	0.0248	0.0634	0.0487	0.0487	TRUE	0.4237
31	0.99796172	0.0248	0.0634	0.0487	0.0487	TRUE	0.4237
32	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
33	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
34	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
35	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
36	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
37	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
38	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
39	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
40	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
41	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
42	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
43	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
44	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
45	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
46	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
47	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
48	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
49	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
50	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
51	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
52	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
53	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
54	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
55	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
56	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
57	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
58	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
59	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
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3	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
4	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
5	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
6	0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
7	0.99796172	0.0355	0.1569	0.1167	0.1167	TRUE	0.6572
8	0.99796172	0.0927	0.096	0.095	0.095	TRUE	1.2452
9	0.99796172	0.0425	0.161	0.1221	0.1221	TRUE	0.7749
10	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
11	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
12	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
13	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
14	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
15	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
16	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
17	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
18	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
19	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
20	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
21	0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
22	0.99796172	0.1354	0.0952	0.1084	0.1084	TRUE	0.5894
23	0.99796172	0.0188	0.0638	0.0463	0.0463	TRUE	0.3773
24	0.99796172	0.0031	0.0861	0.0543	0.0543	TRUE	0.0864
25	0.99796172	0.0031	0.0861	0.0543	0.0543	TRUE	0.0864
26	0.99796172	0.0031	0.0861	0.0543	0.0543	TRUE	0.0864
27	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
28	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
29	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
30	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
31	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
32	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
33	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
34	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
35	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
36	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
37	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
38	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
39	0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
40	0.99796172	0.1128	0.0735	0.0869	0.0869	TRUE	1.4026
41	0.99796172	0.0373	0.0958	0.0751	0.0751	TRUE	0.7971
42	0.99796172	0.0373	0.0958	0.0751	0.0751	TRUE	0.7971
43	0.99796172	0.0373	0.0958	0.0751	0.0751	TRUE	0.7971
44	0.99796172	0.0135	0.0708	0.0483	0.0483	TRUE	0.3424
45	0.99796172	0.0135	0.0708	0.0483	0.0483	TRUE	0.3424
46	0.99796172	0.0135	0.0708	0.0483	0.0483	TRUE	0.3424
47	0.99796172	0.0162	0.0865	0.0603	0.0603	TRUE	0.296
48	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
49	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
50	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
51	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
52	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
53	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
54	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
55	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
56	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
57	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
58	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
59	0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
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3	0.99796172	0.033	0.0644	0.0525	0.0525	TRUE	0.1969
4	0.99796172	0.033	0.0644	0.0525	0.0525	TRUE	0.1969
5	0.99796172	0.0332	0.0644	0.0526	0.0526	TRUE	0.1952
6	0.99796172	0.0332	0.0644	0.0526	0.0526	TRUE	0.1952
7	0.99796172	0.0316	0.089	0.0683	0.0683	TRUE	0.3234
8	0.99796172	0.0358	0.064	0.0524	0.0524	TRUE	0.7117
9	0.99796172	0.0358	0.064	0.0524	0.0524	TRUE	0.7117
10	0.99796172	0.0406	0.1378	0.1049	0.1049	TRUE	0.8973
11	0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
12	0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
13	0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
14	0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
15	0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
16	0.99796172	0.0532	0.1262	0.1011	0.1011	TRUE	0.1735
17	0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
18	0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
19	0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
20	0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
21	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
22	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
23	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
24	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
25	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
26	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
27	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
28	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
29	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
30	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
31	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
32	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
33	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
34	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
35	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
36	0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
37	0.99796172	0.0665	0.0634	0.0646	0.0646	TRUE	0.2512
38	0.99796172	0.0665	0.0634	0.0646	0.0646	TRUE	0.2512
39	0.99796172	0.0222	0.0853	0.062	0.062	TRUE	0.1748
40	0.99796172	0.0222	0.0853	0.062	0.062	TRUE	0.1748
41	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
42	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
43	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
44	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
45	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
46	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
47	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
48	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
49	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
50	0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
51	0.99796172	0.0517	0.0934	0.0786	0.0786	TRUE	0.1983
52	0.99796172	0.0517	0.0934	0.0786	0.0786	TRUE	0.1983
53	0.99796172	0.0505	0.1279	0.1013	0.1013	TRUE	0.1939
54	0.99796172	0.0505	0.1279	0.1013	0.1013	TRUE	0.1939
55	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
56	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
57	0.99796172						
58	0.99796172						
59	0.99796172						
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3	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
4	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
5	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
6	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
7	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
8	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
9	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
10	0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
11	0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
12	0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
13	0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
14	0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
15	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
16	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
17	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
18	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
19	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
20	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
21	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
22	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
23	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
24	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
25	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
26	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
27	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
28	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
29	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
30	0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
31	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
32	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
33	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
34	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
35	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
36	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
37	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
38	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
39	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
40	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
41	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
42	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
43	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
44	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
45	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
46	0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
47	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
48	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
49	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
50	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
51	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
52	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
53	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
54	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
55	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
56	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
57	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
58	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
59	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
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3	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
4	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
5	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
6	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
7	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
8	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
9	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
10	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
11	0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
12	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
13	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
14	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
15	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
16	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
17	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
18	0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
19	0.99796172	0.0623	0.1346	0.1103	0.1103	TRUE	1.2936
20	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
21	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
22	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
23	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
24	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
25	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
26	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
27	0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
28	0.99796172	0.0571	0.0828	0.073	0.073	TRUE	1.1198
29	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
30	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
31	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
32	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
33	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
34	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
35	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
36	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
37	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
38	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
39	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
40	0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
41	0.99796172	0.0633	0.0836	0.0759	0.0759	TRUE	0.8119
42	0.99796172	0.0633	0.0836	0.0759	0.0759	TRUE	0.8119
43	0.99796172	0.063	0.137	0.1124	0.1124	TRUE	0.7054
44	0.99796172	0.3796	0.1445	0.2152	0.2152	TRUE	3.7357
45	0.99796172	0.3796	0.1445	0.2152	0.2152	TRUE	3.7357
46	0.99796172	0.1042	0.1278	0.1199	0.1199	TRUE	1.3928
47	0.99796172	0.1042	0.1278	0.1199	0.1199	TRUE	1.3928
48	0.99796172	0.1042	0.1278	0.1199	0.1199	TRUE	1.3928
49	0.99796172	0.0179	0.0634	0.045	0.045	TRUE	0.3052
50	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
51	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
52	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
53	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
54	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
55	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
56	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
57	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
58	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
59	0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
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3	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
4	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
5	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
6	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
7	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
8	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
9	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
10	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
11	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
12	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
13	0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
14	0.99796172	0.0871	0.156	0.1336	0.1336	TRUE	0.5158
15	0.99796172	0.1861	0.071	0.1079	0.1079	TRUE	0.3378
16	0.99796172	0.0156	0.0978	0.0683	0.0683	TRUE	0.3906
17	0.99796172	0.0124	0.1639	0.1142	0.1142	TRUE	0.4142
18	0.99796172	0.0464	0.0645	0.058	0.058	TRUE	0.5885
19	0.99796172	0.0464	0.0645	0.058	0.058	TRUE	0.5885
20	0.99796172	0.0873	0.1601	0.1365	0.1365	TRUE	1.0664
21	0.99796172	0.0873	0.1601	0.1365	0.1365	TRUE	1.0664
22	0.99796172	0.0504	0.0647	0.0598	0.0598	TRUE	0.6657
23	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
24	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
25	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
26	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
27	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
28	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
29	0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
30	0.99796172	0.0614	0.0742	0.069	0.069	TRUE	0.589
31	0.99796172	0.1744	0.063	0.102	0.102	TRUE	0.5408
32	0.99796172	0.1744	0.063	0.102	0.102	TRUE	0.5408
33	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
34	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
35	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
36	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
37	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
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40	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
41	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
42	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
43	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
44	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
45	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
46	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
47	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
48	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
49	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
50	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
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52	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
53	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
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56	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
57	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
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59	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
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3	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
4	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
5	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
6	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
7	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
8	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
9	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
10	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
11	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
12	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
13	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
14	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
15	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
16	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
17	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
18	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
19	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
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21	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
22	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
23	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
24	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
25	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
26	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
27	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
28	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
29	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
30	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
31	0.99796172	0.2477	0.133	0.168	0.168	TRUE	3.2329
32	0.99796172	0.0739	0.0971	0.0892	0.0892	TRUE	0.3575
33	0.99796172	0.0745	0.0783	0.0766	0.0766	TRUE	0.3259
34	0.99796172	0.0745	0.0783	0.0766	0.0766	TRUE	0.3259
35	0.99796172	0.0769	0.078	0.0771	0.0771	TRUE	0.3403
36	0.99796172	0.0769	0.078	0.0771	0.0771	TRUE	0.3403
37	0.99796172	0.0274	0.1003	0.0747	0.0747	TRUE	0.4968
38	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
39	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
40	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
41	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
42	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
43	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
44	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
45	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
46	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
47	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
48	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
49	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
50	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
51	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
52	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
53	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
54	0.99796172	0.0537	0.0901	0.0775	0.0775	TRUE	0.8934
55	0.99796172	0.0331	0.1395	0.1026	0.1026	TRUE	0.2314
56	0.99796172	0.0331	0.1395	0.1026	0.1026	TRUE	0.2314
57	0.99796172	0.0331	0.1395	0.1026	0.1026	TRUE	0.2314
58	0.99796172	0.0331	0.1395	0.1026	0.1026	TRUE	0.2314
59	0.99796172	0.0331	0.1395	0.1026	0.1026	TRUE	0.2314
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3	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
4	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
5	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
6	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
7	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
8	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
9	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
10	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
11	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
12	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
13	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
14	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
15	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
16	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
17	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
18	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
19	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
20	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
21	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
22	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
23	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
24	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
25	0.99796172	0.1515	0.1034	0.1189	0.1189	TRUE	0.4812
26	0.99796172	0.0634	0.0792	0.0739	0.0739	TRUE	0.5652
27	0.99796172	0.1333	0.0712	0.0919	0.0919	TRUE	1.2929
28	0.99796172	0.1333	0.0712	0.0919	0.0919	TRUE	1.2929
29	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
30	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
31	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
32	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
33	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
34	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
35	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
36	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
37	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
38	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
39	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
40	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
41	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
42	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
43	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
44	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
45	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
46	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
47	0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
48	0.99796172	0.0604	0.0838	0.0754	0.0754	TRUE	1.206
49	0.99796172	0.0577	0.0836	0.0743	0.0743	TRUE	1.1646
50	0.99796172	0.0577	0.0836	0.0743	0.0743	TRUE	1.1646
51	0.99796172	0.0577	0.0836	0.0743	0.0743	TRUE	1.1646
52	0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
53	0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
54	0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
55	0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
56	0.99796172	0.172	0.063	0.0933	0.0933	TRUE	3.6096
57	0.99796172	0.0992	0.1507	0.1347	0.1347	TRUE	1.7485
58	0.99796172	0.0992	0.1507	0.1347	0.1347	TRUE	1.7485
59	NA	10	0.084	1.2226	10	TRUE	36.0827
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2							
3	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
4	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
5	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
6	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
7	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
8	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
9	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
10	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
11	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
12	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
13	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
14	NA	6.2015	0.0919	1.0138	6.2015	TRUE	35.2254
15	NA	10	0.1598	1.2513	10	TRUE	31.4086
16	NA	10	0.1598	1.2513	10	TRUE	31.4086
17	NA	10	0.1628	1.2539	10	TRUE	31.2615
18	NA	10	0.1628	1.2539	10	TRUE	31.2615
19	NA	10	0.1628	1.2539	10	TRUE	31.2615
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Do not distribute

	mean	5%	1%
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miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
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ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
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agagguaguagg	Phvul.006G201700.1	2.5	-1	1	24
ugagguaguagg	Phvul.009G057800.1	2.5	-1	1	22
ugagguaguagg	Phvul.009G057800.1	2.5	-1	1	22
agagguaguagg	Phvul.009G086800.1	2.5	-1	1	24
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
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ugagguaguagg	Phvul.L009543.1	2.5	-1	1	22
ugagguaguagg	Phvul.L009543.1	2.5	-1	1	22
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ugagguaguagg	Phvul.001G077200.2	3	-1	1	22
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ugagguaguagg	Phvul.001G077200.2	3	-1	1	22
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ugagguaguagg	Phvul.001G215300.1	3	-1	1	22
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ugagguaguagg	Phvul.002G267400.1	3	-1	1	22
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agagguaguagg	Phvul.004G044900.1	3	-1	1	24
agagguaguagg	Phvul.006G158900.1	3	-1	1	24
ugagguaguagg	Phvul.008G071966.1	3	-1	1	22
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agagguaguagg	Phvul.008G110200.1	3	-1	1	24
agagguaguagg	Phvul.008G110500.1	3	-1	1	24

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6	ugagguaguagǵ Phvul.008G163350.2	3	-1	1	22
7	ugagguaguagǵ Phvul.008G163350.1	3	-1	1	22
8	ugagguaguagǵ Phvul.008G163350.4	3	-1	1	22
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33	ugagguaguagǵ Phvul.001G022400.1	3.5	-1	1	22
34	ugagguaguagǵ Phvul.001G022400.1	3.5	-1	1	22
35	ugagguaguagǵ Phvul.001G077200.2	3.5	-1	1	22
36	ugagguaguagǵ Phvul.001G077200.2	3.5	-1	1	22
37	ugagguaguagǵ Phvul.001G077200.2	3.5	-1	1	22
38	ugagguaguagǵ Phvul.001G077700.1	3.5	-1	1	22
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41	ugagguaguagǵ Phvul.001G086466.1	3.5	-1	1	22
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46	ugagguaguagǵ Phvul.001G089600.1	3.5	-1	1	22
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56	agagguaguagǵ Phvul.001G121000.1	3.5	-1	1	24
57	agagguaguagǵ Phvul.001G121000.2	3.5	-1	1	24
58	agagguaguagǵ Phvul.001G121000.2	3.5	-1	1	24
59	ugagguaguagǵ Phvul.001G131150.1	3.5	-1	1	22
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4	ugagguaguagξ Phvul.001G131150.1	3.5	-1	1	22
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9	ugagguaguagξ Phvul.001G131150.2	3.5	-1	1	22
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11	ugagguaguagξ Phvul.001G131150.2	3.5	-1	1	22
12	ugagguaguagξ Phvul.001G141000.1	3.5	-1	1	22
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17	ugagguaguagξ Phvul.001G141000.1	3.5	-1	1	22
18	agagguaguagξ Phvul.001G179700.1	3.5	-1	1	24
19	ugagguaguagξ Phvul.001G179700.1	3.5	-1	1	22
20	ugagguaguagξ Phvul.001G179700.1	3.5	-1	1	22
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23	ugagguaguagξ Phvul.001G179700.1	3.5	-1	1	22
24	ugagguaguagξ Phvul.002G042000.2	3.5	-1	1	22
25	ugagguaguagξ Phvul.002G042000.8	3.5	-1	1	22
26	ugagguaguagξ Phvul.002G042000.8	3.5	-1	1	22
27	ugagguaguagξ Phvul.002G042000.7	3.5	-1	1	22
28	ugagguaguagξ Phvul.002G042000.6	3.5	-1	1	22
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30	ugagguaguagξ Phvul.002G042000.5	3.5	-1	1	22
31	ugagguaguagξ Phvul.002G042000.3	3.5	-1	1	22
32	ugagguaguagξ Phvul.002G042000.4	3.5	-1	1	22
33	ugagguaguagξ Phvul.002G042000.4	3.5	-1	1	22
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35	ugagguaguagξ Phvul.002G042000.2	3.5	-1	1	22
36	ugagguaguagξ Phvul.002G042000.8	3.5	-1	1	22
37	ugagguaguagξ Phvul.002G042000.8	3.5	-1	1	22
38	ugagguaguagξ Phvul.002G042000.7	3.5	-1	1	22
39	ugagguaguagξ Phvul.002G042000.6	3.5	-1	1	22
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41	ugagguaguagξ Phvul.002G042000.5	3.5	-1	1	22
42	ugagguaguagξ Phvul.002G042000.3	3.5	-1	1	22
43	ugagguaguagξ Phvul.002G042000.4	3.5	-1	1	22
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46	ugagguaguagξ Phvul.002G068200.1	3.5	-1	1	22
47	ugagguaguagξ Phvul.002G068200.1	3.5	-1	1	22
48	ugagguaguagξ Phvul.002G071800.1	3.5	-1	1	22
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51	ugagguaguagξ Phvul.002G076600.1	3.5	-1	1	22
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54	ugagguaguagξ Phvul.002G076600.1	3.5	-1	1	22
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56	agagguaguagξ Phvul.002G185150.2	3.5	-1	1	24
57	agagguaguagξ Phvul.002G185150.1	3.5	-1	1	24
58	agagguaguagξ Phvul.002G185150.1	3.5	-1	1	24
59	agagguaguagξ Phvul.002G185150.3	3.5	-1	1	24
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7	agagguaguagǵ Phvul.004G044800.1	3.5	-1	1	24
8	agagguaguagǵ Phvul.004G106000.1	3.5	-1	1	24
9	ugagguaguagǵ Phvul.004G133400.1	3.5	-1	1	22
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12	ugagguaguagǵ Phvul.004G176700.1	3.5	-1	1	22
13	ugagguaguagǵ Phvul.004G176700.1	3.5	-1	1	22
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18	agagguaguagǵ Phvul.005G087300.1	3.5	-1	1	24
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32	ugagguaguagξ Phvul.006G168154.1	4.5	-1	1	22
33	ugagguaguagξ Phvul.006G168154.1	4.5	-1	1	22
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35	ugagguaguagξ Phvul.006G168154.1	4.5	-1	1	22
36	ugagguaguagξ Phvul.006G168154.2	4.5	-1	1	22
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38	ugagguaguagξ Phvul.006G193700.1	4.5	-1	1	22
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6	ugagguaguagξ Phvul.011G160800.1	4.5	-1	1	22
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8	ugagguaguagξ Phvul.011G160800.2	4.5	-1	1	22
9	ugagguaguagξ Phvul.011G202700.1	4.5	-1	1	22
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11	ugagguaguagξ Phvul.011G202700.1	4.5	-1	1	22
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25	ugagguaguagξ Phvul.L002051.2	4.5	-1	1	22
26	agagguaguagξ Phvul.L002537.1	4.5	-1	1	24
27	ugagguaguagξ Phvul.L002537.1	4.5	-1	1	22
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30	agagguaguagξ Phvul.L007343.1	4.5	-1	1	24
31	ugagguaguagξ Phvul.008G004400.1	4.75	-1	1	22
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33	agagguaguagξ Phvul.001G020300.1	5	-1	1	24
34	agagguaguagξ Phvul.001G020350.1	5	-1	1	24
35	ugagguaguagξ Phvul.001G022700.1	5	-1	1	22
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59	ugagguaguagξ Phvul.002G243300.1	5	-1	1	22
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36	agagguaguagξ Phvul.003G169700.1	5	-1	1	24
37	agagguaguagξ Phvul.003G169700.1	5	-1	1	24
38	agagguaguagξ Phvul.003G292000.1	5	-1	1	24
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56	ugagguaguagξ Phvul.008G110500.1	5	-1	1	22
57	ugagguaguagξ Phvul.008G110500.1	5	-1	1	22
58	ugagguaguagξ Phvul.008G110500.1	5	-1	1	22
59	ugagguaguagξ Phvul.008G110500.1	5	-1	1	22
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3	ugagguaguagã Phvul.008G125400.2	5	-1	1	22
4	ugagguaguagã Phvul.008G125400.1	5	-1	1	22
5	ugagguaguagã Phvul.008G125400.2	5	-1	1	22
6	ugagguaguagã Phvul.008G125400.1	5	-1	1	22
7	agagguaguagę Phvul.008G229100.1	5	-1	1	24
8	ugagguaguagã Phvul.008G279750.1	5	-1	1	22
9	ugagguaguagã Phvul.008G279750.1	5	-1	1	22
10	ugagguaguagã Phvul.009G010800.1	5	-1	1	22
11	ugagguaguagã Phvul.009G010800.1	5	-1	1	22
12	agagguaguagę Phvul.009G034800.1	5	-1	1	24
13	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
14	ugagguaguagę Phvul.009G060200.2	5	-1	1	22
15	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
16	ugagguaguagę Phvul.009G060200.2	5	-1	1	22
17	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
18	ugagguaguagę Phvul.009G060200.2	5	-1	1	22
19	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
20	ugagguaguagę Phvul.009G060200.2	5	-1	1	22
21	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
22	ugagguaguagę Phvul.009G060200.2	5	-1	1	22
23	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
24	ugagguaguagę Phvul.009G060200.1	5	-1	1	22
25	ugagguaguagę Phvul.009G060200.2	5	-1	1	22
26	ugagguaguagã Phvul.009G115500.1	5	-1	1	22
27	ugagguaguagã Phvul.009G115500.1	5	-1	1	22
28	ugagguaguagę Phvul.009G158700.1	5	-1	1	22
29	ugagguaguagę Phvul.009G158700.1	5	-1	1	22
30	ugagguaguagę Phvul.009G158700.1	5	-1	1	22
31	ugagguaguagę Phvul.009G158700.1	5	-1	1	22
32	ugagguaguagę Phvul.009G158700.1	5	-1	1	22
33	ugagguaguagę Phvul.009G158700.1	5	-1	1	22
34	agagguaguagę Phvul.009G203100.1	5	-1	1	24
35	ugagguaguagę Phvul.009G232500.1	5	-1	1	22
36	ugagguaguagę Phvul.009G232500.1	5	-1	1	22
37	ugagguaguagę Phvul.009G232500.1	5	-1	1	22
38	ugagguaguagę Phvul.009G232500.1	5	-1	1	22
39	ugagguaguagã Phvul.009G255100.1	5	-1	1	22
40	ugagguaguagã Phvul.009G255100.2	5	-1	1	22
41	ugagguaguagã Phvul.009G255100.1	5	-1	1	22
42	ugagguaguagã Phvul.009G255100.2	5	-1	1	22
43	ugagguaguagę Phvul.010G026500.1	5	-1	1	22
44	ugagguaguagę Phvul.010G026500.1	5	-1	1	22
45	ugagguaguagę Phvul.010G026500.1	5	-1	1	22
46	ugagguaguagę Phvul.010G026500.1	5	-1	1	22
47	ugagguaguagã Phvul.010G028900.2	5	-1	1	22
48	ugagguaguagã Phvul.010G028900.1	5	-1	1	22
49	ugagguaguagã Phvul.010G028900.2	5	-1	1	22
50	ugagguaguagã Phvul.010G028900.1	5	-1	1	22
51	ugagguaguagę Phvul.010G067900.1	5	-1	1	22
52	ugagguaguagę Phvul.010G067900.1	5	-1	1	22
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3	ugagguaguagξ Phvul.010G067900.1	5	-1	1	22
4	ugagguaguagξ Phvul.010G067900.1	5	-1	1	22
5	ugagguaguagξ Phvul.010G089200.1	5	-1	1	22
6	ugagguaguagξ Phvul.010G089200.1	5	-1	1	22
7	ugagguaguagξ Phvul.010G089200.2	5	-1	1	22
8	ugagguaguagξ Phvul.010G089200.1	5	-1	1	22
9	ugagguaguagξ Phvul.010G089200.1	5	-1	1	22
10	ugagguaguagξ Phvul.010G089200.2	5	-1	1	22
11	ugagguaguagξ Phvul.010G089200.1	5	-1	1	22
12	ugagguaguagξ Phvul.010G089200.2	5	-1	1	22
13	ugagguaguagξ Phvul.010G089200.2	5	-1	1	22
14	ugagguaguagξ Phvul.010G089200.1	5	-1	1	22
15	ugagguaguagξ Phvul.010G089200.2	5	-1	1	22
16	ugagguaguagξ Phvul.010G094450.1	5	-1	1	22
17	ugagguaguagξ Phvul.010G094450.1	5	-1	1	22
18	ugagguaguagξ Phvul.010G094450.1	5	-1	1	22
19	ugagguaguagξ Phvul.010G094450.1	5	-1	1	22
20	ugagguaguagξ Phvul.010G094450.1	5	-1	1	22
21	ugagguaguagξ Phvul.010G094450.1	5	-1	1	22
22	ugagguaguagξ Phvul.011G001200.2	5	-1	1	22
23	ugagguaguagξ Phvul.011G001200.1	5	-1	1	22
24	ugagguaguagξ Phvul.011G001200.2	5	-1	1	22
25	ugagguaguagξ Phvul.011G001200.1	5	-1	1	22
26	ugagguaguagξ Phvul.011G001200.1	5	-1	1	22
27	ugagguaguagξ Phvul.011G001200.2	5	-1	1	22
28	ugagguaguagξ Phvul.011G001200.1	5	-1	1	22
29	ugagguaguagξ Phvul.011G001200.2	5	-1	1	22
30	ugagguaguagξ Phvul.011G001200.2	5	-1	1	22
31	ugagguaguagξ Phvul.011G001200.1	5	-1	1	22
32	agagguaguagξ Phvul.011G004200.1	5	-1	1	24
33	ugagguaguagξ Phvul.011G203450.1	5	-1	1	22
34	ugagguaguagξ Phvul.011G203450.1	5	-1	1	22
35	ugagguaguagξ Phvul.011G203450.1	5	-1	1	22
36	ugagguaguagξ Phvul.011G203450.1	5	-1	1	22
37	ugagguaguagξ Phvul.011G203450.1	5	-1	1	22
38	ugagguaguagξ Phvul.011G203450.1	5	-1	1	22
39	ugagguaguagç Phvul.L001679.1	5	-1	1	22
40	ugagguaguagç Phvul.L001679.1	5	-1	1	22
41	ugagguaguagç Phvul.L002537.1	5	-1	1	22
42	ugagguaguagç Phvul.L002537.1	5	-1	1	22
43	ugagguaguagç Phvul.L002537.1	5	-1	1	22
44	ugagguaguagç Phvul.L009843.2	5	-1	1	22
45	ugagguaguagç Phvul.L009843.1	5	-1	1	22
46	ugagguaguagç Phvul.L009843.1	5	-1	1	22
47	ugagguaguagç Phvul.L009843.2	5	-1	1	22
48	ugagguaguagç Phvul.L009843.1	5	-1	1	22
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Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
1480	1501	UGAGGUAGU	.....:UCUUAUACA	Cleavage		pacid=371762
1480	1501	UGAGGUAGU	.....:UCUUAUACA	Cleavage		pacid=371762
1331	1352	UGAGGUAGU	.....:GUCCAUACA	Cleavage		pacid=371768
1331	1352	UGAGGUAGU	.....:GUCCAUACA	Cleavage		pacid=371768
1331	1352	UGAGGUAGU	.....:GUCCAUACA	Cleavage		pacid=371768
1331	1352	UGAGGUAGU	.....:GUCCAUACA	Cleavage		pacid=371768
697	720	AGAGGUAGU	...:AGUCCUAGG	Cleavage		pacid=371733
878	899	UGAGGUAGU	.....:GAAGGUUAU	Cleavage		pacid=371486
878	899	UGAGGUAGU	.....:GAAGGUUAU	Cleavage		pacid=371486
2017	2040	AGAGGUAGU	.....:UUCUUUAUG	Cleavage		pacid=371513
1035	1056	UGAGGUAGU	.....:AUGCAAACA	Cleavage		pacid=371429
1035	1056	UGAGGUAGU	.....:AUGCAAACA	Cleavage		pacid=371429
1035	1056	UGAGGUAGU	.....:AUGCAAACA	Cleavage		pacid=371429
1035	1056	UGAGGUAGU	.....:AUGCAAACA	Cleavage		pacid=371429
3821	3842	UGAGGUAGU	.....:GCGCAUGAA	Cleavage		pacid=371789
3821	3842	UGAGGUAGU	.....:GCGCAUGAA	Cleavage		pacid=371789
3821	3842	UGAGGUAGU	.....:GCGCAUGAA	Cleavage		pacid=371789
3821	3842	UGAGGUAGU	.....:GCGCAUGAA	Cleavage		pacid=371789
348	369	UGAGGUAGU	.....:UCCCAUCCAA	Cleavage		pacid=371701
348	369	UGAGGUAGU	.....:UCCCAUCCAA	Cleavage		pacid=371701
348	369	UGAGGUAGU	.....:UCCCAUCCAA	Cleavage		pacid=371701
348	369	UGAGGUAGU	.....:UCCCAUCCAA	Cleavage		pacid=371701
99	120	UGAGGUAGU	...:CGUUGCAAA	Cleavage		pacid=371684
99	120	UGAGGUAGU	...:CGUUGCAAA	Cleavage		pacid=371684
99	120	UGAGGUAGU	...:CGUUGCAAA	Cleavage		pacid=371684
99	120	UGAGGUAGU	...:CGUUGCAAA	Cleavage		pacid=371684
1480	1501	UGAGGUAGU	.....:UCUUAUACA	Cleavage		pacid=371762
1480	1501	UGAGGUAGU	.....:UCUUAUACA	Cleavage		pacid=371762
1480	1501	UGAGGUAGU	.....:UCUUAUACA	Cleavage		pacid=371762
1480	1501	UGAGGUAGU	.....:UCUUAUACA	Cleavage		pacid=371762
806	827	UGAGGUAGU	.....:UGCCAUACA	Cleavage		pacid=371750
806	827	UGAGGUAGU	.....:UGCCAUACA	Cleavage		pacid=371750
806	827	UGAGGUAGU	.....:UGCCAUACA	Cleavage		pacid=371750
806	827	UGAGGUAGU	.....:UGCCAUACA	Cleavage		pacid=371750
1989	2012	AGAGGUAGU	...:AAGUCUAUG	Translation		pacid=371619
442	465	AGAGGUAGU	...:UCAGAUCUG	Cleavage		pacid=371741
3299	3320	UGAGGUAGU	.....:UUCCAUAUA	Cleavage		pacid=371576
3299	3320	UGAGGUAGU	.....:UUCCAUAUA	Cleavage		pacid=371576
3299	3320	UGAGGUAGU	.....:UUCCAUAUA	Cleavage		pacid=371576
3299	3320	UGAGGUAGU	.....:UUCCAUAUA	Cleavage		pacid=371576
1023	1046	AGAGGUAGU	.....:CAAUUGUGI	Cleavage		pacid=371614
927	950	AGAGGUAGU	.....:CAAUUGUGI	Cleavage		pacid=371601

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1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
1298	1319	UGAGGUAGU	::: :: :::::UUUCAUCCA/	Cleavage	pacid=371603
878	899	UGAGGUAGU	::: :: :::::GAAGGUUAU/	Cleavage	pacid=371486
878	899	UGAGGUAGU	::: :: :::::GAAGGUUAU/	Cleavage	pacid=371486
878	899	UGAGGUAGU	::: :: :::::GAAGGUUAU/	Cleavage	pacid=371486
878	899	UGAGGUAGU	::: :: :::::GAAGGUUAU/	Cleavage	pacid=371486
1826	1847	UGAGGUAGU	::: :: :::::UAAUAUGCU/	Cleavage	pacid=371420
1826	1847	UGAGGUAGU	::: :: :::::UAAUAUGCU/	Cleavage	pacid=371420
2732	2753	UGAGGUAGU	::: :: :::::GAGUUUGCA/	Cleavage	pacid=371691
2732	2753	UGAGGUAGU	::: :: :::::GAGUUUGCA/	Cleavage	pacid=371691
348	369	UGAGGUAGU	::: :: :::::UCCCAUCCAA	Cleavage	pacid=371701
348	369	UGAGGUAGU	::: :: :::::UCCCAUCCAA	Cleavage	pacid=371701
2435	2456	UGAGGUAGU	::: :: :::::ACUUAUGUA/	Cleavage	pacid=371684
2435	2456	UGAGGUAGU	::: :: :::::ACUUAUGUA/	Cleavage	pacid=371684
184	205	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371689
184	205	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371689
184	205	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371689
184	205	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371689
16	37	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371701
16	37	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371701
16	37	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371701
16	37	UGAGGUAGU	::: :: :::::CGACAUUAU/	Cleavage	pacid=371701
290	311	UGAGGUAGU	::: :: :::::AUUCUUGCA(	Cleavage	pacid=371710
290	311	UGAGGUAGU	::: :: :::::AUUCUUGCA(	Cleavage	pacid=371710
290	311	UGAGGUAGU	::: :: :::::AUUCUUGCA(	Cleavage	pacid=371710
290	311	UGAGGUAGU	::: :: :::::AUUCUUGCA(	Cleavage	pacid=371710
111	134	AGAGGUAGU	::: :: :::::CCUUCUCUG(	Cleavage	pacid=371699
111	134	AGAGGUAGU	::: :: :::::CCUUCUCUG(	Cleavage	pacid=371699
3957	3977	UGAGGUAGU	::: :: :::::CAUCAU-CAA/	Cleavage	pacid=371677

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3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
3957	3977 UGAGGUAGU	::: ::::: :CAUCAU-CAA	Cleavage	pacid=371677
956	977 UGAGGUAGU	::: ::::: :CAUGACACAA	Cleavage	pacid=371706
956	977 UGAGGUAGU	::: ::::: :CAUGACACAA	Cleavage	pacid=371706
956	977 UGAGGUAGU	::: ::::: :CAUGACACAA	Cleavage	pacid=371706
956	977 UGAGGUAGU	::: ::::: :CAUGACACAA	Cleavage	pacid=371706
143	166 AGAGGUAGU	::: ::::: :CGGAUUGUG	Cleavage	pacid=371689
145	166 UGAGGUAGU	::: ::::: :GAUUGUGCA	Cleavage	pacid=371689
145	166 UGAGGUAGU	::: ::::: :GAUUGUGCA	Cleavage	pacid=371689
145	166 UGAGGUAGU	::: ::::: :GAUUGUGCA	Cleavage	pacid=371689
145	166 UGAGGUAGU	::: ::::: :GAUUGUGCA	Cleavage	pacid=371689
371	392 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
371	392 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
740	761 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
813	834 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
872	893 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
903	924 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
945	966 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
1034	1055 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
371	392 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
371	392 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
740	761 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
813	834 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
872	893 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
903	924 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
945	966 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
1034	1055 UGAGGUAGU	::: ::::: :CAUUGGAUA	Cleavage	pacid=371781
615	636 UGAGGUAGU	::: ::::: :..AAGUGUACA	Cleavage	pacid=371771
615	636 UGAGGUAGU	::: ::::: :..AAGUGUACA	Cleavage	pacid=371771
1331	1352 UGAGGUAGU	::: ::::: :GUCCAUACA	Cleavage	pacid=371768
1331	1352 UGAGGUAGU	::: ::::: :GUCCAUACA	Cleavage	pacid=371768
961	982 UGAGGUAGU	::: ::::: :CAUCAUGUA	Cleavage	pacid=371787
961	982 UGAGGUAGU	::: ::::: :CAUCAUGUA	Cleavage	pacid=371787
961	982 UGAGGUAGU	::: ::::: :CAUCAUGUA	Cleavage	pacid=371787
961	982 UGAGGUAGU	::: ::::: :CAUCAUGUA	Cleavage	pacid=371787
70	93 AGAGGUAGU	::: ::::: : :ACAAUAUG	Cleavage	pacid=371770
70	93 AGAGGUAGU	::: ::::: : :ACAAUAUG	Cleavage	pacid=371770
70	93 AGAGGUAGU	::: ::::: : :ACAAUAUG	Cleavage	pacid=371770



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4	1287	1308 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
5	1360	1381 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
6	1287	1308 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
7	1360	1381 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
8	1287	1308 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
9	1360	1381 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
10	1287	1308 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
11	1360	1381 UGAGGUAGU	::: ::: : ::: ::: : CUCCAUGCAL Cleavage	pacid=371474
12	575	596 UGAGGUAGU	::: ::: : ::: ::: : : : : : AGCUAUACA/ Cleavage	pacid=371471
13	575	596 UGAGGUAGU	::: ::: : ::: ::: : : : : : AGCUAUACA/ Cleavage	pacid=371471
14	1400	1421 UGAGGUAGU	::: ::: : ::: ::: : : : : : CAUUGUAUC/ Cleavage	pacid=371474
15	1400	1421 UGAGGUAGU	::: ::: : ::: ::: : : : : : CAUUGUAUC/ Cleavage	pacid=371474
16	1154	1175 UGAGGUAGU	::: ::: : ::: ::: : : : : : AAAUAUAUG( Cleavage	pacid=371474
17	1154	1175 UGAGGUAGU	::: ::: : ::: ::: : : : : : AAAUAUAUG( Cleavage	pacid=371474
18	1154	1175 UGAGGUAGU	::: ::: : ::: ::: : : : : : AAAUAUAUG( Cleavage	pacid=371474
19	1154	1175 UGAGGUAGU	::: ::: : ::: ::: : : : : : AAAUAUAUG( Cleavage	pacid=371474
20	389	412 AGAGGUAGU	::: ::: : ::: ::: : : : : : CUAGCCAUGC Cleavage	pacid=371474
21	1354	1377 AGAGGUAGU	::: ::: : ::: ::: : : : : : CUAGCCAUGC Cleavage	pacid=371451
22	1492	1515 AGAGGUAGU	::: ::: : ::: ::: : : : : : CUAGCCAUGC Cleavage	pacid=371451
23	763	784 UGAGGUAGU	::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage	pacid=371631
24	763	784 UGAGGUAGU	::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage	pacid=371631
25	763	784 UGAGGUAGU	::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage	pacid=371631
26	763	784 UGAGGUAGU	::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage	pacid=371631
27	724	747 AGAGGUAGU	::: ::: : ::: ::: : : : : : CAUACAAUGC Cleavage	pacid=371634
28	1991	2012 UGAGGUAGU	::: ::: : ::: ::: : : : : : GUCUAUGCA/ Translation	pacid=371619
29	1991	2012 UGAGGUAGU	::: ::: : ::: ::: : : : : : GUCUAUGCA/ Translation	pacid=371619
30	1035	1057 AGAGGUAGU	::: ::: : ::: ::: : : : : : UAUACUAUG( Translation	pacid=371623
31	1488	1511 AGAGGUAGU	::: ::: : ::: ::: : : : : : UCAACUAUG( Cleavage	pacid=371545
32	1497	1518 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
33	1539	1560 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
34	1497	1518 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
35	1539	1560 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
36	1497	1518 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
37	1539	1560 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
38	1497	1518 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
39	1539	1560 UGAGGUAGU	::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage	pacid=371529
40	854	875 UGAGGUAGU	::: ::: : ::: ::: : : : : : GAAUAUACA( Translation	pacid=371522
41	854	875 UGAGGUAGU	::: ::: : ::: ::: : : : : : GAAUAUACA( Translation	pacid=371522
42	10	32 UGAGGUAGU	::: ::: : ::: ::: : : : : : AACUACAACA Cleavage	pacid=371524
43	190	212 UGAGGUAGU	::: ::: : ::: ::: : : : : : AACUACAACA Cleavage	pacid=371524
44	190	212 UGAGGUAGU	::: ::: : ::: ::: : : : : : AACUACAACA Cleavage	pacid=371524
45	10	32 UGAGGUAGU	::: ::: : ::: ::: : : : : : AACUACAACA Cleavage	pacid=371524
46	190	212 UGAGGUAGU	::: ::: : ::: ::: : : : : : AACUACAACA Cleavage	pacid=371524
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190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
500	521 UGAGGUAGU :: : ::::: : UAUUUUAUA Translation	pacid=371722
500	521 UGAGGUAGU :: : ::::: : UAUUUUAUA Translation	pacid=371722
1609	1630 UGAGGUAGU ::::: : : : UAUUGUACA/ Cleavage	pacid=371714
1609	1630 UGAGGUAGU ::::: : : : UAUUGUACA/ Cleavage	pacid=371714
716	739 AGAGGUAGU: : ::::: : : : AUAGUUAUG Cleavage	pacid=371719
716	739 AGAGGUAGU: : ::::: : : : AUAGUUAUG Cleavage	pacid=371719
824	847 AGAGGUAGU: : ::::: : : : AUAGUUAUG Cleavage	pacid=371719
824	847 AGAGGUAGU: : ::::: : : : AUAGUUAUG Cleavage	pacid=371719
379	402 AGAGGUAGU, : ::::: : : : CGAGUUAUA( Cleavage	pacid=371660
379	402 AGAGGUAGU, : ::::: : : : CGAGUUAUA( Cleavage	pacid=371660
609	630 UGAGGUAGU ::::: : : : GACUAUGCC/ Cleavage	pacid=371662
609	630 UGAGGUAGU ::::: : : : GACUAUGCC/ Cleavage	pacid=371662
557	580 AGAGGUAGU, : ::::: : : : AGAGUUUUA Cleavage	pacid=371662
388	409 UGAGGUAGU ... : : : : GGCUUGACA( Cleavage	pacid=371654
388	409 UGAGGUAGU ... : : : : GGCUUGACA( Cleavage	pacid=371654
2987	3008 UGAGGUAGU : : : : : : ACCUGUAUC/ Cleavage	pacid=371649
2987	3008 UGAGGUAGU : : : : : : ACCUGUAUC/ Cleavage	pacid=371649
2987	3008 UGAGGUAGU : : : : ~ : ACCUGUAUC/ Cleavage	pacid=371649
2987	3008 UGAGGUAGU : : : : ~ : ACCUGUAUC/ Cleavage	pacid=371649
2341	2362 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2361	2382 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2341	2362 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2361	2382 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2361	2382 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2341	2362 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2361	2382 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2341	2362 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
2361	2382 UGAGGUAGU : : : : ~ : ACCUGUGCU/ Cleavage	pacid=371589
3008	3029 UGAGGUAGU :: : : : : : : AAGCAUUAU/ Translation	pacid=371595
3008	3029 UGAGGUAGU :: : : : : ~ : AAGCAUUAU/ Translation	pacid=371595
3008	3029 UGAGGUAGU :: : : : : ~ : AAGCAUUAU/ Translation	pacid=371595
3008	3029 UGAGGUAGU :: : : : : ~ : AAGCAUUAU/ Translation	pacid=371595
1469	1490 UGAGGUAGU ..... : : : : CGUUAUACA/ Translation	pacid=371599
1469	1490 UGAGGUAGU ..... : : : : CGUUAUACA/ Translation	pacid=371599
866	887 UGAGGUAGU ..... : : : : CCUUAUACA/ Cleavage	pacid=371576
883	904 UGAGGUAGU ..... : : : : CCUUAUACA/ Cleavage	pacid=371576
1146	1167 UGAGGUAGU ..... : : : : CCUUAUACA/ Cleavage	pacid=371576
866	887 UGAGGUAGU ..... : : : : CCUUAUACA/ Cleavage	pacid=371576
883	904 UGAGGUAGU ..... : : : : CCUUAUACA/ Cleavage	pacid=371576
1146	1167 UGAGGUAGU ..... : : : : CCUUAUACA/ Cleavage	pacid=371576
593	614 UGAGGUAGU .. : : : : : : AGUGAUUCA/ Translation	pacid=371587



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886	907 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371426
892	913 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371425
886	907 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371425
892	913 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371425
886	907 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371426
892	913 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371425
886	907 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371425
892	913 UGAGGUAGU .....	::GGCCAUGCA/ Cleavage	pacid=371425
2329	2350 UGAGGUAGU .....	::AAUCGUGCA/ Cleavage	pacid=371429
2329	2350 UGAGGUAGU .....	::AAUCGUGCA/ Cleavage	pacid=371429
2329	2350 UGAGGUAGU .....	::AAUCGUGCA/ Cleavage	pacid=371429
2329	2350 UGAGGUAGU .....	::AAUCGUGCA/ Cleavage	pacid=371429
3280	3301 UGAGGUAGU .....	::UACUAUACU/ Cleavage	pacid=371551
3280	3301 UGAGGUAGU .....	::UACUAUACU/ Cleavage	pacid=371551
3280	3301 UGAGGUAGU .....	::UACUAUACU/ Cleavage	pacid=371551
3280	3301 UGAGGUAGU .....	::UACUAUACU/ Cleavage	pacid=371551
278	299 UGAGGUAGU .....	::AACCAAACAA Cleavage	pacid=371552
278	299 UGAGGUAGU .....	::AACCAAACAA Cleavage	pacid=371552
278	299 UGAGGUAGU .....	::AACCAAACAA Cleavage	pacid=371552
278	299 UGAGGUAGU .....	::AACCAAACAA Cleavage	pacid=371552
405	426 UGAGGUAGU .....	::UGCUAUACA/ Cleavage	pacid=371559
410	431 UGAGGUAGU .....	::UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	::UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	::UGCUAUACA/ Cleavage	pacid=371559
410	431 UGAGGUAGU .....	::UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	::UGCUAUACA/ Cleavage	pacid=371559
25	46 UGAGGUAGU .....	::CAUCAUUUA/ Cleavage	pacid=371573
25	46 UGAGGUAGU .....	::CAUCAUUUA/ Cleavage	pacid=371573
25	46 UGAGGUAGU .....	::CAUCAUUUA/ Cleavage	pacid=371573
25	46 UGAGGUAGU .....	::CAUCAUUUA/ Cleavage	pacid=371573
317	340 AGAGGUAGU .....	::AAAUCUCUU( Cleavage	pacid=371549
317	340 AGAGGUAGU .....	::AAAUCUCUU( Cleavage	pacid=371549
28	48 UGAGGUAGU .....	::CACUAUAUA/ Cleavage	pacid=371700
28	48 UGAGGUAGU .....	::CACUAUAUA/ Cleavage	pacid=371700
1608	1629 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1614	1635 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1617	1638 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1670	1691 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1608	1629 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1614	1635 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1617	1638 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1670	1691 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703
1608	1629 UGAGGUAGU .....	::GACCAAUAC Cleavage	pacid=371703

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4	1614	1635 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
5	1617	1638 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
6	1670	1691 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
7	1608	1629 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
8	1614	1635 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
9	1617	1638 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
10	1670	1691 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
11	1670	1691 UGAGGUAGU	..... :GACCAAAUAC	Cleavage pacid=371703
12	1388	1412 AGAGGUAGU	..... :UAGGCUAUG	Translation pacid=371689
13	12	33 UGAGGUAGU	..... :AGCCACAGAA	Cleavage pacid=371689
14	12	33 UGAGGUAGU	..... :AGCCACAGAA	Cleavage pacid=371689
15	12	33 UGAGGUAGU	..... :AGCCACAGAA	Cleavage pacid=371689
16	12	33 UGAGGUAGU	..... :AGCCACAGAA	Cleavage pacid=371689
17	12	33 UGAGGUAGU	..... :AGCCACAGAA	Cleavage pacid=371689
18	145	166 UGAGGUAGU	..... :GAUUGUGCA	Cleavage pacid=371689
19	145	166 UGAGGUAGU	..... :GAUUGUGCA	Cleavage pacid=371689
20	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
21	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
22	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
23	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
24	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
25	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
26	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
27	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
28	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
29	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
30	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
31	1118	1139 UGAGGUAGU	..... :UAUCAUACA	Translation pacid=371696
32	40	63 AGAGGUAGU	..... :GGAAAUGUG	Cleavage pacid=371689
33	1077	1098 UGAGGUAGU	..... :CGCUGUGCA	Cleavage pacid=371690
34	1077	1098 UGAGGUAGU	..... :CGCUGUGCA	Cleavage pacid=371690
35	1175	1196 UGAGGUAGU	..... :AGUGAUACA	Cleavage pacid=371755
36	1175	1196 UGAGGUAGU	..... :AGUGAUACA	Cleavage pacid=371755
37	615	636 UGAGGUAGU	..... :AAGUGUACA	Cleavage pacid=371771
38	615	636 UGAGGUAGU	..... :AAGUGUACA	Cleavage pacid=371771
39	615	636 UGAGGUAGU	..... :AAGUGUACA	Cleavage pacid=371771
40	615	636 UGAGGUAGU	..... :AAGUGUACA	Cleavage pacid=371771
41	958	979 UGAGGUAGU	..... :AAUUCUACA	Cleavage pacid=371766
42	958	979 UGAGGUAGU	..... :AAUUCUACA	Cleavage pacid=371766
43	1506	1527 UGAGGUAGU	..... :AACCAAAGAA	Cleavage pacid=371744
44	1506	1527 UGAGGUAGU	..... :AACCAAAGAA	Cleavage pacid=371744
45	1506	1527 UGAGGUAGU	..... :AACCAAAGAA	Cleavage pacid=371744
46	1506	1527 UGAGGUAGU	..... :AACCAAAGAA	Cleavage pacid=371744
47	102	123 UGAGGUAGU	..... :AAUUAUUA	Cleavage pacid=371753
48	102	123 UGAGGUAGU	..... :AAUUAUUA	Cleavage pacid=371753
49	102	123 UGAGGUAGU	..... :AAUUAUUA	Cleavage pacid=371753
50	102	123 UGAGGUAGU	..... :AAUUAUUA	Cleavage pacid=371753
51	628	649 UGAGGUAGU	..... :GAUUAUGUA	Translation pacid=371766
52	628	649 UGAGGUAGU	..... :GAUUAUGUA	Translation pacid=371766
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4	306	327 UGAGGUAGU :::: :GACCAAACAA Cleavage	pacid=371468
5	125	146 UGAGGUAGU :::: :GACUAUAUA(Translation	pacid=371466
6	125	146 UGAGGUAGU :::: :GACUAUAUA(Translation	pacid=371466
7	391	412 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371474
8	391	412 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371474
9	391	412 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371474
10	391	412 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371474
11	391	412 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371474
12	1356	1377 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
13	1494	1515 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
14	1356	1377 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
15	1494	1515 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
16	1356	1377 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
17	1494	1515 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
18	1356	1377 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
19	1494	1515 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
20	1356	1377 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
21	1494	1515 UGAGGUAGU :::: :AGCCAUGCAA Cleavage	pacid=371451
22	726	747 UGAGGUAGU :: :UACAAUGCAA Cleavage	pacid=371634
23	726	747 UGAGGUAGU :: :UACAAUGCAA Cleavage	pacid=371634
24	726	747 UGAGGUAGU :: :UACAAUGCAA Cleavage	pacid=371634
25	726	747 UGAGGUAGU :: :UACAAUGCAA Cleavage	pacid=371634
26	2099	2120 UGAGGUAGU :::: :GUCUAUGUA, Translation	pacid=371618
27	2099	2120 UGAGGUAGU :::: :GUCUAUGUA, Translation	pacid=371618
28	3322	3343 UGAGGUAGU :::: :CACCAUGCAA Cleavage	pacid=371632
29	3322	3343 UGAGGUAGU :::: :CACCAUGCAA Cleavage	pacid=371632
30	3322	3343 UGAGGUAGU :::: :CACCAUGCAA Cleavage	pacid=371632
31	3322	3343 UGAGGUAGU :::: :CACCAUGCAA Cleavage	pacid=371632
32	616	637 UGAGGUAGU :::: :CACCAUAAAC Cleavage	pacid=371624
33	616	637 UGAGGUAGU :::: :CACCAUAAAC Cleavage	pacid=371624
34	616	637 UGAGGUAGU :::: :CACCAUAAAC Cleavage	pacid=371624
35	616	637 UGAGGUAGU :::: :CACCAUAAAC Cleavage	pacid=371624
36	1251	1272 UGAGGUAGU :::: :CACCAUAGAA Cleavage	pacid=371543
37	1251	1272 UGAGGUAGU :::: :CACCAUAGAA Cleavage	pacid=371543
38	1251	1272 UGAGGUAGU :::: :CACCAUAGAA Cleavage	pacid=371543
39	1251	1272 UGAGGUAGU :::: :CACCAUAGAA Cleavage	pacid=371543
40	1073	1096 AGAGGUAGU, : :GACACUAUG( Cleavage	pacid=371538
41	2517	2540 AGAGGUAGU, : :UAAGCGCUG( Cleavage	pacid=371540
42	3256	3279 AGAGGUAGU, : :GAAGCAUUGI Cleavage	pacid=371545
43	196	219 AGAGGUAGU, : :ACAAUUGUG( Translation	pacid=371528
44	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
45	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
46	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
47	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
48	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
49	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
50	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
51	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
52	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
53	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
54	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
55	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
56	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
57	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
58	735	756 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
59	825	846 UGAGGUAGU : : :AGUUAGAU, Cleavage	pacid=371529
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735	756 UGAGGUAGU :... :... :... :AGUUAGAU, Cleavage	pacid=371529
825	846 UGAGGUAGU :... :... :... :AGUUAGAU, Cleavage	pacid=371529
362	383 UGAGGUAGU :... :... :... :AGCUGAACAA, Cleavage	pacid=371534
362	383 UGAGGUAGU :... :... :... :AGCUGAACAA, Cleavage	pacid=371534
910	933 AGAGGUAGU :... :... :... :GGAAGUAUG, Cleavage	pacid=371741
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
160	181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation	pacid=371736
451	472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage	pacid=371712
451	472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage	pacid=371712
451	472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage	pacid=371712
451	472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage	pacid=371712
2070	2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage	pacid=371712
2070	2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage	pacid=371712
2070	2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage	pacid=371712
2070	2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage	pacid=371712
1798	1821 AGAGGUAGU :... :... :... :CUUUUUGUG Cleavage	pacid=371741
267	288 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage	pacid=371733
497	518 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage	pacid=371733
267	288 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage	pacid=371733
497	518 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage	pacid=371733
1188	1209 UGAGGUAGU :... :... :... :AUCUAUAUG, Cleavage	pacid=371727
1188	1209 UGAGGUAGU :... :... :... :AUCUAUAUG, Cleavage	pacid=371727
2074	2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage	pacid=371649
2074	2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage	pacid=371649
2074	2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage	pacid=371649
2074	2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage	pacid=371649
2278	2299 UGAGGUAGU :... :... :... :AGUUUAUA, Translation	pacid=371664
2278	2299 UGAGGUAGU :... :... :... :AGUUUAUA, Translation	pacid=371664
737	764 AGAGGUAGU :... :... :... :UCGAUUGUG Cleavage	pacid=371676
86	108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage	pacid=371665
86	108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage	pacid=371665
86	108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage	pacid=371665
86	108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage	pacid=371665
1385	1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage	pacid=371664
1385	1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage	pacid=371664
1385	1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage	pacid=371664
1385	1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage	pacid=371664

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4	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
5	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
6	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
7	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
8	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
9	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
10	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
11	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
12	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
13	381	402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage	pacid=371660
14	607	630 AGAGGUAGU :..... :..... : CCGACUAUGC Cleavage	pacid=371662
15	609	630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage	pacid=371662
16	609	630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage	pacid=371662
17	609	630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage	pacid=371662
18	609	630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage	pacid=371662
19	609	630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage	pacid=371662
20	914	935 UGAGGUAGU :..... :..... : AAUCAUGUG( Cleavage	pacid=371654
21	914	935 UGAGGUAGU :..... :..... : AAUCAUGUG( Cleavage	pacid=371654
22	914	935 UGAGGUAGU :..... :..... : AAUCAUGUG( Cleavage	pacid=371654
23	914	935 UGAGGUAGU :..... :..... : AAUCAUGUG( Cleavage	pacid=371654
24	914	935 UGAGGUAGU :..... :..... : AAUCAUGUG( Cleavage	pacid=371654
25	48	69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage	pacid=371676
26	48	69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage	pacid=371676
27	48	69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage	pacid=371676
28	48	69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage	pacid=371676
29	48	69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage	pacid=371676
30	48	69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage	pacid=371676
31	42	63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage	pacid=371666
32	42	63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage	pacid=371666
33	42	63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage	pacid=371666
34	42	63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage	pacid=371666
35	42	63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage	pacid=371666
36	559	580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage	pacid=371662
37	559	580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage	pacid=371662
38	559	580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage	pacid=371662
39	559	580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage	pacid=371662
40	559	580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage	pacid=371662
41	559	580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage	pacid=371662
42	337	358 UGAGGUAGU :..... :..... : UGCUAUUAUI Cleavage	pacid=371643
43	337	358 UGAGGUAGU :..... :..... : UGCUAUUAUI Cleavage	pacid=371643
44	496	516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
45	833	853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
46	496	516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
47	833	853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
48	496	516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
49	833	853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
50	496	516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
51	833	853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
52	496	516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
53	833	853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
54	833	853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage	pacid=371669
55	1110	1133 AGAGGUAGU :..... :..... : AAGACAAUG( Cleavage	pacid=371653
56	29	50 UGAGGUAGU :..... :..... : GACUAUGAA( Cleavage	pacid=371643
57	29	50 UGAGGUAGU :..... :..... : GACUAUGAA( Cleavage	pacid=371643
58	29	50 UGAGGUAGU :..... :..... : GACUAUGAA( Cleavage	pacid=371643
59	37	58 UGAGGUAGU :..... :..... : GACUAUGAA( Cleavage	pacid=371660
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37	58	UGAGGUAGU	..... :..... :.....GACUAUGAA( Cleavage	pacid=371660
37	58	UGAGGUAGU	..... :..... :.....GAUUAUGAA( Cleavage	pacid=371647
37	58	UGAGGUAGU	..... :..... :.....GAUUAUGAA( Cleavage	pacid=371647
816	837	UGAGGUAGU	:: : : :.....:AAACAACGCCG Cleavage	pacid=371581
816	837	UGAGGUAGU	:: : : :.....:AAACAACGCCG Cleavage	pacid=371581
816	837	UGAGGUAGU	:: : : :.....:AAACAACGCCG Cleavage	pacid=371581
816	837	UGAGGUAGU	:: : : :.....:AAACAACGCCG Cleavage	pacid=371581
2339	2362	AGAGGUAGU	:: :..... :.....:CAACCUUGUG( Cleavage	pacid=371589
2359	2382	AGAGGUAGU	:: :..... :.....:CAACCUUGUG( Cleavage	pacid=371589
2339	2362	AGAGGUAGU	:: :..... :.....:CAACCUUGUG( Cleavage	pacid=371589
2359	2382	AGAGGUAGU	:: :..... :.....:CAACCUUGUG( Cleavage	pacid=371589
2359	2382	AGAGGUAGU	:: :..... :.....:CAACCUUGUG( Cleavage	pacid=371589
621	644	AGAGGUAGU	:: :..... :..... GAAGGUGUG Cleavage	pacid=371606
617	640	AGAGGUAGU	:: :..... :..... GAAGGUGUG Cleavage	pacid=371606
1243	1266	AGAGGUAGU	:: :..... :.....UAACCUAUG( Cleavage	pacid=371592
393	414	UGAGGUAGU	.....:..... :GGUCAUAUG( Cleavage	pacid=371593
393	414	UGAGGUAGU	.....:..... :GGUCAUAUG( Cleavage	pacid=371593
393	414	UGAGGUAGU	.....:..... :GGUCAUAUG( Cleavage	pacid=371593
393	414	UGAGGUAGU	.....:..... :GGUCAUAUG( Cleavage	pacid=371593
3769	3790	UGAGGUAGU	.....:..... :UUACAUGUG( Cleavage	pacid=371576
3769	3790	UGAGGUAGU	.....:..... :UUACAUGUG( Cleavage	pacid=371576
3769	3790	UGAGGUAGU	.....:..... :UUACAUGUG( Cleavage	pacid=371576
3769	3790	UGAGGUAGU	.....:..... :UUACAUGUG( Cleavage	pacid=371576
830	851	UGAGGUAGU	:..... :.....:UGUCAAAUA( Translation	pacid=371576
847	868	UGAGGUAGU	:..... :.....:UGUCAAAUA( Translation	pacid=371576
1110	1131	UGAGGUAGU	:..... :.....:UGUCAAAUA( Translation	pacid=371576
830	851	UGAGGUAGU	:..... :.....:UGUCAAAUA( Translation	pacid=371576
847	868	UGAGGUAGU	:..... :.....:UGUCAAAUA( Translation	pacid=371576
1110	1131	UGAGGUAGU	:..... :.....:UGUCAAAUA( Translation	pacid=371576
974	995	UGAGGUAGU	..... :.....:AAUUGUCUA( Cleavage	pacid=371580
974	995	UGAGGUAGU	..... :.....:AAUUGUCUA( Cleavage	pacid=371580
1023	1046	AGAGGUAGU	:: :.....:CAAUCCUGL Cleavage	pacid=371596
842	863	UGAGGUAGU	..... :.....:AAUUGUCUA( Cleavage	pacid=371613
842	863	UGAGGUAGU	..... :.....:AAUUGUCUA( Cleavage	pacid=371613
1374	1395	UGAGGUAGU	:: : :.....:AAUGAUUCA( Cleavage	pacid=371588
1374	1395	UGAGGUAGU	:: : :.....:AAUGAUUCA( Cleavage	pacid=371588
79	100	UGAGGUAGU	:: : :.....:CACCAUUCAC Cleavage	pacid=371604
79	100	UGAGGUAGU	:: : :.....:CACCAUUCAC Cleavage	pacid=371604
79	100	UGAGGUAGU	:: : :.....:CACCAUUCAC Cleavage	pacid=371604
79	100	UGAGGUAGU	:: : :.....:CACCAUUCAC Cleavage	pacid=371604
60	81	UGAGGUAGU	:: : :.....:AACUCUAUCA( Cleavage	pacid=371615
61	82	UGAGGUAGU	:: : :.....:AACUCUAUCA( Cleavage	pacid=371615
60	81	UGAGGUAGU	:: : :.....:AACUCUAUCA( Cleavage	pacid=371615

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4	61	82 UGAGGUAGU :::: :. ::::: :::: AACUCUAUCA Cleavage	pacid=371615
5	811	832 UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage	pacid=371610
6	811	832 UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage	pacid=371610
7	811	832 UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage	pacid=371610
8	811	832 UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage	pacid=371610
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10	1742	1763 UGAGGUAGU :::: :. ::::: : AGCCCUGCG Cleavage	pacid=371608
11	1742	1763 UGAGGUAGU :::: :. ::::: : AGCCCUGCG Cleavage	pacid=371608
12	1742	1763 UGAGGUAGU :::: :. ::::: : AGCCCUGCG Cleavage	pacid=371608
13	1742	1763 UGAGGUAGU :::: :. ::::: : AGCCCUGCG Cleavage	pacid=371608
14	1742	1763 UGAGGUAGU :::: :. ::::: : AGCCCUGCG Cleavage	pacid=371608
15	1434	1457 AGAGGUAGU, :::: :. ::::: : UCAACUUGG Cleavage	pacid=371609
16	2135	2158 AGAGGUAGU, :::: :. ::::: : UCAACUUGG Cleavage	pacid=371609
17	2140	2163 AGAGGUAGU, :::: :. ::::: : UCAACUUGG Cleavage	pacid=371609
18	1671	1692 UGAGGUAGU ::::: :. ::::: : AAUUAUGCU Cleavage	pacid=371575
19	1671	1692 UGAGGUAGU ::::: :. ::::: : AAUUAUGCU Cleavage	pacid=371575
20	1671	1692 UGAGGUAGU ::::: :. ::::: : AAUUAUGCU Cleavage	pacid=371575
21	2511	2534 AGAGGUAGU ::::: :. ::::: : AAAUUAAG Cleavage	pacid=371520
22	2873	2894 UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage	pacid=371488
23	2905	2926 UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage	pacid=371488
24	2873	2894 UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage	pacid=371488
25	2905	2926 UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage	pacid=371488
26	2496	2518 UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage	pacid=371517
27	2459	2481 UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage	pacid=371517
28	2496	2518 UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage	pacid=371517
29	2459	2481 UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage	pacid=371517
30	2496	2518 UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage	pacid=371517
31	2459	2481 UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage	pacid=371517
32	1402	1423 UGAGGUAGU :::: :. ::::: : GACAAUAUG Cleavage	pacid=371510
33	1402	1423 UGAGGUAGU :::: :. ::::: : GACAAUAUG Cleavage	pacid=371510
34	158	179 UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage	pacid=371517
35	158	179 UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage	pacid=371517
36	158	179 UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage	pacid=371517
37	158	179 UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage	pacid=371517
38	1956	1977 UGAGGUAGU :::: :. ::::: : AGUCACACAC Translation	pacid=371432
39	1956	1977 UGAGGUAGU :::: :. ::::: : AGUCACACAC Translation	pacid=371432
40	1956	1977 UGAGGUAGU :::: :. ::::: : AGUCACACAC Translation	pacid=371432
41	1956	1977 UGAGGUAGU :::: :. ::::: : AGUCACACAC Translation	pacid=371432
42	3980	4001 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
43	3970	3991 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
44	3992	4013 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
45	3993	4014 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
46	4085	4106 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
47	4062	4083 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
48	4669	4690 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
49	4681	4702 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
50	4774	4795 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
51	3980	4001 UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage	pacid=371431
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3970	3991 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
3992	4013 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
3993	4014 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
4085	4106 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
4062	4083 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
4669	4690 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
4681	4702 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
4774	4795 UGAGGUAGU .....	GAUUAUGCG( Cleavage	pacid=371431
294	317 AGAGGUAGU.....	AAAACUAUG( Cleavage	pacid=371421
793	816 AGAGGUAGU.....	GAAACUAUG( Cleavage	pacid=371424
798	821 AGAGGUAGU.....	GAAACUAUG( Cleavage	pacid=371424
795	816 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
800	821 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
795	816 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
800	821 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
795	816 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
800	821 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
795	816 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
800	821 UGAGGUAGU .....	AACUAUGGA( Cleavage	pacid=371424
1427	1448 UGAGGUAGU .....	UGCCAUACAC Cleavage	pacid=371442
1427	1448 UGAGGUAGU .....	UGCCAUACAC Cleavage	pacid=371442
1427	1448 UGAGGUAGU .....	UGCCAUACAC Cleavage	pacid=371442
1427	1448 UGAGGUAGU .....	UGCCAUACAC Cleavage	pacid=371442
675	696 UGAGGUAGU .....	AAUCAUACU/ Cleavage	pacid=371556
675	696 UGAGGUAGU .....	AAUCAUACU/ Cleavage	pacid=371556
675	696 UGAGGUAGU .....	AAUCAUACU/ Cleavage	pacid=371556
675	696 UGAGGUAGU .....	AAUCAUACU/ Cleavage	pacid=371556
900	921 UGAGGUAGU .....	UAUUCUGCA( Translation	pacid=371548
900	921 UGAGGUAGU .....	UAUUCUGCA( Translation	pacid=371548
900	921 UGAGGUAGU .....	UAUUCUGCA( Translation	pacid=371548
900	921 UGAGGUAGU .....	UAUUCUGCA( Translation	pacid=371548
1830	1851 UGAGGUAGU .....	AUCUAUGUA( Cleavage	pacid=371559
1830	1851 UGAGGUAGU .....	AUCUAUGUA( Cleavage	pacid=371559
175	198 AGAGGUAGU.....	AAACUUAUU( Cleavage	pacid=371562
196	219 AGAGGUAGU.....	AAACUUAUU( Cleavage	pacid=371556
278	299 UGAGGUAGU .....	AACCAAACAA Cleavage	pacid=371552
278	299 UGAGGUAGU .....	AACCAAACAA Cleavage	pacid=371552
405	426 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559
410	431 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559
410	431 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559
405	426 UGAGGUAGU .....	UGCUAUACA/ Cleavage	pacid=371559



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4	405	426 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
5	410	431 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
6	405	426 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
7	405	426 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
8	410	431 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
9	410	431 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
10	405	426 UGAGGUAGU	.....:UGCUAUACA/ Cleavage	pacid=371559
11	294	315 UGAGGUAGU	...:.....:UACUGAACAC/ Cleavage	pacid=371569
12	294	315 UGAGGUAGU	...:.....:UACUGAACAC/ Cleavage	pacid=371569
13	294	315 UGAGGUAGU	...:.....:UACUGAACAC/ Cleavage	pacid=371569
14	294	315 UGAGGUAGU	...:.....:UACUGAACAC/ Cleavage	pacid=371569
15	294	315 UGAGGUAGU	...:.....:UACUGAACAC/ Cleavage	pacid=371569
16	3916	3937 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
17	2706	2727 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
18	3916	3937 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
19	2706	2727 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
20	3916	3937 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
21	2706	2727 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
22	3916	3937 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
23	2706	2727 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
24	3916	3937 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
25	2706	2727 UGAGGUAGU	...:.....:AGUCCUGCAC/ Cleavage	pacid=371443
26	1727	1749 AGAGGUAGU	.....:CAAGCUGU-C Cleavage	pacid=371575
27	1223	1245 UGAGGUAGU	.....:UACUAUAAC/ Translation	pacid=371575
28	1223	1245 UGAGGUAGU	.....:UACUAUAAC/ Translation	pacid=371575
29	79	102 AGAGGUAGU	.....:AAGUCUGUG/ Cleavage	pacid=371789
30	986	1009 UGAGGU--AG	.....:GAAUAUACA/ Cleavage	pacid=371577
31	986	1009 UGAGGU--AG	.....:GAAUAUACA/ Cleavage	pacid=371577
32	753	776 AGAGGUAGU	.....:AAGUCUAUG/ Translation	pacid=371678
33	695	718 AGAGGUAGU	.....:AAGUCUAUG/ Translation	pacid=371680
34	2388	2409 UGAGGUAGU	.....:AAAUCUGUA/ Cleavage	pacid=371676
35	2388	2409 UGAGGUAGU	.....:AAAUCUGUA/ Cleavage	pacid=371676
36	2388	2409 UGAGGUAGU	.....:AAAUCUGUA/ Cleavage	pacid=371676
37	2388	2409 UGAGGUAGU	.....:AAAUCUGUA/ Cleavage	pacid=371676
38	1918	1941 AGAGGUAGU	.....:AUAACUAUG/ Cleavage	pacid=371711
39	1601	1622 UGAGGUAGU	.....:AAUUUUGCAC/ Cleavage	pacid=371696
40	1601	1622 UGAGGUAGU	.....:AAUUUUGCAC/ Cleavage	pacid=371696
41	1983	2004 UGAGGUAGU	.....:AGGUGUAUC/ Cleavage	pacid=371684
42	1983	2004 UGAGGUAGU	.....:AGGUGUAUC/ Cleavage	pacid=371684
43	2640	2661 UGAGGUAGU	.....:AAUUAUGUU/ Cleavage	pacid=371712
44	2640	2661 UGAGGUAGU	.....:AAUUAUGUU/ Cleavage	pacid=371712
45	876	897 UGAGGUAGU	.....:AACUGUACAC/ Translation	pacid=371709
46	876	897 UGAGGUAGU	.....:AACUGUACAC/ Translation	pacid=371709
47	876	897 UGAGGUAGU	.....:AACUGUACAC/ Translation	pacid=371709
48	876	897 UGAGGUAGU	.....:AACUGUACAC/ Translation	pacid=371709
49	2372	2393 UGAGGUAGU	.....:UACUGUGCAC/ Cleavage	pacid=371700
50	2372	2393 UGAGGUAGU	.....:UACUGUGCAC/ Cleavage	pacid=371700
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1237	1258 UGAGGUAGU .....	: : : : : GAUUAUACA( Cleavage	pacid=371711
1237	1258 UGAGGUAGU .....	: : : : : GAUUAUACA( Cleavage	pacid=371711
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
1650	1671 UGAGGUAGU .....	: : : : : AACCAUACUA Cleavage	pacid=371692
254	277 AGAGGUAGU .....	: : : : : GAAAGUGUG( Translation	pacid=371687
1804	1825 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1816	1837 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1804	1825 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1816	1837 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1804	1825 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1816	1837 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1804	1825 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
1816	1837 UGAGGUAGU .....	: : : : : AGCCAUUAUG( Cleavage	pacid=371711
2325	2348 AGAGGUAGU .....	: : : : : UUAACUUAUU( Cleavage	pacid=371711
2445	2468 AGAGGUAGU .....	: : : : : UUAACUUAUU( Cleavage	pacid=371711
1874	1895 UGAGGUAGU .....	: : : : : CACCGUGUA( Cleavage	pacid=371687
1874	1895 UGAGGUAGU .....	: : : : : CACCGUGUA( Cleavage	pacid=371687
1874	1895 UGAGGUAGU .....	: : : : : CACCGUGUA( Cleavage	pacid=371687
1874	1895 UGAGGUAGU .....	: : : : : CACCGUGUA( Cleavage	pacid=371687
615	636 UGAGGUAGU .....	: : : : : GGCUAUACA( Cleavage	pacid=371766
615	636 UGAGGUAGU .....	: : : : : GGCUAUACA( Cleavage	pacid=371766
615	636 UGAGGUAGU .....	: : : : : GGCUAUACA( Cleavage	pacid=371766
615	636 UGAGGUAGU .....	: : : : : GGCUAUACA( Cleavage	pacid=371766
1026	1047 UGAGGUAGU .....	: : : : : AACCAUGUU( Cleavage	pacid=371749
1026	1047 UGAGGUAGU .....	: : : : : AACCAUGUU( Cleavage	pacid=371749
1026	1047 UGAGGUAGU .....	: : : : : AACCAUGUU( Cleavage	pacid=371749
1026	1047 UGAGGUAGU .....	: : : : : AACCAUGUU( Cleavage	pacid=371749
1126	1147 UGAGGUAGU .....	: : : : : GUUUUAUA. Cleavage	pacid=371755
1126	1147 UGAGGUAGU .....	: : : : : GUUUUAUA. Cleavage	pacid=371755
54	75 UGAGGUAGU .....	: : : : : AACUCUUCA( Cleavage	pacid=371767
54	75 UGAGGUAGU .....	: : : : : AACUCUUCA( Cleavage	pacid=371767
54	75 UGAGGUAGU .....	: : : : : AACUCUUCA( Cleavage	pacid=371767
54	75 UGAGGUAGU .....	: : : : : AACUCUUCA( Cleavage	pacid=371767
498	521 AGAGGUAGU .....	: : : : : UAAACUAUG( Translation	pacid=371764
628	649 UGAGGUAGU .....	: : : : : GAUUAUGUA. Translation	pacid=371766
628	649 UGAGGUAGU .....	: : : : : GAUUAUGUA. Translation	pacid=371766
628	649 UGAGGUAGU .....	: : : : : GAUUAUGUA. Translation	pacid=371766



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3	628	649 UGAGGUAGU ..... : .....:GAUUAUGUA Translation	pacid=371766
4	868	889 UGAGGUAGU ..... : ..... :GAUUAUACA/ Cleavage	pacid=371774
5	868	889 UGAGGUAGU ..... : ..... :GAUUAUACA/ Cleavage	pacid=371774
6	169	192 AGAGGUAGU,:::: : ..... :AAAAGGUG( Translation	pacid=371764
7	300	321 UGAGGUAGU ..... : .....:CACUGUGUA/ Cleavage	pacid=371760
8	300	321 UGAGGUAGU ..... : .....:CACUGUGUA/ Cleavage	pacid=371760
9	2595	2616 UGAGGUAGU ..... : ..... :CGUUGUAUA/ Cleavage	pacid=371445
10	2595	2616 UGAGGUAGU ..... : ..... :CGUUGUAUA/ Cleavage	pacid=371445
11	2031	2052 UGAGGUAGU ..... : ..... : GAUCAUGCA/ Cleavage	pacid=371470
12	2031	2052 UGAGGUAGU ..... : ..... : GAUCAUGCA/ Cleavage	pacid=371470
13	2031	2052 UGAGGUAGU ..... : ..... : GAUCAUGCA/ Cleavage	pacid=371470
14	2031	2052 UGAGGUAGU ..... : ..... : GAUCAUGCA/ Cleavage	pacid=371470
15	165	187 UGAGGUAGU ..... : .....:GGCCAUGAA/ Cleavage	pacid=371454
16	165	187 UGAGGUAGU ..... : .....:GGCCAUGAA/ Cleavage	pacid=371454
17	165	187 UGAGGUAGU ..... : .....:GGCCAUGAA/ Cleavage	pacid=371454
18	165	187 UGAGGUAGU ..... : .....:GGCCAUGAA/ Cleavage	pacid=371454
19	1526	1547 UGAGGUAGU ..... : .....:GACUGUAAA/ Cleavage	pacid=371467
20	1526	1547 UGAGGUAGU ..... : .....:GACUGUAAA/ Cleavage	pacid=371467
21	575	596 UGAGGUAGU ..... : .....:AGCUAUACA/ Cleavage	pacid=371471
22	575	596 UGAGGUAGU ..... : .....:AGCUAUACA/ Cleavage	pacid=371471
23	575	596 UGAGGUAGU ..... : .....:AGCUAUACA/ Cleavage	pacid=371471
24	575	596 UGAGGUAGU ..... : .....:AGCUAUACA/ Cleavage	pacid=371471
25	9208	9231 AGAGGUAGU,:: ..... : .....:AGCACUGUG( Cleavage	pacid=371454
26	9208	9231 AGAGGUAGU,:: ..... : .....:AGCACUGUG( Cleavage	pacid=371454
27	9208	9231 AGAGGUAGU,:: ..... : .....:AGCACUGUG( Cleavage	pacid=371454
28	143	166 AGAGGUAGU,:::: : ..... :AAAUAUGI Cleavage	pacid=371469
29	420	443 AGAGGUAGU,:::: : ..... :GAAUUGGAG( Cleavage	pacid=371446
30	349	373 AGAGGUAGU, ..... : .....:CUAGUUAUG( Translation	pacid=371637
31	4084	4104 UGAGGUAGU ..... : .....:AAUCAUGCG- Cleavage	pacid=371622
32	4084	4104 UGAGGUAGU ..... : .....:AAUCAUGCG- Cleavage	pacid=371622
33	4084	4104 UGAGGUAGU ..... : .....:AAUCAUGCG- Cleavage	pacid=371622
34	4084	4104 UGAGGUAGU ..... : .....:AAUCAUGCG- Cleavage	pacid=371622
35	2603	2624 UGAGGUAGU ..... : .....:AACCAACCAA Cleavage	pacid=371635
36	2603	2624 UGAGGUAGU ..... : .....:AACCAACCAA Cleavage	pacid=371635
37	2603	2624 UGAGGUAGU ..... : .....:AACCAACCAA Cleavage	pacid=371635
38	2603	2624 UGAGGUAGU ..... : .....:AACCAACCAA Cleavage	pacid=371635
39	971	993 UGAGGUAGU ..... : .....:AGCUCAUGU/ Translation	pacid=371622
40	971	993 UGAGGUAGU ..... : .....:AGCUCAUGU/ Translation	pacid=371622
41	2918	2939 UGAGGUAGU ..... : ..... :AGCUAUUUA/ Cleavage	pacid=371540
42	2918	2939 UGAGGUAGU ..... : ..... :AGCUAUUUA/ Cleavage	pacid=371540
43	297	320 AGAGGUAGU,:::: : ..... :AAAGUUGUU Cleavage	pacid=371538
44	1539	1562 AGAGGUAGU,:::: : ..... : AAAUUAUG( Cleavage	pacid=371546
45	10	32 UGAGGUAGU ..... : .....:AACUACAACA Cleavage	pacid=371524
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190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
10	32 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
10	32 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
190	212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage	pacid=371524
2173	2194 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation	pacid=371530
2213	2234 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation	pacid=371530
2421	2442 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation	pacid=371530
2173	2194 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation	pacid=371530
2213	2234 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation	pacid=371530
2421	2442 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation	pacid=371530
362	383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage	pacid=371534
362	383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage	pacid=371534
362	383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage	pacid=371534
362	383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage	pacid=371534
197	219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage	pacid=371522
197	219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage	pacid=371522
197	219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage	pacid=371522
197	219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage	pacid=371522
44	65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage	pacid=371713
44	65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage	pacid=371713
44	65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage	pacid=371713
44	65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage	pacid=371713
267	288 UGAGGUAGU ::::: : ::::: : GUGCAGGCAI Cleavage	pacid=371730
267	288 UGAGGUAGU ::::: : ::::: : GUGCAGGCAI Cleavage	pacid=371730
1870	1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA Cleavage	pacid=371645
1870	1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA Cleavage	pacid=371645
1870	1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA Cleavage	pacid=371645
1870	1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA Cleavage	pacid=371645
1971	1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
1971	1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
2125	2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
2125	2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
1971	1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
1971	1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
2125	2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648
2125	2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage	pacid=371648

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3	1971	1992 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
4	1971	1992 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
5	2125	2146 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
6	2125	2146 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
7	1971	1992 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
8	1971	1992 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
9	2125	2146 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
10	2125	2146 UGAGGUAGU ::::: :.....: ::AGCCAUUCAᄁ Cleavage	pacid=371648
11	46	69 AGAGGUAGU::::: :. :.....: AAAAUCAUGᄁ Cleavage	pacid=371676
12	165	186 UGAGGUAGU ::: : ::::: :.....: AACCUUCCAG Cleavage	pacid=371643
13	165	186 UGAGGUAGU ::: : ::::: :.....: AACCUUCCAG Cleavage	pacid=371643
14	165	186 UGAGGUAGU ::: : ::::: :.....: AACCUUCCAG Cleavage	pacid=371643
15	165	186 UGAGGUAGU ::: : ::::: :.....: AACCUUCCAG Cleavage	pacid=371643
16	833	854 UGAGGUAGU :::: ::::: :.....: AAUUGCACAᄁ Translation	pacid=371669
17	833	854 UGAGGUAGU :::: ::::: :.....: AAUUGCACAᄁ Translation	pacid=371669
18	365	388 AGAGGUAGU :::: ::::: :.....: CAAACAAUGᄁ Cleavage	pacid=371643
19	1112	1133 UGAGGUAGU ::: ::::: :.....: GACAAUGCAᄁ Cleavage	pacid=371653
20	1112	1133 UGAGGUAGU ::: ::::: :.....: GACAAUGCAᄁ Cleavage	pacid=371653
21	1112	1133 UGAGGUAGU ::: ::::: :.....: GACAAUGCAᄁ Cleavage	pacid=371653
22	1112	1133 UGAGGUAGU ::: ::::: :.....: GACAAUGCAᄁ Cleavage	pacid=371653
23	1112	1133 UGAGGUAGU ::: ::::: :.....: GACAAUGCAᄁ Cleavage	pacid=371653
24	1112	1133 UGAGGUAGU ::: ::::: :.....: GACAAUGCAᄁ Cleavage	pacid=371653
25	1919	1940 UGAGGUAGU ::::: :.....: AACCAAUUACᄁ Cleavage	pacid=371670
26	1919	1940 UGAGGUAGU ::::: :.....: AACCAAUUACᄁ Cleavage	pacid=371670
27	1919	1940 UGAGGUAGU ::::: :.....: AACCAAUUACᄁ Cleavage	pacid=371670
28	1919	1940 UGAGGUAGU ::::: :.....: AACCAAUUACᄁ Cleavage	pacid=371670
29	2013	2037 AGAGGUAGU ::::: : :.....: GAAACUAAUᄁ Cleavage	pacid=371654
30	2548	2571 AGAGGUAGU ::: :.....: : CAAAAUAUGᄁ Cleavage	pacid=371606
31	1653	1676 AGAGGUAGU ::: :.....: : ACAAUAUGᄁ Cleavage	pacid=371606
32	1200	1221 UGAGGUAGU ::::: :.....: AAUUAUAGGᄁ Cleavage	pacid=371586
33	1200	1221 UGAGGUAGU ::::: :.....: AAUUAUAGGᄁ Cleavage	pacid=371586
34	1025	1046 UGAGGUAGU ::: :.....: AAUCCUGUAᄁ Cleavage	pacid=371596
35	1025	1046 UGAGGUAGU ::: :.....: AAUCCUGUAᄁ Cleavage	pacid=371596
36	1025	1046 UGAGGUAGU ::: :.....: AAUCCUGUAᄁ Cleavage	pacid=371596
37	1025	1046 UGAGGUAGU ::: :.....: AAUCCUGUAᄁ Cleavage	pacid=371596
38	1025	1046 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371614
39	1025	1046 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371614
40	1025	1046 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371614
41	1025	1046 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371614
42	929	950 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371601
43	929	950 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371601
44	929	950 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371601
45	929	950 UGAGGUAGU :.....:.....: AAUUGUGUA. Cleavage	pacid=371601
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2973	2994	UGAGGUAGU ..... :GGCUGUGUA, Cleavage	pacid=371589
2979	3000	UGAGGUAGU ..... :GGCUGUGUA, Cleavage	pacid=371589
2973	2994	UGAGGUAGU ..... :GGCUGUGUA, Cleavage	pacid=371589
2979	3000	UGAGGUAGU ..... :GGCUGUGUA, Cleavage	pacid=371589
2270	2293	AGAGGUAGU.....:GAGAUUGUG Cleavage	pacid=371586
2172	2193	UGAGGUAGU ::: :..... :UUCUAUCAAC Cleavage	pacid=371611
2172	2193	UGAGGUAGU ::: :..... :UUCUAUCAAC Cleavage	pacid=371611
1538	1559	UGAGGUAGU ..... :GGCUGUAUA, Cleavage	pacid=371502
1538	1559	UGAGGUAGU ..... :GGCUGUAUA, Cleavage	pacid=371502
612	635	AGAGGUAGU.....:AAAGCUACGC Cleavage	pacid=371497
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
269	290	UGAGGUAGU ::: :..... :AACCCCACAA Translation	pacid=371509
1680	1701	UGAGGUAGU ..... :GACUGUACAC Cleavage	pacid=371502
1680	1701	UGAGGUAGU ..... :GACUGUACAC Cleavage	pacid=371502
290	311	UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage	pacid=371491
290	311	UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage	pacid=371491
290	311	UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage	pacid=371491
290	311	UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage	pacid=371491
767	790	AGAGGUAGU.....:AAGAUUGUG, Translation	pacid=371518
1402	1423	UGAGGUAGU .. :..... :GACAAUAUG, Cleavage	pacid=371510
1402	1423	UGAGGUAGU .. :..... :GACAAUAUG, Cleavage	pacid=371510
1402	1423	UGAGGUAGU .. :..... :GACAAUAUG, Cleavage	pacid=371510
1402	1423	UGAGGUAGU .. :..... :GACAAUAUG, Cleavage	pacid=371510
512	533	UGAGGUAGU ..... :GAUUGUGCA, Translation	pacid=371513
535	556	UGAGGUAGU ..... :GAUUGUGCA, Translation	pacid=371513
512	533	UGAGGUAGU ..... :GAUUGUGCA, Translation	pacid=371513
535	556	UGAGGUAGU ..... :GAUUGUGCA, Translation	pacid=371513
509	530	UGAGGUAGU ..... :AAUCAUACUL Cleavage	pacid=371431
509	530	UGAGGUAGU ..... :AAUCAUACUL Cleavage	pacid=371431
509	530	UGAGGUAGU ..... :AAUCAUACUL Cleavage	pacid=371431
509	530	UGAGGUAGU ..... :AAUCAUACUL Cleavage	pacid=371431
2465	2486	UGAGGUAGU ..... :AGUUAUACA, Cleavage	pacid=371430
2478	2499	UGAGGUAGU ..... :AGUUAUACA, Cleavage	pacid=371430
2465	2486	UGAGGUAGU ..... :AGUUAUACA, Cleavage	pacid=371430
2478	2499	UGAGGUAGU ..... :AGUUAUACA, Cleavage	pacid=371430
1001	1022	UGAGGUAGU ..... :AAUUAUAGA, Cleavage	pacid=371424
1001	1022	UGAGGUAGU ..... :AAUUAUAGA, Cleavage	pacid=371424

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1001	1022	UGAGGUAGU ::::: : :::::AAUUAUAGA/ Cleavage	pacid=371424
1001	1022	UGAGGUAGU ::::: : :::::AAUUAUAGA/ Cleavage	pacid=371424
1340	1361	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1345	1366	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1340	1361	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1345	1366	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1340	1361	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1345	1366	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1340	1361	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1345	1366	UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage	pacid=371424
1562	1583	UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage	pacid=371432
1562	1583	UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage	pacid=371432
1562	1583	UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage	pacid=371432
1562	1583	UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage	pacid=371432
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
534	555	UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage	pacid=371560
589	611	AGAGGUAGU::: : :::::AAUAUUAUG/ Cleavage	pacid=371566
299	320	UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation	pacid=371558
299	320	UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation	pacid=371558
299	320	UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation	pacid=371558
299	320	UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation	pacid=371558
1405	1426	UGAGGUAGU ::::: : :::::GACUGUAAA/ Cleavage	pacid=371574
1405	1426	UGAGGUAGU ::::: : :::::GACUGUAAA/ Cleavage	pacid=371574
1729	1749	UGAGGUAGU ::::: : :::::AGCUGU-CAA Cleavage	pacid=371575
1729	1749	UGAGGUAGU ::::: : :::::AGCUGU-CAA Cleavage	pacid=371575
121	142	UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage	pacid=371790
121	142	UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage	pacid=371790
121	142	UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage	pacid=371790
121	142	UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage	pacid=371790



Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.002G267400.1	Phvul.002G267400	Phvul.002G267400	PF02732
1	Phvul.002G267400.1	Phvul.002G267400	Phvul.002G267400	PF02732
1	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
1	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
1	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
1	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
1	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
1	Phvul.006G201700.1	Phvul.006G201700	Phvul.006G201700	PF12014
1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072
1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072
1	Phvul.009G086800.1	Phvul.009G086800	Phvul.009G086800	PF02990
2	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
2	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
2	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
2	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
1	Phvul.L009543.1	Phvul.L009543	Phvul.L009543	PF00111,PF01
1	Phvul.L009543.1	Phvul.L009543	Phvul.L009543	PF00111,PF01
1	Phvul.L009543.1	Phvul.L009543	Phvul.L009543	PF00111,PF01
1	Phvul.L009543.1	Phvul.L009543	Phvul.L009543	PF00111,PF01
1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170
1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170
1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170
1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170
1	Phvul.001G215300.1	Phvul.001G215300	Phvul.001G215300	PF01501
1	Phvul.001G215300.2	Phvul.001G215300	Phvul.001G215300	PF01501
1	Phvul.001G215300.1	Phvul.001G215300	Phvul.001G215300	PF01501
1	Phvul.001G215300.2	Phvul.001G215300	Phvul.001G215300	PF01501
1	Phvul.002G267400.1	Phvul.002G267400	Phvul.002G267400	PF02732
1	Phvul.002G267400.1	Phvul.002G267400	Phvul.002G267400	PF02732
1	Phvul.002G267400.1	Phvul.002G267400	Phvul.002G267400	PF02732
1	Phvul.002G267400.1	Phvul.002G267400	Phvul.002G267400	PF02732
1	Phvul.002G281100.1	Phvul.002G281100	Phvul.002G281100	PF03016
1	Phvul.002G281100.1	Phvul.002G281100	Phvul.002G281100	PF03016
1	Phvul.002G281100.1	Phvul.002G281100	Phvul.002G281100	PF03016
1	Phvul.002G281100.1	Phvul.002G281100	Phvul.002G281100	PF03016
1	Phvul.004G044900.1	Phvul.004G044900	Phvul.004G044900	PF08263,PF00
2	Phvul.006G158900.1	Phvul.006G158900	Phvul.006G158900	PF15365
2	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
2	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
2	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
2	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
1	Phvul.008G110200.1	Phvul.008G110200	Phvul.008G110200	PF05056
1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500	PF05056

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3	1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350	0
4	1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350	0
5	1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350	0
6	1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350	0
7	1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350	0
8	1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350	0
9	1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350	0
10	1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350	0
11	1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350	0
12	1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350	0
13	1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350	0
14	1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350	0
15	1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350	0
16	1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350	0
17	1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350	0
18	1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350	0
19	1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350	0
20	1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350	0
21	1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350	0
22	1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350	0
23	1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350	0
24	1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350	0
25	1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072
26	1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072
27	1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072
28	1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072
29	1	Phvul.010G058700.1	Phvul.010G058700	Phvul.010G058700	0
30	1	Phvul.010G058700.1	Phvul.010G058700	Phvul.010G058700	0
31	1	Phvul.001G022400.1	Phvul.001G022400	Phvul.001G022400	PF00497,PF00
32	1	Phvul.001G022400.1	Phvul.001G022400	Phvul.001G022400	PF00497,PF00
33	1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170
34	1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170
35	2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF00
36	2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF00
37	1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022
38	1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022
39	1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022
40	1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022
41	1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600	0
42	1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600	0
43	1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600	0
44	1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600	0
45	1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365
46	1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365
47	1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365
48	1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365
49	1	Phvul.001G121000.1	Phvul.001G121000	Phvul.001G121000	PF00682
50	1	Phvul.001G121000.2	Phvul.001G121000	Phvul.001G121000	PF00682
51	1	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
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1	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
2	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
3	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
4	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
5	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
6	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
7	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
8	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
9	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
10	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
11	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF00
12	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
13	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
14	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
15	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
16	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
17	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
18	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
19	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
20	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
21	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
22	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
23	Phvul.002G042000.2	Phvul.002G042000	Phvul.002G042000	0
24	Phvul.002G042000.8	Phvul.002G042000	Phvul.002G042000	0
25	Phvul.002G042000.7	Phvul.002G042000	Phvul.002G042000	0
26	Phvul.002G042000.6	Phvul.002G042000	Phvul.002G042000	0
27	Phvul.002G042000.5	Phvul.002G042000	Phvul.002G042000	0
28	Phvul.002G042000.3	Phvul.002G042000	Phvul.002G042000	0
29	Phvul.002G042000.4	Phvul.002G042000	Phvul.002G042000	0
30	Phvul.002G042000.1	Phvul.002G042000	Phvul.002G042000	0
31	Phvul.002G042000.2	Phvul.002G042000	Phvul.002G042000	0
32	Phvul.002G042000.8	Phvul.002G042000	Phvul.002G042000	0
33	Phvul.002G042000.7	Phvul.002G042000	Phvul.002G042000	0
34	Phvul.002G042000.6	Phvul.002G042000	Phvul.002G042000	0
35	Phvul.002G042000.5	Phvul.002G042000	Phvul.002G042000	0
36	Phvul.002G042000.3	Phvul.002G042000	Phvul.002G042000	0
37	Phvul.002G042000.4	Phvul.002G042000	Phvul.002G042000	0
38	Phvul.002G042000.1	Phvul.002G042000	Phvul.002G042000	0
39	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
40	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
41	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
42	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
43	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF00
44	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF00
45	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF00
46	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF00
47	Phvul.002G185150.2	Phvul.002G185150	Phvul.002G185150	PF00999
48	Phvul.002G185150.1	Phvul.002G185150	Phvul.002G185150	PF00999
49	Phvul.002G185150.3	Phvul.002G185150	Phvul.002G185150	PF00999

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4	1	Phvul.002G304500.1	Phvul.002G304500	Phvul.002G304500	PF07714
5	1	Phvul.003G103100.2	Phvul.003G103100	Phvul.003G103100	PF07496
6	1	Phvul.003G103100.2	Phvul.003G103100	Phvul.003G103100	PF07496
7	1	Phvul.004G044800.1	Phvul.004G044800	Phvul.004G044800	PF08263,PF00
8	1	Phvul.004G106000.1	Phvul.004G106000	Phvul.004G106000	PF01535
9	1	Phvul.004G133400.1	Phvul.004G133400	Phvul.004G133400	PF00571,PF00
10	1	Phvul.004G133400.1	Phvul.004G133400	Phvul.004G133400	PF00571,PF00
11	1	Phvul.004G133400.1	Phvul.004G133400	Phvul.004G133400	PF00571,PF00
12	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
13	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
14	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
15	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
16	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
17	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
18	1	Phvul.005G087300.1	Phvul.005G087300	Phvul.005G087300	PF12609
19	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
20	1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738
21	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
22	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
23	1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738
24	1	Phvul.005G180200.1	Phvul.005G180200	Phvul.005G180200	PF16987
25	1	Phvul.005G180200.1	Phvul.005G180200	Phvul.005G180200	PF16987
26	1	Phvul.005G180200.1	Phvul.005G180200	Phvul.005G180200	PF16987
27	1	Phvul.006G019800.1	Phvul.006G019800	Phvul.006G019800	PF00736
28	1	Phvul.006G019800.1	Phvul.006G019800	Phvul.006G019800	PF00736
29	1	Phvul.006G019800.1	Phvul.006G019800	Phvul.006G019800	PF00736
30	1	Phvul.006G019800.1	Phvul.006G019800	Phvul.006G019800	PF00736
31	1	Phvul.006G019800.1	Phvul.006G019800	Phvul.006G019800	PF00736
32	1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
33	1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
34	1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
35	1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
36	1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
37	1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
38	1	Phvul.006G106900.2	Phvul.006G106900	Phvul.006G106900	PF14365,PF03
39	1	Phvul.006G106900.1	Phvul.006G106900	Phvul.006G106900	PF14365,PF03
40	1	Phvul.006G137200.3	Phvul.006G137200	Phvul.006G137200	PF03765
41	1	Phvul.006G137200.2	Phvul.006G137200	Phvul.006G137200	PF03765
42	1	Phvul.006G137200.2	Phvul.006G137200	Phvul.006G137200	PF03765
43	1	Phvul.007G113800.1	Phvul.007G113800	Phvul.007G113800	PF12697
44	1	Phvul.007G113800.1	Phvul.007G113800	Phvul.007G113800	PF12697
45	1	Phvul.007G211400.1	Phvul.007G211400	Phvul.007G211400	PF00295
46	1	Phvul.007G211400.1	Phvul.007G211400	Phvul.007G211400	PF00295
47	1	Phvul.007G219400.1	Phvul.007G219400	Phvul.007G219400	PF02519
48	1	Phvul.007G219400.1	Phvul.007G219400	Phvul.007G219400	PF02519
49	1	Phvul.007G219400.1	Phvul.007G219400	Phvul.007G219400	PF02519
50	1	Phvul.007G219400.1	Phvul.007G219400	Phvul.007G219400	PF02519
51	1	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
52	1	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
53	1	Phvul.008G107300.1	Phvul.008G107300	Phvul.008G107300	0
54	1	Phvul.008G107300.1	Phvul.008G107300	Phvul.008G107300	0
55	1	Phvul.008G107300.1	Phvul.008G107300	Phvul.008G107300	0
56	1	Phvul.008G115900.1	Phvul.008G115900	Phvul.008G115900	PF08659
57	1	Phvul.008G115900.1	Phvul.008G115900	Phvul.008G115900	PF08659
58	1	Phvul.008G115900.1	Phvul.008G115900	Phvul.008G115900	PF08659
59	1	Phvul.008G257700.2	Phvul.008G257700	Phvul.008G257700	PF01370
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3	Phvul.008G257700.1	Phvul.008G257700	Phvul.008G257700	PF01370
4	Phvul.008G282700.1	Phvul.008G282700	Phvul.008G282700	PF02628
5	Phvul.008G289600.1	Phvul.008G289600	Phvul.008G289600	PF02990
6	Phvul.009G127300.1	Phvul.009G127300	Phvul.009G127300	PF12937
7	Phvul.009G127300.1	Phvul.009G127300	Phvul.009G127300	PF12937
8	Phvul.009G127300.1	Phvul.009G127300	Phvul.009G127300	PF12937
9	Phvul.009G127300.1	Phvul.009G127300	Phvul.009G127300	PF12937
10	Phvul.009G160700.1	Phvul.009G160700	Phvul.009G160700	PF03016
11	Phvul.009G160700.1	Phvul.009G160700	Phvul.009G160700	PF03016
12	Phvul.009G160700.1	Phvul.009G160700	Phvul.009G160700	PF03016
13	Phvul.009G160700.1	Phvul.009G160700	Phvul.009G160700	PF03016
14	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
15	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
16	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
17	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
18	Phvul.011G047100.1	Phvul.011G047100	Phvul.011G047100	PF00170
19	Phvul.011G047100.1	Phvul.011G047100	Phvul.011G047100	PF00170
20	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
21	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
22	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
23	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
24	Phvul.L007343.1	Phvul.L007343	Phvul.L007343	PF07731,PF07
25	Phvul.L007343.1	Phvul.L007343	Phvul.L007343	PF07731,PF07
26	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
27	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
28	Phvul.001G036800.1	Phvul.001G036800	Phvul.001G036800	PF08244,PF00
29	Phvul.001G100700.2	Phvul.001G100700	Phvul.001G100700	PF00076
30	Phvul.001G100700.2	Phvul.001G100700	Phvul.001G100700	PF00076
31	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
32	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
33	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
34	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
35	Phvul.001G247000.1	Phvul.001G247000	Phvul.001G247000	PF00364
36	Phvul.002G004100.1	Phvul.002G004100	Phvul.002G004100	PF03330,PF01
37	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
38	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
39	Phvul.002G212900.1	Phvul.002G212900	Phvul.002G212900	PF12689
40	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
41	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
42	Phvul.003G029000.2	Phvul.003G029000	Phvul.003G029000	PF13646,PF02
43	Phvul.003G029000.1	Phvul.003G029000	Phvul.003G029000	PF13646,PF02

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4	1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
5	1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
6	1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
7	1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
8	1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
9	1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
10	1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
11	1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
12	1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
13	1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF00
14	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
15	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
16	1	Phvul.003G141700.1	Phvul.003G141700	Phvul.003G141700	PF00566
17	1	Phvul.003G141700.1	Phvul.003G141700	Phvul.003G141700	PF00566
18	1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF00
19	1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF00
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21	1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF00
22	1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF00
23	1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF00
24	1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601	PF00076
25	1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800	PF00076
26	1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800	PF00076
27	1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
28	1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
29	1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
30	1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
31	1	Phvul.004G032100.1	Phvul.004G032100	Phvul.004G032100	0
32	1	Phvul.004G044900.1	Phvul.004G044900	Phvul.004G044900	PF08263,PF00
33	1	Phvul.004G044900.1	Phvul.004G044900	Phvul.004G044900	PF08263,PF00
34	1	Phvul.004G163200.1	Phvul.004G163200	Phvul.004G163200	PF00225
35	1	Phvul.005G010700.2	Phvul.005G010700	Phvul.005G010700	PF11717,PF01
36	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
37	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
38	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
39	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
40	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
41	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
42	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
43	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
44	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
45	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
46	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
47	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
48	1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
49	1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
50	1	Phvul.005G081600.1	Phvul.005G081600	Phvul.005G081600	PF13692,PF13
51	1	Phvul.005G081600.1	Phvul.005G081600	Phvul.005G081600	PF13692,PF13
52	1	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
53	1	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
54	1	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
55	1	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
56	1	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
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1 Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634	
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1 Phvul.006G062000.1	Phvul.006G062000	Phvul.006G062000		0
1 Phvul.006G130611.1	Phvul.006G130611	Phvul.006G130611	PF00282	
1 Phvul.006G130611.1	Phvul.006G130611	Phvul.006G130611	PF00282	
1 Phvul.006G192200.2	Phvul.006G192200	Phvul.006G192200	PF00622,PF13	
1 Phvul.006G192200.1	Phvul.006G192200	Phvul.006G192200	PF00622,PF13	
1 Phvul.006G192200.4	Phvul.006G192200	Phvul.006G192200	PF00622,PF13	
1 Phvul.006G192200.3	Phvul.006G192200	Phvul.006G192200	PF00622,PF13	
1 Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570	
1 Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570	
1 Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695	
1 Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695	
1 Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300		0
1 Phvul.007G198500.1	Phvul.007G198500	Phvul.007G198500	PF13414	
1 Phvul.007G198500.1	Phvul.007G198500	Phvul.007G198500	PF13414	
1 Phvul.007G233800.1	Phvul.007G233800	Phvul.007G233800		0
1 Phvul.007G233800.2	Phvul.007G233800	Phvul.007G233800		0
1 Phvul.007G233800.1	Phvul.007G233800	Phvul.007G233800		0
1 Phvul.007G233800.2	Phvul.007G233800	Phvul.007G233800		0
1 Phvul.008G008300.6	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.3	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.5	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.4	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.2	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.6	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.3	Phvul.008G008300	Phvul.008G008300		0
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1 Phvul.008G008300.4	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G008300.2	Phvul.008G008300	Phvul.008G008300		0
1 Phvul.008G009200.2	Phvul.008G009200	Phvul.008G009200	PF07522,PF04	
1 Phvul.008G009200.2	Phvul.008G009200	Phvul.008G009200	PF07522,PF04	
1 Phvul.008G009200.2	Phvul.008G009200	Phvul.008G009200	PF07522,PF04	
1 Phvul.008G009200.2	Phvul.008G009200	Phvul.008G009200	PF07522,PF04	
1 Phvul.008G038300.1	Phvul.008G038300	Phvul.008G038300	PF03105,PF03	
1 Phvul.008G038300.1	Phvul.008G038300	Phvul.008G038300	PF03105,PF03	
2 Phvul.008G093200.3	Phvul.008G093200	Phvul.008G093200	PF00560,PF08	
2 Phvul.008G093200.2	Phvul.008G093200	Phvul.008G093200	PF00560,PF08	
2 Phvul.008G093200.1	Phvul.008G093200	Phvul.008G093200	PF00560,PF08	
2 Phvul.008G093200.3	Phvul.008G093200	Phvul.008G093200	PF00560,PF08	
2 Phvul.008G093200.2	Phvul.008G093200	Phvul.008G093200	PF00560,PF08	
2 Phvul.008G093200.1	Phvul.008G093200	Phvul.008G093200	PF00560,PF08	
2 Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800		0

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3	2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
4	2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
5	2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
6	2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
7	1	Phvul.008G110000.1	Phvul.008G110000	Phvul.008G110000	PF05056
8	1	Phvul.008G110200.1	Phvul.008G110200	Phvul.008G110200	PF05056
9	1	Phvul.008G110200.1	Phvul.008G110200	Phvul.008G110200	PF05056
10	1	Phvul.008G110200.1	Phvul.008G110200	Phvul.008G110200	PF05056
11	1	Phvul.008G110400.1	Phvul.008G110400	Phvul.008G110400	PF05056
12	1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500	PF05056
13	1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500	PF05056
14	1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500	PF05056
15	1	Phvul.008G199500.1	Phvul.008G199500	Phvul.008G199500	0
16	1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
17	1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
18	1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
19	1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
20	1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
21	1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
22	1	Phvul.009G026200.1	Phvul.009G026200	Phvul.009G026200	PF02362,PF06
23	1	Phvul.009G026200.1	Phvul.009G026200	Phvul.009G026200	PF02362,PF06
24	1	Phvul.009G040800.3	Phvul.009G040800	Phvul.009G040800	0
25	1	Phvul.009G040800.1	Phvul.009G040800	Phvul.009G040800	0
26	1	Phvul.009G040800.1	Phvul.009G040800	Phvul.009G040800	0
27	1	Phvul.009G040800.2	Phvul.009G040800	Phvul.009G040800	0
28	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
29	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
30	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
31	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
32	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
33	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
34	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
35	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
36	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
37	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
38	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
39	1	Phvul.009G246900.4	Phvul.009G246900	Phvul.009G246900	PF00153
40	1	Phvul.009G246900.3	Phvul.009G246900	Phvul.009G246900	PF00153
41	1	Phvul.009G246900.1	Phvul.009G246900	Phvul.009G246900	PF00153
42	1	Phvul.009G246900.1	Phvul.009G246900	Phvul.009G246900	PF00153
43	1	Phvul.009G246900.2	Phvul.009G246900	Phvul.009G246900	PF00153
44	1	Phvul.009G246900.4	Phvul.009G246900	Phvul.009G246900	PF00153
45	1	Phvul.009G246900.3	Phvul.009G246900	Phvul.009G246900	PF00153
46	1	Phvul.009G246900.3	Phvul.009G246900	Phvul.009G246900	PF00153
47	1	Phvul.009G246900.1	Phvul.009G246900	Phvul.009G246900	PF00153
48	1	Phvul.009G246900.2	Phvul.009G246900	Phvul.009G246900	PF00153
49	1	Phvul.009G246900.2	Phvul.009G246900	Phvul.009G246900	PF00153
50	1	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
51	1	Phvul.010G048400.3	Phvul.010G048400	Phvul.010G048400	PF08879
52	1	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
53	1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
54	1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
55	1	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
56	1	Phvul.010G048400.3	Phvul.010G048400	Phvul.010G048400	PF08879
57	1	Phvul.010G048400.3	Phvul.010G048400	Phvul.010G048400	PF08879
58	1	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
59	1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
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3	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
4	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
5	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
6	Phvul.010G048400.3	Phvul.010G048400	Phvul.010G048400	PF08879
7	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
8	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
9	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
10	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
11	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
12	Phvul.010G116400.1	Phvul.010G116400	Phvul.010G116400	PF05659,PF04
13	Phvul.011G013800.1	Phvul.011G013800	Phvul.011G013800	PF00642,PF00
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15	Phvul.011G013800.1	Phvul.011G013800	Phvul.011G013800	PF00642,PF00
16	Phvul.011G013800.1	Phvul.011G013800	Phvul.011G013800	PF00642,PF00
17	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
18	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
19	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
20	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
21	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
22	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
23	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
24	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
25	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
26	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
27	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
28	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
29	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
30	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
31	Phvul.011G190200.3	Phvul.011G190200	Phvul.011G190200	PF05033,PF00
32	Phvul.011G190200.2	Phvul.011G190200	Phvul.011G190200	PF05033,PF00
33	Phvul.001G098600.1	Phvul.001G098600	Phvul.001G098600	PF05553
34	Phvul.001G098600.1	Phvul.001G098600	Phvul.001G098600	PF05553
35	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818
36	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
37	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
38	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
39	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818
40	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
41	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
42	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
43	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818
44	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
45	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
46	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
47	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818



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4	1	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
5	1	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
6	1	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
7	1	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818
8	1	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
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10	1	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
11	1	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
12	1	Phvul.001G147800.2	Phvul.001G147800	Phvul.001G147800	0
13					
14	1	Phvul.001G173900.1	Phvul.001G173900	Phvul.001G173900	PF13911
15	1	Phvul.001G173900.1	Phvul.001G173900	Phvul.001G173900	PF13911
16	1	Phvul.001G173900.1	Phvul.001G173900	Phvul.001G173900	PF13911
17	1	Phvul.001G173900.1	Phvul.001G173900	Phvul.001G173900	PF13911
18	1	Phvul.001G173900.1	Phvul.001G173900	Phvul.001G173900	PF13911
19	1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
20	1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
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22	1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
23	1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
24	1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
25	1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
26	1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
27	1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
28	1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
29	1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
30	1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
31	1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03
32	1	Phvul.001G260300.1	Phvul.001G260300	Phvul.001G260300	PF04564
33					
34	1	Phvul.001G268700.1	Phvul.001G268700	Phvul.001G268700	PF08100,PF00
35	1	Phvul.001G268700.1	Phvul.001G268700	Phvul.001G268700	PF08100,PF00
36	2	Phvul.002G058900.1	Phvul.002G058900	Phvul.002G058900	PF13912
37	2	Phvul.002G058900.1	Phvul.002G058900	Phvul.002G058900	PF13912
38	1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
39	1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
40	1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
41	1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
42	1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
43	1	Phvul.002G163400.1	Phvul.002G163400	Phvul.002G163400	PF03106
44	1	Phvul.002G163400.1	Phvul.002G163400	Phvul.002G163400	PF03106
45	1	Phvul.002G163400.1	Phvul.002G163400	Phvul.002G163400	PF03106
46	1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738
47	1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738
48	1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738
49	1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738
50	1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738
51	1	Phvul.002G216700.3	Phvul.002G216700	Phvul.002G216700	PF00010
52	1	Phvul.002G216700.2	Phvul.002G216700	Phvul.002G216700	PF00010
53	1	Phvul.002G216700.3	Phvul.002G216700	Phvul.002G216700	PF00010
54	1	Phvul.002G216700.2	Phvul.002G216700	Phvul.002G216700	PF00010
55	1	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657
56	1	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657
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3	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
4	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
5	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
6	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
7	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
8	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
9	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
10	Phvul.002G290904.1	Phvul.002G290904	Phvul.002G290904	PF11940
11	Phvul.002G290904.1	Phvul.002G290904	Phvul.002G290904	PF11940
12	Phvul.002G309100.1	Phvul.002G309100	Phvul.002G309100	PF00481
13	Phvul.002G309100.1	Phvul.002G309100	Phvul.002G309100	PF00481
14	Phvul.002G320900.1	Phvul.002G320900	Phvul.002G320900	PF03152
15	Phvul.002G320900.1	Phvul.002G320900	Phvul.002G320900	PF03152
16	Phvul.002G320900.1	Phvul.002G320900	Phvul.002G320900	PF03152
17	Phvul.002G320900.1	Phvul.002G320900	Phvul.002G320900	PF03152
18	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
19	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
20	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
21	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
22	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
23	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
24	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
25	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
26	Phvul.003G032300.1	Phvul.003G032300	Phvul.003G032300	PF15628
27	Phvul.003G032300.1	Phvul.003G032300	Phvul.003G032300	PF15628
28	Phvul.003G057700.1	Phvul.003G057700	Phvul.003G057700	PF13641
29	Phvul.003G057700.1	Phvul.003G057700	Phvul.003G057700	PF13641
30	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
31	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
32	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
33	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
34	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
35	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
36	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
37	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
38	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
39	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
40	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
41	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
42	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
43	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
44	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
45	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
46	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
47	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
48	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
49	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
50	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF00

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6	1	Phvul.003G280100.2	Phvul.003G280100	Phvul.003G280100 PF03141
7	1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601 PF00076
8	1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601 PF00076
9	1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601 PF00076
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11	1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601 PF00076
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13	1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800 PF00076
14	1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800 PF00076
15	1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800 PF00076
16	1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800 PF00076
17	1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800 PF00076
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42	1	Phvul.005G006400.1	Phvul.005G006400	Phvul.005G006400 PF12796
43	1	Phvul.005G006400.1	Phvul.005G006400	Phvul.005G006400 PF12796
44	1	Phvul.005G006400.1	Phvul.005G006400	Phvul.005G006400 PF12796
45	1	Phvul.005G014300.2	Phvul.005G014300	Phvul.005G014300 PF00808
46	1	Phvul.005G056400.1	Phvul.005G056400	Phvul.005G056400 PF00651
47	1	Phvul.005G095300.1	Phvul.005G095300	Phvul.005G095300 PF00311
48	1	Phvul.005G100300.1	Phvul.005G100300	Phvul.005G100300 PF10551
49	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100 PF01738
50	1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100 PF01738
51	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100 PF01738
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53	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100 PF01738
54	1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100 PF01738
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56	1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100 PF01738
57	1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100 PF01738
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59	1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100 PF01738
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1	Phvul.006G113800.2	Phvul.006G113800	Phvul.006G113800	PF14227,PF02
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1	Phvul.006G113800.1	Phvul.006G113800	Phvul.006G113800	PF14227,PF02
1	Phvul.006G121500.1	Phvul.006G121500	Phvul.006G121500	PF00955
1	Phvul.006G121500.2	Phvul.006G121500	Phvul.006G121500	PF00955
1	Phvul.006G121500.1	Phvul.006G121500	Phvul.006G121500	PF00955
1	Phvul.006G121500.2	Phvul.006G121500	Phvul.006G121500	PF00955
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2	Phvul.006G158900.1	Phvul.006G158900	Phvul.006G158900	PF15365
1	Phvul.006G168154.1	Phvul.006G168154	Phvul.006G168154	PF00450
1	Phvul.006G168154.2	Phvul.006G168154	Phvul.006G168154	PF00450
1	Phvul.006G168154.1	Phvul.006G168154	Phvul.006G168154	PF00450
1	Phvul.006G168154.2	Phvul.006G168154	Phvul.006G168154	PF00450
1	Phvul.006G193700.1	Phvul.006G193700	Phvul.006G193700	PF04641,PF15
1	Phvul.006G193700.1	Phvul.006G193700	Phvul.006G193700	PF04641,PF15
1	Phvul.007G012500.1	Phvul.007G012500	Phvul.007G012500	PF00326,PF02
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1	Phvul.007G015000.1	Phvul.007G015000	Phvul.007G015000	PF03634
1	Phvul.007G034000.1	Phvul.007G034000	Phvul.007G034000	PF03034
1	Phvul.007G051100.1	Phvul.007G051100	Phvul.007G051100	PF01657,PF07
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7	1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
8	1	Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570
9	1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
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11	1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
12	1	Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570
13	1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
14	1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
15	1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
16	1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
17	1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
18	1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
19	1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
20	1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
21	1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
22	1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
23	1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
24	1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
25	1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
26	1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
27	1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
28	1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
29	1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
30	1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
31	1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
32	1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
33	1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
34	1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
35	1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
36	1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
37	1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
38	1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
39	1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
40	1	Phvul.007G189000.1	Phvul.007G189000	Phvul.007G189000	0
41	1	Phvul.007G189000.1	Phvul.007G189000	Phvul.007G189000	0
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43	1	Phvul.007G189000.1	Phvul.007G189000	Phvul.007G189000	0
44	1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
45	1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
46	1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
47	1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
48	1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
49	1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
50	1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
51	1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
52	1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
53	1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
54	1	Phvul.007G210400.1	Phvul.007G210400	Phvul.007G210400	PF04043,PF01
55	1	Phvul.007G275700.1	Phvul.007G275700	Phvul.007G275700	PF00045
56	1	Phvul.007G275700.1	Phvul.007G275700	Phvul.007G275700	PF00045
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58	1	Phvul.007G276200.1	Phvul.007G276200	Phvul.007G276200	PF00045
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3	1 Phvul.007G276300.1	Phvul.007G276300	Phvul.007G276300	PF00045
4	1 Phvul.008G003900.1	Phvul.008G003900	Phvul.008G003900	0
5	1 Phvul.008G003900.1	Phvul.008G003900	Phvul.008G003900	0
6	1 Phvul.008G003900.1	Phvul.008G003900	Phvul.008G003900	0
7	1 Phvul.008G003900.1	Phvul.008G003900	Phvul.008G003900	0
8	1 Phvul.008G008300.6	Phvul.008G008300	Phvul.008G008300	0
9	1 Phvul.008G008300.3	Phvul.008G008300	Phvul.008G008300	0
10	1 Phvul.008G008300.5	Phvul.008G008300	Phvul.008G008300	0
11	1 Phvul.008G008300.4	Phvul.008G008300	Phvul.008G008300	0
12	1 Phvul.008G008300.2	Phvul.008G008300	Phvul.008G008300	0
13	1 Phvul.008G012100.1	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
14	1 Phvul.008G012100.2	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
15	1 Phvul.008G048200.1	Phvul.008G048200	Phvul.008G048200	PF02536
16	1 Phvul.008G069000.1	Phvul.008G069000	Phvul.008G069000	0
17	1 Phvul.008G069000.1	Phvul.008G069000	Phvul.008G069000	0
18	1 Phvul.008G069000.1	Phvul.008G069000	Phvul.008G069000	0
19	1 Phvul.008G069000.1	Phvul.008G069000	Phvul.008G069000	0
20	2 Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
21	2 Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
22	2 Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
23	2 Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
24	2 Phvul.008G093200.3	Phvul.008G093200	Phvul.008G093200	PF00560,PF08
25	2 Phvul.008G093200.2	Phvul.008G093200	Phvul.008G093200	PF00560,PF08
26	2 Phvul.008G093200.1	Phvul.008G093200	Phvul.008G093200	PF00560,PF08
27	2 Phvul.008G093200.3	Phvul.008G093200	Phvul.008G093200	PF00560,PF08
28	2 Phvul.008G093200.2	Phvul.008G093200	Phvul.008G093200	PF00560,PF08
29	2 Phvul.008G093200.1	Phvul.008G093200	Phvul.008G093200	PF00560,PF08
30	1 Phvul.008G110000.1	Phvul.008G110000	Phvul.008G110000	PF05056
31	1 Phvul.008G110000.1	Phvul.008G110000	Phvul.008G110000	PF05056
32	1 Phvul.008G110100.1	Phvul.008G110100	Phvul.008G110100	PF05056
33	1 Phvul.008G110400.1	Phvul.008G110400	Phvul.008G110400	PF05056
34	1 Phvul.008G110400.1	Phvul.008G110400	Phvul.008G110400	PF05056
35	1 Phvul.008G118900.1	Phvul.008G118900	Phvul.008G118900	PF00026
36	1 Phvul.008G118900.1	Phvul.008G118900	Phvul.008G118900	PF00026
37	1 Phvul.008G157900.1	Phvul.008G157900	Phvul.008G157900	0
38	1 Phvul.008G157900.1	Phvul.008G157900	Phvul.008G157900	0
39	1 Phvul.008G157900.1	Phvul.008G157900	Phvul.008G157900	0
40	1 Phvul.008G157900.1	Phvul.008G157900	Phvul.008G157900	0
41	1 Phvul.008G206400.5	Phvul.008G206400	Phvul.008G206400	PF01575
42	1 Phvul.008G206400.1	Phvul.008G206400	Phvul.008G206400	PF01575
43	1 Phvul.008G206400.5	Phvul.008G206400	Phvul.008G206400	PF01575



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4	1	Phvul.008G206400.1	Phvul.008G206400	Phvul.008G206400	PF01575
5	1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
6	1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
7	1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
8					
9	1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
10	1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
11	1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
12					
13	1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
14	1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
15	1	Phvul.008G274900.1	Phvul.008G274900	Phvul.008G274900	PF00076
16	1	Phvul.008G274900.2	Phvul.008G274900	Phvul.008G274900	PF00076
17					
18	1	Phvul.008G274900.3	Phvul.008G274900	Phvul.008G274900	PF00076
19	1	Phvul.008G282700.1	Phvul.008G282700	Phvul.008G282700	PF02628
20	1	Phvul.008G282700.1	Phvul.008G282700	Phvul.008G282700	PF02628
21					
22	1	Phvul.009G106700.1	Phvul.009G106700	Phvul.009G106700	PF00249
23	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
24	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
25					
26	1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
27	1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
28	1	Phvul.009G173100.1	Phvul.009G173100	Phvul.009G173100	PF00069
29					
30	1	Phvul.009G173100.3	Phvul.009G173100	Phvul.009G173100	PF00069
31	1	Phvul.009G173100.1	Phvul.009G173100	Phvul.009G173100	PF00069
32	1	Phvul.009G173100.3	Phvul.009G173100	Phvul.009G173100	PF00069
33					
34	1	Phvul.009G232500.1	Phvul.009G232500	Phvul.009G232500	PF01301
35	1	Phvul.009G232500.1	Phvul.009G232500	Phvul.009G232500	PF01301
36	1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
37					
38	1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
39	1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
40	1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
41					
42	1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
43	1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
44					
45	1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
46	1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
47	1	Phvul.010G043700.5	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
48	1	Phvul.010G043700.6	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
49					
50	1	Phvul.010G043700.4	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
51	1	Phvul.010G043700.1	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
52	1	Phvul.010G043700.3	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
53					
54	1	Phvul.010G043700.2	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
55	1	Phvul.010G043700.9	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
56	1	Phvul.010G043700.8	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
57	1	Phvul.010G043700.7	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
58					
59	1	Phvul.010G043700.5	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
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1	Phvul.010G043700.6	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
2	Phvul.010G043700.4	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
3	Phvul.010G043700.1	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
4	Phvul.010G043700.3	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
5	Phvul.010G043700.2	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
6	Phvul.010G043700.9	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
7	Phvul.010G043700.8	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
8	Phvul.010G043700.7	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
9	Phvul.010G070600.1	Phvul.010G070600	Phvul.010G070600	PF00010
10	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
11	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
12	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
13	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
14	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
15	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
16	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
17	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
18	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
19	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
20	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
21	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
22	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
23	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
24	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
25	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
26	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
27	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
28	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
29	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
30	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
31	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
32	Phvul.011G061600.1	Phvul.011G061600	Phvul.011G061600	PF05368
33	Phvul.011G061600.1	Phvul.011G061600	Phvul.011G061600	PF05368
34	Phvul.011G114700.1	Phvul.011G114700	Phvul.011G114700	PF05938
35	Phvul.011G123000.1	Phvul.011G123000	Phvul.011G123000	PF05938
36	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
37	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
38	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
39	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
40	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
41	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
42	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
43	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112

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4	1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
5	1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
6	1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
7	1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
8	1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
9	1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
10	1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
11	1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
12	1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
13	1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
14	1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
15	1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
16	1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
17	1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
18	1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
19	1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
20	1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
21	1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
22	1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
23	1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
24	1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
25	1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
26	1	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
27	2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
28	2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
29	1	Phvul.L007343.1	Phvul.L007343	Phvul.L007343	PF07731,PF07
30	1	Phvul.008G004400.1	Phvul.008G004400	Phvul.008G004400	PF00107,PF16
31	1	Phvul.008G004400.1	Phvul.008G004400	Phvul.008G004400	PF00107,PF16
32	1	Phvul.001G020300.1	Phvul.001G020300	Phvul.001G020300	PF01734
33	1	Phvul.001G020350.1	Phvul.001G020350	Phvul.001G020350	PF01734
34	1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
35	1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
36	1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
37	1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
38	2	Phvul.001G036800.1	Phvul.001G036800	Phvul.001G036800	PF08244,PF00
39	1	Phvul.001G057800.1	Phvul.001G057800	Phvul.001G057800	PF10058
40	1	Phvul.001G057800.1	Phvul.001G057800	Phvul.001G057800	PF10058
41	2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF00
42	2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF00
43	1	Phvul.001G097800.1	Phvul.001G097800	Phvul.001G097800	PF16177,PF13
44	1	Phvul.001G097800.1	Phvul.001G097800	Phvul.001G097800	PF16177,PF13
45	1	Phvul.001G109300.2	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
46	1	Phvul.001G109300.1	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
47	1	Phvul.001G109300.2	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
48	1	Phvul.001G109300.1	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
49	1	Phvul.001G114900.1	Phvul.001G114900	Phvul.001G114900	PF01042,PF01
50	1	Phvul.001G114900.1	Phvul.001G114900	Phvul.001G114900	PF01042,PF01
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1	Phvul.001G123000.2	Phvul.001G123000	Phvul.001G123000	PF01055
2	Phvul.001G123000.2	Phvul.001G123000	Phvul.001G123000	PF01055
3	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
4	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
5	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
6	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
7	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
8	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
9	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
10	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
11	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
12	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
13	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
14	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
15	Phvul.001G159300.1	Phvul.001G159300	Phvul.001G159300	PF03195
16	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
17	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
18	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
19	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
20	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
21	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
22	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
23	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
24	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
25	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
26	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
27	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
28	Phvul.001G214300.2	Phvul.001G214300	Phvul.001G214300	PF05691
29	Phvul.001G214300.1	Phvul.001G214300	Phvul.001G214300	PF05691
30	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
31	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
32	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
33	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
34	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
35	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
36	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
37	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
38	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
39	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
40	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
41	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
42	Phvul.002G058900.1	Phvul.002G058900	Phvul.002G058900	PF13912
43	Phvul.002G058900.1	Phvul.002G058900	Phvul.002G058900	PF13912
44	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
45	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
46	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
47	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
48	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
49	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657
50	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657
51	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657

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4	1	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657
5	1	Phvul.002G253100.1	Phvul.002G253100	Phvul.002G253100	PF00415
6	1	Phvul.002G253100.1	Phvul.002G253100	Phvul.002G253100	PF00415
7	1	Phvul.002G262600.1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00
8	1	Phvul.002G290000.3	Phvul.002G290000	Phvul.002G290000	PF00010
9	1	Phvul.002G290000.3	Phvul.002G290000	Phvul.002G290000	PF00010
10	1	Phvul.003G022200.1	Phvul.003G022200	Phvul.003G022200	PF10508
11	1	Phvul.003G022200.1	Phvul.003G022200	Phvul.003G022200	PF10508
12	1	Phvul.003G022200.1	Phvul.003G022200	Phvul.003G022200	PF10508
13	1	Phvul.003G022200.1	Phvul.003G022200	Phvul.003G022200	PF10508
14	1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
15	1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
16	1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
17	1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
18	1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
19	1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
20	1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
21	1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
22	1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
23	1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
24	1	Phvul.003G088200.1	Phvul.003G088200	Phvul.003G088200	PF02893,PF00
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26	1	Phvul.003G088200.1	Phvul.003G088200	Phvul.003G088200	PF02893,PF00
27	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
28	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
29	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
30	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
31	1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
32	1	Phvul.003G119100.3	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
33	1	Phvul.003G119100.2	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
34	1	Phvul.003G119100.1	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
35	1	Phvul.003G119100.1	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
36	1	Phvul.003G169700.1	Phvul.003G169700	Phvul.003G169700	PF03016
37	1	Phvul.003G292000.1	Phvul.003G292000	Phvul.003G292000	PF00852
38	1	Phvul.004G058600.1	Phvul.004G058600	Phvul.004G058600	PF04193
39	1	Phvul.004G058600.1	Phvul.004G058600	Phvul.004G058600	PF04193
40	1	Phvul.004G121666.1	Phvul.004G121666	Phvul.004G121666	PF02874,PF00
41	1	Phvul.004G121666.1	Phvul.004G121666	Phvul.004G121666	PF02874,PF00
42	1	Phvul.004G121666.1	Phvul.004G121666	Phvul.004G121666	PF02874,PF00
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44	1	Phvul.004G121666.1	Phvul.004G121666	Phvul.004G121666	PF02874,PF00
45	1	Phvul.004G133700.1	Phvul.004G133700	Phvul.004G133700	PF02213,PF02
46	1	Phvul.004G133700.1	Phvul.004G133700	Phvul.004G133700	PF02213,PF02
47	1	Phvul.004G133700.1	Phvul.004G133700	Phvul.004G133700	PF02213,PF02
48	1	Phvul.004G133700.1	Phvul.004G133700	Phvul.004G133700	PF02213,PF02
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51	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
52	1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
53	1	Phvul.005G056400.1	Phvul.005G056400	Phvul.005G056400	PF00651
54	1	Phvul.005G056400.1	Phvul.005G056400	Phvul.005G056400	PF00651
55	1	Phvul.005G056400.1	Phvul.005G056400	Phvul.005G056400	PF00651
56	1	Phvul.005G088800.1	Phvul.005G088800	Phvul.005G088800	PF11883,PF08
57	1	Phvul.005G095600.1	Phvul.005G095600	Phvul.005G095600	PF13419
58	1	Phvul.005G095600.1	Phvul.005G095600	Phvul.005G095600	PF13419
59	1	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
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4	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
5	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
6	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
7	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
8	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
9	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
10	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
11	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
12	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
13	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
14	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
15	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
16	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
17	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
18	Phvul.005G101400.3	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
19	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
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21	Phvul.005G101400.3	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
22	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
23	Phvul.005G101400.1	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
24	Phvul.005G130100.1	Phvul.005G130100	Phvul.005G130100	0
25	Phvul.005G130100.1	Phvul.005G130100	Phvul.005G130100	0
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28	Phvul.005G173200.1	Phvul.005G173200	Phvul.005G173200	0
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32	Phvul.006G143300.1	Phvul.006G143300	Phvul.006G143300	0
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35	Phvul.006G143300.1	Phvul.006G143300	Phvul.006G143300	0
36	Phvul.006G168163.1	Phvul.006G168163	Phvul.006G168163	PF00450
37	Phvul.006G168163.1	Phvul.006G168163	Phvul.006G168163	PF00450
38	Phvul.007G035900.2	Phvul.007G035900	Phvul.007G035900	PF00085,PF04
39	Phvul.007G035900.2	Phvul.007G035900	Phvul.007G035900	PF00085,PF04
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41	Phvul.007G035900.2	Phvul.007G035900	Phvul.007G035900	PF00085,PF04
42	Phvul.007G069900.3	Phvul.007G069900	Phvul.007G069900	PF13041
43	Phvul.007G069900.5	Phvul.007G069900	Phvul.007G069900	PF13041
44	Phvul.007G069900.1	Phvul.007G069900	Phvul.007G069900	PF13041
45	Phvul.007G069900.4	Phvul.007G069900	Phvul.007G069900	PF13041
46	Phvul.007G069900.3	Phvul.007G069900	Phvul.007G069900	PF13041
47	Phvul.007G069900.5	Phvul.007G069900	Phvul.007G069900	PF13041
48	Phvul.007G069900.1	Phvul.007G069900	Phvul.007G069900	PF13041
49	Phvul.007G069900.4	Phvul.007G069900	Phvul.007G069900	PF13041

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4	1	Phvul.007G069900.5	Phvul.007G069900	Phvul.007G069900 PF13041
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6	1	Phvul.007G069900.4	Phvul.007G069900	Phvul.007G069900 PF13041
7	1	Phvul.007G069900.3	Phvul.007G069900	Phvul.007G069900 PF13041
8	1	Phvul.007G069900.5	Phvul.007G069900	Phvul.007G069900 PF13041
9	1	Phvul.007G069900.1	Phvul.007G069900	Phvul.007G069900 PF13041
10	1	Phvul.007G069900.4	Phvul.007G069900	Phvul.007G069900 PF13041
11	1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300 PF12646
12	1	Phvul.007G114100.1	Phvul.007G114100	Phvul.007G114100 PF00628
13	1	Phvul.007G114100.1	Phvul.007G114100	Phvul.007G114100 PF00628
14	1	Phvul.007G114100.1	Phvul.007G114100	Phvul.007G114100 PF00628
15	1	Phvul.007G114100.1	Phvul.007G114100	Phvul.007G114100 PF00628
16	1	Phvul.007G184600.1	Phvul.007G184600	Phvul.007G184600 PF07714,PF14
17	1	Phvul.007G184600.1	Phvul.007G184600	Phvul.007G184600 PF07714,PF14
18	1	Phvul.007G192300.1	Phvul.007G192300	Phvul.007G192300 PF04564,PF00
19	1	Phvul.007G210400.1	Phvul.007G210400	Phvul.007G210400 PF04043,PF01
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26	1	Phvul.007G215300.1	Phvul.007G215300	Phvul.007G215300 PF00628,PF00
27	1	Phvul.007G215300.1	Phvul.007G215300	Phvul.007G215300 PF00628,PF00
28	1	Phvul.007G215300.1	Phvul.007G215300	Phvul.007G215300 PF00628,PF00
29	1	Phvul.007G215300.1	Phvul.007G215300	Phvul.007G215300 PF00628,PF00
30	1	Phvul.007G251800.1	Phvul.007G251800	Phvul.007G251800 PF00085,PF00
31	2	Phvul.008G043400.1	Phvul.008G043400	Phvul.008G043400 PF08263,PF13
32	2	Phvul.008G043400.1	Phvul.008G043400	Phvul.008G043400 PF08263,PF13
33	1	Phvul.008G067300.1	Phvul.008G067300	Phvul.008G067300 PF00249
34	1	Phvul.008G067300.1	Phvul.008G067300	Phvul.008G067300 PF00249
35	1	Phvul.008G110100.1	Phvul.008G110100	Phvul.008G110100 PF05056
36	1	Phvul.008G110100.1	Phvul.008G110100	Phvul.008G110100 PF05056
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38	1	Phvul.008G110100.1	Phvul.008G110100	Phvul.008G110100 PF05056
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59	1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500 PF05056
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1 Phvul.008G125400.2	Phvul.008G125400	Phvul.008G125400	PF08513,PF00
1 Phvul.008G125400.1	Phvul.008G125400	Phvul.008G125400	PF08513,PF00
1 Phvul.008G229100.1	Phvul.008G229100	Phvul.008G229100	PF02225,PF05
1 Phvul.008G279750.1	Phvul.008G279750	Phvul.008G279750	PF03552
1 Phvul.008G279750.1	Phvul.008G279750	Phvul.008G279750	PF03552
1 Phvul.009G010800.1	Phvul.009G010800	Phvul.009G010800	PF00246
1 Phvul.009G010800.1	Phvul.009G010800	Phvul.009G010800	PF00246
1 Phvul.009G034800.1	Phvul.009G034800	Phvul.009G034800	0
1 Phvul.009G060200.1	Phvul.009G060200	Phvul.009G060200	PF01565,PF09
1 Phvul.009G060200.2	Phvul.009G060200	Phvul.009G060200	PF01565,PF09
1 Phvul.009G060200.1	Phvul.009G060200	Phvul.009G060200	PF01565,PF09
1 Phvul.009G060200.2	Phvul.009G060200	Phvul.009G060200	PF01565,PF09
1 Phvul.009G060200.1	Phvul.009G060200	Phvul.009G060200	PF01565,PF09
1 Phvul.009G060200.2	Phvul.009G060200	Phvul.009G060200	PF01565,PF09
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1 Phvul.009G232500.1	Phvul.009G232500	Phvul.009G232500	PF01301
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1 Phvul.009G255100.1	Phvul.009G255100	Phvul.009G255100	PF02466
1 Phvul.009G255100.2	Phvul.009G255100	Phvul.009G255100	PF02466
1 Phvul.009G255100.1	Phvul.009G255100	Phvul.009G255100	PF02466
1 Phvul.009G255100.2	Phvul.009G255100	Phvul.009G255100	PF02466
1 Phvul.010G026500.1	Phvul.010G026500	Phvul.010G026500	0
1 Phvul.010G026500.1	Phvul.010G026500	Phvul.010G026500	0
1 Phvul.010G026500.1	Phvul.010G026500	Phvul.010G026500	0
1 Phvul.010G026500.1	Phvul.010G026500	Phvul.010G026500	0
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1 Phvul.010G028900.1	Phvul.010G028900	Phvul.010G028900	PF01582,PF00
1 Phvul.010G028900.2	Phvul.010G028900	Phvul.010G028900	PF01582,PF00
1 Phvul.010G028900.1	Phvul.010G028900	Phvul.010G028900	PF01582,PF00
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1 Phvul.010G067900.1	Phvul.010G067900	Phvul.010G067900	PF00069



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4	1	Phvul.010G067900.1	Phvul.010G067900	Phvul.010G067900	PF00069
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6	2	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
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13	2	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
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22	1	Phvul.011G001200.2	Phvul.011G001200	Phvul.011G001200	PF02383
23	1	Phvul.011G001200.1	Phvul.011G001200	Phvul.011G001200	PF02383
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26	1	Phvul.011G001200.2	Phvul.011G001200	Phvul.011G001200	PF02383
27	1	Phvul.011G001200.1	Phvul.011G001200	Phvul.011G001200	PF02383
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31	1	Phvul.011G001200.1	Phvul.011G001200	Phvul.011G001200	PF02383
32	1	Phvul.011G004200.1	Phvul.011G004200	Phvul.011G004200	0
33	1	Phvul.011G203450.1	Phvul.011G203450	Phvul.011G203450	PF05678
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35	1	Phvul.011G203450.1	Phvul.011G203450	Phvul.011G203450	PF05678
36	1	Phvul.011G203450.1	Phvul.011G203450	Phvul.011G203450	PF05678
37	1	Phvul.011G203450.1	Phvul.011G203450	Phvul.011G203450	PF05678
38	1	Phvul.L001679.1	Phvul.L001679	Phvul.L001679	PF00168
39	1	Phvul.L001679.1	Phvul.L001679	Phvul.L001679	PF00168
40	2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
41	2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
42	1	Phvul.L009843.2	Phvul.L009843	Phvul.L009843	PF00153
43	1	Phvul.L009843.1	Phvul.L009843	Phvul.L009843	PF00153
44	1	Phvul.L009843.2	Phvul.L009843	Phvul.L009843	PF00153
45	1	Phvul.L009843.1	Phvul.L009843	Phvul.L009843	PF00153
46	1	Phvul.L009843.1	Phvul.L009843	Phvul.L009843	PF00153
47	1	Phvul.L009843.1	Phvul.L009843	Phvul.L009843	PF00153
48	1	Phvul.L009843.1	Phvul.L009843	Phvul.L009843	PF00153
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Panther	KOG	KEGG	KOG	GO	Best-hit-arabi-
PTHR13451,P <sup>-</sup>		0	0 K10882	GO:0004518,(	AT2G22140.1
PTHR13451,P <sup>-</sup>		0	0 K10882	GO:0004518,(	AT2G22140.1
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PTHR33917,P <sup>-</sup>		0	0	0	0 AT4G33630.1
PTHR13600,P <sup>-</sup>		0	0	0 GO:0032259,(	AT5G42760.1
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PTHR10766,P <sup>-</sup>		0	0 K17086	GO:0016021	AT5G10840.1
PTHR22849,P <sup>-</sup>		0 6.3.2.19		0 GO:0016567,(	AT1G76390.1
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PTHR22849,P <sup>-</sup>		0 6.3.2.19		0 GO:0016567,(	AT1G76390.1
PTHR11908,P <sup>-</sup>		0 1.17.1.4	K00106	GO:0051536,(	AT4G34890.1
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PTHR11183,P <sup>-</sup>	KOG1950	2.4.1.123	K18819	GO:0016757	AT2G47180.1
PTHR11183,P <sup>-</sup>	KOG1950	2.4.1.123	K18819	GO:0016757	AT2G47180.1
PTHR11183,P <sup>-</sup>	KOG1950	2.4.1.123	K18819	GO:0016757	AT2G47180.1
PTHR11183,P <sup>-</sup>	KOG1950	2.4.1.123	K18819	GO:0016757	AT2G47180.1
PTHR13451,P <sup>-</sup>		0	0 K10882	GO:0004518,(	AT2G22140.1
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PTHR11062,P <sup>-</sup>	KOG1021	2.4.2.41		0	0 AT5G61840.1
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PTHR27004,P <sup>-</sup>	KOG0472	2.7.11.1		0 GO:0005515	AT2G34930.1
PTHR33670,P <sup>-</sup>		0	0	0	0 AT3G21570.1
PTHR33463,P <sup>-</sup>	KOG1947		0	0	0 AT1G61300.1
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PTHR10457,P <sup>-</sup> KOG0631	2.7.1.46	K12446		GO:0005524 AT4G16130.1
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PTHR31719,P <sup>-</sup>	0	0	0	0 GO:0006355,(AT2G33480.2
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PTHR19229,P <sup>-</sup> KOG0059	3.6.3.25	K05643		GO:0005524,(AT2G41700.1

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5	PTHR19229,P <sup>-</sup> KOG0059	3.6.3.25	K05643	GO:0005524,(AT2G41700.1
6	PTHR19229,P <sup>-</sup> KOG0059	3.6.3.25	K05643	GO:0005524,(AT2G41700.1
7	PTHR19229,P <sup>-</sup> KOG0059	3.6.3.25	K05643	GO:0005524,(AT2G41700.1
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9	PTHR19229,P <sup>-</sup> KOG0059	3.6.3.25	K05643	GO:0005524,(AT2G41700.1
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11	PTHR19229,P <sup>-</sup> KOG0059	3.6.3.25	K05643	GO:0005524,(AT2G41700.1
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18	PTHR23293,P <sup>-</sup> KOG2644	2.7.7.2		0 GO:0008152,(AT5G03430.1
19	PTHR23293,P <sup>-</sup> KOG2644	2.7.7.2		0 GO:0008152,(AT5G03430.1
20	PTHR23293,P <sup>-</sup> KOG2644	2.7.7.2		0 GO:0008152,(AT5G03430.1
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24	PTHR13115,P <sup>-</sup>	0	0	0 AT5G43630.1
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44	PTHR13115,P <sup>-</sup>	0	0	0 AT5G43630.1
45	PTHR10438,P <sup>-</sup> KOG0907	1.6.5.4	K03671	GO:0045454,(AT5G39950.1
46	PTHR10438,P <sup>-</sup> KOG0907	1.6.5.4	K03671	GO:0045454,(AT5G39950.1
47	PTHR31928,P <sup>-</sup>	0	0	0 AT1G70340.1
48	PTHR31928,P <sup>-</sup>	0	0	0 AT1G70340.1
49	PTHR31928,P <sup>-</sup>	0	0	0 AT1G70340.1
50	PTHR10201,P <sup>-</sup>	0 3.4.24.23		0 GO:0031012,(AT1G70170.1
51	PTHR10201,P <sup>-</sup>	0 3.4.24.23		0 GO:0031012,(AT1G70170.1
52	PTHR10201,P <sup>-</sup>	0 3.4.24.23		0 GO:0031012,(AT1G70170.1
53	PTHR10201,P <sup>-</sup>	0 3.4.24.23		0 GO:0031012,(AT1G70170.1
54	PTHR10201,P <sup>-</sup>	0 3.4.24.23		0 GO:0031012,(AT1G70170.1
55	PTHR10201,P <sup>-</sup>	0 3.4.24.23		0 GO:0031012,(AT1G70170.1
56	PTHR10110,P <sup>-</sup> KOG1965		0	0 GO:0055085,(AT2G01980.1
57	PTHR10110,P <sup>-</sup> KOG1965		0	0 GO:0055085,(AT2G01980.1
58	PTHR10110,P <sup>-</sup> KOG1965		0	0 GO:0055085,(AT2G01980.1
59	PTHR10110,P <sup>-</sup> KOG1965		0	0 GO:0055085,(AT2G01980.1
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3	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,(AT3G13690.1
4	PTHR23336,P <sup>-</sup>	0	0	0 GO:0008270 AT3G62900.1
5	PTHR23336,P <sup>-</sup>	0	0	0 GO:0008270 AT3G62900.1
6	PTHR27004,P <sup>-</sup> KOG0472	2.7.11.1		0 GO:0005515 AT2G34930.1
7	PTHR24015,P <sup>-</sup>	0	0	0 0 AT4G21190.1
8	PTHR11689,P <sup>-</sup>	0	0 K05016	GO:0055085,(AT5G49890.1
9	PTHR11689,P <sup>-</sup>	0	0 K05016	GO:0055085,(AT5G49890.1
10	PTHR10438,P <sup>-</sup> KOG0907	3.5.1.52		0 GO:0045454,(AT4G29670.1
11	PTHR10438,P <sup>-</sup> KOG0907	3.5.1.52		0 GO:0045454,(AT4G29670.1
12	PTHR10438,P <sup>-</sup> KOG0907	3.5.1.52		0 GO:0045454,(AT4G29670.1
13	PTHR10438,P <sup>-</sup> KOG0907	3.5.1.52		0 GO:0045454,(AT4G29670.1
14	PTHR33090	0	0	0 0 AT4G10265.1
15	PTHR17630 KOG3043	3.1.1.45		0 GO:0016787 AT2G32520.1
16	PTHR17630 KOG3043	3.1.1.45		0 GO:0016787 AT2G32520.1
17	PTHR17630 KOG3043	3.1.1.45		0 GO:0016787 AT2G32520.1
18	PTHR17630 KOG3043	3.1.1.45		0 GO:0016787 AT2G32520.1
19	PTHR33137,P <sup>-</sup>	0	0 K14972	0 AT1G15780.1
20	PTHR33137,P <sup>-</sup>	0	0 K14972	0 AT1G15780.1
21	PTHR11595,P <sup>-</sup> KOG1668		0 K03232	GO:0006414,(AT5G12110.1
22	PTHR11595,P <sup>-</sup> KOG1668		0 K03232	GO:0006414,(AT5G12110.1
23	PTHR11595,P <sup>-</sup> KOG1668		0 K03232	GO:0006414,(AT5G12110.1
24	PTHR11595,P <sup>-</sup> KOG1668		0 K03232	GO:0006414,(AT5G12110.1
25	PTHR19241,P <sup>-</sup>	0 3.6.3.34		0 GO:0016887,(AT2G29940.1
26	PTHR19241,P <sup>-</sup>	0 3.6.3.34		0 GO:0016887,(AT2G29940.1
27	PTHR19241,P <sup>-</sup>	0 3.6.3.34		0 GO:0016887,(AT2G29940.1
28	PTHR19241,P <sup>-</sup>	0 3.6.3.34		0 GO:0016887,(AT2G29940.1
29	PTHR31589,P <sup>-</sup>	0	0	0 0 AT5G18460.1
30	PTHR31589,P <sup>-</sup>	0	0	0 0 AT5G18460.1
31	PTHR23324,P <sup>-</sup>	0	0	0 0 AT5G47730.1
32	PTHR23324,P <sup>-</sup>	0	0	0 0 AT5G47730.1
33	PTHR10992,P <sup>-</sup> KOG1454		0	0 0 AT5G38520.1
34	PTHR10992,P <sup>-</sup> KOG1454		0	0 0 AT5G38520.1
35	PTHR31375,P <sup>-</sup>	0 3.2.1.15		0 GO:0005975,(AT1G02460.1
36	PTHR31375,P <sup>-</sup>	0 3.2.1.15		0 GO:0005975,(AT1G02460.1
37	PTHR31374,P <sup>-</sup>	0	0 K14488	GO:0009733 AT3G09870.1
38	PTHR31374,P <sup>-</sup>	0	0 K14488	GO:0009733 AT3G09870.1
39	PTHR33463,P <sup>-</sup> KOG1947		0	0 0 AT1G61300.1
40	PTHR33463,P <sup>-</sup> KOG1947		0	0 0 AT1G61300.1
41	PTHR35731,P <sup>-</sup>	0	0	0 0 AT3G09050.1
42	PTHR35731,P <sup>-</sup>	0	0	0 0 AT3G09050.1
43	PTHR24322,P <sup>-</sup> KOG0725	1.1.1.206	K08081	0 AT5G06060.1
44	PTHR24322,P <sup>-</sup> KOG0725	1.1.1.206	K08081	0 AT5G06060.1
45	PTHR10366,P <sup>-</sup> KOG1502	1.2.1.44		0 GO:0050662,(AT5G58490.1
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PTHR10366,P <sup>-</sup>	KOG1502	1.2.1.44		0	GO:0050662,(AT5G58490.1
PTHR10366,P <sup>-</sup>	KOG1502	1.2.1.44		0	GO:0050662,(AT5G58490.1
PTHR10366,P <sup>-</sup>	KOG1502	1.2.1.44		0	GO:0050662,(AT5G58490.1
PTHR23289,P <sup>-</sup>		0	0 K02259		GO:0055114,(AT5G56090.1
PTHR10766,P <sup>-</sup>		0	0 K17086		GO:0016021 AT4G12650.1
PTHR12874	KOG2997		0 K10295		GO:0005515 AT1G21760.1
PTHR12874	KOG2997		0 K10295		GO:0005515 AT1G21760.1
PTHR12874	KOG2997		0 K10295		GO:0005515 AT1G21760.1
PTHR12874	KOG2997		0 K10295		GO:0005515 AT1G21760.1
PTHR11062,P <sup>-</sup>	KOG1021	2.4.2.41		0	0 AT5G61840.1
PTHR11062,P <sup>-</sup>	KOG1021	2.4.2.41		0	0 AT5G61840.1
PTHR11062,P <sup>-</sup>	KOG1021	2.4.2.41		0	0 AT5G61840.1
PTHR11062,P <sup>-</sup>	KOG1021	2.4.2.41		0	0 AT5G61840.1
PTHR23155,P <sup>-</sup>	KOG4658		0		0 GO:0043531 AT3G14470.1
PTHR23155,P <sup>-</sup>	KOG4658		0		0 GO:0043531 AT3G14470.1
PTHR23155,P <sup>-</sup>	KOG4658		0		0 GO:0043531 AT3G14470.1
PTHR23155,P <sup>-</sup>	KOG4658		0		0 GO:0043531 AT3G14470.1
	0	0	0		0 GO:0043565,(AT4G36730.1
	0	0	0		0 GO:0043565,(AT4G36730.1
PTHR11139,P <sup>-</sup>		0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
PTHR11139,P <sup>-</sup>		0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
PTHR11139,P <sup>-</sup>		0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
PTHR11139,P <sup>-</sup>		0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
PTHR11709,P <sup>-</sup>		0 1.10.3.2	K05909		GO:0055114,(AT2G29130.1
PTHR11709,P <sup>-</sup>		0 1.10.3.2	K05909		GO:0055114,(AT2G29130.1
PTHR31471,P <sup>-</sup>		0	0	0	0 AT1G45207.2
PTHR31471,P <sup>-</sup>		0	0	0	0 AT1G45207.2
PTHR31953,P <sup>-</sup>		0 3.2.1.153,3.2.	K01193		0 AT3G13790.1
PTHR16105,P <sup>-</sup>		0	0 K13157		GO:0003676 AT1G09230.1
PTHR16105,P <sup>-</sup>		0	0 K13157		GO:0003676 AT1G09230.1
PTHR33044,P <sup>-</sup>		0	0	0	0 AT2G48140.1
PTHR33044,P <sup>-</sup>		0	0	0	0 AT2G48140.1
PTHR33044,P <sup>-</sup>		0	0	0	0 AT2G48140.1
PTHR33044,P <sup>-</sup>		0	0	0	0 AT2G48140.1
PTHR18866,P <sup>-</sup>		0	0	0	0 AT3G56130.1
PTHR31692,P <sup>-</sup>		0	0	0	0 AT4G17030.1
PTHR23083,P <sup>-</sup>		0	0	0	0 AT4G37460.1
PTHR23083,P <sup>-</sup>		0	0	0	0 AT4G37460.1
PTHR17901,P <sup>-</sup>	KOG4549	3.1.3.48	K17619		GO:0016791 AT2G14110.1
PTHR22870,P <sup>-</sup>		0	0	0	0 AT3G26100.2
PTHR22870,P <sup>-</sup>		0	0	0	0 AT3G26100.2
PTHR10648,P <sup>-</sup>		0	0 K03456		GO:0005515 AT3G25800.1
PTHR10648,P <sup>-</sup>		0	0 K03456		GO:0005515 AT3G25800.1



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3	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
4	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
5	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
6	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
7	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
8	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
9	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
10	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
11	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
12	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
13	PTHR18919,P <sup>-</sup>	0 2.3.1.9	K00626	GO:0016747,(AT5G47720.2
14	PTHR24089,P <sup>-</sup> KOG0752		0 K15108	0 AT5G48970.1
15	PTHR24089,P <sup>-</sup> KOG0752		0 K15108	0 AT5G48970.1
16	PTHR22957,P <sup>-</sup> KOG1091		0 K18469	0 AT4G29950.1
17	PTHR22957,P <sup>-</sup> KOG1091		0 K18469	0 AT4G29950.1
18	PTHR22957,P <sup>-</sup> KOG1091		0 K18469	0 AT4G29950.1
19	PTHR11588,P <sup>-</sup>	0	0 K07374	GO:0003924,(AT1G04820.1
20	PTHR11588,P <sup>-</sup>	0	0 K07374	GO:0003924,(AT1G04820.1
21	PTHR11588,P <sup>-</sup>	0	0 K07374	GO:0003924,(AT1G04820.1
22	PTHR11588,P <sup>-</sup>	0	0 K07374	GO:0003924,(AT1G04820.1
23	PTHR11588,P <sup>-</sup>	0	0 K07374	GO:0003924,(AT1G04820.1
24	PTHR24012,P <sup>-</sup>	0	0	0 GO:0003676 AT1G49600.1
25	PTHR24012,P <sup>-</sup> KOG0148		0	0 GO:0003676 AT3G19130.1
26	PTHR24012,P <sup>-</sup> KOG0148		0	0 GO:0003676 AT3G19130.1
27	PTHR24012,P <sup>-</sup> KOG0148		0	0 GO:0003676 AT3G19130.1
28	PTHR32212,P <sup>-</sup>	0	0	0 GO:0005515 AT3G49030.1
29	PTHR32212,P <sup>-</sup>	0	0	0 GO:0005515 AT3G49030.1
30	PTHR32212,P <sup>-</sup>	0	0	0 GO:0005515 AT3G49030.1
31	PTHR32212,P <sup>-</sup>	0	0	0 GO:0005515 AT3G49030.1
32	PTHR32212,P <sup>-</sup>	0	0	0 GO:0005515 AT3G49030.1
33	0	0	0	0 0 0
34	0	0	0	0 0 0
35	PTHR27004,P <sup>-</sup> KOG0472	2.7.11.1		0 GO:0005515 AT2G34930.1
36	PTHR27004,P <sup>-</sup> KOG0472	2.7.11.1		0 GO:0005515 AT2G34930.1
37	PTHR24115,P <sup>-</sup>	0 3.6.4.4	K10393	GO:0008017,(AT3G16060.1
38	PTHR10615,P <sup>-</sup> KOG2747	2.3.1.48	K11308	GO:0016747,(AT5G64610.1
39	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
40	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
41	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
42	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
43	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
44	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
45	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
46	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
47	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
48	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
49	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
50	PTHR24286,P <sup>-</sup> KOG0157		0	0 GO:0055114,(AT3G14620.1
51	PTHR12526,P <sup>-</sup> KOG0853	2.4.1.132,2.4.	K03843	0 AT1G78800.1
52	PTHR12526,P <sup>-</sup> KOG0853	2.4.1.132,2.4.	K03843	0 AT1G78800.1
53	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
54	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
55	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
56	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
57	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
58	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
59	PTHR31072,P <sup>-</sup>	0	0	0 0 AT3G15030.2
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3	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2	
4	PTHR37716,P <sup>-</sup>	0	0	0	0 AT2G01870.1	
5	PTHR37716,P <sup>-</sup>	0	0	0	0 AT2G01870.1	
6	PTHR37716,P <sup>-</sup>	0	0	0	0 AT2G01870.1	
7	PTHR11999,P <sup>-</sup>	0	4.1.1.28,4.1.1 K01592	GO:0030170,(	AT2G20340.1	
8	PTHR11999,P <sup>-</sup>	0	4.1.1.28,4.1.1 K01592	GO:0030170,(	AT2G20340.1	
9	PTHR11999,P <sup>-</sup>	0	4.1.1.28,4.1.1 K01592	GO:0030170,(	AT2G20340.1	
10	PTHR12381,P <sup>-</sup>	0	0 K15047	GO:0005515	0	
11	PTHR12381,P <sup>-</sup>	0	0 K15047	GO:0005515	0	
12	PTHR12381,P <sup>-</sup>	0	0 K15047	GO:0005515	0	
13	PTHR12381,P <sup>-</sup>	0	0 K15047	GO:0005515	0	
14	PTHR12381,P <sup>-</sup>	0	0 K15047	GO:0005515	0	
15	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1	
16	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1	
17	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1	
18	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1	
19	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1	
20	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1	
21		0	0	0	0 AT5G27390.1	
22	0	0	0	0	0 AT3G05625.1	
23	0	0	0	0	0 AT3G05625.1	
24	PTHR33416,P <sup>-</sup>	0	0	0	0 AT3G10650.1	
25	PTHR33416,P <sup>-</sup>	0	0	0	0 AT3G10650.1	
26	PTHR33416,P <sup>-</sup>	0	0	0	0 AT3G10650.1	
27	PTHR33416,P <sup>-</sup>	0	0	0	0 AT3G10650.1	
28	PTHR33416,P <sup>-</sup>	0	0	0	0 AT3G10650.1	
29	PTHR33416,P <sup>-</sup>	0	0	0	0 AT3G10650.1	
30	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
31	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
32	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
33	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
34	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
35	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
36	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
37	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
38	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
39	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
40	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
41	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
42	PTHR32059,P <sup>-</sup>	0	0	0	0 AT5G16210.1	
43	PTHR23240,P <sup>-</sup> KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1	
44	PTHR23240,P <sup>-</sup> KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1	
45	PTHR23240,P <sup>-</sup> KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1	
46	PTHR23240,P <sup>-</sup> KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1	
47	PTHR23240,P <sup>-</sup> KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1	
48	PTHR10783,P <sup>-</sup>	0	0	0	GO:0016021 AT3G29060.1	
49	PTHR10783,P <sup>-</sup>	0	0	0	GO:0016021 AT3G29060.1	
50	PTHR10783,P <sup>-</sup>	0	0	0	GO:0016021 AT3G29060.1	
51	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
52	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
53	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
54	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
55	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
56	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
57	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
58	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
59	PTHR13480 KOG2932		0 K15685		0 AT5G01160.1	
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3	PTHR13480	KOG2932	0	K15685	0 AT5G01160.1
4	PTHR13480	KOG2932	0	K15685	0 AT5G01160.1
5	PTHR13480	KOG2932	0	K15685	0 AT5G01160.1
6	PTHR13480	KOG2932	0	K15685	0 AT5G01160.1
7	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
8	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
9	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
10	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
11	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
12	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
13	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
14	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
15	PTHR13343,P <sup>-</sup>	0	0	0	0 AT3G59300.1
16	PTHR11926,P <sup>-</sup>	KOG1192	0	0	GO:0016758,(AT3G21780.1
17	PTHR11926,P <sup>-</sup>	KOG1192	0	0	GO:0016758,(AT3G21780.1
18	PTHR11926,P <sup>-</sup>	KOG1192	0	0	GO:0016758,(AT3G21780.1
19	PTHR11926,P <sup>-</sup>	KOG1192	0	0	GO:0016758,(AT3G21780.1
20	PTHR11926,P <sup>-</sup>	KOG1192	0	0	GO:0016758,(AT3G21780.1
21	PTHR11926,P <sup>-</sup>	KOG1192	0	0	GO:0016758,(AT3G21780.1
22	PTHR31384,P <sup>-</sup>	0	0	0	GO:0003677,(AT1G77850.1
23	PTHR31384,P <sup>-</sup>	0	0	0	GO:0003677,(AT1G77850.1
24	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1
25	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1
26	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1
27	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1
28	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
29	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
30	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
31	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
32	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
33	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
34	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
35	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
36	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
37	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
38	PTHR10972,P <sup>-</sup>	0	0	0	0 AT4G08180.2
39	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
40	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
41	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
42	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
43	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
44	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
45	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
46	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
47	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
48	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
49	PTHR24089,P <sup>-</sup>	0	0	0	0 AT5G48970.1
50	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
51	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
52	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
53	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
54	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
55	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
56	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
57	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
58	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
59	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
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3	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
4	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
5	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
6	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
7	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
8	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
9	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
10	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
11	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
12	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
13	PTHR31602,P <sup>-</sup>	0	0	0	GO:0032502,(AT4G37740.1
14	PTHR22849,P <sup>-</sup>	0	6.3.2.19	0	GO:0016567,(AT1G76390.1
15	PTHR22849,P <sup>-</sup>	0	6.3.2.19	0	GO:0016567,(AT1G76390.1
16	PTHR22849,P <sup>-</sup>	0	6.3.2.19	0	GO:0016567,(AT1G76390.1
17	PTHR22849,P <sup>-</sup>	0	6.3.2.19	0	GO:0016567,(AT1G76390.1
18	PTHR22849,P <sup>-</sup>	0	6.3.2.19	0	GO:0016567,(AT1G76390.1
19	PTHR24009,P <sup>-</sup>	0	0	0	GO:0046872,(AT3G51950.2
20	PTHR24009,P <sup>-</sup>	0	0	0	GO:0046872,(AT3G51950.2
21	PTHR24009,P <sup>-</sup>	0	0	0	GO:0046872,(AT3G51950.2
22	PTHR24009,P <sup>-</sup>	0	0	0	GO:0046872,(AT3G51950.2
23	PTHR24009,P <sup>-</sup>	0	0	0	GO:0046872,(AT3G51950.2
24	0	0	0	0	AT3G06985.1
25	0	0	0	0	AT3G06985.1
26	0	0	0	0	AT3G06985.1
27	0	0	0	0	AT3G06985.1
28	0	0	0	0	AT3G06985.1
29					
30	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
31	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
32	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
33	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
34	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
35	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
36	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
37					
38	PTHR10173,P <sup>-</sup> KOG0856	1.8.4.12	K07305		GO:0055114,(AT1G53670.1
39	PTHR10173,P <sup>-</sup> KOG0856	1.8.4.12	K07305		GO:0055114,(AT1G53670.1
40	PTHR10173,P <sup>-</sup> KOG0856	1.8.4.12	K07305		GO:0055114,(AT1G53670.1
41	PTHR10173,P <sup>-</sup> KOG0856	1.8.4.12	K07305		GO:0055114,(AT1G53670.1
42	PTHR10173,P <sup>-</sup> KOG0856	1.8.4.12	K07305		GO:0055114,(AT1G53670.1
43	PTHR22884,P <sup>-</sup> KOG1082	2.1.1.43	K11420		GO:0034968,(AT5G04940.2
44	PTHR22884,P <sup>-</sup> KOG1082	2.1.1.43	K11420		GO:0034968,(AT5G04940.2
45					
46	PTHR33265,P <sup>-</sup>	0	0	0	AT1G52140.1
47	PTHR33265,P <sup>-</sup>	0	0	0	AT1G52140.1
48	PTHR12460 KOG2669		0	K15559	AT5G65180.1
49	PTHR12460 KOG2669		0	K15559	AT5G65180.1
50	PTHR12460 KOG2669		0	K15559	AT5G65180.1
51	PTHR12460 KOG2669		0	K15559	AT5G65180.1
52	PTHR12460 KOG2669		0	K15559	AT5G65180.1
53	PTHR12460 KOG2669		0	K15559	AT5G65180.1
54	PTHR12460 KOG2669		0	K15559	AT5G65180.1
55	PTHR12460 KOG2669		0	K15559	AT5G65180.1
56	PTHR12460 KOG2669		0	K15559	AT5G65180.1
57	PTHR12460 KOG2669		0	K15559	AT5G65180.1
58	PTHR12460 KOG2669		0	K15559	AT5G65180.1
59	PTHR12460 KOG2669		0	K15559	AT5G65180.1
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3	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
4	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
5	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
6	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
7	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
8	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
9	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
10	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
11	PTHR12460	KOG2669	0	K15559	0 AT5G65180.1
12	PTHR31447,P	KOG4176	0	0	0 AT4G02940.1
13	PTHR28630,P	KOG4498	0	0	0 AT2G37240.1
14	PTHR28630,P	KOG4498	0	0	0 AT2G37240.1
15	PTHR28630,P	KOG4498	0	0	0 AT2G37240.1
16	PTHR28630,P	KOG4498	0	0	0 AT2G37240.1
17	PTHR28630,P	KOG4498	0	0	0 AT2G37240.1
18	PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(AT5G03430.1
19	PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(AT5G03430.1
20	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
21	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
22	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
23	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
24	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
25	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
26	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
27	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
28	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
29	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
30	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
31	PTHR12121,P	KOG0620	3.1.13.4	K12603	0 AT3G58580.1
32	PTHR22849,P	0	6.3.2.19	0	GO:0016567,(AT1G24330.1
33	PTHR11746,P	KOG3178	0	0	GO:0046983,(AT4G35160.1
34	PTHR11746,P	KOG3178	0	0	GO:0046983,(AT4G35160.1
35	PTHR26374,P	0	0	0	0 AT3G60580.1
36	PTHR26374,P	0	0	0	0 AT3G60580.1
37	PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(AT5G39950.1
38	PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(AT5G39950.1
39	PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(AT5G39950.1
40	PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(AT5G39950.1
41	PTHR32096,P	0	0	0	GO:0043565,(AT4G11070.1
42	PTHR32096,P	0	0	0	GO:0043565,(AT4G11070.1
43	PTHR12953	KOG1396	0	0	0 AT4G23950.1
44	PTHR12953	KOG1396	0	0	0 AT4G23950.1
45	PTHR12953	KOG1396	0	0	0 AT4G23950.1
46	PTHR12953	KOG1396	0	0	0 AT4G23950.1
47	PTHR23042,P	0	0	0	GO:0046983 AT4G37850.1
48	PTHR23042,P	0	0	0	GO:0046983 AT4G37850.1
49	PTHR23042,P	0	0	0	GO:0046983 AT4G37850.1
50	PTHR23042,P	0	0	0	GO:0046983 AT4G37850.1
51	PTHR23042,P	0	0	0	GO:0046983 AT4G37850.1
52	PTHR22835,P	0	3.1.1.3	0	GO:0016788 AT1G29670.1
53	PTHR22835,P	0	3.1.1.3	0	GO:0016788 AT1G29670.1
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3	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
4	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
5	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
6	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
7	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
8	PTHR10791,P <sup>-</sup> KOG1623		0 K15382	GO:0016021	AT5G50800.1
9	PTHR10791,P <sup>-</sup> KOG1623		0 K15382	GO:0016021	AT5G50800.1
10	PTHR10791,P <sup>-</sup> KOG1623		0 K15382	GO:0016021	AT5G50800.1
11	PTHR10791,P <sup>-</sup> KOG1623		0 K15382	GO:0016021	AT5G50800.1
12	PTHR11533,P <sup>-</sup>	0 3.4.11.14	K01256	GO:0006508	AT1G63770.3
13	PTHR11533,P <sup>-</sup>	0 3.4.11.14	K01256	GO:0006508	AT1G63770.3
14	PTHR13832,P <sup>-</sup> KOG0698	3.1.3.16	K14497	GO:0003824,(	AT4G26080.1
15	PTHR13832,P <sup>-</sup> KOG0698	3.1.3.16	K14497	GO:0003824,(	AT4G26080.1
16	PTHR12555,P <sup>-</sup> KOG1816		0 K14016	GO:0006511	AT2G21270.3
17	PTHR12555,P <sup>-</sup> KOG1816		0 K14016	GO:0006511	AT2G21270.3
18	PTHR12555,P <sup>-</sup> KOG1816		0 K14016	GO:0006511	AT2G21270.3
19	PTHR12555,P <sup>-</sup> KOG1816		0 K14016	GO:0006511	AT2G21270.3
20	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
21	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
22	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
23	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
24	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
25	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
26	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
27	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
28	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
29	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
30	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
31	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
32	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
33	PTHR24089,P <sup>-</sup> KOG0749		0 K05863		0 AT5G17400.1
34	PTHR10359,P <sup>-</sup>	0 4.2.99.18		0	0 AT5G04560.2
35	PTHR10359,P <sup>-</sup>	0 4.2.99.18		0	0 AT5G04560.2
36	PTHR10859 KOG2978	2.4.1.83	K00721		0 AT1G20575.1
37	PTHR10859 KOG2978	2.4.1.83	K00721		0 AT1G20575.1
38	PTHR34775,P <sup>-</sup>	0	0	0	0 AT2G16270.1
39	PTHR34775,P <sup>-</sup>	0	0	0	0 AT2G16270.1
40	PTHR34775,P <sup>-</sup>	0	0	0	0 AT2G16270.1
41	PTHR34775,P <sup>-</sup>	0	0	0	0 AT2G16270.1
42	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0030246,(	AT3G13750.1
43	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0030246,(	AT3G13750.1
44	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0030246,(	AT3G13750.1
45	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0030246,(	AT3G13750.1
46	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
47	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
48	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
49	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
50	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
51	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
52	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
53	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
54	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
55	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
56	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
57	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
58	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
59	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT5G66900.1
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3	PTHR23155,P <sup>-</sup>	KOG4658	0	0	GO:0043531	AT5G66900.1
4	PTHR10108,P <sup>-</sup>	0 2.1.1.41		0	GO:0008168	AT1G31850.2
5	PTHR10108,P <sup>-</sup>	0 2.1.1.41		0	GO:0008168	AT1G31850.2
6	PTHR24012,P <sup>-</sup>	0	0	0	GO:0003676	AT1G49600.1
7	PTHR24012,P <sup>-</sup>	0	0	0	GO:0003676	AT1G49600.1
8	PTHR24012,P <sup>-</sup>	0	0	0	GO:0003676	AT1G49600.1
9	PTHR24012,P <sup>-</sup>	0	0	0	GO:0003676	AT1G49600.1
10	PTHR24012,P <sup>-</sup>	0	0	0	GO:0003676	AT1G49600.1
11	PTHR24012,P <sup>-</sup>	0	0	0	GO:0003676	AT1G49600.1
12	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
13	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
14	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
15	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
16	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
17	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
18	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
19	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
20	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
21	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
22	PTHR24012,P <sup>-</sup>	KOG0148	0	0	GO:0003676	AT3G19130.1
23	0	0	0	0	0	0
24	0	0	0	0	0	0
25	0	0	0	0	0	0
26	0	0	0	0	0	0
27	0	0	0	0	0	0
28	PTHR27004,P <sup>-</sup>	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
29	PTHR27004,P <sup>-</sup>	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
30	PTHR34482,P <sup>-</sup>	0	0	0	0	AT3G29750.1
31	PTHR34482,P <sup>-</sup>	0	0	0	0	AT3G29750.1
32	PTHR34482,P <sup>-</sup>	0	0	0	0	AT3G29750.1
33	PTHR34482,P <sup>-</sup>	0	0	0	0	AT3G29750.1
34	PTHR34482,P <sup>-</sup>	0	0	0	0	AT3G29750.1
35	PTHR33374,P <sup>-</sup>	0	0	0	0	AT3G61640.1
36	PTHR33374,P <sup>-</sup>	0	0	0	0	AT3G61640.1
37	PTHR33374,P <sup>-</sup>	0	0	0	0	AT3G61640.1
38	PTHR33374,P <sup>-</sup>	0	0	0	0	AT3G61640.1
39	PTHR33374,P <sup>-</sup>	0	0	0	0	AT3G61640.1
40	PTHR33374,P <sup>-</sup>	0	0	0	0	AT3G61640.1
41	PTHR24193,P <sup>-</sup>	KOG4214	0	0	0	AT2G17390.1
42	PTHR24193,P <sup>-</sup>	KOG4214	0	0	0	AT2G17390.1
43	PTHR24193,P <sup>-</sup>	KOG4214	0	0	0	AT2G17390.1
44	PTHR24193,P <sup>-</sup>	KOG4214	0	0	0	AT2G17390.1
45	PTHR10252,P <sup>-</sup>	0	0	0	0	AT3G12480.1
46	PTHR35918,P <sup>-</sup>	0	0	0	GO:0005515	AT1G04390.1
47	PTHR30523,P <sup>-</sup>	0 4.1.1.31	K01595	GO:0015977,(	AT2G42600.2	
48	PTHR31973,P <sup>-</sup>	0	0	0	0	AT1G64260.1
49	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
50	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
51	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
52	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
53	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
54	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
55	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
56	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
57	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
58	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
59	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
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3	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787 AT2G32520.1
4	PTHR17630	KOG3043	3.1.1.45	0	GO:0016787 AT2G32520.1
5	PTHR10593,P <sup>-</sup>			0	0 AT5G22890.1
6	PTHR10593,P <sup>-</sup>			0	0 AT5G22890.1
7	PTHR14095,P <sup>-</sup>			0	0 AT5G28850.2
8	PTHR14095,P <sup>-</sup>			0	0 AT5G28850.2
9	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
10	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
11	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
12	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
13	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
14	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
15	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
16	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
17	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
18	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
19	PTHR13215,P <sup>-</sup>			0	GO:0006355,(AT4G00980.1
20	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
21	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
22	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
23	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
24	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
25	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
26	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
27	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
28	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
29	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
30	PTHR11453,P <sup>-</sup>			0	GO:0016021,(AT3G62270.1
31	PTHR33670,P <sup>-</sup>			0	0 AT3G21570.1
32	PTHR11802,P <sup>-</sup>	KOG1282		0	K16296 GO:0006508,(AT5G09640.1
33	PTHR11802,P <sup>-</sup>	KOG1282		0	K16296 GO:0006508,(AT5G09640.1
34	PTHR11802,P <sup>-</sup>	KOG1282		0	K16296 GO:0006508,(AT5G09640.1
35	PTHR11802,P <sup>-</sup>	KOG1282		0	K16296 GO:0006508,(AT5G09640.1
36	PTHR11802,P <sup>-</sup>	KOG1282		0	K16296 GO:0006508,(AT5G09640.1
37	PTHR13063,P <sup>-</sup>	KOG3039		0	K13125 GO:0050999 AT1G61620.1
38	PTHR13063,P <sup>-</sup>	KOG3039		0	K13125 GO:0050999 AT1G61620.1
39	PTHR11757,P <sup>-</sup>		0 3.4.21.83	K01354	GO:0008236,(AT1G50380.1
40	PTHR11757,P <sup>-</sup>		0 3.4.21.83	K01354	GO:0008236,(AT1G50380.1
41	PTHR11757,P <sup>-</sup>		0 3.4.21.83	K01354	GO:0008236,(AT1G50380.1
42	PTHR11757,P <sup>-</sup>		0 3.4.21.83	K01354	GO:0008236,(AT1G50380.1
43	PTHR31072,P <sup>-</sup>			0	0 AT5G23280.1
44	PTHR31072,P <sup>-</sup>			0	0 AT5G23280.1
45	PTHR15362,P <sup>-</sup>		0 2.7.8.8	K08730	GO:0006659 AT1G15110.1
46	PTHR27002	KOG1187	2.7.10.2		0 GO:0006468,(AT4G05200.1
47	PTHR27002	KOG1187	2.7.10.2		0 GO:0006468,(AT4G05200.1
48	PTHR27002	KOG1187	2.7.10.2		0 GO:0006468,(AT4G05200.1
49	PTHR27002	KOG1187	2.7.10.2		0 GO:0006468,(AT4G05200.1
50	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
51	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
52	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
53	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
54	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
55	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
56	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
57	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
58	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
59	PTHR10638,P <sup>-</sup>			0	0 K00276 GO:0055114,(AT4G14940.1
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3	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
4	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
5	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
6	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
7	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
8	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
9	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
10	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
11	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
12	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
13	PTHR33059,P <sup>-</sup>	0	0	0	0 AT3G22550.1
14	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1
15	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1
16	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1
17	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1
18	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1
19	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1		0	0 AT5G62180.1
20	PTHR11972,P <sup>-</sup> KOG0039	1.16.1.7		0	GO:0055114,(AT1G01580.1
21	PTHR11972,P <sup>-</sup> KOG0039	1.16.1.7		0	GO:0055114,(AT1G01580.1
22	PTHR11972,P <sup>-</sup> KOG0039	1.16.1.7		0	GO:0055114,(AT1G01580.1
23	PTHR11972,P <sup>-</sup> KOG0039	1.16.1.7		0	GO:0055114,(AT1G01580.1
24	PTHR11972,P <sup>-</sup> KOG0039	1.16.1.7		0	GO:0055114,(AT1G01580.1
25	PTHR11972,P <sup>-</sup> KOG0039	1.16.1.7		0	GO:0055114,(AT1G01580.1
26	PTHR35732,P <sup>-</sup>	0	0	0	0 AT3G10405.1
27	PTHR35732,P <sup>-</sup>	0	0	0	0 AT3G10405.1
28	PTHR35732,P <sup>-</sup>	0	0	0	0 AT3G10405.1
29	PTHR35732,P <sup>-</sup>	0	0	0	0 AT3G10405.1
30	PTHR35732,P <sup>-</sup>	0	0	0	0 AT3G10405.1
31	PTHR11260,P <sup>-</sup> KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
32	PTHR11260,P <sup>-</sup> KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
33	PTHR11260,P <sup>-</sup> KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
34	PTHR11260,P <sup>-</sup> KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
35	PTHR11260,P <sup>-</sup> KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
36	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1
37	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1
38	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1
39	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1
40	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1
41	PTHR37764,P <sup>-</sup>	0	0	0	0 AT5G27390.1
42	PTHR33592	0	0	0	0 AT2G31345.1
43	PTHR33592	0	0	0	0 AT2G31345.1
44	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
45	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
46	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
47	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
48	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
49	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
50	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
51	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
52	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
53	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
54	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.1
55	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0004857,(AT3G05610.1	
56	0	0	0	0	0
57	0	0	0	0	0
58	0	0	0	0	0
59	0	0	0	0	0
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3	0	0	0	0	0	0
4	0	0	0	0	0	0
5	0	0	0	0	0	0
6	0	0	0	0	0	0
7	PTHR35313,P <sup>-</sup>	0	0	0	0	AT5G13390.1
8	PTHR35313,P <sup>-</sup>	0	0	0	0	AT5G13390.1
9	PTHR35313,P <sup>-</sup>	0	0	0	0	AT5G13390.1
10	PTHR35313,P <sup>-</sup>	0	0	0	0	AT5G13390.1
11	PTHR35313,P <sup>-</sup>	0	0	0	0	AT5G13390.1
12	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
13	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
14	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
15	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
16	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
17	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
18	PTHR32059,P <sup>-</sup>	0	0	0	0	AT5G16210.1
19	PTHR10221,P <sup>-</sup> KOG2549		0 K03131		GO:0006352,(	AT1G04950.1
20	PTHR10221,P <sup>-</sup> KOG2549		0 K03131		GO:0006352,(	AT1G04950.1
21	PTHR13068,P <sup>-</sup>	0	0 K15032		GO:0006355,(	AT3G18870.1
22	PTHR13068,P <sup>-</sup>	0	0 K15032		GO:0006355,(	AT3G18870.1
23	PTHR35410,P <sup>-</sup>	0	0	0	0	0
24	PTHR35410,P <sup>-</sup>	0	0	0	0	0
25	PTHR35410,P <sup>-</sup>	0	0	0	0	0
26	PTHR35410,P <sup>-</sup>	0	0	0	0	0
27	PTHR35410,P <sup>-</sup>	0	0	0	0	0
28	PTHR33463,P <sup>-</sup> KOG1947		0	0	0	AT1G61300.1
29	PTHR33463,P <sup>-</sup> KOG1947		0	0	0	AT1G61300.1
30	PTHR33463,P <sup>-</sup> KOG1947		0	0	0	AT1G61300.1
31	PTHR33463,P <sup>-</sup> KOG1947		0	0	0	AT1G61300.1
32	PTHR33463,P <sup>-</sup> KOG1947		0	0	0	AT1G61300.1
33	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
34	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
35	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
36	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
37	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
38	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
39	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
40	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(	AT3G47570.1
41	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
42	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
43	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
44	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
45	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
46	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
47	PTHR33103,P <sup>-</sup>	0	0	0	0	AT5G01120.1
48	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,(	AT5G02190.1
49	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,(	AT5G02190.1
50	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,(	AT5G02190.1
51	0	0	0	0	0	0
52	0	0	0	0	0	0
53	0	0	0	0	0	0
54	0	0	0	0	0	0
55	0	0	0	0	0	0
56	PTHR13078	0 4.2.1.119		0	0	AT5G60335.1
57	PTHR13078	0 4.2.1.119		0	0	AT5G60335.1
58	PTHR13078	0 4.2.1.119		0	0	AT5G60335.1
59	PTHR13078	0 4.2.1.119		0	0	AT5G60335.1
60						

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3	PTHR13078	0 4.2.1.119		0		0 AT5G60335.1
4						
5	0	0	0	0	0	0
6	0	0	0	0	0	0
7	0	0	0	0	0	0
8	0	0	0	0	0	0
9						
10	PTHR22950,P <sup>-</sup> KOG1303		0	0		0 AT2G39890.1
11	PTHR22950,P <sup>-</sup> KOG1303		0	0		0 AT2G39890.1
12	PTHR22950,P <sup>-</sup> KOG1303		0	0		0 AT2G39890.1
13	PTHR22950,P <sup>-</sup> KOG1303		0	0		0 AT2G39890.1
14	PTHR24012,P <sup>-</sup> KOG4205		0 K14411		GO:0003676	AT3G07810.1
15	PTHR24012,P <sup>-</sup> KOG4205		0 K14411		GO:0003676	AT3G07810.1
16	PTHR24012,P <sup>-</sup> KOG4205		0 K14411		GO:0003676	AT3G07810.1
17	PTHR23289,P <sup>-</sup>	0	0 K02259		GO:0055114,(	AT5G56090.1
18	PTHR23289,P <sup>-</sup>	0	0 K02259		GO:0055114,(	AT5G56090.1
19	PTHR10641,P <sup>-</sup> KOG0048		0	0		0 AT4G32730.2
20	PTHR10972,P <sup>-</sup>	0	0	0		0 AT4G08180.2
21	PTHR10972,P <sup>-</sup>	0	0	0		0 AT4G08180.2
22	PTHR10972,P <sup>-</sup>	0	0	0		0 AT4G08180.2
23	PTHR10972,P <sup>-</sup>	0	0	0		0 AT4G08180.2
24	PTHR13902 KOG0198	2.7.11.1		0	GO:0006468,(	AT3G48260.1
25	PTHR13902 KOG0198	2.7.11.1		0	GO:0006468,(	AT3G48260.1
26	PTHR13902 KOG0198	2.7.11.1		0	GO:0006468,(	AT3G48260.1
27	PTHR13902 KOG0198	2.7.11.1		0	GO:0006468,(	AT3G48260.1
28	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0	GO:0005975,(	AT4G26140.1
29	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0	GO:0005975,(	AT4G26140.1
30	PTHR11746,P <sup>-</sup> KOG3178	2.1.1.68	K13066		GO:0046983,(	AT5G54160.1
31	PTHR11746,P <sup>-</sup> KOG3178	2.1.1.68	K13066		GO:0046983,(	AT5G54160.1
32	PTHR11746,P <sup>-</sup> KOG3178	2.1.1.68	K13066		GO:0046983,(	AT5G54160.1
33	PTHR11746,P <sup>-</sup> KOG3178	2.1.1.68	K13066		GO:0046983,(	AT5G54160.1
34	PTHR32387,P <sup>-</sup>	0	0 K17592			0 AT3G48770.1
35	PTHR32387,P <sup>-</sup>	0	0 K17592			0 AT3G48770.1
36	PTHR32387,P <sup>-</sup>	0	0 K17592			0 AT3G48770.1
37	PTHR32387,P <sup>-</sup>	0	0 K17592			0 AT3G48770.1
38	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
39	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
40	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
41	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
42	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
43	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
44	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
45	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
46	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
47	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
48	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
49	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
50	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
51	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
52	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
53	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
54	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
55	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
56	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
57	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
58	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
59	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(	AT3G60240.4
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3	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
4	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
5	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
6	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
7	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
8	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
9	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
10	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
11	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
12	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
13	PTHR23253,P <sup>-</sup> KOG0401		0	0	GO:0005515,(AT3G60240.4
14	PTHR12565,P <sup>-</sup>	0	0	0	GO:0046983 AT4G00050.1
15	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
16	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
17	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
18	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
19	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
20	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
21	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
22	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
23	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
24	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
25	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
26	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
27	PTHR13299,P <sup>-</sup> KOG4546		0	0	AT2G45690.1
28	PTHR11771,P <sup>-</sup>	0 1.13.11.58		0	GO:0055114,(AT1G55020.1
29	PTHR11771,P <sup>-</sup>	0 1.13.11.58		0	GO:0055114,(AT1G55020.1
30	PTHR11771,P <sup>-</sup>	0 1.13.11.58		0	GO:0055114,(AT1G55020.1
31	PTHR11771,P <sup>-</sup>	0 1.13.11.58		0	GO:0055114,(AT1G55020.1
32	PTHR11771,P <sup>-</sup>	0 1.13.11.58		0	GO:0055114,(AT1G55020.1
33	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT3G57330.1
34	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT3G57330.1
35	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT3G57330.1
36	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT3G57330.1
37	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT3G57330.1
38	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT3G57330.1
39	PTHR11139,P <sup>-</sup>	0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
40	PTHR11139,P <sup>-</sup>	0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
41	PTHR11139,P <sup>-</sup>	0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
42	PTHR11139,P <sup>-</sup>	0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
43	PTHR11139,P <sup>-</sup>	0 2.7.11.1	K08873		GO:0005515,(AT1G50030.1
44	PTHR14194,P <sup>-</sup> KOG1203		0	0	AT3G46780.1
45	PTHR14194,P <sup>-</sup> KOG1203		0	0	AT3G46780.1
46	PTHR31232	0	0	0	AT1G04645.1
47	PTHR31232	0	0	0	AT4G16195.1
48	PTHR31232	0	0	0	AT4G16195.1
49	0	0	0	0	AT3G06985.1
50	0	0	0	0	AT3G06985.1
51	0	0	0	0	AT3G06985.1
52	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
53	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
54	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
55	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
56	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
57	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
58	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
59	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787 AT4G00590.1
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3	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
4	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
5	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
6	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
7	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
8	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
9	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
10	PTHR10188,P <sup>-</sup> KOG1592	3.4.19.5,3.5.1		0	GO:0016787	AT4G00590.1
11	0	0	0	0	0	0
12	0	0	0	0	0	0
13	0	0	0	0	0	0
14	0	0	0	0	0	0
15	0	0	0	0	0	0
16	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
17	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
18	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
19	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
20	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
21	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
22	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
23	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
24	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
25	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
26	PTHR23076,P <sup>-</sup> KOG0737		0	0	GO:0006508,(	AT3G04340.1
27	PTHR14089,P <sup>-</sup>	0	0 K12872	0	GO:0003676	AT1G07360.1
28	PTHR14089,P <sup>-</sup>	0	0 K12872	0	GO:0003676	AT1G07360.1
29	PTHR14089,P <sup>-</sup>	0	0 K12872	0	GO:0003676	AT1G07360.1
30	PTHR14089,P <sup>-</sup>	0	0 K12872	0	GO:0003676	AT1G07360.1
31	PTHR11709,P <sup>-</sup>	0 1.10.3.2	K05909	0	GO:0055114,(	AT2G29130.1
32	PTHR11695,P <sup>-</sup>	0 1.1.1.54,1.3.1		0	GO:0055114,(	AT1G65560.1
33	PTHR11695,P <sup>-</sup>	0 1.1.1.54,1.3.1		0	GO:0055114,(	AT1G65560.1
34	PTHR11695,P <sup>-</sup>	0 1.1.1.54,1.3.1		0	GO:0055114,(	AT1G65560.1
35	PTHR32176 KOG0513		0	0	GO:0006629	AT2G26560.1
36	PTHR32176 KOG0513		0	0	GO:0006629	AT2G26560.1
37						
38	PTHR31471,P <sup>-</sup>	0	0	0	0	AT1G45207.2
39	PTHR31471,P <sup>-</sup>	0	0	0	0	AT1G45207.2
40	PTHR31471,P <sup>-</sup>	0	0	0	0	AT1G45207.2
41	PTHR31471,P <sup>-</sup>	0	0	0	0	AT1G45207.2
42	PTHR31471,P <sup>-</sup>	0	0	0	0	AT1G45207.2
43	PTHR31953,P <sup>-</sup>	0 3.2.1.153,3.2.	K01193	0		AT3G13790.1
44	PTHR22166,P <sup>-</sup> KOG2846		0	0	0	AT4G31080.1
45	PTHR22166,P <sup>-</sup> KOG2846		0	0	0	AT4G31080.1
46	PTHR22166,P <sup>-</sup> KOG2846		0	0	0	AT4G31080.1
47	PTHR10457,P <sup>-</sup> KOG0631	2.7.1.46	K12446	0	GO:0005524	AT4G16130.1
48	PTHR10457,P <sup>-</sup> KOG0631	2.7.1.46	K12446	0	GO:0005524	AT4G16130.1
49	PTHR24095,P <sup>-</sup>	0 6.2.1.1	K01895	0	GO:0008152,(	AT5G36880.2
50	PTHR24095,P <sup>-</sup>	0 6.2.1.1	K01895	0	GO:0008152,(	AT5G36880.2
51	PTHR24095,P <sup>-</sup>	0 6.2.1.1	K01895	0	GO:0008152,(	AT5G36880.2
52	PTHR23326,P <sup>-</sup> KOG2150		0 K12580	0	GO:0006355,(	AT5G18230.1
53	PTHR23326,P <sup>-</sup> KOG2150		0 K12580	0	GO:0006355,(	AT5G18230.1
54	PTHR23326,P <sup>-</sup> KOG2150		0 K12580	0	GO:0006355,(	AT5G18230.1
55	PTHR23326,P <sup>-</sup> KOG2150		0 K12580	0	GO:0006355,(	AT5G18230.1
56	PTHR23326,P <sup>-</sup> KOG2150		0 K12580	0	GO:0006355,(	AT5G18230.1
57	PTHR12196 KOG2316	6.3.1.14	K06927	0	0	AT3G04480.1
58	PTHR12196 KOG2316	6.3.1.14	K06927	0	0	AT3G04480.1
59	PTHR12196 KOG2316	6.3.1.14	K06927	0	0	AT3G04480.1
60						

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2					
3	PTHR22762,P <sup>-</sup>	0 3.2.1.20		0 GO:0005975,(	AT5G63840.1
4	PTHR22762,P <sup>-</sup>	0 3.2.1.20		0 GO:0005975,(	AT5G63840.1
5					
6	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
7	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
8					
9	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
10	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
11	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
12	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
13	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
14	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
15	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1
16					
17	PTHR31529,P <sup>-</sup>	0	0	0	AT2G42430.1
18	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
19	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
20	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
21	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
22	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
23	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
24	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
25	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
26	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
27	PTHR31314,P <sup>-</sup>	0	0	0	AT4G28610.1
28					
29	PTHR31268,P <sup>-</sup>	0 2.4.1.67	K06611		0 AT4G01970.1
30	PTHR31268,P <sup>-</sup>	0 2.4.1.67	K06611		0 AT4G01970.1
31	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02519	GO:0005525	AT4G11160.1
32	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02519	GO:0005525	AT4G11160.1
33	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02519	GO:0005525	AT4G11160.1
34	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02519	GO:0005525	AT4G11160.1
35	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02519	GO:0005525	AT4G11160.1
36	PTHR23083,P <sup>-</sup>	0	0	0	AT4G37460.1
37	PTHR23083,P <sup>-</sup>	0	0	0	AT4G37460.1
38	PTHR23083,P <sup>-</sup>	0	0	0	AT4G37460.1
39	PTHR23083,P <sup>-</sup>	0	0	0	AT4G37460.1
40	PTHR23083,P <sup>-</sup>	0	0	0	AT4G37460.1
41					
42	PTHR24015,P <sup>-</sup>	0	0	0	AT3G22690.2
43	PTHR24015,P <sup>-</sup>	0	0	0	AT3G22690.2
44	PTHR24015,P <sup>-</sup>	0	0	0	AT3G22690.2
45	PTHR24015,P <sup>-</sup>	0	0	0	AT3G22690.2
46	PTHR24015,P <sup>-</sup>	0	0	0	AT3G22690.2
47	PTHR26374,P <sup>-</sup>	0	0	0	AT3G60580.1
48	PTHR26374,P <sup>-</sup>	0	0	0	AT3G60580.1
49					
50	PTHR31867,P <sup>-</sup>	0	0	0	AT1G12560.1
51	PTHR31867,P <sup>-</sup>	0	0	0	AT1G12560.1
52	PTHR31867,P <sup>-</sup>	0	0	0	AT1G12560.1
53	PTHR31867,P <sup>-</sup>	0	0	0	AT1G12560.1
54					
55	PTHR10366,P <sup>-</sup>	0 1.1.1.133	K12451		0 AT1G63000.1
56	PTHR22835,P <sup>-</sup>	0 3.1.1.3		0 GO:0016788	AT1G29670.1
57	PTHR22835,P <sup>-</sup>	0 3.1.1.3		0 GO:0016788	AT1G29670.1
58	PTHR22835,P <sup>-</sup>	0 3.1.1.3		0 GO:0016788	AT1G29670.1
59	PTHR22835,P <sup>-</sup>	0 3.1.1.3		0 GO:0016788	AT1G29670.1
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3	PTHR22835,P <sup>-</sup>	0 3.1.1.3		0 GO:0016788	AT1G29670.1
4	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
5	PTHR22870,P <sup>-</sup>	0	0	0	0 AT3G26100.2
6	PTHR23315,P <sup>-</sup>	0	0	0 GO:0005515	AT2G22125.1
7	PTHR11514,P <sup>-</sup>	0	0	0 GO:0046983	AT5G41315.1
8	PTHR11514,P <sup>-</sup>	0	0	0 GO:0046983	AT5G41315.1
9	PTHR23315,P <sup>-</sup>	0	0	0 GO:0043248	AT1G23180.1
10	PTHR23315,P <sup>-</sup>	0	0	0 GO:0043248	AT1G23180.1
11	PTHR22762,P <sup>-</sup>	0 3.2.1.177,3.2. K15925		GO:0005975,(AT1G68560.1	
12	PTHR22762,P <sup>-</sup>	0 3.2.1.177,3.2. K15925		GO:0005975,(AT1G68560.1	
13	PTHR22762,P <sup>-</sup>	0 3.2.1.177,3.2. K15925		GO:0005975,(AT1G68560.1	
14	PTHR22762,P <sup>-</sup>	0 3.2.1.177,3.2. K15925		GO:0005975,(AT1G68560.1	
15	PTHR31642,P <sup>-</sup>	0 2.3.1.99		0 GO:0016747	AT4G13840.1
16	PTHR31642,P <sup>-</sup>	0 2.3.1.99		0 GO:0016747	AT4G13840.1
17	PTHR31642,P <sup>-</sup>	0 2.3.1.99		0 GO:0016747	AT4G13840.1
18	PTHR31642,P <sup>-</sup>	0 2.3.1.99		0 GO:0016747	AT4G13840.1
19	PTHR10774,P <sup>-</sup> KOG1032		0	0 GO:0005515	AT1G03370.1
20	PTHR10774,P <sup>-</sup> KOG1032		0	0 GO:0005515	AT1G03370.1
21	PTHR24089,P <sup>-</sup> KOG0752		0 K15108		0 AT5G48970.1
22	PTHR24089,P <sup>-</sup> KOG0752		0 K15108		0 AT5G48970.1
23	PTHR24089,P <sup>-</sup> KOG0752		0 K15108		0 AT5G48970.1
24	PTHR24089,P <sup>-</sup> KOG0752		0 K15108		0 AT5G48970.1
25	PTHR16166,P <sup>-</sup> KOG1809		0	0	0 AT1G48090.1
26	PTHR16166,P <sup>-</sup> KOG1809		0	0	0 AT1G48090.1
27	PTHR16166,P <sup>-</sup> KOG1809		0	0	0 AT1G48090.1
28	PTHR11062,P <sup>-</sup> KOG1021	2.4.2.41	K18789		0 AT5G33290.1
29	PTHR11929,P <sup>-</sup>	0	0	0 GO:0016020,(AT3G19280.1	
30	PTHR13131,P <sup>-</sup> KOG2913		0 K12386		0 AT5G40670.1
31	PTHR15184,P <sup>-</sup>	0 3.6.3.14	K02112	GO:0046034,(ATCG00480.1	
32	PTHR15184,P <sup>-</sup>	0 3.6.3.14	K02112	GO:0046034,(ATCG00480.1	
33	PTHR15184,P <sup>-</sup>	0 3.6.3.14	K02112	GO:0046034,(ATCG00480.1	
34	PTHR15184,P <sup>-</sup>	0 3.6.3.14	K02112	GO:0046034,(ATCG00480.1	
35	PTHR14445,P <sup>-</sup>	0	0	0 GO:0005515,(AT5G08430.1	
36	PTHR14445,P <sup>-</sup>	0	0	0 GO:0005515,(AT5G08430.1	
37	PTHR14445,P <sup>-</sup>	0	0	0 GO:0005515,(AT5G08430.1	
38	PTHR14445,P <sup>-</sup>	0	0	0 GO:0005515,(AT5G08430.1	
39	PTHR10438,P <sup>-</sup> KOG0907	3.5.1.52		0 GO:0045454,(AT4G29670.1	
40	PTHR10438,P <sup>-</sup> KOG0907	3.5.1.52		0 GO:0045454,(AT4G29670.1	
41	PTHR35918,P <sup>-</sup>	0	0	0 GO:0005515	AT1G04390.1
42	PTHR35918,P <sup>-</sup>	0	0	0 GO:0005515	AT1G04390.1
43	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0004674,(AT4G21380.1	
44	PTHR22749,P <sup>-</sup> KOG2914	2.7.1.26		0	0 AT4G21470.1
45	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
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3	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
4	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
5	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
6	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
7	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
8	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
9	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
10	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
11	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
12	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
13	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
14	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
15	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
16	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
17	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G15030.2
18	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
19	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
20	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
21	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
22	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
23	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
24	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
25	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,(	AT5G44240.2
26	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G22890.1
27	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G22890.1
28	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G22890.1
29	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G22890.1
30	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G22890.1
31	PTHR10285,P <sup>-</sup> KOG2878	2.7.1.31	K15918	0	AT1G80380.2
32	PTHR10285,P <sup>-</sup> KOG2878	2.7.1.31	K15918	0	AT1G80380.2
33	PTHR10285,P <sup>-</sup> KOG2878	2.7.1.31	K15918	0	AT1G80380.2
34	PTHR10285,P <sup>-</sup> KOG2878	2.7.1.31	K15918	0	AT1G80380.2
35	PTHR10285,P <sup>-</sup> KOG2878	2.7.1.31	K15918	0	AT1G80380.2
36	0	0	0	0	0 AT1G12064.1
37	0	0	0	0	0 AT1G12064.1
38	0	0	0	0	0 AT1G12064.1
39	0	0	0	0	0 AT1G12064.1
40	0	0	0	0	0 AT1G12064.1
41	0	0	0	0	0 AT1G12064.1
42	PTHR11802,P <sup>-</sup> KOG1282		0 K16296	GO:0006508,(	AT1G73300.1
43	PTHR11802,P <sup>-</sup> KOG1282		0 K16296	GO:0006508,(	AT1G73300.1
44	PTHR22897 KOG1731	1.8.3.2	K10758	GO:0045454,(	AT1G15020.2
45	PTHR22897 KOG1731	1.8.3.2	K10758	GO:0045454,(	AT1G15020.2
46	PTHR22897 KOG1731	1.8.3.2	K10758	GO:0045454,(	AT1G15020.2
47	PTHR22897 KOG1731	1.8.3.2	K10758	GO:0045454,(	AT1G15020.2
48	PTHR22897 KOG1731	1.8.3.2	K10758	GO:0045454,(	AT1G15020.2
49	PTHR22897 KOG1731	1.8.3.2	K10758	GO:0045454,(	AT1G15020.2
50	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
51	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
52	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
53	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
54	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
55	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
56	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
57	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
58	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
59	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
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3	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
4	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
5	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
6	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
7	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
8	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
9	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
10	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
11	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
13	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G55630.1
14	PTHR35732,P <sup>-</sup>	0	0	0	0 AT3G10405.1
15	PTHR15856,P <sup>-</sup> KOG1844		0	0	GO:0005515 AT1G33420.1
16	PTHR15856,P <sup>-</sup> KOG1844		0	0	GO:0005515 AT1G33420.1
17	PTHR15856,P <sup>-</sup> KOG1844		0	0	GO:0005515 AT1G33420.1
18	PTHR15856,P <sup>-</sup> KOG1844		0	0	GO:0005515 AT1G33420.1
19	PTHR15856,P <sup>-</sup> KOG1844		0	0	GO:0005515 AT1G33420.1
20	PTHR23257,P <sup>-</sup> KOG0192	2.7.11.1		0	GO:0006468,(AT1G08720.1
21	PTHR23257,P <sup>-</sup> KOG0192	2.7.11.1		0	GO:0006468,(AT1G08720.1
22	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0	GO:0016567,(AT3G54790.1
23	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
24	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
25	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
26	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
27	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
28	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
29	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
30	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
31	PTHR31707,P <sup>-</sup>	0 3.1.1.11	K01051		GO:0004857,(AT3G05610.1
32	PTHR13561,P <sup>-</sup>	0	0 K10728		GO:0005515 AT4G02110.1
33	PTHR13561,P <sup>-</sup>	0	0 K10728		GO:0005515 AT4G02110.1
34	PTHR13561,P <sup>-</sup>	0	0 K10728		GO:0005515 AT4G02110.1
35	PTHR13561,P <sup>-</sup>	0	0 K10728		GO:0005515 AT4G02110.1
36	PTHR13561,P <sup>-</sup>	0	0 K10728		GO:0005515 AT4G02110.1
37	PTHR22912,P <sup>-</sup>	0 1.8.1.9	K00384		GO:0045454,(AT2G41680.1
38	PTHR27004,P <sup>-</sup> KOG0472		0	0	GO:0005515 AT1G47890.1
39	PTHR27004,P <sup>-</sup> KOG0472		0	0	GO:0005515 AT1G47890.1
40	PTHR10641,P <sup>-</sup> KOG0048		0 K09422		0 AT3G61250.1
41	PTHR10641,P <sup>-</sup> KOG0048		0 K09422		0 AT3G61250.1
42	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
43	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
44	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
45	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
46	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
47	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
48	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
49	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
50	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
51	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
52	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
53	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01150.1
54	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
55	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
56	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
57	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
58	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
59	PTHR33103,P <sup>-</sup>	0	0	0	0 AT5G01120.1
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3	PTHR22847,P <sup>-</sup> KOG0266		0	0 GO:0005515	AT2G32700.6
4	PTHR22847,P <sup>-</sup> KOG0266		0	0 GO:0005515	AT2G32700.6
5	PTHR22847,P <sup>-</sup> KOG0266		0	0 GO:0005515	AT2G32700.6
6	PTHR22847,P <sup>-</sup> KOG0266		0	0 GO:0005515	AT2G32700.6
7	PTHR22847,P <sup>-</sup> KOG0266		0	0 GO:0005515	AT2G32700.6
8	PTHR10795,P <sup>-</sup>	0 3.4.21.25		0 GO:0006508,(	AT5G59100.1
9	PTHR13301,P <sup>-</sup>	0 2.4.1.12		0 GO:0030244,(	AT1G55850.1
10	PTHR13301,P <sup>-</sup>	0 2.4.1.12		0 GO:0030244,(	AT1G55850.1
11	PTHR11705,P <sup>-</sup> KOG2650	3.4.17.1		0 GO:0008270,(	AT5G42320.1
12	PTHR11705,P <sup>-</sup> KOG2650	3.4.17.1		0 GO:0008270,(	AT5G42320.1
13	PTHR12791,P <sup>-</sup>	0	0 K08505	0 AT4G14600.1	
14	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
15	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
16	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
17	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
18	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
19	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
20	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
21	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
22	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
23	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
24	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
25	PTHR13878,P <sup>-</sup> KOG1231	1.5.99.12		0 GO:0055114,(	AT1G75450.1
26	PTHR23500,P <sup>-</sup> KOG0254		0	0 GO:0055085,(	AT4G35300.1
27	PTHR23500,P <sup>-</sup> KOG0254		0	0 GO:0055085,(	AT4G35300.1
28	PTHR33880,P <sup>-</sup>	0	0	0 AT4G14100.1	
29	PTHR33880,P <sup>-</sup>	0	0	0 AT4G14100.1	
30	PTHR33880,P <sup>-</sup>	0	0	0 AT4G14100.1	
31	PTHR33880,P <sup>-</sup>	0	0	0 AT4G14100.1	
32	PTHR33880,P <sup>-</sup>	0	0	0 AT4G14100.1	
33	PTHR33880,P <sup>-</sup>	0	0	0 AT4G14100.1	
34	PTHR31673,P <sup>-</sup>	0	0	0 GO:0031225,(	AT5G60920.1
35	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0005975,(	AT4G26140.1
36	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0005975,(	AT4G26140.1
37	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0005975,(	AT4G26140.1
38	PTHR23421,P <sup>-</sup>	0 3.2.1.23		0 GO:0005975,(	AT4G26140.1
39	PTHR15371,P <sup>-</sup>	0	0	0 AT4G16160.1	
40	PTHR15371,P <sup>-</sup>	0	0	0 AT4G16160.1	
41	PTHR15371,P <sup>-</sup>	0	0	0 AT4G16160.1	
42	PTHR15371,P <sup>-</sup>	0	0	0 AT4G16160.1	
43	0	0	0	0	0
44	0	0	0	0	0
45	0	0	0	0	0
46	0	0	0	0	0
47	PTHR11017,P <sup>-</sup>	0	0	0 GO:0007165,(	AT5G36930.2
48	PTHR11017,P <sup>-</sup>	0	0	0 GO:0007165,(	AT5G36930.2
49	PTHR11017,P <sup>-</sup>	0	0	0 GO:0007165,(	AT5G36930.2
50	PTHR11017,P <sup>-</sup>	0	0	0 GO:0007165,(	AT5G36930.2
51	PTHR13902,P <sup>-</sup>	0 2.7.11.1	K08867	GO:0006468,(	AT3G51630.1
52	PTHR13902,P <sup>-</sup>	0 2.7.11.1	K08867	GO:0006468,(	AT3G51630.1
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3	PTHR13902,P <sup>-</sup>	0 2.7.11.1	K08867	GO:0006468,(	AT3G51630.1
4	PTHR13902,P <sup>-</sup>	0 2.7.11.1	K08867	GO:0006468,(	AT3G51630.1
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6	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
7	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
8					
9	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
10	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
11	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
12	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
13	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
14	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
15	PTHR13299,P <sup>-</sup> KOG4546		0	0	0 AT2G45690.1
16					
17	PTHR30573,P <sup>-</sup>	0 2.5.1.72		0	0 AT5G50210.1
18	PTHR30573,P <sup>-</sup>	0 2.5.1.72		0	0 AT5G50210.1
19	PTHR30573,P <sup>-</sup>	0 2.5.1.72		0	0 AT5G50210.1
20	PTHR30573,P <sup>-</sup>	0 2.5.1.72		0	0 AT5G50210.1
21					
22	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
23	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
24	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
25	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
26	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
27	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
28	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
29	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
30	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
31	PTHR11200,P <sup>-</sup>	0	0	0 GO:0042578	AT1G22620.1
32					
33	PTHR15852,P <sup>-</sup>	0 5.3.4.1		0	0 AT5G61670.1
34	PTHR33624,P <sup>-</sup>	0	0	0	0 AT3G56710.1
35	PTHR33624,P <sup>-</sup>	0	0	0	0 AT3G56710.1
36	PTHR33624,P <sup>-</sup>	0	0	0	0 AT3G56710.1
37	PTHR33624,P <sup>-</sup>	0	0	0	0 AT3G56710.1
38	PTHR33624,P <sup>-</sup>	0	0	0	0 AT3G56710.1
39	PTHR10774,P <sup>-</sup>	0	0	0 GO:0005515	AT1G03370.1
40	PTHR10774,P <sup>-</sup>	0	0	0 GO:0005515	AT1G03370.1
41					
42	PTHR14089,P <sup>-</sup>	0	0 K12872	GO:0003676	AT1G07360.1
43	PTHR14089,P <sup>-</sup>	0	0 K12872	GO:0003676	AT1G07360.1
44	PTHR24089,P <sup>-</sup> KOG0749		0	0	0 AT5G13490.1
45	PTHR24089,P <sup>-</sup> KOG0749		0	0	0 AT5G13490.1
46	PTHR24089,P <sup>-</sup> KOG0749		0	0	0 AT5G13490.1
47	PTHR24089,P <sup>-</sup> KOG0749		0	0	0 AT5G13490.1
48	PTHR24089,P <sup>-</sup> KOG0749		0	0	0 AT5G13490.1
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arabi-symbol	arabi-defline	ID
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
	0 Plant protein of unknown function (DUF936)	Phvul.002G07
	0 Plant protein of unknown function (DUF936)	Phvul.002G07
	0 Plant protein of unknown function (DUF936)	Phvul.002G07
	0 Plant protein of unknown function (DUF936)	Phvul.002G07
EX1	Protein of unknown function (DUF3506)	Phvul.006G20
	0 Leucine carboxyl methyltransferase	Phvul.009G05
	0 Leucine carboxyl methyltransferase	Phvul.009G05
	0 Endomembrane protein 70 protein family	Phvul.009G08
	0 ARM repeat superfamily protein	Phvul.010G11
	0 ARM repeat superfamily protein	Phvul.010G11
	0 ARM repeat superfamily protein	Phvul.010G11
	0 ARM repeat superfamily protein	Phvul.010G11
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L009543
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L009543
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L009543
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L009543
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
GUT1	Exostosin family protein	Phvul.002G28
GUT1	Exostosin family protein	Phvul.002G28
GUT1	Exostosin family protein	Phvul.002G28
GUT1	Exostosin family protein	Phvul.002G28
	0 disease resistance family protein / LRR family protein	Phvul.004G04
	0	0 Phvul.006G15
	0 LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
	0 LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
	0 LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
	0 LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
	0 Protein of unknown function (DUF674)	Phvul.008G11
	0 Protein of unknown function (DUF674)	Phvul.008G11

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	0 ARM repeat superfamily protein	Phvul.008G16
	0 ARM repeat superfamily protein	Phvul.008G16
	0 ARM repeat superfamily protein	Phvul.008G16
	0 ARM repeat superfamily protein	Phvul.008G16
	0 ARM repeat superfamily protein	Phvul.008G16
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	0 ARM repeat superfamily protein	Phvul.008G16
	0 ARM repeat superfamily protein	Phvul.008G16
	0 Leucine carboxyl methyltransferase	Phvul.009G05
	0 Leucine carboxyl methyltransferase	Phvul.009G05
	0 Leucine carboxyl methyltransferase	Phvul.009G05
	0 Leucine carboxyl methyltransferase	Phvul.009G05
	0	0 0
	0	0 0
	ATGLR3.2,ATGLUR2,GLR3.2, glutamate receptor 2	Phvul.001G02
	ATGLR3.2,ATGLUR2,GLR3.2, glutamate receptor 2	Phvul.001G02
	ATBZIP9,BZIP9,BZO2H2 basic leucine zipper 9	Phvul.001G07
	ATBZIP9,BZIP9,BZO2H2 basic leucine zipper 9	Phvul.001G07
	ARA1,ATISA1,ISA1 arabinose kinase	Phvul.001G07
	ARA1,ATISA1,ISA1 arabinose kinase	Phvul.001G07
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ARP2,ATARP2,WRM actin related protein 2	Phvul.001G08
	ANAC041,NAC041 NAC domain containing protein 41	Phvul.001G09
	ANAC041,NAC041 NAC domain containing protein 41	Phvul.001G09
	ANAC041,NAC041 NAC domain containing protein 41	Phvul.001G09
	ANAC041,NAC041 NAC domain containing protein 41	Phvul.001G09
	0 Aldolase superfamily protein	Phvul.001G12
	0 Aldolase superfamily protein	Phvul.001G12
	ABCA1,AtABCA1 ATP-binding cassette A1	Phvul.001G13

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ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13
SPL9	squamosa promoter binding protein-like 9	Phvul.001G14
SPL9	squamosa promoter binding protein-like 9	Phvul.001G14
SPL9	squamosa promoter binding protein-like 9	Phvul.001G14
SPL9	squamosa promoter binding protein-like 9	Phvul.001G14
	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
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TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
TZP	zinc knuckle (CCHC-type) family protein	Phvul.002G04
ATH2,ATTRX2,ATTRXH2,TRX	thioredoxin 2	Phvul.002G06
ATH2,ATTRX2,ATTRXH2,TRX	thioredoxin 2	Phvul.002G06
	0 Plant protein of unknown function (DUF936)	Phvul.002G07
	0 Plant protein of unknown function (DUF936)	Phvul.002G07
MMP	matrix metalloproteinase	Phvul.002G07
MMP	matrix metalloproteinase	Phvul.002G07
MMP	matrix metalloproteinase	Phvul.002G07
MMP	matrix metalloproteinase	Phvul.002G07
ATNHX7,ATSOS1,SOS1	sodium proton exchanger, putative (NHX7) (SOS1)	Phvul.002G18
ATNHX7,ATSOS1,SOS1	sodium proton exchanger, putative (NHX7) (SOS1)	Phvul.002G18
ATNHX7,ATSOS1,SOS1	sodium proton exchanger, putative (NHX7) (SOS1)	Phvul.002G18



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3		0 Protein kinase protein with adenine nucleotide alpha	Phvul.002G30
4		0 CW-type Zinc Finger	Phvul.003G10
5		0 CW-type Zinc Finger	Phvul.003G10
6		0 disease resistance family protein / LRR family protein	Phvul.004G04
7			
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9	emb1417	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.004G10
10	ATCLC-C,CLC-C	chloride channel C	Phvul.004G13
11	ATCLC-C,CLC-C	chloride channel C	Phvul.004G13
12	ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
13	ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
14	ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
15	ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
16			
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18		0 Wound-responsive family protein	Phvul.005G08
19		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
20		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
21		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
22		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
23		0	0 Phvul.005G18
24		0	0 Phvul.005G18
25			
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27		0 Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
28		0 Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
29		0 Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
30		0 Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
31			
32	ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
33	ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
34	ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
35	ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
36			
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38		0 Protein of Unknown Function (DUF239)	Phvul.006G10
39		0 Protein of Unknown Function (DUF239)	Phvul.006G10
40		0 Sec14p-like phosphatidylinositol transfer family prote	Phvul.006G13
41		0 Sec14p-like phosphatidylinositol transfer family prote	Phvul.006G13
42		0 alpha/beta-Hydrolases superfamily protein	Phvul.007G11
43		0 alpha/beta-Hydrolases superfamily protein	Phvul.007G11
44		0 Pectin lyase-like superfamily protein	Phvul.007G21
45		0 Pectin lyase-like superfamily protein	Phvul.007G21
46		0 SAUR-like auxin-responsive protein family	Phvul.007G21
47		0 SAUR-like auxin-responsive protein family	Phvul.007G21
48		0 LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
49		0 LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
50		0	0 0
51		0	0 0
52		0 NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G11
53		0 NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G11
54		0 NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
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	0 NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
	0 NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
	0 NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
COX15	cytochrome c oxidase 15	Phvul.008G28
	0 Endomembrane protein 70 protein family	Phvul.008G28
ATFBP7,FBP7	F-box protein 7	Phvul.009G12
ATFBP7,FBP7	F-box protein 7	Phvul.009G12
ATFBP7,FBP7	F-box protein 7	Phvul.009G12
ATFBP7,FBP7	F-box protein 7	Phvul.009G12
GUT1	Exostosin family protein	Phvul.009G16
GUT1	Exostosin family protein	Phvul.009G16
GUT1	Exostosin family protein	Phvul.009G16
GUT1	Exostosin family protein	Phvul.009G16
	0 NB-ARC domain-containing disease resistance protei	Phvul.010G06
	0 NB-ARC domain-containing disease resistance protei	Phvul.010G06
	0 NB-ARC domain-containing disease resistance protei	Phvul.010G06
	0 NB-ARC domain-containing disease resistance protei	Phvul.010G06
GBF1	G-box binding factor 1	Phvul.011G04
GBF1	G-box binding factor 1	Phvul.011G04
TOR	target of rapamycin	Phvul.011G05
TOR	target of rapamycin	Phvul.011G05
TOR	target of rapamycin	Phvul.011G05
TOR	target of rapamycin	Phvul.011G05
ATLAC2,LAC2	laccase 2	Phvul.L00734:
ATLAC2,LAC2	laccase 2	Phvul.L00734:
	0 Remorin family protein	Phvul.001G02
	0 Remorin family protein	Phvul.001G02
ATBFRUCT1,ATCWINV1	Glycosyl hydrolases family 32 protein	Phvul.001G03
	0 RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.001G10
	0 RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.001G10
EDA4	Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
EDA4	Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
EDA4	Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
EDA4	Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
	0 biotin/lipoyl attachment domain-containing protein	Phvul.001G24
AT-EXPR,ATEXLB1,ATEXPR1,	expansin-like B1	Phvul.002G00
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
	0 Haloacid dehalogenase-like hydrolase (HAD) superfan	Phvul.002G21
	0 Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
	0 Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
PDF1,PP2AA2,PR 65	protein phosphatase 2A subunit A2	Phvul.003G02
PDF1,PP2AA2,PR 65	protein phosphatase 2A subunit A2	Phvul.003G02

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3		0 Thiolase family protein	Phvul.003G08
4		0 Thiolase family protein	Phvul.003G08
5		0 Thiolase family protein	Phvul.003G08
6		0 Thiolase family protein	Phvul.003G08
7		0 Thiolase family protein	Phvul.003G08
8		0 Thiolase family protein	Phvul.003G08
9		0 Thiolase family protein	Phvul.003G08
10		0 Thiolase family protein	Phvul.003G08
11		0 Thiolase family protein	Phvul.003G08
12		0 Thiolase family protein	Phvul.003G08
13		0 Thiolase family protein	Phvul.003G08
14		0 Mitochondrial substrate carrier family protein	Phvul.003G10
15		0 Mitochondrial substrate carrier family protein	Phvul.003G10
16		0 Ypt/Rab-GAP domain of gyp1p superfamily protein	Phvul.003G14
17		0 Ypt/Rab-GAP domain of gyp1p superfamily protein	Phvul.003G14
18		0 Ypt/Rab-GAP domain of gyp1p superfamily protein	Phvul.003G14
19	TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
20	TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
21	TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
22	TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
23	TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
24	ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
25	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
26	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
27	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
28		0 FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
29		0 FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
30		0 FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
31		0 FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
32		0 FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
33		0	0
34		0	0
35		0 disease resistance family protein / LRR family protein	Phvul.004G04
36		0 disease resistance family protein / LRR family protein	Phvul.004G04
37		0 ATP binding microtubule motor family protein	Phvul.004G16
38		0 ATP binding microtubule motor family protein	Phvul.004G16
39	HAM1	histone acetyltransferase of the MYST family 1	Phvul.005G01
40	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
41	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
42	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
43	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
44	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
45	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
46	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
47	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
48	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
49	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
50	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide	Phvul.005G01
51		0 UDP-Glycosyltransferase superfamily protein	Phvul.005G08
52		0 UDP-Glycosyltransferase superfamily protein	Phvul.005G08
53		0 UDP-Glycosyltransferase superfamily protein	Phvul.005G08
54	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
55	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
56	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
57	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
58	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
59	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
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MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
	0	0 0
	0	0 0
	0 Pyridoxal phosphate (PLP)-dependent transferases	suPhvul.006G13
	0 Pyridoxal phosphate (PLP)-dependent transferases	suPhvul.006G13
	0	0 Phvul.006G19
	0	0 Phvul.006G19
	0	0 Phvul.006G19
	0	0 Phvul.006G19
	0 Protein of unknown function (DUF581)	Phvul.007G05
	0 Protein of unknown function (DUF581)	Phvul.007G05
AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
	0 Mog1/PsbP/DUF1795-like photosystem II reaction ce	Phvul.007G18
	0 Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.007G19
	0 Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.007G19
	0	0 0
	0	0 0
	0	0 0
	0	0 0
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
	0 HEAT repeat-containing protein	Phvul.008G00
AtLIG6,LIG6	DNA LIGASE 6	Phvul.008G00
AtLIG6,LIG6	DNA LIGASE 6	Phvul.008G00
AtLIG6,LIG6	DNA LIGASE 6	Phvul.008G00
AtLIG6,LIG6	DNA LIGASE 6	Phvul.008G00
	0 EXS (ERD1/XPR1/SYG1) family protein	Phvul.008G03
	0 EXS (ERD1/XPR1/SYG1) family protein	Phvul.008G03
	0 Leucine-rich repeat protein kinase family protein	Phvul.008G09
	0 Leucine-rich repeat protein kinase family protein	Phvul.008G09
	0 Leucine-rich repeat protein kinase family protein	Phvul.008G09
	0 Leucine-rich repeat protein kinase family protein	Phvul.008G09
	0 Leucine-rich repeat protein kinase family protein	Phvul.008G09
	0 Leucine-rich repeat protein kinase family protein	Phvul.008G09
	0 RING/U-box superfamily protein	Phvul.008G10

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3		0 RING/U-box superfamily protein	Phvul.008G10
4		0 RING/U-box superfamily protein	Phvul.008G10
5		0 RING/U-box superfamily protein	Phvul.008G10
6		0 RING/U-box superfamily protein	Phvul.008G10
7		0 Protein of unknown function (DUF674)	Phvul.008G11
8		0 Protein of unknown function (DUF674)	Phvul.008G11
9		0 Protein of unknown function (DUF674)	Phvul.008G11
10		0 Protein of unknown function (DUF674)	Phvul.008G11
11		0 Protein of unknown function (DUF674)	Phvul.008G11
12		0 Protein of unknown function (DUF674)	Phvul.008G11
13		0 Protein of unknown function (DUF674)	Phvul.008G11
14		0 Protein of unknown function (DUF674)	Phvul.008G11
15		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.008G19
16	UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
17	UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
18	UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
19	UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
20	UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
21	UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
22	ARF17	auxin response factor 17	Phvul.009G02
23	ARF17	auxin response factor 17	Phvul.009G02
24			
25		0 vacuolar iron transporter (VIT) family protein	Phvul.009G04
26		0 vacuolar iron transporter (VIT) family protein	Phvul.009G04
27		0 vacuolar iron transporter (VIT) family protein	Phvul.009G04
28	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
29	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
30	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
31	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
32	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
33	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
34	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
35	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
36	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
37	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
38	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
39		0 Mitochondrial substrate carrier family protein	Phvul.009G24
40		0 Mitochondrial substrate carrier family protein	Phvul.009G24
41		0 Mitochondrial substrate carrier family protein	Phvul.009G24
42		0 Mitochondrial substrate carrier family protein	Phvul.009G24
43		0 Mitochondrial substrate carrier family protein	Phvul.009G24
44		0 Mitochondrial substrate carrier family protein	Phvul.009G24
45		0 Mitochondrial substrate carrier family protein	Phvul.009G24
46		0 Mitochondrial substrate carrier family protein	Phvul.009G24
47		0 Mitochondrial substrate carrier family protein	Phvul.009G24
48		0 Mitochondrial substrate carrier family protein	Phvul.009G24
49	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
50	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
51	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
52	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
53	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
54	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
55	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
56	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
57	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
58	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
59	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
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3	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
4	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
5	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
6	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
7	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
8	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
9	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
10	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
11	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
12	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
13	AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
14		0 ARM repeat superfamily protein	Phvul.010G11
15		0 ARM repeat superfamily protein	Phvul.010G11
16		0 ARM repeat superfamily protein	Phvul.010G11
17		0 ARM repeat superfamily protein	Phvul.010G11
18		0 ARM repeat superfamily protein	Phvul.010G11
19		0 Zinc finger (CCCH-type) family protein / RNA recogniti	Phvul.011G01
20		0 Zinc finger (CCCH-type) family protein / RNA recogniti	Phvul.011G01
21		0 Zinc finger (CCCH-type) family protein / RNA recogniti	Phvul.011G01
22		0 Zinc finger (CCCH-type) family protein / RNA recogniti	Phvul.011G01
23		0 Zinc finger (CCCH-type) family protein / RNA recogniti	Phvul.011G01
24	LCR44	low-molecular-weight cysteine-rich 44	0
25	LCR44	low-molecular-weight cysteine-rich 44	0
26	LCR44	low-molecular-weight cysteine-rich 44	0
27	LCR44	low-molecular-weight cysteine-rich 44	0
28	LCR44	low-molecular-weight cysteine-rich 44	0
29		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
30		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
31		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
32		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
33		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
34		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
35		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
36		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
37	ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
38	ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
39	ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
40	ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
41	ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
42	ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
43	SUVH1	SU(VAR)3-9 homolog 1	Phvul.011G19
44	SUVH1	SU(VAR)3-9 homolog 1	Phvul.011G19
45		0	0 Phvul.001G09
46		0	0 Phvul.001G09
47		0 ENTH/VHS family protein	Phvul.001G10
48		0 ENTH/VHS family protein	Phvul.001G10
49		0 ENTH/VHS family protein	Phvul.001G10
50		0 ENTH/VHS family protein	Phvul.001G10
51		0 ENTH/VHS family protein	Phvul.001G10
52		0 ENTH/VHS family protein	Phvul.001G10
53		0 ENTH/VHS family protein	Phvul.001G10
54		0 ENTH/VHS family protein	Phvul.001G10
55		0 ENTH/VHS family protein	Phvul.001G10
56		0 ENTH/VHS family protein	Phvul.001G10
57		0 ENTH/VHS family protein	Phvul.001G10
58		0 ENTH/VHS family protein	Phvul.001G10
59		0 ENTH/VHS family protein	Phvul.001G10
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3	0 ENTH/VHS family protein	Phvul.001G10
4	0 ENTH/VHS family protein	Phvul.001G10
5	0 ENTH/VHS family protein	Phvul.001G10
6	0 ENTH/VHS family protein	Phvul.001G10
7	0 ENTH/VHS family protein	Phvul.001G10
8	0 ENTH/VHS family protein	Phvul.001G10
9	0 ENTH/VHS family protein	Phvul.001G10
10	0 ENTH/VHS family protein	Phvul.001G10
11	0 ENTH/VHS family protein	Phvul.001G10
12	0 ENTH/VHS family protein	Phvul.001G10
13	0 oxidoreductase, 2OG-Fe(II) oxygenase family protein	Phvul.001G14
14	0 Thioredoxin superfamily protein	Phvul.001G17
15	0 Thioredoxin superfamily protein	Phvul.001G17
16	0 Thioredoxin superfamily protein	Phvul.001G17
17	0 Thioredoxin superfamily protein	Phvul.001G17
18	0 Thioredoxin superfamily protein	Phvul.001G17
19	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
20	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
21	0 phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
22	0 DNase I-like superfamily protein	Phvul.001G20
23	0 DNase I-like superfamily protein	Phvul.001G20
24	0 DNase I-like superfamily protein	Phvul.001G20
25	0 DNase I-like superfamily protein	Phvul.001G20
26	0 DNase I-like superfamily protein	Phvul.001G20
27	0 DNase I-like superfamily protein	Phvul.001G20
28	0 DNase I-like superfamily protein	Phvul.001G20
29	0 DNase I-like superfamily protein	Phvul.001G20
30	0 DNase I-like superfamily protein	Phvul.001G20
31	0 DNase I-like superfamily protein	Phvul.001G20
32	0 DNase I-like superfamily protein	Phvul.001G20
33	0 ARM repeat superfamily protein	Phvul.001G26
34	0 O-methyltransferase family protein	Phvul.001G26
35	0 O-methyltransferase family protein	Phvul.001G26
36	0 O-methyltransferase family protein	Phvul.001G26
37	0 C2H2-like zinc finger protein	Phvul.002G05
38	0 C2H2-like zinc finger protein	Phvul.002G05
39	ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2	Phvul.002G06
40	ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2	Phvul.002G06
41	ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2	Phvul.002G06
42	ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2	Phvul.002G06
43	ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2	Phvul.002G06
44	AtWRKY41,WRKY41 WRKY family transcription factor	Phvul.002G16
45	AtWRKY41,WRKY41 WRKY family transcription factor	Phvul.002G16
46	AtWRKY41,WRKY41 WRKY family transcription factor	Phvul.002G16
47	0 Galactose-binding protein	Phvul.002G16
48	0 Galactose-binding protein	Phvul.002G16
49	0 Galactose-binding protein	Phvul.002G16
50	0 Galactose-binding protein	Phvul.002G16
51	0 Galactose-binding protein	Phvul.002G16
52	0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.002G21
53	0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.002G21
54	0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.002G21
55	0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.002G21
56	0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.002G21
57	0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
58	0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
59	0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
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3		0 Regulator of chromosome condensation (RCC1) family	Phvul.002G25
4		0 Regulator of chromosome condensation (RCC1) family	Phvul.002G25
5		0 Regulator of chromosome condensation (RCC1) family	Phvul.002G25
6		0 Regulator of chromosome condensation (RCC1) family	Phvul.002G25
7		0 Regulator of chromosome condensation (RCC1) family	Phvul.002G25
8		0 Nodulin MtN3 family protein	Phvul.002G28
9		0 Nodulin MtN3 family protein	Phvul.002G28
10		0 Nodulin MtN3 family protein	Phvul.002G28
11		0 Nodulin MtN3 family protein	Phvul.002G28
12		0 Nodulin MtN3 family protein	Phvul.002G28
13		0 Peptidase M1 family protein	Phvul.002G29
14		0 Peptidase M1 family protein	Phvul.002G29
15		0 Peptidase M1 family protein	Phvul.002G29
16	ABI1,AtABI1	Protein phosphatase 2C family protein	Phvul.002G30
17	ABI1,AtABI1	Protein phosphatase 2C family protein	Phvul.002G30
18	UFD1	ubiquitin fusion degradation 1	Phvul.002G32
19	UFD1	ubiquitin fusion degradation 1	Phvul.002G32
20	UFD1	ubiquitin fusion degradation 1	Phvul.002G32
21	UFD1	ubiquitin fusion degradation 1	Phvul.002G32
22	UFD1	ubiquitin fusion degradation 1	Phvul.002G32
23	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
24	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
25	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
26	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
27	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
28	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
29	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
30	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
31	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
32	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
33	ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
34	DME	HhH-GPD base excision DNA repair family protein	Phvul.003G03
35	DME	HhH-GPD base excision DNA repair family protein	Phvul.003G03
36		0 Nucleotide-diphospho-sugar transferases superfamily	Phvul.003G05
37		0 Nucleotide-diphospho-sugar transferases superfamily	Phvul.003G05
38		0	0
39		0	0
40		0	0
41		0	0
42		0	0
43		0	0
44		0	0
45	BGAL1	beta galactosidase 1	Phvul.003G13
46	BGAL1	beta galactosidase 1	Phvul.003G13
47	BGAL1	beta galactosidase 1	Phvul.003G13
48	BGAL1	beta galactosidase 1	Phvul.003G13
49		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
50		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
51		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
52		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
53		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
54		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
55		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
56		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
57		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
58		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
59		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
60			

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3		0 Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
4		0 S-adenosyl-L-methionine-dependent methyltransferase	Phvul.003G28
5		0 S-adenosyl-L-methionine-dependent methyltransferase	Phvul.003G28
6			
7	ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
8	ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
9	ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
10	ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
11	ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
12	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
13	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
14	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
15	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
16	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
17	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
18	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
19	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
20	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
21	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
22	ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
23		0	0 0
24		0	0 0
25		0	0 0
26		0	0 0
27		0	0 0
28		0 disease resistance family protein / LRR family protein	Phvul.004G04
29		0 disease resistance family protein / LRR family protein	Phvul.004G04
30			
31		0 Eukaryotic aspartyl protease family protein	Phvul.004G05
32		0 Eukaryotic aspartyl protease family protein	Phvul.004G05
33		0 Eukaryotic aspartyl protease family protein	Phvul.004G05
34		0 Eukaryotic aspartyl protease family protein	Phvul.004G05
35		0 Eukaryotic aspartyl protease family protein	Phvul.004G05
36	AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
37	AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
38	AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
39	AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
40	AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
41	AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
42	AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
43	AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
44	AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
45	AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
46	NF-YC11	nuclear factor Y, subunit C11	Phvul.005G01
47		0 BTB/POZ domain-containing protein	Phvul.005G05
48			
49	ATPPC2,PPC2	phosphoenolpyruvate carboxylase 2	Phvul.005G09
50		0 MuDR family transposase	Phvul.005G10
51		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
52		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
53		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
54		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
55		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
56		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
57		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
58		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
59		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
60			

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2			
3		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
4		0 alpha/beta-Hydrolases superfamily protein	Phvul.005G11
5		0 C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
6		0 C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
7		0 Calcium-binding EF-hand family protein	Phvul.006G10
8		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
9		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
10		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
11		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
12		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
13		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
14		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
15		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
16		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
17		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
18		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
19		0 zinc knuckle (CCHC-type) family protein	Phvul.006G11
20		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
21		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
22		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
23		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
24		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
25		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
26		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
27		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
28		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
29		0 HCO <sub>3</sub> <sup>-</sup> transporter family	Phvul.006G12
30		0	0 Phvul.006G15
31			
32	SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
33	SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
34	SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
35	SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
36	SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
37			
38		0 phosphoinositide binding	Phvul.006G19
39		0 phosphoinositide binding	Phvul.006G19
40		0 Prolyl oligopeptidase family protein	Phvul.007G01
41		0 Prolyl oligopeptidase family protein	Phvul.007G01
42		0 Prolyl oligopeptidase family protein	Phvul.007G01
43		0 Prolyl oligopeptidase family protein	Phvul.007G01
44		0 TCP family transcription factor	Phvul.007G01
45		0 TCP family transcription factor	Phvul.007G01
46		0 phosphatidyl serine synthase family protein	Phvul.007G03
47			
48			
49	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
50	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
51	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
52	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
53	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
54	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
55	AO1,ATAO1	amine oxidase 1	Phvul.007G05
56	AO1,ATAO1	amine oxidase 1	Phvul.007G05
57	AO1,ATAO1	amine oxidase 1	Phvul.007G05
58	AO1,ATAO1	amine oxidase 1	Phvul.007G05
59	AO1,ATAO1	amine oxidase 1	Phvul.007G05
60			

1			
2			
3		0 Protein of unknown function (DUF581)	Phvul.007G05
4		0 Protein of unknown function (DUF581)	Phvul.007G05
5		0 Protein of unknown function (DUF581)	Phvul.007G05
6		0 Protein of unknown function (DUF581)	Phvul.007G05
7		0 Protein of unknown function (DUF581)	Phvul.007G05
8		0 Protein of unknown function (DUF581)	Phvul.007G05
9		0 Protein of unknown function (DUF581)	Phvul.007G05
10		0 Protein of unknown function (DUF581)	Phvul.007G05
11		0 Protein of unknown function (DUF581)	Phvul.007G05
12		0 Protein of unknown function (DUF581)	Phvul.007G05
13		0 Protein of unknown function (DUF581)	Phvul.007G05
14	AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
15	AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
16	AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
17	AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
18	AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
19	AtCXE20,CXE20	carboxyesterase 20	Phvul.007G06
20	ATFRO2,FRD1,FRO2	ferric reduction oxidase 2	Phvul.007G07
21	ATFRO2,FRD1,FRO2	ferric reduction oxidase 2	Phvul.007G07
22	ATFRO2,FRD1,FRO2	ferric reduction oxidase 2	Phvul.007G07
23	ATFRO2,FRD1,FRO2	ferric reduction oxidase 2	Phvul.007G07
24	ATFRO2,FRD1,FRO2	ferric reduction oxidase 2	Phvul.007G07
25			
26		0	0 Phvul.007G09
27		0	0 Phvul.007G09
28		0	0 Phvul.007G09
29		0	0 Phvul.007G09
30		0	0 Phvul.007G09
31	ATGST11,ATGSTF7,ATGSTF8	glutathione S-transferase 7	Phvul.007G10
32	ATGST11,ATGSTF7,ATGSTF8	glutathione S-transferase 7	Phvul.007G10
33	ATGST11,ATGSTF7,ATGSTF8	glutathione S-transferase 7	Phvul.007G10
34	ATGST11,ATGSTF7,ATGSTF8	glutathione S-transferase 7	Phvul.007G10
35	ATGST11,ATGSTF7,ATGSTF8	glutathione S-transferase 7	Phvul.007G10
36		0 Mog1/PsbP/DUF1795-like photosystem II reaction ce	Phvul.007G18
37		0 Mog1/PsbP/DUF1795-like photosystem II reaction ce	Phvul.007G18
38		0 Mog1/PsbP/DUF1795-like photosystem II reaction ce	Phvul.007G18
39		0 Mog1/PsbP/DUF1795-like photosystem II reaction ce	Phvul.007G18
40		0 Mog1/PsbP/DUF1795-like photosystem II reaction ce	Phvul.007G18
41			
42		0	0 0
43		0	0 0
44		0 Protein kinase superfamily protein	Phvul.007G20
45		0 Protein kinase superfamily protein	Phvul.007G20
46		0 Protein kinase superfamily protein	Phvul.007G20
47		0 Protein kinase superfamily protein	Phvul.007G20
48		0 Protein kinase superfamily protein	Phvul.007G20
49		0 Protein kinase superfamily protein	Phvul.007G20
50		0 Protein kinase superfamily protein	Phvul.007G20
51		0 Protein kinase superfamily protein	Phvul.007G20
52		0 Protein kinase superfamily protein	Phvul.007G20
53		0 Protein kinase superfamily protein	Phvul.007G20
54		0 Protein kinase superfamily protein	Phvul.007G20
55		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
56		0	0 Phvul.007G27
57		0	0 Phvul.007G27
58		0	0 Phvul.007G27
59		0	0 Phvul.007G27
60			

1				
2				
3		0	0	Phvul.007G27
4		0	0	Phvul.007G27
5		0	0	Phvul.007G27
6		0	0	Phvul.007G27
7	NEF1	no exine formation 1		Phvul.008G00
8	NEF1	no exine formation 1		Phvul.008G00
9	NEF1	no exine formation 1		Phvul.008G00
10	NEF1	no exine formation 1		Phvul.008G00
11	NEF1	no exine formation 1		Phvul.008G00
12		0 HEAT repeat-containing protein		Phvul.008G00
13		0 HEAT repeat-containing protein		Phvul.008G00
14		0 HEAT repeat-containing protein		Phvul.008G00
15		0 HEAT repeat-containing protein		Phvul.008G00
16		0 HEAT repeat-containing protein		Phvul.008G00
17		0 HEAT repeat-containing protein		Phvul.008G00
18		0 HEAT repeat-containing protein		Phvul.008G00
19	ATTA6,TAF6,TAFII59	TATA BOX ASSOCIATED FACTOR II 59		Phvul.008G01
20	ATTA6,TAF6,TAFII59	TATA BOX ASSOCIATED FACTOR II 59		Phvul.008G01
21		0 Mitochondrial transcription termination factor family		Phvul.008G04
22		0	0	0
23		0	0	0
24		0	0	0
25		0	0	0
26		0	0	0
27		0	0	0
28		0 LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
29		0 LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
30		0 LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
31		0 LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
32		0 LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
33		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
34		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
35		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
36		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
37		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
38		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
39		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
40		0 Leucine-rich repeat protein kinase family protein		Phvul.008G09
41		0 Protein of unknown function (DUF674)		Phvul.008G11
42		0 Protein of unknown function (DUF674)		Phvul.008G11
43		0 Protein of unknown function (DUF674)		Phvul.008G11
44		0 Protein of unknown function (DUF674)		Phvul.008G11
45		0 Protein of unknown function (DUF674)		Phvul.008G11
46		0 Protein of unknown function (DUF674)		Phvul.008G11
47		0 Protein of unknown function (DUF674)		Phvul.008G11
48	ATASP38,EMB24,PCS1	Eukaryotic aspartyl protease family protein		Phvul.008G11
49	ATASP38,EMB24,PCS1	Eukaryotic aspartyl protease family protein		Phvul.008G11
50		0	0	0
51		0	0	0
52		0	0	0
53		0	0	0
54		0	0	0
55		0 Thioesterase superfamily protein		Phvul.008G20
56		0 Thioesterase superfamily protein		Phvul.008G20
57		0 Thioesterase superfamily protein		Phvul.008G20
58		0 Thioesterase superfamily protein		Phvul.008G20
59		0 Thioesterase superfamily protein		Phvul.008G20
60				

1			
2			
3		0 Thioesterase superfamily protein	Phvul.008G20
4		0	0
5		0	0
6		0	0
7		0	0
8		0	0
9		0	0
10	ATPROT1,PROT1	proline transporter 1	Phvul.008G22
11	ATPROT1,PROT1	proline transporter 1	Phvul.008G22
12	ATPROT1,PROT1	proline transporter 1	Phvul.008G22
13	ATPROT1,PROT1	proline transporter 1	Phvul.008G22
14	ATPROT1,PROT1	proline transporter 1	Phvul.008G22
15		0 RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.008G27
16		0 RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.008G27
17		0 RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.008G27
18		0 RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.008G27
19	COX15	cytochrome c oxidase 15	Phvul.008G28
20	COX15	cytochrome c oxidase 15	Phvul.008G28
21			
22	ATMYB3R-1,ATMYB3R1,MYI	Homeodomain-like protein	Phvul.009G10
23	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
24	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
25	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
26	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
27	ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
28	WNK3	with no lysine (K) kinase 3	Phvul.009G17
29	WNK3	with no lysine (K) kinase 3	Phvul.009G17
30	WNK3	with no lysine (K) kinase 3	Phvul.009G17
31	WNK3	with no lysine (K) kinase 3	Phvul.009G17
32	WNK3	with no lysine (K) kinase 3	Phvul.009G17
33	BGAL12	beta-galactosidase 12	Phvul.009G23
34	BGAL12	beta-galactosidase 12	Phvul.009G23
35	ATOMT1,OMT1	O-methyltransferase 1	Phvul.009G25
36	ATOMT1,OMT1	O-methyltransferase 1	Phvul.009G25
37	ATOMT1,OMT1	O-methyltransferase 1	Phvul.009G25
38	ATOMT1,OMT1	O-methyltransferase 1	Phvul.009G25
39	ATOMT1,OMT1	O-methyltransferase 1	Phvul.009G25
40	ATOMT1,OMT1	O-methyltransferase 1	Phvul.009G25
41		0 DNA binding;ATP binding	Phvul.010G03
42		0 DNA binding;ATP binding	Phvul.010G03
43		0 DNA binding;ATP binding	Phvul.010G03
44		0 DNA binding;ATP binding	Phvul.010G03
45		0 DNA binding;ATP binding	Phvul.010G03
46		0 DNA binding;ATP binding	Phvul.010G03
47	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
48	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
49	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
50	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
51	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
52	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
53	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
54	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
55	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
56	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
57	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
58	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
59	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
60			



1			
2			
3	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
4	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
5	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
6	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
7	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
8	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
9	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
10	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
11	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
12	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
13	CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
14	UNE10	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.010G07
15	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
16	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
17	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
18	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
19	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
20	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
21	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
22	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
23	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
24	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
25	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
26	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
27	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
28	ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
29	ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
30	ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
31	ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
32	ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
33	ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
34	ACA11	autoinhibited Ca <sup>2+</sup> -ATPase 11	Phvul.011G01
35	ACA11	autoinhibited Ca <sup>2+</sup> -ATPase 11	Phvul.011G01
36	ACA11	autoinhibited Ca <sup>2+</sup> -ATPase 11	Phvul.011G01
37	ACA11	autoinhibited Ca <sup>2+</sup> -ATPase 11	Phvul.011G01
38	ACA11	autoinhibited Ca <sup>2+</sup> -ATPase 11	Phvul.011G01
39	TOR	target of rapamycin	Phvul.011G05
40	TOR	target of rapamycin	Phvul.011G05
41	TOR	target of rapamycin	Phvul.011G05
42	TOR	target of rapamycin	Phvul.011G05
43	TOR	target of rapamycin	Phvul.011G05
44	PTAC16	plastid transcriptionally active 16	Phvul.011G06
45	PTAC16	plastid transcriptionally active 16	Phvul.011G06
46		0 Plant self-incompatibility protein S1 family	Phvul.011G11
47		0 Plant self-incompatibility protein S1 family	Phvul.011G12
48		0 Plant self-incompatibility protein S1 family	Phvul.011G12
49	LCR44	low-molecular-weight cysteine-rich 44	0
50	LCR44	low-molecular-weight cysteine-rich 44	0
51	LCR44	low-molecular-weight cysteine-rich 44	0
52		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
53		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
54		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
55		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
56		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
57		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
58		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
59		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
60		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16



1			
2			
3		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
4		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
5		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
6		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
7		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
8		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
9		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
10		0 N-terminal nucleophile aminohydrolases (Ntn hydrolase)	Phvul.011G16
11		0	0 0
12		0	0 0
13		0	0 0
14		0	0 0
15		0	0 0
16	emb2458	FtsH extracellular protease family	Phvul.L00205:
17	emb2458	FtsH extracellular protease family	Phvul.L00205:
18	emb2458	FtsH extracellular protease family	Phvul.L00205:
19	emb2458	FtsH extracellular protease family	Phvul.L00205:
20	emb2458	FtsH extracellular protease family	Phvul.L00205:
21	emb2458	FtsH extracellular protease family	Phvul.L00205:
22	emb2458	FtsH extracellular protease family	Phvul.L00205:
23	emb2458	FtsH extracellular protease family	Phvul.L00205:
24	emb2458	FtsH extracellular protease family	Phvul.L00205:
25	emb2458	FtsH extracellular protease family	Phvul.L00205:
26	emb2458	FtsH extracellular protease family	Phvul.L00205:
27		0 CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253:
28		0 CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253:
29		0 CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253:
30		0 CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253:
31	ATLAC2,LAC2	laccase 2	Phvul.L00734:
32		0 Zinc-binding dehydrogenase family protein	Phvul.008G00
33		0 Zinc-binding dehydrogenase family protein	Phvul.008G00
34		0 Zinc-binding dehydrogenase family protein	Phvul.008G00
35	PLA IIA,PLA2A,PLP2	phospholipase A 2A	Phvul.001G02
36	PLA IIA,PLA2A,PLP2	phospholipase A 2A	Phvul.001G02
37		0 Remorin family protein	Phvul.001G02
38		0 Remorin family protein	Phvul.001G02
39		0 Remorin family protein	Phvul.001G02
40		0 Remorin family protein	Phvul.001G02
41		0 Remorin family protein	Phvul.001G02
42		0 Remorin family protein	Phvul.001G02
43	ATBFRUCT1,ATCWINV1	Glycosyl hydrolases family 32 protein	Phvul.001G03
44		0 Protein of unknown function (DUF2296)	Phvul.001G05
45		0 Protein of unknown function (DUF2296)	Phvul.001G05
46		0 Protein of unknown function (DUF2296)	Phvul.001G05
47	ARA1,ATISA1,ISA1	arabinose kinase	Phvul.001G07
48	ARA1,ATISA1,ISA1	arabinose kinase	Phvul.001G07
49	ACS	acetyl-CoA synthetase	Phvul.001G09
50	ACS	acetyl-CoA synthetase	Phvul.001G09
51		0 transcription regulator NOT2/NOT3/NOT5 family prot	Phvul.001G10
52		0 transcription regulator NOT2/NOT3/NOT5 family prot	Phvul.001G10
53		0 transcription regulator NOT2/NOT3/NOT5 family prot	Phvul.001G10
54		0 transcription regulator NOT2/NOT3/NOT5 family prot	Phvul.001G10
55		0 transcription regulator NOT2/NOT3/NOT5 family prot	Phvul.001G10
56		0 transcription regulator NOT2/NOT3/NOT5 family prot	Phvul.001G10
57		0 endoribonucleases	Phvul.001G11
58		0 endoribonucleases	Phvul.001G11
59		0 endoribonucleases	Phvul.001G11
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PSL5,RSW3	Glycosyl hydrolases family 31 protein	Phvul.001G12
PSL5,RSW3	Glycosyl hydrolases family 31 protein	Phvul.001G12
	0 NB-ARC domain-containing disease resistance protei	Phvul.001G13
	0 NB-ARC domain-containing disease resistance protei	Phvul.001G13
	0 NB-ARC domain-containing disease resistance protei	Phvul.001G13
	0 NB-ARC domain-containing disease resistance protei	Phvul.001G13
	0 NB-ARC domain-containing disease resistance protei	Phvul.001G13
	0 NB-ARC domain-containing disease resistance protei	Phvul.001G13
ASL18,LBD16	lateral organ boundaries-domain 16	Phvul.001G15
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtSTS,STS	stachyose synthase	Phvul.001G21
AtSTS,STS	stachyose synthase	Phvul.001G21
	0 Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
	0 Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
	0 Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
	0 Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
	0	0 Phvul.002G04
	0	0 Phvul.002G04
	0	0 Phvul.002G04
	0	0 Phvul.002G04
	0 C2H2-like zinc finger protein	Phvul.002G05
	0 C2H2-like zinc finger protein	Phvul.002G05
ATEXP7,ATEXPA7,ATHEXP	Al expansin A7	Phvul.002G15
ATEXP7,ATEXPA7,ATHEXP	Al expansin A7	Phvul.002G15
ATEXP7,ATEXPA7,ATHEXP	Al expansin A7	Phvul.002G15
ATEXP7,ATEXPA7,ATHEXP	Al expansin A7	Phvul.002G15
NRS/ER,UER1	nucleotide-rhamnose synthase/epimerase-reductase	Phvul.002G15
	0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
	0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
	0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24

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3		0 GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
4		0 Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
5		0 Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
6		0 Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
7	CSI1	binding	Phvul.002G26
8	GL3,MYC6.2	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G29
9	GL3,MYC6.2	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G29
10		0 ARM repeat superfamily protein	Phvul.003G02
11		0 ARM repeat superfamily protein	Phvul.003G02
12		0 ARM repeat superfamily protein	Phvul.003G02
13		0 ARM repeat superfamily protein	Phvul.003G02
14	ATXYL1,TRG1,XYL1	alpha-xylosidase 1	Phvul.003G03
15	ATXYL1,TRG1,XYL1	alpha-xylosidase 1	Phvul.003G03
16	ATXYL1,TRG1,XYL1	alpha-xylosidase 1	Phvul.003G03
17	ATXYL1,TRG1,XYL1	alpha-xylosidase 1	Phvul.003G03
18	ATXYL1,TRG1,XYL1	alpha-xylosidase 1	Phvul.003G03
19		0 HXXXD-type acyl-transferase family protein	Phvul.003G05
20		0 HXXXD-type acyl-transferase family protein	Phvul.003G05
21		0 HXXXD-type acyl-transferase family protein	Phvul.003G05
22		0 HXXXD-type acyl-transferase family protein	Phvul.003G05
23		0 HXXXD-type acyl-transferase family protein	Phvul.003G05
24		0 C2 calcium/lipid-binding and GRAM domain containin	Phvul.003G08
25		0 C2 calcium/lipid-binding and GRAM domain containin	Phvul.003G08
26		0 Mitochondrial substrate carrier family protein	Phvul.003G10
27		0 Mitochondrial substrate carrier family protein	Phvul.003G10
28		0 Mitochondrial substrate carrier family protein	Phvul.003G10
29		0 Mitochondrial substrate carrier family protein	Phvul.003G10
30		0 Mitochondrial substrate carrier family protein	Phvul.003G10
31		0 Mitochondrial substrate carrier family protein	Phvul.003G10
32		0 calcium-dependent lipid-binding family protein	Phvul.003G11
33		0 calcium-dependent lipid-binding family protein	Phvul.003G11
34		0 calcium-dependent lipid-binding family protein	Phvul.003G11
35		0 calcium-dependent lipid-binding family protein	Phvul.003G11
36	XGD1	xylogalacturonan deficient 1	Phvul.003G16
37	ATFUT11,FUCT1,FUCTA,FUT	fucosyltransferase 11	Phvul.003G29
38		0 PQ-loop repeat family protein / transmembrane fami	Phvul.004G05
39		0 ATP synthase subunit beta	Phvul.004G12
40		0 ATP synthase subunit beta	Phvul.004G12
41		0 ATP synthase subunit beta	Phvul.004G12
42		0 ATP synthase subunit beta	Phvul.004G12
43		0 ATP synthase subunit beta	Phvul.004G12
44		0 ATP synthase subunit beta	Phvul.004G12
45		0 SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
46		0 SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
47		0 SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
48		0 SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
49		0 SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
50		0 SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
51	ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
52	ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
53		0 BTB/POZ domain-containing protein	Phvul.005G05
54		0 BTB/POZ domain-containing protein	Phvul.005G05
55		0 BTB/POZ domain-containing protein	Phvul.005G05
56	ARK3,RK3	receptor kinase 3	Phvul.005G08
57	ATFMN/FHY,FMN/FHY	riboflavin kinase/FMN hydrolase	Phvul.005G09
58	MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
59			
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3		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
4		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
5		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
6		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
7		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
8		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
9		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
10		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
11		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
12		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
13		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
14		0	0 Phvul.007G09
15		0 RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
16		0 RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
17		0 RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
18		0 RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
19		0 RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
20	ATEDR1,EDR1	Protein kinase superfamily protein	Phvul.007G18
21	ATEDR1,EDR1	Protein kinase superfamily protein	Phvul.007G18
22		0 ARM repeat superfamily protein	Phvul.007G19
23		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
24		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
25		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
26		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
27		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
28		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
29		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
30		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
31		0 Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
32		0 transcription coactivators	Phvul.007G21
33		0 transcription coactivators	Phvul.007G21
34		0 transcription coactivators	Phvul.007G21
35		0 transcription coactivators	Phvul.007G21
36		0 transcription coactivators	Phvul.007G21
37	NTRC	NADPH-dependent thioredoxin reductase C	Phvul.007G25
38	AtRLP7,RLP7	receptor like protein 7	Phvul.008G04
39	AtRLP7,RLP7	receptor like protein 7	Phvul.008G04
40	AtMYB17,MYB17	myb domain protein 17	Phvul.008G06
41	AtMYB17,MYB17	myb domain protein 17	Phvul.008G06
42		0 Protein of unknown function (DUF674)	Phvul.008G11
43		0 Protein of unknown function (DUF674)	Phvul.008G11
44		0 Protein of unknown function (DUF674)	Phvul.008G11
45		0 Protein of unknown function (DUF674)	Phvul.008G11
46		0 Protein of unknown function (DUF674)	Phvul.008G11
47		0 Protein of unknown function (DUF674)	Phvul.008G11
48		0 Protein of unknown function (DUF674)	Phvul.008G11
49		0 Protein of unknown function (DUF674)	Phvul.008G11
50		0 Protein of unknown function (DUF674)	Phvul.008G11
51		0 Protein of unknown function (DUF674)	Phvul.008G11
52		0 Protein of unknown function (DUF674)	Phvul.008G11
53		0 Protein of unknown function (DUF674)	Phvul.008G11
54		0 Protein of unknown function (DUF674)	Phvul.008G11
55		0 Protein of unknown function (DUF674)	Phvul.008G11
56		0 Protein of unknown function (DUF674)	Phvul.008G11
57		0 Protein of unknown function (DUF674)	Phvul.008G11
58		0 Protein of unknown function (DUF674)	Phvul.008G11
59		0 Protein of unknown function (DUF674)	Phvul.008G11
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3	LUH	LEUNIG_homolog	Phvul.008G12
4	LUH	LEUNIG_homolog	Phvul.008G12
5	LUH	LEUNIG_homolog	Phvul.008G12
6	LUH	LEUNIG_homolog	Phvul.008G12
7	LUH	LEUNIG_homolog	Phvul.008G12
8			
9		0 Subtilisin-like serine endopeptidase family protein	Phvul.008G22
10	ATCSLE1,CSLE1	cellulose synthase like E1	Phvul.008G27
11	ATCSLE1,CSLE1	cellulose synthase like E1	Phvul.008G27
12			
13		0 Zn-dependent exopeptidases superfamily protein	Phvul.009G01
14		0 Zn-dependent exopeptidases superfamily protein	Phvul.009G01
15		0 Target SNARE coiled-coil domain protein	Phvul.009G03
16	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
17	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
18	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
19	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
20	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
21	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
22	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
23	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
24	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
25	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
26	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
27	TMT2	tonoplast monosaccharide transporter2	Phvul.009G11
28	TMT2	tonoplast monosaccharide transporter2	Phvul.009G11
29			
30		0 transferases, transferring glycosyl groups	0
31		0 transferases, transferring glycosyl groups	0
32		0 transferases, transferring glycosyl groups	0
33		0 transferases, transferring glycosyl groups	0
34		0 transferases, transferring glycosyl groups	0
35	COB	COBRA-like extracellular glycosyl-phosphatidyl inositol	Phvul.009G20
36	BGAL12	beta-galactosidase 12	Phvul.009G23
37	BGAL12	beta-galactosidase 12	Phvul.009G23
38	BGAL12	beta-galactosidase 12	Phvul.009G23
39	BGAL12	beta-galactosidase 12	Phvul.009G23
40	BGAL12	beta-galactosidase 12	Phvul.009G23
41	ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase subunit OXA1	Phvul.009G25
42	ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase subunit OXA1	Phvul.009G25
43	ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase subunit OXA1	Phvul.009G25
44	ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase subunit OXA1	Phvul.009G25
45	ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase subunit OXA1	Phvul.009G25
46			
47		0	0 0
48		0	0 0
49		0	0 0
50		0	0 0
51		0	0 0
52		0 Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
53		0 Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
54		0 Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
55		0 Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
56		0 Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
57	ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
58	ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
59			
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3	ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
4	ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
5	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
6	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
7	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
8	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
9	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
10	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
11	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
12	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
13	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
14	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
15	ATPEX16,PEX16,SSE,SSE1	shrunk seed protein (SSE1)	Phvul.010G08
16	OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
17	OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
18	OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
19	OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
20	OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
21	OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
22	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
23	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
24	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
25	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
26	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
27	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
28	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
29	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
30	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
31	ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
32		0	0 Phvul.011G00
33			
34	SIB1	sigma factor binding protein 1	Phvul.011G20
35	SIB1	sigma factor binding protein 1	Phvul.011G20
36	SIB1	sigma factor binding protein 1	Phvul.011G20
37	SIB1	sigma factor binding protein 1	Phvul.011G20
38	SIB1	sigma factor binding protein 1	Phvul.011G20
39		0 C2 calcium/lipid-binding and GRAM domain containin	Phvul.L001679
40		0 C2 calcium/lipid-binding and GRAM domain containin	Phvul.L001679
41			
42		0 CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L002537
43		0 CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L002537
44	AAC2	ADP/ATP carrier 2	Phvul.L009843
45	AAC2	ADP/ATP carrier 2	Phvul.L009843
46	AAC2	ADP/ATP carrier 2	Phvul.L009843
47	AAC2	ADP/ATP carrier 2	Phvul.L009843
48	AAC2	ADP/ATP carrier 2	Phvul.L009843
49			
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Annot_defline	IDENTIFIER	NAME	DESCRIPTION
K10882 - cros:	Phvul.002G26	Cell cycle orga	component EME1 of MUS81-EME1 Holliday junction clea
K10882 - cros:	Phvul.002G26	Cell cycle orga	component EME1 of MUS81-EME1 Holliday junction clea
PF06075 - Plai	Phvul.002G07	Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi	
PF06075 - Plai	Phvul.002G07	Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi	
PF06075 - Plai	Phvul.002G07	Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi	
PF06075 - Plai	Phvul.002G07	Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi	
PTHR33917:Sf	Phvul.006G20	not assigned.	ã (original description: pacid=37173374 transcript=Phvul.)
PTHR13600:Sf	Phvul.009G05	not assigned.	r no hits & (original description: pacid=37148617 transcri
PTHR13600:Sf	Phvul.009G05	not assigned.	r no hits & (original description: pacid=37148617 transcri
PTHR10766:Sf	Phvul.009G08	not assigned.	ã (original description: pacid=37151360 transcript=Phvul.)
PTHR22849//I	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR22849//I	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR22849//I	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR22849//I	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
1.17.1.4 - Xan	Phvul.L00954:	Redox homeo	xanthine dehydrogenase (original description: pacid=371
1.17.1.4 - Xan	Phvul.L00954:	Redox homeo	xanthine dehydrogenase (original description: pacid=371
1.17.1.4 - Xan	Phvul.L00954:	Redox homeo	xanthine dehydrogenase (original description: pacid=371
1.17.1.4 - Xan	Phvul.L00954:	Redox homeo	xanthine dehydrogenase (original description: pacid=371
PTHR22952//I	Phvul.001G07	RNA biosynth	transcription factor (bZIP9/10/25) (original description: p
PTHR22952//I	Phvul.001G07	RNA biosynth	transcription factor (bZIP9/10/25) (original description: p
PTHR22952//I	Phvul.001G07	RNA biosynth	transcription factor (bZIP9/10/25) (original description: p
PTHR22952//I	Phvul.001G07	RNA biosynth	transcription factor (bZIP9/10/25) (original description: p
PTHR11183//I	Phvul.001G21	Carbohydrate	galactinol synthase (original description: pacid=3716845
PTHR11183//I	Phvul.001G21	Carbohydrate	galactinol synthase (original description: pacid=3716845
PTHR11183//I	Phvul.001G21	Carbohydrate	galactinol synthase (original description: pacid=3716845
PTHR11183//I	Phvul.001G21	Carbohydrate	galactinol synthase (original description: pacid=3716845
K10882 - cros:	Phvul.002G26	Cell cycle orga	component EME1 of MUS81-EME1 Holliday junction clea
K10882 - cros:	Phvul.002G26	Cell cycle orga	component EME1 of MUS81-EME1 Holliday junction clea
K10882 - cros:	Phvul.002G26	Cell cycle orga	component EME1 of MUS81-EME1 Holliday junction clea
K10882 - cros:	Phvul.002G26	Cell cycle orga	component EME1 of MUS81-EME1 Holliday junction clea
PTHR11062:Sf	Phvul.002G28	Cell wall orga	xylosyltransferase (IRX10) (original description: pacid=37
PTHR11062:Sf	Phvul.002G28	Cell wall orga	xylosyltransferase (IRX10) (original description: pacid=37
PTHR11062:Sf	Phvul.002G28	Cell wall orga	xylosyltransferase (IRX10) (original description: pacid=37
PTHR11062:Sf	Phvul.002G28	Cell wall orga	xylosyltransferase (IRX10) (original description: pacid=37
PF00560//PFC	Phvul.004G04	not assigned.	ã (original description: pacid=37161946 transcript=Phvul.)
PF15365 - Pro	Phvul.006G15	not assigned.	r no hits & (original description: pacid=37174157 transcri
KOG1947 - Lei	Phvul.008G07	not assigned.	r no hits & (original description: pacid=37157631 transcri
KOG1947 - Lei	Phvul.008G07	not assigned.	r no hits & (original description: pacid=37157631 transcri
KOG1947 - Lei	Phvul.008G07	not assigned.	r no hits & (original description: pacid=37157631 transcri
KOG1947 - Lei	Phvul.008G07	not assigned.	r no hits & (original description: pacid=37157631 transcri
PTHR33103:Sf	Phvul.008G11	not assigned.	r no hits & (original description: pacid=37161406 transcri
PTHR33103:Sf	Phvul.008G11	not assigned.	r no hits & (original description: pacid=37160139 transcri

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3 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
4 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
5 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
6 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
7 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
8 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
9 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
10 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
11 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
12 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
13 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
14 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
15 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
16 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
17 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
18 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
19 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
20 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
21 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
22 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
23 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371  
24 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri  
25 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri  
26 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri  
27 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri  
28 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri  
29 0 Phvul.010G05not assigned.r no hits & (original description: pacid=37142098 transcri  
30 0 Phvul.010G05not assigned.r no hits & (original description: pacid=37142098 transcri  
31 PF01094 - RecPhvul.001G02Solute transpcligand-gated cation channel (GLR) (original description: ꝑ  
32 PF01094 - RecPhvul.001G02Solute transpcligand-gated cation channel (GLR) (original description: ꝑ  
33 PTHR22952//IPhvul.001G07RNA biosynthtranscription factor (bZIP9/10/25) (original description: ꝑ  
34 PTHR22952//IPhvul.001G07RNA biosynthtranscription factor (bZIP9/10/25) (original description: ꝑ  
35 K12446 - L-arçPhvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=3716845ç  
36 K12446 - L-arçPhvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=3716845ç  
37 PTHR11937:SlPhvul.001G08not assigned.ç (original description: pacid=37168999 transcript=Phvul.ç  
38 PTHR11937:SlPhvul.001G08not assigned.ç (original description: pacid=37168999 transcript=Phvul.ç  
39 PTHR11937:SlPhvul.001G08not assigned.ç (original description: pacid=37168999 transcript=Phvul.ç  
40 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.ç  
41 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.ç  
42 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.ç  
43 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.ç  
44 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37  
45 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37  
46 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37  
47 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37  
48 PTHR10277//IPhvul.001G12Amino acid m-hydroxymethylglutaryl-CoA lyase (original description: ꝑ  
49 PTHR10277//IPhvul.001G12Amino acid m-hydroxymethylglutaryl-CoA lyase (original description: ꝑ  
50 K05643 - ATP-Phvul.001G13Solute transpçsubfamily ABCA transporter (original description: pacid=

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2  
3 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
4 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
5 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
6 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
7 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
8 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
9 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
10 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
11 K05643 - ATP-Phvul.001G13 Solute transp<sub>c</sub> subfamily ABCA transporter (original description: pacid=  
12 PF03110 - SBFPhvul.001G14 RNA biosynth<sub>e</sub> transcription factor (SBP) (original description: pacid=37  
13 PF03110 - SBFPhvul.001G14 RNA biosynth<sub>e</sub> transcription factor (SBP) (original description: pacid=37  
14 PF03110 - SBFPhvul.001G14 RNA biosynth<sub>e</sub> transcription factor (SBP) (original description: pacid=37  
15 PF03110 - SBFPhvul.001G14 RNA biosynth<sub>e</sub> transcription factor (SBP) (original description: pacid=37  
16 PF03110 - SBFPhvul.001G14 RNA biosynth<sub>e</sub> transcription factor (SBP) (original description: pacid=37  
17 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
18 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
19 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
20 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
21 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
22 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
23 2.7.7.2 - FAD<sub>s</sub>Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri  
24 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
25 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
26 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
27 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
28 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
29 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
30 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
31 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
32 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
33 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
34 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
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37 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
38 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
39 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
40 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
41 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
42 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
43 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
44 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio  
45 PTHR10438:SlPhvul.002G06 Redox homeo H-type thioredoxin (original description: pacid=3717719!  
46 PTHR10438:SlPhvul.002G06 Redox homeo H-type thioredoxin (original description: pacid=3717719!  
47 PF06075 - PlalPhvul.002G07 Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi  
48 PF06075 - PlalPhvul.002G07 Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi  
49 3.4.24.23 - MzPhvul.002G07 Protein homeo Matrixin-type metalloprotease (original description: paci  
50 3.4.24.23 - MzPhvul.002G07 Protein homeo Matrixin-type metalloprotease (original description: paci  
51 3.4.24.23 - MzPhvul.002G07 Protein homeo Matrixin-type metalloprotease (original description: paci  
52 3.4.24.23 - MzPhvul.002G07 Protein homeo Matrixin-type metalloprotease (original description: paci  
53 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
54 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
55 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
56 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
57 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
58 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
59 PTHR10110:SlPhvul.002G18 External stim<sub>i</sub> sodium:proton antiporter (SOS1) (original description: p  
60



2.7.11.1 - NonPhvul.002G30Protein modif protein kinase (PERK-related) (original description: pacid  
 PTHR23336:SIPhvul.003G10not assigned.r no hits & (original description: pacid=37147291 transcri  
 PTHR23336:SIPhvul.003G10not assigned.r no hits & (original description: pacid=37147291 transcri  
 PF00560//PFPhvul.004G04not assigned.ã (original description: pacid=37161823 transcript=Phvul.  
 PF01535 - PPPhvul.004G10not assigned.ã (original description: pacid=37161859 transcript=Phvul.  
 PTHR11689:SIPhvul.004G13Solute transpñanion channel / anion:proton antiporter (CLC) (original d  
 PTHR11689:SIPhvul.004G13Solute transpñanion channel / anion:proton antiporter (CLC) (original d  
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:  
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:  
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:  
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:  
 PF12609 - WoPhvul.005G08not assigned.r no hits & (original description: pacid=37154279 transcri  
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri  
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri  
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri  
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri  
 K14972 - PAX-Phvul.005G18RNA biosynthcomponent MED15 of tail module of MEDIATOR transcri  
 K14972 - PAX-Phvul.005G18RNA biosynthcomponent MED15 of tail module of MEDIATOR transcri  
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy  
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy  
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy  
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy  
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=  
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=  
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=  
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=  
 PF14365 - DorPhvul.006G10not assigned.r no hits & (original description: pacid=37172094 transcri  
 PF14365 - DorPhvul.006G10not assigned.r no hits & (original description: pacid=37172094 transcri  
 PTHR23324//IPhvul.006G13not assigned.r no hits & (original description: pacid=37171658 transcri  
 PTHR23324//IPhvul.006G13not assigned.r no hits & (original description: pacid=37171658 transcri  
 PTHR10992:SIPhvul.007G11Coenzyme mechlorophyll dephytylase (CLD) (original description: pacid  
 PTHR10992:SIPhvul.007G11Coenzyme mechlorophyll dephytylase (CLD) (original description: pacid  
 PTHR31375:SIPhvul.007G21Enzyme classii Polygalacturonase At1g48100 OS=Arabidopsis thaliana (:  
 PTHR31375:SIPhvul.007G21Enzyme classii Polygalacturonase At1g48100 OS=Arabidopsis thaliana (:  
 K14488 - SAUIPhvul.007G21not assigned.r no hits & (original description: pacid=37166206 transcri  
 K14488 - SAUIPhvul.007G21not assigned.r no hits & (original description: pacid=37166206 transcri  
 KOG1947 - LeiPhvul.008G07not assigned.r no hits & (original description: pacid=37157631 transcri  
 KOG1947 - LeiPhvul.008G07not assigned.r no hits & (original description: pacid=37157631 transcri  
 O Phvul.008G10not assigned.r no hits & (original description: pacid=37160112 transcri  
 O Phvul.008G10not assigned.r no hits & (original description: pacid=37160112 transcri  
 K08081 - TropPhvul.008G11Enzyme classii Enzyme classification.EC\_1 oxidoreductases.EC\_1.1 oxid  
 K08081 - TropPhvul.008G11Enzyme classii Enzyme classification.EC\_1 oxidoreductases.EC\_1.1 oxid  
 PTHR10366:SIPhvul.008G25not assigned.ã (original description: pacid=37158298 transcript=Phvul.

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3 PTHR10366:SlPhvul.008G25 not assigned.ã (original description: pacid=37158298 transcript=Phvul.  
4 PTHR10366:SlPhvul.008G25 not assigned.ã (original description: pacid=37158298 transcript=Phvul.  
5 PTHR10366:SlPhvul.008G25 not assigned.ã (original description: pacid=37158298 transcript=Phvul.  
6 K02259 - cytoPhvul.008G28 Cellular respir component COX15 of cytochrome c oxidase assembly (o  
7 PTHR10766:SlPhvul.008G28 not assigned.ã (original description: pacid=37158021 transcript=Phvul.  
8 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi  
9 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi  
10 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi  
11 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi  
12 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37  
13 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37  
14 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37  
15 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37  
16 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.  
17 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.  
18 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.  
19 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.  
20 PF00170 - bZlIPhvul.011G04 not assigned.r no hits & (original description: pacid=37157418 transcri  
21 PF00170 - bZlIPhvul.011G04 not assigned.r no hits & (original description: pacid=37157418 transcri  
22 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**  
23 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**  
24 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**  
25 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**  
26 PTHR11709//IPhvul.L00734:Cell wall orgar lignin laccase (original description: pacid=37178902 tran  
27 PTHR11709//IPhvul.L00734:Cell wall orgar lignin laccase (original description: pacid=37178902 tran  
28 **PTHR31471:SlPhvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri**  
29 **PTHR31471:SlPhvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri**  
30 3.2.1.153 - FrPhvul.001G03 Carbohydrate acid beta-fructofuranosidase (CWIN) (original descriptio  
31 K13157 - U11,Phvul.001G10 RNA processir protein factor U11/U12-65K of U11/U12 small nuclear ri  
32 K13157 - U11,Phvul.001G10 RNA processir protein factor U11/U12-65K of U11/U12 small nuclear ri  
33 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri  
34 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri  
35 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri  
36 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri  
37 PTHR18866//IPhvul.001G24 Lipid metaboli acetyl-CoA carboxylase regulator (BADDC) (original descriq  
38 PF01357//PFCPhvul.002G00 Cell wall orgar beta-like-class expansin (original description: pacid=371  
39 PTHR23083//IPhvul.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvul.  
40 PTHR23083//IPhvul.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvul.  
41 K17619 - magPhvul.002G21 not assigned.r no hits & (original description: pacid=37177891 transcri  
42 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.  
43 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.  
44 K03456 - serirPhvul.003G02 Protein modif scaffold component A of PP2A phosphatase complexes (  
45 K03456 - serirPhvul.003G02 Protein modif scaffold component A of PP2A phosphatase complexes (  
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K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
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K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:  
K15108 - solu:Phvul.003G10Solute transp:solute transporter (MTCC) (original description: pacid=3:  
K15108 - solu:Phvul.003G10Solute transp:solute transporter (MTCC) (original description: pacid=3:  
PTHR22957:SI:Phvul.003G14Vesicle traffi:RAB-GTPase-activating protein (RAB-GAP) (original descr  
PTHR22957:SI:Phvul.003G14Vesicle traffi:RAB-GTPase-activating protein (RAB-GAP) (original descr  
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc  
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc  
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc  
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc  
PTHR24012:SI:Phvul.003G29not assigned.ã (original description: pacid=37147487 transcript=Phvul.  
PTHR24012:SI:Phvul.003G29RNA processir:mRNA-binding regulatory factor (RBP45/47) (original des  
PTHR24012:SI:Phvul.003G29RNA processir:mRNA-binding regulatory factor (RBP45/47) (original des  
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri  
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri  
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri  
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri  
0 Phvul.004G03not assigned.r no hits & (original description: pacid=37163425 transcri  
PF00560//PFC:Phvul.004G04not assigned.ã (original description: pacid=37161946 transcript=Phvul.  
PF00560//PFC:Phvul.004G04not assigned.ã (original description: pacid=37161946 transcript=Phvul.  
K10393 - kine:Phvul.004G16Cytoskeleton :motor protein (Kinesin-13) (original description: pacid=3  
K11308 - histc:Phvul.005G01Chromatin orç:acetyltransferase component HAM of NuA4 histone acet  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic  
2.4.1.132 - GC:Phvul.005G08Protein modif:alpha-1,3/1,6-mannosyltransferase (ALG2) (original desc  
2.4.1.132 - GC:Phvul.005G08Protein modif:alpha-1,3/1,6-mannosyltransferase (ALG2) (original desc  
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37  
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37  
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37  
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37  
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37

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3 PTHR31072:SI Phvul.005G09 RNA biosynthesis transcription factor (TCP) (original description: pacid=37  
4 0 Phvul.006G06 not assigned.r no hits & (original description: pacid=37172254 transcri  
5 0 Phvul.006G06 not assigned.r no hits & (original description: pacid=37172254 transcri  
6 4.1.1.28 - AroI Phvul.006G13 Secondary aromatic L-amino acid decarboxylase (original descriptio  
7 4.1.1.28 - AroI Phvul.006G13 Secondary aromatic L-amino acid decarboxylase (original descriptio  
8 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri  
9 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri  
10 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri  
11 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri  
12 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri  
13 PF04570 - zinc Phvul.007G05 Multi-process SnRK1-interacting factor (FLZ) (original description: pacid  
14 PF04570 - zinc Phvul.007G05 Multi-process SnRK1-interacting factor (FLZ) (original description: pacid  
15 PTHR23024:SI Phvul.007G06 not assigned.a (original description: pacid=37166219 transcript=Phvul.  
16 PTHR23024:SI Phvul.007G06 not assigned.a (original description: pacid=37166219 transcript=Phvul.  
17 PTHR37764:SI Phvul.007G18 not assigned.r no hits & (original description: pacid=37166249 transcri  
18 PF13414 - TPF Phvul.007G19 not assigned.r no hits & (original description: pacid=37165459 transcri  
19 PF13414 - TPF Phvul.007G19 not assigned.r no hits & (original description: pacid=37165459 transcri  
20 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori  
21 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori  
22 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori  
23 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori  
24 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
25 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
26 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
27 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
28 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
29 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
30 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
31 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
32 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
33 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
34 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
35 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
36 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
37 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
38 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
39 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
40 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
41 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
42 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578  
43 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578  
44 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578  
45 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578  
46 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578  
47 PTHR10783:SI Phvul.008G03 Nutrient uptake phosphate transporter (PHO1) (original description: paci  
48 PTHR10783:SI Phvul.008G03 Nutrient uptake phosphate transporter (PHO1) (original description: paci  
49 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
50 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
51 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
52 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
53 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
54 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
55 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
56 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
57 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715  
58 K15685 - E3 ubiquitin ligase (HAKAI) (original description: pacid=3  
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3 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
4 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
5 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
6 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
7 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
8 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
9 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
10 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
11 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
12 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
13 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig  
14 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371  
15 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371  
16 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371  
17 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371  
18 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371  
19 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:  
20 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:  
21 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:  
22 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:  
23 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:  
24 0 Phvul.011G12 not assigned.r no hits & (original description: pacid=37155251 transcri  
25 0 Phvul.011G12 not assigned.r no hits & (original description: pacid=37155251 transcri  
26 0 Phvul.011G12 not assigned.r no hits & (original description: pacid=37155251 transcri  
27 0 Phvul.011G12 not assigned.r no hits & (original description: pacid=37155251 transcri  
28 0 Phvul.011G12 not assigned.r no hits & (original description: pacid=37155251 transcri  
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30 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
31 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
32 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
33 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
34 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
35 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
36 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
37 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
38 PTHR10173:SlPhvul.011G17 not assigned.a (original description: pacid=37157390 transcript=Phvul.l  
39 PTHR10173:SlPhvul.011G17 not assigned.a (original description: pacid=37157390 transcript=Phvul.l  
40 PTHR10173:SlPhvul.011G17 not assigned.a (original description: pacid=37157390 transcript=Phvul.l  
41 PTHR10173:SlPhvul.011G17 not assigned.a (original description: pacid=37157390 transcript=Phvul.l  
42 PTHR10173:SlPhvul.011G17 not assigned.a (original description: pacid=37157390 transcript=Phvul.l  
43 PTHR22884:SlPhvul.011G19Chromatin org methylated DNA binding component SUVH1/3 of SUVH-l  
44 PTHR22884:SlPhvul.011G19Chromatin org methylated DNA binding component SUVH1/3 of SUVH-l  
45 PF05553 - CotPhvul.001G09 not assigned.r no hits & (original description: pacid=37170071 transcri  
46 PF05553 - CotPhvul.001G09 not assigned.r no hits & (original description: pacid=37170071 transcri  
47 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
48 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
49 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
50 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
51 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
52 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
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54 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
55 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
56 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
57 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
58 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
59 K15559 - reguPhvul.001G10 not assigned.r no hits & (original description: pacid=37170360 transcri  
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K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri  
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K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri  
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K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri  
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri  
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri  
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri  
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PTHR31447:SIPhvul.001G14RNA processir N6-methyladenosine demethylase (ALKBH10) (original d  
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.  
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.  
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.  
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2.7.7.2 - FAD ðPhvul.001G17not assigned.r no hits & (original description: pacid=37168919 transcri  
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K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or  
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or  
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or  
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K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or  
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or  
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or  
PTHR22849:SIPhvul.001G26not assigned.ã (original description: pacid=37168993 transcript=Phvul.  
PTHR11746:SIPhvul.001G26Enzyme classii Acetylserotonin O-methyltransferase OS=Arabidopsis th  
PTHR11746:SIPhvul.001G26Enzyme classii Acetylserotonin O-methyltransferase OS=Arabidopsis th  
PF13912 - C2FPhvul.002G05RNA biosynthç C2H2 zinc finger transcription factor (original descriptio  
PF13912 - C2FPhvul.002G05RNA biosynthç C2H2 zinc finger transcription factor (original descriptio  
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!  
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!  
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!  
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!  
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!  
PF03106 - WRPhvul.002G16RNA biosynthç transcription factor (WRKY) (original description: pacid=:  
PF03106 - WRPhvul.002G16RNA biosynthç transcription factor (WRKY) (original description: pacid=:  
PTHR12953 - IPhvul.002G16Cytoskeleton çregulatory factor (SUN3/4/5) nuclear shape determinatiç  
PTHR12953 - IPhvul.002G16Cytoskeleton çregulatory factor (SUN3/4/5) nuclear shape determinatiç  
PTHR12953 - IPhvul.002G16Cytoskeleton çregulatory factor (SUN3/4/5) nuclear shape determinatiç  
PTHR12953 - IPhvul.002G16Cytoskeleton çregulatory factor (SUN3/4/5) nuclear shape determinatiç  
PTHR23042:SIPhvul.002G21Nutrient uptalçbHLH-IVa-class iron homeostasis regulator (original desc  
PTHR23042:SIPhvul.002G21Nutrient uptalçbHLH-IVa-class iron homeostasis regulator (original desc  
PTHR23042:SIPhvul.002G21Nutrient uptalçbHLH-IVa-class iron homeostasis regulator (original desc  
PTHR23042:SIPhvul.002G21Nutrient uptalçbHLH-IVa-class iron homeostasis regulator (original desc  
PTHR22835//IPhvul.002G24not assigned.ã (original description: pacid=37176697 transcript=Phvul.  
PTHR22835//IPhvul.002G24not assigned.ã (original description: pacid=37176697 transcript=Phvul.

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3 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.  
4 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.  
5 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.  
6 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.  
7 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
8 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
9 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
10 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
11 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
12 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
13 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã  
14 3.4.11.14 - CyPhvul.002G29 not assigned.ã (original description: pacid=37176433 transcript=Phvul.  
15 3.4.11.14 - CyPhvul.002G29 not assigned.ã (original description: pacid=37176433 transcript=Phvul.  
16 PTHR13832//IPhvul.002G30 Protein modif clade A phosphatase (original description: pacid=371752  
17 PTHR13832//IPhvul.002G30 Protein modif clade A phosphatase (original description: pacid=371752  
18 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (  
19 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (  
20 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (  
21 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (  
22 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (  
23 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
24 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
25 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
26 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
27 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
28 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
29 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
30 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
31 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
32 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
33 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
34 K05863 - soluIPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3  
35 PTHR10359:SlPhvul.003G03 Chromatin orç methylcytosine-specific DNA glycosylase (ROS1) (original  
36 PTHR10359:SlPhvul.003G03 Chromatin orç methylcytosine-specific DNA glycosylase (ROS1) (original  
37 K00721 - dolipPhvul.003G05 Protein modif catalytic component DPMS1 of DPMS dolichol-phosphat  
38 K00721 - dolipPhvul.003G05 Protein modif catalytic component DPMS1 of DPMS dolichol-phosphat  
39 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri  
40 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri  
41 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri  
42 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri  
43 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3  
44 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3  
45 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3  
46 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3  
47 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
48 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
49 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
50 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
51 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
52 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
53 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
54 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
55 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
56 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
57 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
58 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
59 PTHR23155//IPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.  
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3 K01061 - carb Phvul.005G11 not assigned.r no hits & (original description: pacid=37152909 transcri  
4 K01061 - carb Phvul.005G11 not assigned.r no hits & (original description: pacid=37152909 transcri  
5 PTHR10593//IPhvu.005G13RNA biosynth C2H2 zinc finger transcription factor (original descriptio  
6 PTHR10593//IPhvu.005G13RNA biosynth C2H2 zinc finger transcription factor (original descriptio  
7 K11583 - serir Phvul.006G10 Protein modif regulatory component B2 of PP2A phosphatase complex  
8 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
9 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
10 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
11 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
12 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
13 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
14 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
15 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
16 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
17 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
18 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
19 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.  
20 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
21 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
22 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
23 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
24 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
25 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
26 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
27 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
28 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
29 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
30 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:  
31 PF15365 - Pro Phvul.006G15 not assigned.r no hits & (original description: pacid=37174157 transcri  
32 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371  
33 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371  
34 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371  
35 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371  
36 K13125 - nitri Phvul.006G19 not assigned.a (original description: pacid=37172724 transcript=Phvu.  
37 K13125 - nitri Phvul.006G19 not assigned.a (original description: pacid=37172724 transcript=Phvu.  
38 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri  
39 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri  
40 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri  
41 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri  
42 PTHR31072:SI Phvul.007G01 Multi-process CHE circadian clock repression factor (original descriptio  
43 PTHR31072:SI Phvul.007G01 Multi-process CHE circadian clock repression factor (original descriptio  
44 2.7.8.8 - CDP- (Phvul.007G03 Lipid metaboli base-exchange-type phosphatidylserine synthase (origin  
45 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665  
46 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665  
47 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665  
48 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665  
49 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
50 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
51 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
52 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
53 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
54 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
55 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
56 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
57 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
58 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
59 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri  
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PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic  
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic  
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic  
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic  
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic  
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic  
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.  
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.  
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.  
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.  
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.  
PTHR11972//IPhvul.007G07Nutrient uptal metal ion-chelate reductase (FRO) (original description: |  
PTHR11972//IPhvul.007G07Nutrient uptal metal ion-chelate reductase (FRO) (original description: |  
PTHR11972//IPhvul.007G07Nutrient uptal metal ion-chelate reductase (FRO) (original description: |  
PTHR11972//IPhvul.007G07Nutrient uptal metal ion-chelate reductase (FRO) (original description: |  
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri  
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri  
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri  
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri  
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |  
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |  
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |  
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |  
PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri  
PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri  
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PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri  
0 Phvul.007G18not assigned.r no hits & (original description: pacid=37164309 transcri  
0 Phvul.007G18not assigned.r no hits & (original description: pacid=37164309 transcri  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio  
PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
PF00045 - HerPhvul.007G27not assigned.ã (original description: pacid=37164350 transcript=Phvul.  
PF00045 - HerPhvul.007G27not assigned.ã (original description: pacid=37164350 transcript=Phvul.  
PF00045 - HerPhvul.007G27not assigned.ã (original description: pacid=37166099 transcript=Phvul.



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3 PF00045 - HerPhvul.007G27 not assigned.a (original description: pacid=37166099 transcript=Phvul.  
4 PF00045 - HerPhvul.007G27 not assigned.a (original description: pacid=37164734 transcript=Phvul.  
5 PF00045 - HerPhvul.007G27 not assigned.a (original description: pacid=37164734 transcript=Phvul.  
6 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci  
7 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci  
8 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci  
9 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci  
10 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci  
11 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci  
12 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
13 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
14 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
15 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
16 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
17 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
18 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri  
19 K03131 - tran:Phvul.008G01 RNA biosynthcomponent TAF6 of TFIIId basal transcription regulation c  
20 K03131 - tran:Phvul.008G01 RNA biosynthcomponent TAF6 of TFIIId basal transcription regulation c  
21 PTHR13068//lPhvul.008G04 RNA biosynthtranscription factor (mTERF) (original description: pacid=  
22 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri  
23 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri  
24 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri  
25 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri  
26 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri  
27 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri  
28 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri  
29 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri  
30 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri  
31 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
32 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
33 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
34 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
35 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
36 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
37 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
38 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
39 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
40 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715  
41 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37158099 transcri  
42 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37158099 transcri  
43 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37159657 transcri  
44 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37161383 transcri  
45 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37161383 transcri  
46 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37161383 transcri  
47 PTHR13683:SlPhvul.008G11 Protein home pepsin-type protease (original description: pacid=37158  
48 PTHR13683:SlPhvul.008G11 Protein home pepsin-type protease (original description: pacid=37158  
49 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri  
50 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri  
51 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri  
52 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri  
53 4.2.1.119 - EnPhvul.008G20 Lipid metaboli hydroxyacyl-ACP dehydratase (mtHD) (original descripti  
54 4.2.1.119 - EnPhvul.008G20 Lipid metaboli hydroxyacyl-ACP dehydratase (mtHD) (original descripti  
55 4.2.1.119 - EnPhvul.008G20 Lipid metaboli hydroxyacyl-ACP dehydratase (mtHD) (original descripti  
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3 4.2.1.119 - EnPhvul.008G20Lipid metabol hydroxyacyl-ACP dehydratase (mtHD) (original descriptio  
4 0 Phvul.008G22not assigned.r no hits & (original description: pacid=37161082 transcri  
5 0 Phvul.008G22not assigned.r no hits & (original description: pacid=37161082 transcri  
6 0 Phvul.008G22not assigned.r no hits & (original description: pacid=37161082 transcri  
7 0 Phvul.008G22not assigned.r no hits & (original description: pacid=37161082 transcri  
8  
9 PTHR22950:SlPhvul.008G22Solute transp( proline transporter (ProT) (original description: pacid=37  
10 PTHR22950:SlPhvul.008G22Solute transp( proline transporter (ProT) (original description: pacid=37  
11 PTHR22950:SlPhvul.008G22Solute transp( proline transporter (ProT) (original description: pacid=37  
12 PTHR22950:SlPhvul.008G22Solute transp( proline transporter (ProT) (original description: pacid=37  
13 PTHR24012:SlPhvul.008G27not assigned.a (original description: pacid=37160931 transcript=Phvul.  
14 PTHR24012:SlPhvul.008G27not assigned.a (original description: pacid=37160931 transcript=Phvul.  
15 PTHR24012:SlPhvul.008G27not assigned.a (original description: pacid=37160931 transcript=Phvul.  
16 PTHR24012:SlPhvul.008G27not assigned.a (original description: pacid=37160931 transcript=Phvul.  
17 K02259 - cytoPhvul.008G28Cellular respir component COX15 of cytochrome c oxidase assembly (o  
18 K02259 - cytoPhvul.008G28Cellular respir component COX15 of cytochrome c oxidase assembly (o  
19 PTHR10641:SlPhvul.009G10RNA biosynth( transcription factor (MYB) (original description: pacid=37  
20 PTHR10972:SlPhvul.009G12not assigned.a (original description: pacid=37148875 transcript=Phvul.  
21 PTHR10972:SlPhvul.009G12not assigned.a (original description: pacid=37148875 transcript=Phvul.  
22 PTHR10972:SlPhvul.009G12not assigned.a (original description: pacid=37148875 transcript=Phvul.  
23 PTHR10972:SlPhvul.009G12not assigned.a (original description: pacid=37148875 transcript=Phvul.  
24 K08867 - WNkPhvul.009G17Protein modif( protein kinase (MAP3K-WNK) (original description: pacid  
25 K08867 - WNkPhvul.009G17Protein modif( protein kinase (MAP3K-WNK) (original description: pacid  
26 K08867 - WNkPhvul.009G17Protein modif( protein kinase (MAP3K-WNK) (original description: pacid  
27 K08867 - WNkPhvul.009G17Protein modif( protein kinase (MAP3K-WNK) (original description: pacid  
28 PTHR23421:SlPhvul.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37  
29 PTHR23421:SlPhvul.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37  
30 K13066 - caff(Phvul.009G25Enzyme classii( Enzyme classification.EC\_2 transferases.EC\_2.1 transfera  
31 K13066 - caff(Phvul.009G25Enzyme classii( Enzyme classification.EC\_2 transferases.EC\_2.1 transfera  
32 K13066 - caff(Phvul.009G25Enzyme classii( Enzyme classification.EC\_2 transferases.EC\_2.1 transfera  
33 K13066 - caff(Phvul.009G25Enzyme classii( Enzyme classification.EC\_2 transferases.EC\_2.1 transfera  
34 K17592 - sacsiPhvul.010G03not assigned.a (original description: pacid=37143296 transcript=Phvul.  
35 K17592 - sacsiPhvul.010G03not assigned.a (original description: pacid=37143296 transcript=Phvul.  
36 K17592 - sacsiPhvul.010G03not assigned.a (original description: pacid=37143296 transcript=Phvul.  
37 K17592 - sacsiPhvul.010G03not assigned.a (original description: pacid=37143296 transcript=Phvul.  
38 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
39 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
40 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
41 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
42 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
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44 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
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46 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
47 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
48 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
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51 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
52 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
53 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
54 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
55 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
56 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
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59 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
60

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3 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
4 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
5 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
6 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
7 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
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11 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
12 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
13 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi  
14 PTHR12565:SlPhvul.010G07RNA biosynth transcription factor (bHLH) (original description: pacid=3  
15 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.  
16 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.  
17 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.  
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27 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.  
28 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC\_1 oxidoreductases.EC\_1.13 oxi  
29 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC\_1 oxidoreductases.EC\_1.13 oxi  
30 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC\_1 oxidoreductases.EC\_1.13 oxi  
31 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC\_1 oxidoreductases.EC\_1.13 oxi  
32 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig  
33 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig  
34 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig  
35 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig  
36 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548  
37 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548  
38 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548  
39 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548  
40 PTHR14194:SlPhvul.011G06RNA biosynth TAC16 cofactor of plastid-encoded RNA polymerase (orig  
41 PTHR14194:SlPhvul.011G06RNA biosynth TAC16 cofactor of plastid-encoded RNA polymerase (orig  
42 PF05938 - PlaiPhvul.011G11not assigned.a (original description: pacid=37156233 transcript=Phvul.  
43 PF05938 - PlaiPhvul.011G12not assigned.a (original description: pacid=37155659 transcript=Phvul.  
44 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri  
45 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri  
46 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
47 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
48 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
49 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
50 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
51 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
52 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
53 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
54 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
55 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
56 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
57 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
58 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
59 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
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3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
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 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
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 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s  
 0 Phvul.011G20not assigned.r no hits & (original description: pacid=37156963 transcri  
 0 Phvul.011G20not assigned.r no hits & (original description: pacid=37156963 transcri  
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 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.  
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.  
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.  
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.  
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 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.  
 K12872 - pre-iPhvul.L00253:RNA processir component MAC5 of non-snRNP MOS4-associated comp  
 K12872 - pre-iPhvul.L00253:RNA processir component MAC5 of non-snRNP MOS4-associated comp  
 K12872 - pre-iPhvul.L00253:RNA processir component MAC5 of non-snRNP MOS4-associated comp  
 PTHR11709//I Phvul.L00734:Cell wall orgar lignin laccase (original description: pacid=37178902 tran  
 PTHR11695//I Phvul.008G00Enzyme classii 2-alkenal reductase (NADP(+)-dependent) OS=Nicotiana  
 PTHR11695//I Phvul.008G00Enzyme classii 2-alkenal reductase (NADP(+)-dependent) OS=Nicotiana  
 KOG0513 - Ca Phvul.001G02Lipid metaboli phospholipase A2 (pPLA2-II) (original description: pacid=  
 KOG0513 - Ca Phvul.001G02Lipid metaboli phospholipase A2 (pPLA2-II) (original description: pacid=  
 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri  
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 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri  
 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri  
 3.2.1.153 - Fr Phvul.001G03Carbohydrate acid beta-fructofuranosidase (CWIN) (original descriptio  
 PTHR22166:SI Phvul.001G05Cell cycle orgã ER cisternae formation factor (LUNAPARK) (original desc  
 PTHR22166:SI Phvul.001G05Cell cycle orgã ER cisternae formation factor (LUNAPARK) (original desc  
 K12446 - L-arã Phvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=37168452  
 K12446 - L-arã Phvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=37168452  
 K01895 - acet Phvul.001G09Lipid metaboli acetyl-CoA synthetase (original description: pacid=37171  
 K01895 - acet Phvul.001G09Lipid metaboli acetyl-CoA synthetase (original description: pacid=37171  
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿  
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿  
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿  
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿  
 6.3.1.14 - Dipł Phvul.001G11Protein biosyr diphthamide synthetase (DPH6) (original description: pa  
 6.3.1.14 - Dipł Phvul.001G11Protein biosyr diphthamide synthetase (DPH6) (original description: pa



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3 PTHR22762//IPhvu.001G12 not assigned.ã (original description: pacid=37171176 transcript=Phvu.0  
4 PTHR22762//IPhvu.001G12 not assigned.ã (original description: pacid=37171176 transcript=Phvu.0  
5 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.0  
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8 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.0  
9 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.0  
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16 PTHR31529:SIPhvu.001G15RNA biosynth transcription factor (AS2/LOB) (original description: paci  
17 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
18 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
19 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
20 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
21 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
22 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
23 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
24 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
25 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
26 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
27 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3  
28 2.4.1.67 - GalãPhvu.001G21Carbohydrate stachyose synthase (original description: pacid=3717114  
29 2.4.1.67 - GalãPhvu.001G21Carbohydrate stachyose synthase (original description: pacid=3717114  
30 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac  
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32 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac  
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35 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.0  
36 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.0  
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38 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.0  
39 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
40 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
41 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
42 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
43 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
44 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
45 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371  
46 PF13912 - C2IPhvu.002G05RNA biosynth C2H2 zinc finger transcription factor (original descriptio  
47 PF13912 - C2IPhvu.002G05RNA biosynth C2H2 zinc finger transcription factor (original descriptio  
48 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767  
49 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767  
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55 1.1.1.133 - dT Phvu.002G15Carbohydrate UDP-L-rhamnose synthase (original description: pacid=3  
56 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.0  
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59 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.0  
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2  
3 PTHR22835//IPhvu.002G24not assigned.ã (original description: pacid=37176697 transcript=Phvu.  
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5 PTHR22870:SIPhvu.002G25not assigned.ã (original description: pacid=37177422 transcript=Phvu.  
6 PTHR23315:SIPhvu.002G26Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (origi  
7 PTHR11514:SIPhvu.002G29RNA biosynthetranscription factor (bHLH) (original description: pacid=3  
8 PTHR11514:SIPhvu.002G29RNA biosynthetranscription factor (bHLH) (original description: pacid=3  
9 PTHR23315:SIPhvu.003G02not assigned.r no hits & (original description: pacid=37144503 transcri  
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11 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470  
12 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470  
13 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470  
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15 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714  
16 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714  
17 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714  
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19 PTHR10774//IPhvu.003G08not assigned.ã (original description: pacid=37146764 transcript=Phvu.  
20 PTHR10774//IPhvu.003G08not assigned.ã (original description: pacid=37146764 transcript=Phvu.  
21 K15108 - soluIPhvu.003G10Solute transpcsolute transporter (MTCC) (original description: pacid=3  
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25 PTHR16166:SIPhvu.003G11not assigned.r no hits & (original description: pacid=37145453 transcri  
26 PTHR16166:SIPhvu.003G11not assigned.r no hits & (original description: pacid=37145453 transcri  
27 PTHR16166:SIPhvu.003G11not assigned.r no hits & (original description: pacid=37145453 transcri  
28 K18789 - xyloçPhvu.003G16Cell wall orgar xylogalacturonan xylosyltransferase (original description  
29 K00753 - glyccPhvu.003G29Protein modif alpha-1,3-fucosyltransferase (original description: pacid=  
30 K12386 - cystiPhvu.004G05not assigned.ã (original description: pacid=37163777 transcript=Phvu.  
31 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth  
32 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth  
33 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth  
34 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth  
35 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.  
36 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.  
37 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.  
38 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.  
39 PTHR10438:SIPhvu.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=  
40 PTHR10438:SIPhvu.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=  
41 PF00651 - BTEPhvu.005G05not assigned.ã (original description: pacid=37154040 transcript=Phvu.  
42 PF00651 - BTEPhvu.005G05not assigned.ã (original description: pacid=37154040 transcript=Phvu.  
43 PF00954//PFPhvu.005G08Protein modif protein kinase (SD-1) (original description: pacid=371538  
44 2.7.1.26 - RibcPhvu.005G09not assigned.ã (original description: pacid=37154603 transcript=Phvu.  
45 PTHR31072:SIPhvu.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
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3 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
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6 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
7 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
8 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
9 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
10 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
11 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
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14 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
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17 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37  
18 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
19 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
20 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
21 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
22 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
23 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
24 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase  
25 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptio  
26 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptio  
27 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptio  
28 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptio  
29 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptio  
30 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 t  
31 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 t  
32 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 t  
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36 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri  
37 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri  
38 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri  
39 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri  
40 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri  
41 K16296 - serirPhvul.006G16Protein home-serine carboxypeptidase (original description: pacid=371  
42 K16296 - serirPhvul.006G16Protein home-serine carboxypeptidase (original description: pacid=371  
43 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc  
44 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc  
45 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc  
46 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc  
47 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc  
48 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc  
49 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
50 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
51 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
52 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
53 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
54 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
55 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
56 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
57 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
58 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
59 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.i  
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3 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
4 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
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8 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
9 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
10 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
11 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
12 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.  
13 PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri  
14 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci  
15 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci  
16 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci  
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19 PTHR23257//IPhvul.007G18Protein modif protein kinase (MAP3K-RAF) (original description: pacid=  
20 PTHR23257//IPhvul.007G18Protein modif protein kinase (MAP3K-RAF) (original description: pacid=  
21 PTHR23315:SIPhvul.007G19not assigned.ã (original description: pacid=37164330 transcript=Phvul.  
22 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
23 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
24 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
25 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
26 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
27 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
28 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
29 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
30 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165  
31 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o  
32 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o  
33 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o  
34 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o  
35 PTHR22912:SIPhvul.007G25Redox homeo NADPH-dependent thioredoxin reductase (original descr  
36 PTHR27004:SIPhvul.008G04not assigned.ã (original description: pacid=37160665 transcript=Phvul.  
37 PTHR27004:SIPhvul.008G04not assigned.ã (original description: pacid=37160665 transcript=Phvul.  
38 PTHR10641//IPhvul.008G06RNA biosynthe transcription factor (MYB) (original description: pacid=37  
39 PTHR10641//IPhvul.008G06RNA biosynthe transcription factor (MYB) (original description: pacid=37  
40 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37159657 transcri  
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43 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37159657 transcri  
44 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri  
45 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri  
46 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri  
47 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri  
48 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri  
49 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri  
50 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
51 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
52 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
53 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
54 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
55 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
56 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
57 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
58 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
59 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri  
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3 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p  
4 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p  
5 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p  
6 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p  
7 PTHR10795//IPhvu.008G22Protein home protease (SBT4) (original description: pacid=37158609 tr  
8 PTHR13301//IPhvu.008G27not assigned.ã (original description: pacid=37161159 transcript=Phvu.1  
9 PTHR13301//IPhvu.008G27not assigned.ã (original description: pacid=37161159 transcript=Phvu.1  
10 3.4.17.1 - CarłPhvu.009G01Protein home M14 carboxypeptidase (original description: pacid=3715  
11 3.4.17.1 - CarłPhvu.009G01Protein home M14 carboxypeptidase (original description: pacid=3715  
12 K08505 - protPhvu.009G03Vesicle trafficlSFT12 group Qc-type SNARE protein (original description  
13 PTHR13878:SİPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37:  
14 PTHR13878:SİPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37:  
15 PTHR13878:SİPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37:  
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24 PTHR13878:SİPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37:  
25 PTHR13878:SİPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37:  
26 PTHR23500:SİPhvu.009G11Solute transpcomonosaccharide transporter (AZT) (original description:  
27 PTHR23500:SİPhvu.009G11Solute transpcomonosaccharide transporter (AZT) (original description:  
28 0 Phvu.009G15not assigned.ã (original description: pacid=37149132 transcript=Phvu.1  
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31 0 Phvu.009G15not assigned.ã (original description: pacid=37149132 transcript=Phvu.1  
32 PTHR31673:SİPhvu.009G20Cell wall orgar COB cellulose microfibrils and hemicellulose interaction  
33 PTHR23421:SİPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3:  
34 PTHR23421:SİPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3:  
35 PTHR23421:SİPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3:  
36 PTHR23421:SİPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3:  
37 PTHR15371:SİPhvu.009G25not assigned.ã (original description: pacid=37151366 transcript=Phvu.1  
38 PTHR15371:SİPhvu.009G25not assigned.ã (original description: pacid=37151366 transcript=Phvu.1  
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45 PF00931//PFCPhvu.010G02External stimleffector receptor (NLR) (original description: pacid=3714  
46 PF00931//PFCPhvu.010G02External stimleffector receptor (NLR) (original description: pacid=3714  
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49 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid  
50 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid  
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3 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid  
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5 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0  
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15 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0  
16 2.5.1.72 - QuiiPhvu.010G09not assigned.ã (original description: pacid=37143242 transcript=Phvu.0  
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21 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
22 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
23 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
24 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
25 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
26 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
27 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
28 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
29 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
30 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
31 PTHR11200:SIPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or  
32 5.3.4.1 - ProtePhvu.011G00not assigned.ã (original description: pacid=37156678 transcript=Phvu.0  
33 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa  
34 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa  
35 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa  
36 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa  
37 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa  
38 PTHR10774//IPhvu.L00167not assigned.ã (original description: pacid=37157494 transcript=Phvu.0  
39 PTHR10774//IPhvu.L00167not assigned.ã (original description: pacid=37157494 transcript=Phvu.0  
40 K12872 - pre-iPhvu.L00253RNA processir component MAC5 of non-snRNP MOS4-associated comp  
41 K12872 - pre-iPhvu.L00253RNA processir component MAC5 of non-snRNP MOS4-associated comp  
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9 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &  
10 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &  
11 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &  
12 :in EXECUTER 1, chloroplastic OS=Arabidopsis thaliana (sp|q93yw0|exec1\_arath : 424.0)  
13 1)  
14 1)  
15 1)  
16 :membrane 9 superfamily member 9 OS=Arabidopsis thaliana (sp|q9c5n2|tmn9\_arath : 972.0)  
17 ot-version=v2.1) &  
18 ot-version=v2.1) &  
19 ot-version=v2.1) &  
20 ot-version=v2.1) &  
21 ot-version=v2.1) &  
22 .2.1) &  
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28 !.v2.1 annot-version=v2.1) &  
29 !.v2.1 annot-version=v2.1) &  
30 !.v2.1 annot-version=v2.1) &  
31 !.v2.1 annot-version=v2.1) &  
32 rsion=v2.1) &  
33 rsion=v2.1) &  
34 rsion=v2.1) &  
35 rsion=v2.1) &  
36 rsion=v2.1) &  
37 rsion=v2.1) &  
38 rsion=v2.1) &  
39 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &  
40 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &  
41 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &  
42 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &  
43 not-version=v2.1) &  
44 not-version=v2.1) &  
45 not-version=v2.1) &  
46 not-version=v2.1) &  
47 not-version=v2.1) &  
48 not-version=v2.1) &  
49 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 499.0)  
50 1)  
51 1)  
52 1)  
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3 annot-version=v2.1) &  
4 annot-version=v2.1) &  
5 annot-version=v2.1) &  
6 annot-version=v2.1) &  
7 annot-version=v2.1) &  
8 annot-version=v2.1) &  
9 annot-version=v2.1) &  
10 annot-version=v2.1) &  
11 annot-version=v2.1) &  
12 not-version=v2.1) &  
13 not-version=v2.1) &  
14 not-version=v2.1) &  
15 not-version=v2.1) &  
16 not-version=v2.1) &  
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18 1)  
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23 1)  
24 0.8.v2.1 annot-version=v2.1) &  
25 0.8.v2.1 annot-version=v2.1) &  
26 0.8.v2.1 annot-version=v2.1) &  
27 0.8.v2.1 annot-version=v2.1) &  
28 0.8.v2.1 annot-version=v2.1) &  
29 0.8.v2.1 annot-version=v2.1) &  
30 0.8.v2.1 annot-version=v2.1) &  
31 0.8.v2.1 annot-version=v2.1) &  
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34 0.8.v2.1 annot-version=v2.1) &  
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36 0.8.v2.1 annot-version=v2.1) &  
37 0.8.v2.1 annot-version=v2.1) &  
38 0.8.v2.1 annot-version=v2.1) &  
39 0.8.v2.1 annot-version=v2.1) &  
40 0.8.v2.1 annot-version=v2.1) &  
41 0.8.v2.1 annot-version=v2.1) &  
42 0.8.v2.1 annot-version=v2.1) &  
43 0.8.v2.1 annot-version=v2.1) &  
44 0.8.v2.1 annot-version=v2.1) &  
45 rsion=v2.1) &  
46 rsion=v2.1) &  
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48 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &  
49 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &  
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51 ..1 annot-version=v2.1) &  
52 ..1 annot-version=v2.1) &  
53 ..1 annot-version=v2.1) &  
54 ..1 annot-version=v2.1) &  
55 ..1 annot-version=v2.1) &  
56 v2.1 annot-version=v2.1) &  
57 v2.1 annot-version=v2.1) &  
58 v2.1 annot-version=v2.1) &  
59 v2.1 annot-version=v2.1) &  
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3 1 annot-version=v2.1) &  
4 1)  
5 1)  
6 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 539.0)  
7 atricopeptide repeat-containing protein At4g21190 OS=Arabidopsis thaliana (sp|q8lg95|pp332\_ara  
8 4G133400.1.v2.1 annot-version=v2.1) &  
9 4G133400.1.v2.1 annot-version=v2.1) &  
10 annot-version=v2.1) &  
11 annot-version=v2.1) &  
12 annot-version=v2.1) &  
13 annot-version=v2.1) &  
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16 1)  
17 1)  
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21 1)  
22 1)  
23 1)  
24 locus=Phvul.005G180200 ID=Phvul.005G180200.1.v2.1 annot-version=v2.1) &  
25 locus=Phvul.005G180200 ID=Phvul.005G180200.1.v2.1 annot-version=v2.1) &  
26 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &  
27 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &  
28 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &  
29 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &  
30 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &  
31 annot-version=v2.1) &  
32 annot-version=v2.1) &  
33 annot-version=v2.1) &  
34 annot-version=v2.1) &  
35 1)  
36 1)  
37 1)  
38 1)  
39 1 annot-version=v2.1) &  
40 1 annot-version=v2.1) &  
41 : 205.1) (original description: pacid=37166776 transcript=Phvul.007G211400.1 locus=Phvul.007G21  
42 : 205.1) (original description: pacid=37166776 transcript=Phvul.007G211400.1 locus=Phvul.007G21  
43 1)  
44 1)  
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47 1)  
48 1)  
49 1)  
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51 1)  
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54 1)  
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56 tura stramonium (sp|p50165|trnh\_datst : 311.0) (original description: pacid=37158053 transcript=  
57 tura stramonium (sp|p50165|trnh\_datst : 311.0) (original description: pacid=37158053 transcript=  
58 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1\_arath : 214.0)  
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 3 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1\_arath : 214.0)  
 4 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1\_arath : 214.0)  
 5 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1\_arath : 214.0)  
 6 Phvul.008G282700.1.v2.1 annot-version=v2.1) &  
 7  
 8 membrane 9 superfamily member 12 OS=Arabidopsis thaliana (sp|f4jre0|tmn12\_arath : 1080.0)  
 9 ul.009G127300.1.v2.1 annot-version=v2.1) &  
 10 ul.009G127300.1.v2.1 annot-version=v2.1) &  
 11 ul.009G127300.1.v2.1 annot-version=v2.1) &  
 12 ul.009G127300.1.v2.1 annot-version=v2.1) &  
 13 not-version=v2.1) &  
 14 not-version=v2.1) &  
 15 not-version=v2.1) &  
 16 not-version=v2.1) &  
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3 annot-version=v2.1) &  
4 annot-version=v2.1) &  
5 annot-version=v2.1) &  
6 annot-version=v2.1) &  
7 annot-version=v2.1) &  
8 annot-version=v2.1) &  
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12 annot-version=v2.1) &  
13 annot-version=v2.1) &  
14 annot-version=v2.1) &  
15 annot-version=v2.1) &  
16 .41700.1.v2.1 annot-version=v2.1) &  
17 .41700.1.v2.1 annot-version=v2.1) &  
18 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &  
19 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &  
20 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &  
21 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &  
22 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &  
23 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &  
24 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
25 G294800.4.v2.1 annot-version=v2.1) &  
26 G294800.4.v2.1 annot-version=v2.1) &  
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28 1)  
29 1)  
30 1)  
31 1)  
32 1)  
33 1)  
34 1)  
35 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 499.0)  
36 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 499.0)  
37 annot-version=v2.1) &  
38 :=Phvul.005G010700 ID=Phvul.005G010700.2.v2.1 annot-version=v2.1) &  
39  
40 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
41 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
42 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
43 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
44 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
45 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
46 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
47 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
48 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
49 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
50 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c  
51 081600.1.v2.1 annot-version=v2.1) &  
52 081600.1.v2.1 annot-version=v2.1) &  
53 not-version=v2.1) &  
54 not-version=v2.1) &  
55 not-version=v2.1) &  
56 not-version=v2.1) &  
57 not-version=v2.1) &  
58 not-version=v2.1) &  
59 not-version=v2.1) &  
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3 not-version=v2.1) &  
4 1)  
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6 1)  
7 l1.1.v2.1 annot-version=v2.1) &  
8 l1.1.v2.1 annot-version=v2.1) &  
9 1)  
10 1)  
11 1)  
12 1)  
13 1)  
14 1)  
15 1 annot-version=v2.1) &  
16 1 annot-version=v2.1) &  
17 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1\_acter : 319.0)  
18 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1\_acter : 319.0)  
19 1)  
20 1)  
21 1)  
22 1)  
23 1)  
24 vl.007G233800.2.v2.1 annot-version=v2.1) &  
25 vl.007G233800.2.v2.1 annot-version=v2.1) &  
26 vl.007G233800.2.v2.1 annot-version=v2.1) &  
27 vl.007G233800.2.v2.1 annot-version=v2.1) &  
28 vl.007G233800.2.v2.1 annot-version=v2.1) &  
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43 ion=v2.1) &  
44 ion=v2.1) &  
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46 ion=v2.1) &  
47 ion=v2.1) &  
48 .1 annot-version=v2.1) &  
49 .1 annot-version=v2.1) &  
50 rt-version=v2.1) &  
51 rt-version=v2.1) &  
52 rt-version=v2.1) &  
53 rt-version=v2.1) &  
54 rt-version=v2.1) &  
55 rt-version=v2.1) &  
56 rt-version=v2.1) &  
57 rt-version=v2.1) &  
58 rt-version=v2.1) &  
59 nnot-version=v2.1) &  
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3 nnot-version=v2.1) &  
4 nnot-version=v2.1) &  
5 nnot-version=v2.1) &  
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7 1)  
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9 1)  
10 1)  
11 1)  
12 1)  
13 1)  
14 1)

15 aracterized protein At3g49140 OS=Arabidopsis thaliana (sp|q0wmn5|y3913\_arath : 104.0)  
16 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu  
17 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu  
18 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu  
19 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu  
20  
21 not-version=v2.1) &  
22 not-version=v2.1) &  
23 2.1 annot-version=v2.1) &  
24 2.1 annot-version=v2.1) &  
25 2.1 annot-version=v2.1) &  
26  
27 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
28 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
29 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
30 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
31 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
32 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
33 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
34 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
35 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
36 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
37 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
38 not-version=v2.1) &  
39 not-version=v2.1) &  
40 not-version=v2.1) &  
41 not-version=v2.1) &  
42 not-version=v2.1) &  
43 not-version=v2.1) &  
44 not-version=v2.1) &  
45 not-version=v2.1) &  
46 not-version=v2.1) &  
47 not-version=v2.1) &  
48 not-version=v2.1) &  
49 vul.010G048400.4.v2.1 annot-version=v2.1) &  
50 vul.010G048400.4.v2.1 annot-version=v2.1) &  
51 vul.010G048400.4.v2.1 annot-version=v2.1) &  
52 vul.010G048400.4.v2.1 annot-version=v2.1) &  
53 vul.010G048400.4.v2.1 annot-version=v2.1) &  
54 vul.010G048400.4.v2.1 annot-version=v2.1) &  
55 vul.010G048400.4.v2.1 annot-version=v2.1) &  
56 vul.010G048400.4.v2.1 annot-version=v2.1) &  
57 vul.010G048400.4.v2.1 annot-version=v2.1) &  
58 vul.010G048400.4.v2.1 annot-version=v2.1) &  
59 vul.010G048400.4.v2.1 annot-version=v2.1) &  
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3 vul.010G048400.4.v2.1 annot-version=v2.1) &  
4 vul.010G048400.4.v2.1 annot-version=v2.1) &  
5 vul.010G048400.4.v2.1 annot-version=v2.1) &  
6 vul.010G048400.4.v2.1 annot-version=v2.1) &  
7 vul.010G048400.4.v2.1 annot-version=v2.1) &  
8 vul.010G048400.4.v2.1 annot-version=v2.1) &  
9 vul.010G048400.4.v2.1 annot-version=v2.1) &  
10 vul.010G048400.4.v2.1 annot-version=v2.1) &  
11 vul.010G048400.4.v2.1 annot-version=v2.1) &  
12 vul.010G048400.4.v2.1 annot-version=v2.1) &  
13 ot-version=v2.1) &  
14 ot-version=v2.1) &  
15 ot-version=v2.1) &  
16 ot-version=v2.1) &  
17 1.v2.1 annot-version=v2.1) &  
18 1.v2.1 annot-version=v2.1) &  
19 1.v2.1 annot-version=v2.1) &  
20 1.v2.1 annot-version=v2.1) &  
21 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
22 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
23 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
24 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
25 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
26 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
27 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
28 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
29 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
30 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
31 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
32 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
33 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
34 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
35 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
36 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
37 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r  
38 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r  
39 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r  
40 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r  
41 )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
42 )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
43 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
44 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
45 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
46 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
47 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
48 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
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55 1) )200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &  
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3 1)  
4 1)  
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10 1)  
11 1)  
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20 1)  
21  
22 hvul.001G200700.5.v2.1 annot-version=v2.1) &  
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26 hvul.001G200700.5.v2.1 annot-version=v2.1) &  
27 hvul.001G200700.5.v2.1 annot-version=v2.1) &  
28 hvul.001G200700.5.v2.1 annot-version=v2.1) &  
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30 hvul.001G200700.5.v2.1 annot-version=v2.1) &  
31 hvul.001G200700.5.v2.1 annot-version=v2.1) &  
32 x domain-containing protein 6 OS=Arabidopsis thaliana (sp|o48700|pub6\_arath : 901.0)  
33  
34 ie transferring one-carbon group(50.2.1 : 212.4) (original description: pacid=37169062 transcript=Pl  
35 ie transferring one-carbon group(50.2.1 : 212.4) (original description: pacid=37169062 transcript=Pl  
36 J).1.v2.1 annot-version=v2.1) &  
37 J).1.v2.1 annot-version=v2.1) &  
38 rsion=v2.1) &  
39 rsion=v2.1) &  
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41 rsion=v2.1) &  
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43 annot-version=v2.1) &  
44 annot-version=v2.1) &  
45 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &  
46 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &  
47 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &  
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49  
50 216700.3.v2.1 annot-version=v2.1) &  
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53 216700.3.v2.1 annot-version=v2.1) &  
54  
55 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
56 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
57  
58  
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3 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 108.0)  
4 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 108.0)  
5 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 108.0)  
6 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 108.0)  
7  
8 v2.1 annot-version=v2.1) &  
9 v2.1 annot-version=v2.1) &  
10 v2.1 annot-version=v2.1) &  
11 v2.1 annot-version=v2.1) &  
12  
13 mycin-sensitive aminopeptidase OS=Arabidopsis thaliana (sp|q8h0s9|psa\_arath : 805.0)  
14 mycin-sensitive aminopeptidase OS=Arabidopsis thaliana (sp|q8h0s9|psa\_arath : 805.0)  
15  
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17 version=v2.1) &  
18  
19 |ul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &  
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22 |ul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &  
23  
24 |not-version=v2.1) &  
25 |not-version=v2.1) &  
26 |not-version=v2.1) &  
27 |not-version=v2.1) &  
28 |not-version=v2.1) &  
29 |not-version=v2.1) &  
30 |not-version=v2.1) &  
31 |not-version=v2.1) &  
32 |not-version=v2.1) &  
33 |not-version=v2.1) &  
34 |not-version=v2.1) &  
35 |03G032300.1.v2.1 annot-version=v2.1) &  
36 |03G032300.1.v2.1 annot-version=v2.1) &  
37  
38 |.1 locus=Phvul.003G057700 ID=Phvul.003G057700.1.v2.1 annot-version=v2.1) &  
39 |.1 locus=Phvul.003G057700 ID=Phvul.003G057700.1.v2.1 annot-version=v2.1) &  
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41 |1)  
42 |1)  
43 |1)  
44 |1)  
45 |not-version=v2.1) &  
46 |not-version=v2.1) &  
47 |not-version=v2.1) &  
48 |not-version=v2.1) &  
49 |not-version=v2.1) &  
50  
51 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
52 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
53 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
54 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
55 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
56 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
57 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
58 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
59 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42\_arath : 431.0)  
60

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3 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|dr142\_arath : 431.0)  
4 able methyltransferase PMT20 OS=Arabidopsis thaliana (sp|q9c6s7|pmtk\_arath : 983.0)  
5 able methyltransferase PMT20 OS=Arabidopsis thaliana (sp|q9c6s7|pmtk\_arath : 983.0)  
6 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
7 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
8 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
9 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
10 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
11 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b\_arath : 97.4)  
12 G294800.4.v2.1 annot-version=v2.1) &  
13 G294800.4.v2.1 annot-version=v2.1) &  
14 G294800.4.v2.1 annot-version=v2.1) &  
15 G294800.4.v2.1 annot-version=v2.1) &  
16 G294800.4.v2.1 annot-version=v2.1) &  
17 G294800.4.v2.1 annot-version=v2.1) &  
18 G294800.4.v2.1 annot-version=v2.1) &  
19 G294800.4.v2.1 annot-version=v2.1) &  
20 G294800.4.v2.1 annot-version=v2.1) &  
21 G294800.4.v2.1 annot-version=v2.1) &  
22 G294800.4.v2.1 annot-version=v2.1) &  
23 1)  
24 1)  
25 1)  
26 1)  
27 1)  
28 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 539.0)  
29 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 539.0)  
30 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 539.0)  
31 1)  
32 1)  
33 1)  
34 1)  
35 1)  
36 1)  
37 1)  
38 1)  
39 1)  
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41 sion=v2.1) &  
42 sion=v2.1) &  
43 sion=v2.1) &  
44 sion=v2.1) &  
45 sion=v2.1) &  
46 05G014300 ID=Phvul.005G014300.2.v2.1 annot-version=v2.1) &  
47 POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439\_arath : 760  
48 on=v2.1) &  
49 1)  
50 1)  
51 1)  
52 1)  
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3 1)  
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6 J.1.v2.1 annot-version=v2.1) &  
7 J.1.v2.1 annot-version=v2.1) &  
8 ) ID=Phvul.006G105800.1.v2.1 annot-version=v2.1) &  
9 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
10 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
11 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
12 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
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14 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
15 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
16 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
17 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
18 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
19 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp\_arath : 80.  
20 rot-version=v2.1) &  
21 rot-version=v2.1) &  
22 rot-version=v2.1) &  
23 rot-version=v2.1) &  
24 rot-version=v2.1) &  
25 rot-version=v2.1) &  
26 rot-version=v2.1) &  
27 rot-version=v2.1) &  
28 rot-version=v2.1) &  
29 rot-version=v2.1) &  
30 rot-version=v2.1) &  
31 1)  
32 ot-version=v2.1) &  
33 ot-version=v2.1) &  
34 ot-version=v2.1) &  
35 ot-version=v2.1) &  
36 ot-version=v2.1) &  
37 )iquitin-protein ligase CSU1 OS=Arabidopsis thaliana (sp|q9sy88|csu1\_arath : 419.0)  
38 )iquitin-protein ligase CSU1 OS=Arabidopsis thaliana (sp|q9sy88|csu1\_arath : 419.0)  
39 1)  
40 1)  
41 1)  
42 1)  
43 1)  
44 1)  
45 I.0.1.v2.1 annot-version=v2.1) &  
46 I.0.1.v2.1 annot-version=v2.1) &  
47 I.007G034000.2.v2.1 annot-version=v2.1) &  
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49 version=v2.1) &  
50 version=v2.1) &  
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54 i6600.1.v2.1 annot-version=v2.1) &  
55 i6600.1.v2.1 annot-version=v2.1) &  
56 i6600.1.v2.1 annot-version=v2.1) &  
57 i6600.1.v2.1 annot-version=v2.1) &  
58 i6600.1.v2.1 annot-version=v2.1) &  
59 i6600.1.v2.1 annot-version=v2.1) &  
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3 1 annot-version=v2.1) &  
4 1 annot-version=v2.1) &  
5 1 annot-version=v2.1) &  
6 1 annot-version=v2.1) &  
7 1 annot-version=v2.1) &  
8 1 annot-version=v2.1) &  
9 1 annot-version=v2.1) &  
10 1 annot-version=v2.1) &  
11 1 annot-version=v2.1) &  
12 1 annot-version=v2.1) &  
13 1 annot-version=v2.1) &  
14 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1\_acter : 319.0)  
15 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1\_acter : 319.0)  
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17 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1\_acter : 319.0)  
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20 1.v2.1 annot-version=v2.1) &  
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22 1.v2.1 annot-version=v2.1) &  
23 1.v2.1 annot-version=v2.1) &  
24 1.v2.1 annot-version=v2.1) &  
25 1)  
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28 1)  
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31 1.v2.1 annot-version=v2.1) &  
32 1.v2.1 annot-version=v2.1) &  
33 1.v2.1 annot-version=v2.1) &  
34 1.v2.1 annot-version=v2.1) &  
35 1.v2.1 annot-version=v2.1) &  
36 1)  
37 1)  
38 1)  
39 1)  
40 1)  
41 1)  
42 1)  
43 1)  
44 10.2.v2.1 annot-version=v2.1) &  
45 10.2.v2.1 annot-version=v2.1) &  
46 10.2.v2.1 annot-version=v2.1) &  
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49 10.2.v2.1 annot-version=v2.1) &  
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53 10.2.v2.1 annot-version=v2.1) &  
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55 -version=v2.1) &  
56 nin-2 OS=Pisum sativum (sp|p08688|alb2\_pea : 223.0)  
57 nin-2 OS=Pisum sativum (sp|p08688|alb2\_pea : 223.0)  
58 nin-2 OS=Pisum sativum (sp|p08688|alb2\_pea : 223.0)  
59 nin-2 OS=Pisum sativum (sp|p08688|alb2\_pea : 253.0)  
60

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3 min-2 OS=Pisum sativum (sp|p08688|alb2\_pea : 253.0)  
4 min-2 OS=Pisum sativum (sp|p08688|alb2\_pea : 222.0)  
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6  
7 .1 annot-version=v2.1) &  
8 .1 annot-version=v2.1) &  
9 .1 annot-version=v2.1) &  
10 .1 annot-version=v2.1) &  
11 .1 annot-version=v2.1) &  
12  
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14 1)  
15 1)  
16 1)  
17 1)  
18 1)  
19 12100 ID=Phvul.008G012100.2.v2.1 annot-version=v2.1) &  
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21 annot-version=v2.1) &  
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42 1)  
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47 1)  
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51 1)  
52 1)  
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54 1)  
55 1)  
56 00.6.v2.1 annot-version=v2.1) &  
57 00.6.v2.1 annot-version=v2.1) &  
58 00.6.v2.1 annot-version=v2.1) &  
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3 00.6.v2.1 annot-version=v2.1) &  
4 1)  
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6 1)  
7 1)  
8 1)  
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10 not-version=v2.1) &  
11 not-version=v2.1) &  
12 not-version=v2.1) &  
13 not-version=v2.1) &  
14  
15 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1\_arath : 211.0)  
16 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1\_arath : 211.0)  
17 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1\_arath : 211.0)  
18 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1\_arath : 211.0)  
19 'hvul.008G282700.1.v2.1 annot-version=v2.1) &  
20 'hvul.008G282700.1.v2.1 annot-version=v2.1) &  
21  
22 not-version=v2.1) &  
23 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
24 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
25 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
26 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
27 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c\_arath : 1134.0)  
28 1 annot-version=v2.1) &  
29 1 annot-version=v2.1) &  
30 1 annot-version=v2.1) &  
31 1 annot-version=v2.1) &  
32 1 annot-version=v2.1) &  
33 not-version=v2.1) &  
34 not-version=v2.1) &  
35  
36 'um basilicum (sp|q9xgw0|comt1\_ociba : 362.0) (original description: pacid=37151728 transcript=Pr  
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38 'um basilicum (sp|q9xgw0|comt1\_ociba : 362.0) (original description: pacid=37151728 transcript=Pr  
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40  
41 'escription available(sp|f4jts8|nov\_arath : 150.0)  
42 'escription available(sp|f4jts8|nov\_arath : 150.0)  
43 'escription available(sp|f4jts8|nov\_arath : 150.0)  
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46 'escription available(sp|f4jts8|nov\_arath : 150.0)  
47 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
48 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
49 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
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51 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
52 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
53 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
54 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
55 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
56 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
57 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
58 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
59 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
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 3 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 4 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 5 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 6 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 7 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 8 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 9 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 10 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 11 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 12 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 13 'hvul.010G043700.9.v2.1 annot-version=v2.1) &  
 14 nnot-version=v2.1) &  
 15 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 16 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 17 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 18 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 19 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 20 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 21 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 22 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 23 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 24 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 25 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 26 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 27 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)  
 28 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx\_soybn : 884.0) (original d  
 29 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx\_soybn : 884.0) (original d  
 30 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx\_soybn : 884.0) (original d  
 31 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx\_soybn : 884.0) (original d  
 32 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx\_soybn : 884.0) (original d  
 33 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx\_soybn : 884.0) (original d  
 34 /ul.011G013900.1.v2.1 annot-version=v2.1) &  
 35 /ul.011G013900.1.v2.1 annot-version=v2.1) &  
 36 /ul.011G013900.1.v2.1 annot-version=v2.1) &  
 37 /ul.011G013900.1.v2.1 annot-version=v2.1) &  
 38 /ul.011G013900.1.v2.1 annot-version=v2.1) &  
 39 /ersion=v2.1) &  
 40 /ersion=v2.1) &  
 41 /ersion=v2.1) &  
 42 /ersion=v2.1) &  
 43 /ersion=v2.1) &  
 44 vul.011G061600.1.v2.1 annot-version=v2.1) &  
 45 vul.011G061600.1.v2.1 annot-version=v2.1) &  
 46 tein homolog 5 OS=Arabidopsis thaliana (sp|o23020|sph5\_arath : 90.5)  
 47 tein homolog 5 OS=Arabidopsis thaliana (sp|o23020|sph5\_arath : 90.9)  
 48  
 49 1)  
 50 1)  
 51  
 52 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 53 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 54 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 55 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 56 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 57 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 58 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 59 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
 60

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2  
3 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
4 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
5 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
6 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
7 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
8 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
9 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01  
10 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

11 1)  
12 1)  
13 1)  
14 1)  
15 1)

16 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
17 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
18 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
19 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
20 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
21 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
22 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
23 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
24 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
25 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
26 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi  
27 ul.L002537.1.v2.1 annot-version=v2.1) &  
28 ul.L002537.1.v2.1 annot-version=v2.1) &  
29 ul.L002537.1.v2.1 annot-version=v2.1) &  
30 ul.L002537.1.v2.1 annot-version=v2.1) &  
31

32 loreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tr  
33 loreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tr  
34 loreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tr  
35 annot-version=v2.1) &  
36 annot-version=v2.1) &  
37

38 1)  
39 1)  
40 1)  
41 1)  
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43 0.1.v2.1 annot-version=v2.1) &  
44 J57800.1.v2.1 annot-version=v2.1) &  
45 J57800.1.v2.1 annot-version=v2.1) &  
46 sion=v2.1) &  
47 sion=v2.1) &  
48 sion=v2.1) &  
49 -version=v2.1) &  
50 -version=v2.1) &  
51 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &  
52 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &  
53 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &  
54 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &  
55 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &  
56 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &  
57 2.1 annot-version=v2.1) &  
58 2.1 annot-version=v2.1) &  
59 2.1 annot-version=v2.1) &  
60

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 2  
 3 α-glucosidase OS=Spinacia oleracea (sp|o04893|aglu\_spiol : 80.9)  
 4 α-glucosidase OS=Spinacia oleracea (sp|o04893|aglu\_spiol : 80.9)  
 5  
 6 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 7 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 8 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 9 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 10 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 11 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 12 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 13 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 14 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 15 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 339.0)  
 16 .1 annot-version=v2.1) &  
 17 nnot-version=v2.1) &  
 18 nnot-version=v2.1) &  
 19 nnot-version=v2.1) &  
 20 nnot-version=v2.1) &  
 21 nnot-version=v2.1) &  
 22 nnot-version=v2.1) &  
 23 nnot-version=v2.1) &  
 24 nnot-version=v2.1) &  
 25 nnot-version=v2.1) &  
 26 nnot-version=v2.1) &  
 27 nnot-version=v2.1) &  
 28 :rsion=v2.1) &  
 29 :rsion=v2.1) &  
 30  
 31 2.1 annot-version=v2.1) &  
 32 2.1 annot-version=v2.1) &  
 33 2.1 annot-version=v2.1) &  
 34 2.1 annot-version=v2.1) &  
 35  
 36 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1\_arath : 275.0)  
 37 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1\_arath : 275.0)  
 38 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1\_arath : 275.0)  
 39 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1\_arath : 275.0)  
 40  
 41 ot-version=v2.1) &  
 42 ot-version=v2.1) &  
 43 ot-version=v2.1) &  
 44 ot-version=v2.1) &  
 45  
 46 J.1.v2.1 annot-version=v2.1) &  
 47 J.1.v2.1 annot-version=v2.1) &  
 48  
 49 ersion=v2.1) &  
 50 ersion=v2.1) &  
 51 ersion=v2.1) &  
 52 ersion=v2.1) &  
 53 ersion=v2.1) &  
 54  
 55 annot-version=v2.1) &  
 56 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
 57 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
 58 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
 59 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
 60

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 2  
 3 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15\_arath : 284.0)  
 4 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 98.6)  
 5 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 98.6)  
 6 ul.002G262600.2.v2.1 annot-version=v2.1) &  
 7 nnot-version=v2.1) &  
 8 nnot-version=v2.1) &  
 9 1)  
 10 1)  
 11 ersion=v2.1) &  
 12 ersion=v2.1) &  
 13 ersion=v2.1) &  
 14 ersion=v2.1) &  
 15 ersion=v2.1) &  
 16 ersion=v2.1) &  
 17 ersion=v2.1) &  
 18 ersion=v2.1) &  
 19 ersion=v2.1) &  
 20 ersion=v2.1) &  
 21 ersion=v2.1) &  
 22 ersion=v2.1) &  
 23 ersion=v2.1) &  
 24 id GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1\_arath : :  
 25 id GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1\_arath : :  
 26 annot-version=v2.1) &  
 27 annot-version=v2.1) &  
 28 annot-version=v2.1) &  
 29 annot-version=v2.1) &  
 30 annot-version=v2.1) &  
 31 1)  
 32 1)  
 33 1)  
 34 1)  
 35 1)  
 36 ).1.v2.1 annot-version=v2.1) &  
 37 annot-version=v2.1) &  
 38 nosin homolog OS=Arabidopsis thaliana (sp|p57758|ctns\_arath : 317.0)  
 39 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &  
 40 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &  
 41 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &  
 42 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &  
 43 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &  
 44 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &  
 45 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843\_arath : 311.0)  
 46 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843\_arath : 311.0)  
 47 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843\_arath : 311.0)  
 48 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843\_arath : 311.0)  
 49 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843\_arath : 311.0)  
 50 annot-version=v2.1) &  
 51 annot-version=v2.1) &  
 52 POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439\_arath : 760  
 53 POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439\_arath : 760  
 54 ersion=v2.1) &  
 55 ctional riboflavin kinase/FMN phosphatase OS=Arabidopsis thaliana (sp|q84md8|fhyrk\_arath : 248  
 56 not-version=v2.1) &  
 57  
 58  
 59  
 60

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3 not-version=v2.1) &  
4 not-version=v2.1) &  
5 not-version=v2.1) &  
6 not-version=v2.1) &  
7 not-version=v2.1) &  
8 not-version=v2.1) &  
9 not-version=v2.1) &  
10 not-version=v2.1) &  
11 not-version=v2.1) &  
12 not-version=v2.1) &  
13 not-version=v2.1) &  
14 not-version=v2.1) &  
15 not-version=v2.1) &  
16 not-version=v2.1) &  
17  
18 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
19 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
20 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
21 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
22 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
23 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
24 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &  
25  
26 J.1.v2.1 annot-version=v2.1) &  
27 J.1.v2.1 annot-version=v2.1) &  
28 J.1.v2.1 annot-version=v2.1) &  
29 J.1.v2.1 annot-version=v2.1) &  
30  
31 n=v2.1) &  
32 n=v2.1) &  
33 n=v2.1) &  
34 n=v2.1) &  
35  
36 1)  
37 1)  
38 1)  
39 1)  
40  
41 ot-version=v2.1) &  
42 ot-version=v2.1) &  
43  
44 035900.2.v2.1 annot-version=v2.1) &  
45 035900.2.v2.1 annot-version=v2.1) &  
46 035900.2.v2.1 annot-version=v2.1) &  
47 035900.2.v2.1 annot-version=v2.1) &  
48  
49 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
50 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
51 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
52 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
53 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
54 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
55 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
56 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
57 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
58 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
59 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara**  
60

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3 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
4 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
5 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
6 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
7 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
8 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
9 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
10 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
11 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
12 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
13 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81\_ara  
14 1)

15 ..1 annot-version=v2.1) &

16 ..1 annot-version=v2.1) &

17 ..1 annot-version=v2.1) &

18 ..1 annot-version=v2.1) &

19 ..1 annot-version=v2.1) &

20 annot-version=v2.1) &

21 annot-version=v2.1) &

22 x domain-containing protein 3 OS=Arabidopsis thaliana (sp|q8gww5|pub3\_arath : 647.0)

23 :-version=v2.1) &

24 :-version=v2.1) &

25 :-version=v2.1) &

26 :-version=v2.1) &

27 :-version=v2.1) &

28 :-version=v2.1) &

29 :-version=v2.1) &

30 :-version=v2.1) &

31 :-version=v2.1) &

32 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

33 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

34 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

35 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

36 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

37 51800.1.v2.1 annot-version=v2.1) &

38 51800.1.v2.1 annot-version=v2.1) &

39 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

40 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

41 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

42 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

43 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

44 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

45 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

46 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

47 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

48 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6\_arath : 408.0)

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8 n=v2.1) &  
9 lose synthase-like protein E6 OS=Oryza sativa subsp. japonica (sp|q651x6|csle6\_orysj : 667.0)  
10 lose synthase-like protein E6 OS=Oryza sativa subsp. japonica (sp|q651x6|csle6\_orysj : 667.0)  
11 t-version=v2.1) &  
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26 1.v2.1 annot-version=v2.1) &  
27 1.v2.1 annot-version=v2.1) &  
28 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141\_arath : 263.0)  
29 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141\_arath : 263.0)  
30 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141\_arath : 263.0)  
31 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141\_arath : 263.0)  
32 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141\_arath : 263.0)  
33 )3100 ID=Phvul.009G203100.1.v2.1 annot-version=v2.1) &  
34 rot-version=v2.1) &  
35 rot-version=v2.1) &  
36 rot-version=v2.1) &  
37 rot-version=v2.1) &  
38 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162\_arath : 18  
39 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162\_arath : 18  
40 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162\_arath : 18  
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xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16\_arath : 380.0)

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olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada\_arath : 152.0)

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nain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1\_arath : 135.0)

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0G135701.1.v2.1 annot-version=v2.1) &  
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	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
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3	uagcuuaucağa	Phvul.004G023066.1	3	-1	1	22
4	uagcuuaucağa	Phvul.004G023066.1	3	-1	1	22
5	uagcuuaucağa	Phvul.004G023066.1	3	-1	1	23
6	uagcuuaucağa	Phvul.002G097400.1	3.5	-1	1	22
7	uagcuuaucağa	Phvul.002G097400.1	3.5	-1	1	22
8	uagcuuaucağa	Phvul.002G097400.1	3.5	-1	1	23
9	uagcuuaucağa	Phvul.006G008480.2	3.5	-1	1	22
10	uagcuuaucağa	Phvul.006G008480.1	3.5	-1	1	22
11	uagcuuaucağa	Phvul.006G008480.2	3.5	-1	1	22
12	uagcuuaucağa	Phvul.006G008480.1	3.5	-1	1	22
13	uagcuuaucağa	Phvul.006G008480.2	3.5	-1	1	22
14	uagcuuaucağa	Phvul.006G008480.1	3.5	-1	1	23
15	uagcuuaucağa	Phvul.006G008480.2	3.5	-1	1	23
16	uagcuuaucağa	Phvul.006G029000.1	3.5	-1	1	22
17	uagcuuaucağa	Phvul.006G029000.1	3.5	-1	1	22
18	uagcuuaucağa	Phvul.006G029000.1	3.5	-1	1	23
19	uagcuuaucağa	Phvul.006G110300.1	3.5	-1	1	22
20	uagcuuaucağa	Phvul.006G110300.1	3.5	-1	1	22
21	uagcuuaucağa	Phvul.006G110300.1	3.5	-1	1	23
22	uagcuuaucağa	Phvul.007G191600.1	3.5	-1	1	22
23	uagcuuaucağa	Phvul.007G191600.1	3.5	-1	1	22
24	uagcuuaucağa	Phvul.007G191600.1	3.5	-1	1	23
25	uagcuuaucağa	Phvul.001G070000.1	4	-1	1	22
26	uagcuuaucağa	Phvul.001G070000.1	4	-1	1	22
27	uagcuuaucağa	Phvul.001G070000.1	4	-1	1	23
28	uagcuuaucağa	Phvul.001G264600.2	4	-1	1	22
29	uagcuuaucağa	Phvul.001G264600.1	4	-1	1	22
30	uagcuuaucağa	Phvul.001G264600.2	4	-1	1	22
31	uagcuuaucağa	Phvul.001G264600.1	4	-1	1	22
32	uagcuuaucağa	Phvul.001G264600.2	4	-1	1	23
33	uagcuuaucağa	Phvul.001G264600.1	4	-1	1	23
34	uagcuuaucağa	Phvul.002G153500.1	4	-1	1	22
35	uagcuuaucağa	Phvul.002G153500.1	4	-1	1	22
36	uagcuuaucağa	Phvul.002G153500.1	4	-1	1	23
37	uagcuuaucağa	Phvul.003G092500.1	4	-1	1	22
38	uagcuuaucağa	Phvul.003G092500.1	4	-1	1	22
39	uagcuuaucağa	Phvul.004G000300.1	4	-1	1	22
40	uagcuuaucağa	Phvul.004G000300.1	4	-1	1	22
41	uagcuuaucağa	Phvul.004G000300.1	4	-1	1	23
42	uagcuuaucağa	Phvul.004G126100.1	4	-1	1	22
43	uagcuuaucağa	Phvul.004G126100.1	4	-1	1	22
44	uagcuuaucağa	Phvul.004G126100.1	4	-1	1	23
45	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
46	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
47	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
48	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
49	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
50	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
51	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
52	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
53	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
54	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
55	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
56	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
57	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
58	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22
59	uagcuuaucağa	Phvul.005G063700.2	4	-1	1	22
60	uagcuuaucağa	Phvul.005G063700.1	4	-1	1	22

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3	uagcuuaucağa Phvul.005G063700.1	4	-1	1	23
4	uagcuuaucağa Phvul.007G020600.1	4	-1	1	22
5	uagcuuaucağa Phvul.007G020600.1	4	-1	1	22
6	uagcuuaucağa Phvul.007G020700.1	4	-1	1	22
7	uagcuuaucağa Phvul.007G020700.1	4	-1	1	22
8	uagcuuaucağa Phvul.007G020700.1	4	-1	1	22
9	uagcuuaucağa Phvul.007G080800.1	4	-1	1	22
10	uagcuuaucağa Phvul.007G080800.1	4	-1	1	22
11	uagcuuaucağa Phvul.007G080800.1	4	-1	1	22
12	uagcuuaucağa Phvul.007G080800.1	4	-1	1	23
13	uagcuuaucağa Phvul.007G254000.2	4	-1	1	22
14	uagcuuaucağa Phvul.007G254000.1	4	-1	1	22
15	uagcuuaucağa Phvul.007G254000.2	4	-1	1	22
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19	uagcuuaucağa Phvul.007G254000.1	4	-1	1	23
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47	uagcuuaucağa Phvul.007G072700.12	5	-1	1	22
48	uagcuuaucağa Phvul.007G072700.13	5	-1	1	22
49	uagcuuaucağa Phvul.007G072700.10	5	-1	1	22
50	uagcuuaucağa Phvul.007G072700.10	5	-1	1	22
51	uagcuuaucağa Phvul.007G072700.11	5	-1	1	22
52	uagcuuaucağa Phvul.007G215400.1	5	-1	1	22
53	uagcuuaucağa Phvul.007G215400.1	5	-1	1	22
54	uagcuuaucağa Phvul.007G215400.1	5	-1	1	23
55	uagcuuaucağa Phvul.007G249800.1	5	-1	1	22
56	uagcuuaucağa Phvul.007G249800.1	5	-1	1	22
57	uagcuuaucağa Phvul.007G249800.1	5	-1	1	22
58	uagcuuaucağa Phvul.007G249800.1	5	-1	1	23
59	uagcuuaucağa Phvul.008G074600.3	5	-1	1	22
60	uagcuuaucağa Phvul.008G074600.2	5	-1	1	22

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2	uagcuuaucağa Phvul.008G074600.4	5	-1	1	22
3	uagcuuaucağa Phvul.008G074600.1	5	-1	1	22
4	uagcuuaucağa Phvul.008G074600.3	5	-1	1	22
5					
6	uagcuuaucağa Phvul.008G074600.2	5	-1	1	22
7	uagcuuaucağa Phvul.008G074600.4	5	-1	1	22
8	uagcuuaucağa Phvul.008G074600.1	5	-1	1	22
9					
10	uagcuuaucağa Phvul.008G123400.1	5	-1	1	22
11	uagcuuaucağa Phvul.008G123400.1	5	-1	1	22
12	uagcuuaucağa Phvul.008G129500.1	5	-1	1	22
13	uagcuuaucağa Phvul.008G129500.1	5	-1	1	22
14	uagcuuaucağa Phvul.008G129500.1	5	-1	1	22
15	uagcuuaucağa Phvul.008G129500.1	5	-1	1	23
16	uagcuuaucağa Phvul.008G164600.1	5	-1	1	22
17	uagcuuaucağa Phvul.008G164600.1	5	-1	1	22
18	uagcuuaucağa Phvul.008G164600.1	5	-1	1	22
19	uagcuuaucağa Phvul.008G164600.1	5	-1	1	23
20	uagcuuaucağa Phvul.008G225300.1	5	-1	1	23
21	uagcuuaucağa Phvul.008G230200.1	5	-1	1	23
22	uagcuuaucağa Phvul.008G230200.1	5	-1	1	23
23	uagcuuaucağa Phvul.009G030500.1	5	-1	1	22
24	uagcuuaucağa Phvul.009G030500.1	5	-1	1	22
25	uagcuuaucağa Phvul.009G030500.1	5	-1	1	22
26	uagcuuaucağa Phvul.009G030500.1	5	-1	1	23
27	uagcuuaucağa Phvul.009G099700.1	5	-1	1	22
28	uagcuuaucağa Phvul.009G099700.1	5	-1	1	22
29	uagcuuaucağa Phvul.009G099700.1	5	-1	1	22
30	uagcuuaucağa Phvul.009G099700.1	5	-1	1	23
31	uagcuuaucağa Phvul.009G233000.1	5	-1	1	22
32	uagcuuaucağa Phvul.009G233000.1	5	-1	1	22
33	uagcuuaucağa Phvul.009G233000.1	5	-1	1	22
34	uagcuuaucağa Phvul.009G233000.1	5	-1	1	23
35	uagcuuaucağa Phvul.010G021700.1	5	-1	1	22
36	uagcuuaucağa Phvul.010G021700.1	5	-1	1	22
37	uagcuuaucağa Phvul.010G021700.1	5	-1	1	22
38	uagcuuaucağa Phvul.010G021700.1	5	-1	1	23
39	uagcuuaucağa Phvul.010G104900.2	5	-1	1	22
40	uagcuuaucağa Phvul.010G104900.2	5	-1	1	22
41	uagcuuaucağa Phvul.010G104900.2	5	-1	1	22
42	uagcuuaucağa Phvul.010G104900.2	5	-1	1	23
43	uagcuuaucağa Phvul.010G129400.1	5	-1	1	22
44	uagcuuaucağa Phvul.010G129400.1	5	-1	1	22
45	uagcuuaucağa Phvul.010G129400.1	5	-1	1	22
46	uagcuuaucağa Phvul.010G129400.1	5	-1	1	23
47	uagcuuaucağa Phvul.010G157900.4	5	-1	1	22
48	uagcuuaucağa Phvul.010G157900.3	5	-1	1	22
49	uagcuuaucağa Phvul.010G157900.2	5	-1	1	22
50	uagcuuaucağa Phvul.010G157900.2	5	-1	1	22
51	uagcuuaucağa Phvul.010G157900.4	5	-1	1	22
52	uagcuuaucağa Phvul.010G157900.3	5	-1	1	22
53	uagcuuaucağa Phvul.010G157900.2	5	-1	1	22
54	uagcuuaucağa Phvul.010G157900.2	5	-1	1	22
55	uagcuuaucağa Phvul.010G157900.4	5	-1	1	23
56	uagcuuaucağa Phvul.010G157900.3	5	-1	1	23
57	uagcuuaucağa Phvul.010G157900.2	5	-1	1	23
58	uagcuuaucağa Phvul.010G157900.2	5	-1	1	23
59	uagcuuaucağa Phvul.011G006200.1	5	-1	1	22
60	uagcuuaucağa Phvul.011G006200.1	5	-1	1	22
	uagcuuaucağa Phvul.011G006200.1	5	-1	1	23

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2	uagcuuaucağa	Phvul.011G161100.1	5	-1	1	22
3	uagcuuaucağa	Phvul.011G161100.1	5	-1	1	22
4	uagcuuaucağa	Phvul.011G161100.1	5	-1	1	23
5						
6	uagcuuaucağa	Phvul.011G161900.1	5	-1	1	22
7	uagcuuaucağa	Phvul.011G161900.1	5	-1	1	22
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Do not distribute

Target_start	Target_end	miRNA_alignment	Target_alignment	Inhibition	Target_Desc.
1193	1214	UAGCUUAUC/	.....: :AGCACAUUG	Cleavage	pacid=371638
1193	1214	UAGCUUAUC/	.....: :AGCACAUUG	Cleavage	pacid=371638
1192	1214	UAGCUUAUC/	.....: AAGCACAUUC	Cleavage	pacid=371638
1039	1060	UAGCUUAUC/	.....:UGAUGAUC	Cleavage	pacid=371751
1039	1060	UAGCUUAUC/	.....:UGAUGAUC	Cleavage	pacid=371751
1038	1060	UAGCUUAUC/	.....: CUGAUGAUC/	Cleavage	pacid=371751
2781	2802	UAGCUUAUC/	.....: :AGAACAUUU	Cleavage	pacid=371720
2784	2805	UAGCUUAUC/	.....: :AGAACAUUU	Cleavage	pacid=371720
2781	2802	UAGCUUAUC/	.....: :AGAACAUUU	Cleavage	pacid=371720
2784	2805	UAGCUUAUC/	.....: :AGAACAUUU	Cleavage	pacid=371720
2780	2802	UAGCUUAUC/	.....: :UAGAACAUI	Cleavage	pacid=371720
2783	2805	UAGCUUAUC/	.....: :UAGAACAUI	Cleavage	pacid=371720
811	832	UAGCUUAUC/	.....:CCCUCUCAG	Cleavage	pacid=371735
811	832	UAGCUUAUC/	.....:CCCUCUCAG	Cleavage	pacid=371735
810	832	UAGCUUAUC/	.....: UCCUCCUCA	Cleavage	pacid=371735
1572	1594	UAGCUUAUC/	.....: :UUGACAGUC/	Cleavage	pacid=371722
1572	1594	UAGCUUAUC/	.....: :UUGACAGUC/	Cleavage	pacid=371722
1571	1594	UAGCUUAUC/	.....: :UUUGACAGU	Cleavage	pacid=371722
3701	3722	UAGCUUAUC/	.....: : UGAACAUC	Cleavage	pacid=371651
3701	3722	UAGCUUAUC/	.....: : UGAACAUC	Cleavage	pacid=371651
3700	3722	UAGCUUAUC/	.....: :UUGAACAUC/	Cleavage	pacid=371651
263	284	UAGCUUAUC/	.....:UCCUAGUC	Translation	pacid=371681
263	284	UAGCUUAUC/	.....:UCCUAGUC	Translation	pacid=371681
262	284	UAGCUUAUC/	.....: CUCCUAGUC	Translation	pacid=371681
835	856	UAGCUUAUC/	.....:UCAAACUGU	Cleavage	pacid=371688
871	892	UAGCUUAUC/	.....:UCAAACUGU	Cleavage	pacid=371688
835	856	UAGCUUAUC/	.....:UCAAACUGU	Cleavage	pacid=371688
871	892	UAGCUUAUC/	.....:UCAAACUGU	Cleavage	pacid=371688
834	856	UAGCUUAUC/	.....:UCAAACUGU	Cleavage	pacid=371688
870	892	UAGCUUAUC/	.....:UCAAACUGU	Cleavage	pacid=371688
483	504	UAGCUUAUC/	.....:ACAACCUCAU	Cleavage	pacid=371764
483	504	UAGCUUAUC/	.....:ACAACCUCAU	Cleavage	pacid=371764
482	504	UAGCUUAUC/	.....:AACAACCUCA	Cleavage	pacid=371764
2079	2100	UAGCUUAUC/	.....: :UGCACAUC	Cleavage	pacid=371447
2079	2100	UAGCUUAUC/	.....: :UGCACAUC	Cleavage	pacid=371447
1281	1302	UAGCUUAUC/	.....: :AGUUCAUC	Cleavage	pacid=371616
1281	1302	UAGCUUAUC/	.....: :AGUUCAUC	Cleavage	pacid=371616
1280	1302	UAGCUUAUC/	.....: :CAGUUCAUC/	Cleavage	pacid=371616
3452	3473	UAGCUUAUC/	.....: :AUAACUUC	Cleavage	pacid=371630
3452	3473	UAGCUUAUC/	.....: :AUAACUUC	Cleavage	pacid=371630
3451	3473	UAGCUUAUC/	.....: :GAUAACUUC/	Cleavage	pacid=371630
1823	1846	UAGCUUAUC/	.....: :AUAACAUCCA	Cleavage	pacid=371529
1823	1846	UAGCUUAUC/	.....: :AUAACAUCCA	Cleavage	pacid=371529
1823	1846	UAGCUUAUC/	.....: :AUAACAUCCA	Cleavage	pacid=371529



1			
2	2296	2317 UAGCUUAUC/ :: : :::::::::::GCAGAAACAC	Cleavage pacid=371754
3	2295	2317 UAGCUUAUC/ :: : :::::::::::UGCAGAAAC/	Cleavage pacid=371754
4	831	852 UAGCUUAUC/ :::::::::::UAGUGAUCA	(Translation pacid=371478
5	831	852 UAGCUUAUC/ :::::::::::UAGUGAUCA	(Translation pacid=371478
6	294	315 UAGCUUAUC/ :::::::::::UGGACAUUG/	Cleavage pacid=371458
7	294	315 UAGCUUAUC/ :::::::::::UGGACAUUG/	Cleavage pacid=371458
8	293	315 UAGCUUAUC/ :::::::::::GUGGACAUU/	Cleavage pacid=371458
9	125	146 UAGCUUAUC/ :::::::::::UGAGCACUG/	Cleavage pacid=371449
10	125	146 UAGCUUAUC/ :::::::::::UGAGCACUG/	Cleavage pacid=371449
11	124	146 UAGCUUAUC/ :::::::::::AUGAGCACU/	Cleavage pacid=371449
12	780	801 UAGCUUAUC/ :::::::::::UAGUGAUCA	(Translation pacid=371620
13	780	801 UAGCUUAUC/ :::::::::::UAGUGAUCA	(Translation pacid=371620
14	714	734 UAGCUUAUC/ :::::::::::ACAGCA-CAGI	Cleavage pacid=371638
15	714	734 UAGCUUAUC/ :::::::::::ACAGCA-CAGI	Cleavage pacid=371638
16	713	734 UAGCUUAUC/ :::::::::::CACAGCA-CA/	Cleavage pacid=371638
17	1341	1362 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
18	1258	1279 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
19	1418	1439 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
20	1414	1435 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
21	1341	1362 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
22	1258	1279 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
23	1418	1439 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
24	1414	1435 UAGCUUAUC/ :::::::::::UCGACACUG/	Cleavage pacid=371615
25	1340	1362 UAGCUUAUC/ :::::::::::AUCGACACU/	Cleavage pacid=371615
26	1257	1279 UAGCUUAUC/ :::::::::::AUCGACACU/	Cleavage pacid=371615
27	1417	1439 UAGCUUAUC/ :::::::::::AUCGACACU/	Cleavage pacid=371615
28	1413	1435 UAGCUUAUC/ :::::::::::AUCGACACU/	Cleavage pacid=371615
29	1969	1990 UAGCUUAUC/ :::::::::::GCACUAUCAC	Cleavage pacid=371732
30	1969	1990 UAGCUUAUC/ :::::::::::GCACUAUCAC	Cleavage pacid=371732
31	1968	1990 UAGCUUAUC/ :::::::::::UGCACUAUC/	Cleavage pacid=371732
32	441	462 UAGCUUAUC/ :::::::::::CCAAGAUCAU	Cleavage pacid=371725
33	671	692 UAGCUUAUC/ :::::::::::CCAAGAUCAU	Cleavage pacid=371725
34	441	462 UAGCUUAUC/ :::::::::::CCAAGAUCAU	Cleavage pacid=371725
35	671	692 UAGCUUAUC/ :::::::::::CCAAGAUCAU	Cleavage pacid=371725
36	440	462 UAGCUUAUC/ :::::::::::ACCAAGAUCA	Cleavage pacid=371725
37	670	692 UAGCUUAUC/ :::::::::::ACCAAGAUCA	Cleavage pacid=371725
38	454	475 UAGCUUAUC/ :::::::::::UCAGCAUCG/	(Translation pacid=371642
39	454	475 UAGCUUAUC/ :::::::::::UCAGCAUCG/	(Translation pacid=371642
40	453	475 UAGCUUAUC/ :::::::::::UUCAGCAUC/	(Translation pacid=371642
41	1920	1941 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663
42	1924	1945 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663
43	1993	2014 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663
44	2005	2026 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663
45	2005	2026 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663
46	2009	2030 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663
47	2009	2030 UAGCUUAUC/ :::::::::::UGAGCAUAG/	(Cleavage pacid=371663



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2	2097	2118 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
3	2101	2122 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
4	1920	1941 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
5	1924	1945 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
6	1993	2014 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
7	2005	2026 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
8				
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10	2005	2026 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
11	2009	2030 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
12	2009	2030 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
13				
14	2097	2118 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
15	2101	2122 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
16	1629	1650 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
17				
18	1827	1848 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
19	1831	1852 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
20	1828	1849 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
21				
22	1832	1853 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
23	1997	2018 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
24	1629	1650 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
25				
26	1827	1848 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
27	1831	1852 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
28	1828	1849 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
29				
30	1832	1853 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
31	1997	2018 UAGCUUAUC/	::: : ::UGAGCAUAG(Cleavage	pacid=371663
32	1728	1749 UAGCUUAUC/	::: : ::UCCAUAUGA(Cleavage	pacid=371580
33	1728	1749 UAGCUUAUC/	::: : ::UCCAUAUGA(Cleavage	pacid=371580
34				
35	1146	1167 UAGCUUAUC/	::: : ::UCGUCAUCG(Cleavage	pacid=371506
36	1146	1167 UAGCUUAUC/	::: : ::UCGUCAUCG(Cleavage	pacid=371506
37	1145	1167 UAGCUUAUC/	::: : ::UUCGUCAUC(Cleavage	pacid=371506
38				
39	750	771 UAGCUUAUC/	::: : ::AAGACGUCAC(Cleavage	pacid=371507
40	751	772 UAGCUUAUC/	::: : ::AAGACGUCAC(Cleavage	pacid=371507
41	750	771 UAGCUUAUC/	::: : ::AAGACGUCAC(Cleavage	pacid=371507
42	751	772 UAGCUUAUC/	::: : ::AAGACGUCAC(Cleavage	pacid=371507
43	786	807 UAGCUUAUC/	::: : ::UAGUGAUCA(Translation	pacid=371493
44	786	807 UAGCUUAUC/	::: : ::UAGUGAUCA(Translation	pacid=371493
45				
46	2152	2173 UAGCUUAUC/	::: : ::UCUGCAUCA(Cleavage	pacid=371502
47	2237	2258 UAGCUUAUC/	::: : ::UCUGCAUCA(Cleavage	pacid=371502
48	2326	2347 UAGCUUAUC/	::: : ::UCUGCAUCA(Cleavage	pacid=371502
49				
50	2152	2173 UAGCUUAUC/	::: : ::UCUGCAUCA(Cleavage	pacid=371502
51	2237	2258 UAGCUUAUC/	::: : ::UCUGCAUCA(Cleavage	pacid=371502
52	2326	2347 UAGCUUAUC/	::: : ::UCUGCAUCA(Cleavage	pacid=371502
53				
54	2151	2173 UAGCUUAUC/	::: : ::AUCUGCAUCA(Cleavage	pacid=371502
55	2236	2258 UAGCUUAUC/	::: : ::AUCUGCAUCA(Cleavage	pacid=371502
56	2325	2347 UAGCUUAUC/	::: : ::AUCUGCAUCA(Cleavage	pacid=371502
57				
58	908	929 UAGCUUAUC/	::: : ::GGAAAUAUA(Cleavage	pacid=371432
59	908	929 UAGCUUAUC/	::: : ::GGAAAUAUA(Cleavage	pacid=371432
60	1518	1539 UAGCUUAUC/	::: : ::CCAGCAUCUC(Cleavage	pacid=371552



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2	1518	1539 UAGCUUAUC/	::: ::: ::: ::: ::: ::: CCAGCAUCUC	Cleavage pacid=371552
3	1517	1539 UAGCUUAUC/	::: ::: ::: ::: ::: ::: ACCAGCAUCU	Cleavage pacid=371552
4	752	773 UAGCUUAUC/	::: : ::: ::: ::: ::: UCAGGAGCA	Translation pacid=371566
5	752	773 UAGCUUAUC/	::: : ::: ::: ::: ::: UCAGGAGCA	Translation pacid=371566
6	751	773 UAGCUUAUC/	::: : ::: ::: ::: ::: CUCAGGAGC	Translation pacid=371566
7	3	24 UAGCUUAUC/	::: ::: ::: ::: ::: CACACAUCAU	Cleavage pacid=371555
8	3	24 UAGCUUAUC/	::: ::: ::: ::: ::: CACACAUCAU	Cleavage pacid=371555
9	2	24 UAGCUUAUC/	::: ::: ::: ::: ::: ACACACAUCA	Cleavage pacid=371555
10	2751	2772 UAGCUUAUC/	::: ::: ::: ::: ::: UCUACAUGA	Translation pacid=371559
11	2751	2772 UAGCUUAUC/	::: ::: ::: ::: ::: UCUACAUGA	Translation pacid=371559
12	2750	2772 UAGCUUAUC/	::: ::: ::: ::: ::: GUCUACAUG	Translation pacid=371559
13	1565	1586 UAGCUUAUC/	::: ::: ::: ::: ::: GCAGUGGCA	Cleavage pacid=371701
14	1565	1586 UAGCUUAUC/	::: ::: ::: ::: ::: GCAGUGGCA	Cleavage pacid=371701
15	1564	1586 UAGCUUAUC/	::: ::: ::: ::: ::: AGCAGUGGC	Cleavage pacid=371701
16	1691	1712 UAGCUUAUC/	::: ::: ::: ::: ::: UUGGAAUUG	Cleavage pacid=371762
17	1829	1850 UAGCUUAUC/	::: ::: ::: ::: ::: UUGGAAUUG	Cleavage pacid=371762
18	1691	1712 UAGCUUAUC/	::: ::: ::: ::: ::: UUGGAAUUG	Cleavage pacid=371762
19	1829	1850 UAGCUUAUC/	::: ::: ::: ::: ::: UUGGAAUUG	Cleavage pacid=371762
20	1690	1712 UAGCUUAUC/	::: ::: ::: ::: ::: GUUGGAAUU	Cleavage pacid=371762
21	1828	1850 UAGCUUAUC/	::: ::: ::: ::: ::: GUUGGAAUU	Cleavage pacid=371762
22	133	154 UAGCUUAUC/	::: ::: ::: ::: ::: ACAACAUGA	Translation pacid=371760
23	133	154 UAGCUUAUC/	::: ::: ::: ::: ::: ACAACAUGA	Translation pacid=371760
24	132	154 UAGCUUAUC/	::: ::: ::: ::: ::: UACAACAUG	Translation pacid=371760
25	863	884 UAGCUUAUC/	::: ::: ::: ::: ::: UUGGCUUCA	Cleavage pacid=371776
26	863	884 UAGCUUAUC/	::: ::: ::: ::: ::: UUGGCUUCA	Cleavage pacid=371776
27	862	884 UAGCUUAUC/	::: ::: ::: ::: ::: UUUGGCUUC	Cleavage pacid=371776
28	685	707 UAGCUUAUC/	::: ::: ::: ::: ::: AUUUCAUCA	Translation pacid=371755
29	726	748 UAGCUUAUC/	::: ::: ::: ::: ::: AUUUCAUCA	Translation pacid=371755
30	685	707 UAGCUUAUC/	::: ::: ::: ::: ::: AUUUCAUCA	Translation pacid=371755
31	726	748 UAGCUUAUC/	::: ::: ::: ::: ::: AUUUCAUCA	Translation pacid=371755
32	1047	1068 UAGCUUAUC/	::: ::: ::: ::: ::: UUGACAUUG	Cleavage pacid=371444
33	1047	1068 UAGCUUAUC/	::: ::: ::: ::: ::: UUGACAUUG	Cleavage pacid=371444
34	1046	1068 UAGCUUAUC/	::: ::: ::: ::: ::: UUUGACAUU	Cleavage pacid=371444
35	768	790 UAGCUUAUC/	::: ::: ::: ::: ::: GUCUACUUC	Translation pacid=371478
36	630	651 UAGCUUAUC/	::: ::: ::: ::: ::: UCUGCAUCA	Cleavage pacid=371479
37	630	651 UAGCUUAUC/	::: ::: ::: ::: ::: UCUGCAUCA	Cleavage pacid=371479
38	845	866 UAGCUUAUC/	::: ::: ::: ::: ::: ACAACAUGA	Cleavage pacid=371457
39	845	866 UAGCUUAUC/	::: ::: ::: ::: ::: ACAACAUGA	Cleavage pacid=371457
40	844	866 UAGCUUAUC/	::: ::: ::: ::: ::: UACAACAUG	Cleavage pacid=371457
41	1335	1356 UAGCUUAUC/	::: ::: ::: ::: ::: UUAACAUCC	Cleavage pacid=371619
42	1438	1459 UAGCUUAUC/	::: ::: ::: ::: ::: UUAACAUCC	Cleavage pacid=371619
43	1523	1544 UAGCUUAUC/	::: ::: ::: ::: ::: UUAACAUCC	Cleavage pacid=371619
44	1335	1356 UAGCUUAUC/	::: ::: ::: ::: ::: UUAACAUCC	Cleavage pacid=371619
45	1438	1459 UAGCUUAUC/	::: ::: ::: ::: ::: UUAACAUCC	Cleavage pacid=371619
46	1523	1544 UAGCUUAUC/	::: ::: ::: ::: ::: UUAACAUCC	Cleavage pacid=371619
47	1334	1356 UAGCUUAUC/	::: ::: ::: ::: ::: GUUAACAUC	Cleavage pacid=371619

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2	1437	1459	UAGCUUAUC/:::..... ::: ::::GUUAACAUC	Cleavage pacid=371619
3	1522	1544	UAGCUUAUC/:::..... ::: ::::GUUAACAUC	Cleavage pacid=371619
4	1415	1436	UAGCUUAUC/.....:..... :.....UUGGUGUUG	Cleavage pacid=371625
5	1415	1436	UAGCUUAUC/.....:..... :.....UUGGUGUUG	Cleavage pacid=371625
6	1415	1436	UAGCUUAUC/.....:..... :.....UUGGUGUUG	Cleavage pacid=371625
7	1415	1436	UAGCUUAUC/.....:..... :.....UUGGUGUUG	Cleavage pacid=371625
8	1415	1436	UAGCUUAUC/.....:..... :.....UUGGUGUUG	Cleavage pacid=371625
9	1414	1436	UAGCUUAUC/.....:..... :.....GUUGGUGUU	Cleavage pacid=371625
10	1414	1436	UAGCUUAUC/.....:..... :.....GUUGGUGUU	Cleavage pacid=371625
11	1345	1366	UAGCUUAUC/ :::: : : :::: ::::GCAGCAACAC	Cleavage pacid=371625
12	1345	1366	UAGCUUAUC/ :::: : : :::: ::::GCAGCAACAC	Cleavage pacid=371625
13	1344	1366	UAGCUUAUC/ :::: : : :::: ::::AGCAGCAACA	Cleavage pacid=371625
14	636	657	UAGCUUAUC/:::.....:..... : :UCCACAUCAG	Cleavage pacid=371531
15	636	657	UAGCUUAUC/:::.....:..... : :UCCACAUCAG	Cleavage pacid=371531
16	167	188	UAGCUUAUC/::: : : : : :::: :UCAAGAUUC	Cleavage pacid=371718
17	167	188	UAGCUUAUC/::: : : : : :::: :UCAAGAUUC	Cleavage pacid=371718
18	166	188	UAGCUUAUC/ :::: : : : : :::: :UCAAGAUUC	Cleavage pacid=371718
19	606	627	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
20	709	730	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
21	721	742	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
22	736	757	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
23	741	762	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
24	849	870	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
25	895	916	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
26	606	627	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
27	709	730	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
28	721	742	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
29	736	757	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
30	741	762	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
31	849	870	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
32	895	916	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
33	471	492	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
34	652	673	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
35	744	765	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
36	1237	1258	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
37	471	492	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
38	652	673	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
39	744	765	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
40	1237	1258	UAGCUUAUC/ :::: : : : : :::: :GAAACGUCG	Cleavage pacid=371640
41	327	348	UAGCUUAUC/ :.....:..... : :GCGGCAUCAC	Cleavage pacid=371657
42	327	348	UAGCUUAUC/ :.....:..... : :GCGGCAUCAC	Cleavage pacid=371657
43	326	348	UAGCUUAUC/ :.....:..... : :CGCGCAUCA	Cleavage pacid=371657
44	1317	1338	UAGCUUAUC/.....:..... : : : : : : : :UUGAUUUU	Cleavage pacid=371655
45	1317	1338	UAGCUUAUC/.....:..... : : : : : : : :UUGAUUUU	Cleavage pacid=371655
46	1316	1338	UAGCUUAUC/ :.....:..... : : : : : : : :AUUGAUUU	Cleavage pacid=371655
47	463	484	UAGCUUAUC/ :. : : : : : : : : :AUAGAAGCAC	Cleavage pacid=371610
48	1712	1733	UAGCUUAUC/ :. : : : : : : : : :AUAGAAGCAC	Cleavage pacid=371610

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2	3970	3991 UAGCUUAUC/ .. : .. : AUAGAAGCAC	Cleavage	pacid=371610
3	4017	4038 UAGCUUAUC/ .. : .. : AUAGAAGCAC	Cleavage	pacid=371610
4	463	484 UAGCUUAUC/ .. : .. : AUAGAAGCAC	Cleavage	pacid=371610
5	1712	1733 UAGCUUAUC/ .. : .. : AUAGAAGCAC	Cleavage	pacid=371610
6	3970	3991 UAGCUUAUC/ .. : .. : AUAGAAGCAC	Cleavage	pacid=371610
7	4017	4038 UAGCUUAUC/ .. : .. : AUAGAAGCAC	Cleavage	pacid=371610
8				
9	1321	1342 UAGCUUAUC/ .. : .. : AAAUAUCAC	Cleavage	pacid=371593
10	1321	1342 UAGCUUAUC/ .. : .. : AAAUAUCAC	Cleavage	pacid=371593
11	1781	1802 UAGCUUAUC/ .. : .. : CUAGCAUCAC	Cleavage	pacid=371590
12	1781	1802 UAGCUUAUC/ .. : .. : CUAGCAUCAC	Cleavage	pacid=371590
13	1780	1802 UAGCUUAUC/ .. : .. : UCUAGCAUCAC	Cleavage	pacid=371590
14	1544	1565 UAGCUUAUC/ .. : .. : UUGGUAUCU	Translation	pacid=371606
15	1544	1565 UAGCUUAUC/ .. : .. : UUGGUAUCU	Translation	pacid=371606
16	1543	1565 UAGCUUAUC/ .. : .. : AUUGGUAUCU	Translation	pacid=371606
17	955	979 UAGCUUAUC/ .. : .. : GUUCACAUU	Cleavage	pacid=371603
18	500	522 UAGCUUAUC/ .. : .. : GUCCUAAUCAC	Cleavage	pacid=371593
19	382	403 UAGCUUAUC/ .. : .. : GAAACAUCAL	Cleavage	pacid=371512
20	382	403 UAGCUUAUC/ .. : .. : GAAACAUCAL	Cleavage	pacid=371512
21	381	403 UAGCUUAUC/ .. : .. : AGAAACAUCAC	Cleavage	pacid=371512
22	5344	5365 UAGCUUAUC/ .. : .. : UGUUCAUCG	Cleavage	pacid=371485
23	5344	5365 UAGCUUAUC/ .. : .. : UGUUCAUCG	Cleavage	pacid=371485
24	5343	5365 UAGCUUAUC/ .. : .. : CUGUUCAUC	Cleavage	pacid=371485
25	926	947 UAGCUUAUC/ .. : .. : AUGACAUCAC	Cleavage	pacid=371519
26	926	947 UAGCUUAUC/ .. : .. : AUGACAUCAC	Cleavage	pacid=371519
27	925	947 UAGCUUAUC/ .. : .. : GAUGACAUCAC	Cleavage	pacid=371519
28	1319	1340 UAGCUUAUC/ .. : .. : ACAAUAAUAC	Cleavage	pacid=371431
29	1319	1340 UAGCUUAUC/ .. : .. : ACAAUAAUAC	Cleavage	pacid=371431
30	1318	1340 UAGCUUAUC/ .. : .. : AACAAUAAUAC	Cleavage	pacid=371431
31	142	163 UAGCUUAUC/ .. : .. : UCGACAUCUC	Cleavage	pacid=371436
32	142	163 UAGCUUAUC/ .. : .. : UCGACAUCUC	Cleavage	pacid=371436
33	141	163 UAGCUUAUC/ .. : .. : GUCGACAUCU	Cleavage	pacid=371436
34	532	553 UAGCUUAUC/ .. : .. : ACAACAACAG	Translation	pacid=371440
35	532	553 UAGCUUAUC/ .. : .. : ACAACAACAG	Translation	pacid=371440
36	531	553 UAGCUUAUC/ .. : .. : GACAACAACA	Translation	pacid=371440
37	1994	2014 UAGCUUAUC/ .. : .. : UCAG-AUCAG	Cleavage	pacid=371441
38	2056	2076 UAGCUUAUC/ .. : .. : UCAG-AUCAG	Cleavage	pacid=371441
39	2070	2090 UAGCUUAUC/ .. : .. : UCAG-AUCAG	Cleavage	pacid=371441
40	1994	2014 UAGCUUAUC/ .. : .. : UCAG-AUCAG	Cleavage	pacid=371441
41	2056	2076 UAGCUUAUC/ .. : .. : UCAG-AUCAG	Cleavage	pacid=371441
42	2070	2090 UAGCUUAUC/ .. : .. : UCAG-AUCAG	Cleavage	pacid=371441
43	1993	2014 UAGCUUAUC/ .. : .. : AUCAG-AUCA	Cleavage	pacid=371441
44	2055	2076 UAGCUUAUC/ .. : .. : AUCAG-AUCA	Cleavage	pacid=371441
45	2069	2090 UAGCUUAUC/ .. : .. : AUCAG-AUCA	Cleavage	pacid=371441
46	1207	1229 UAGCUUAUC/ .. : .. : CUAAUAUCAC	Cleavage	pacid=371561
47	1207	1229 UAGCUUAUC/ .. : .. : CUAAUAUCAC	Cleavage	pacid=371561
48	1206	1229 UAGCUUAUC/ .. : .. : ACUAAUAUCAC	Cleavage	pacid=371561

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470	491 UAGCUUAUC/::: :: ..: :::::::::::UCACCAAUGC Cleavage	pacid=371556
470	491 UAGCUUAUC/::: :: ..: :::::::::::UCACCAAUGC Cleavage	pacid=371556
469	491 UAGCUUAUC/ ::: :: ..: :::::::::::UUCACCAAUC Cleavage	pacid=371556
413	434 UAGCUUAUC/::: : ..: :::::::::::UCAUCUGUG(Cleavage	pacid=371568
413	434 UAGCUUAUC/::: : ..: :::::::::::UCAUCUGUG(Cleavage	pacid=371568

Do not distribute

Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.004G023066.1	Phvul.004G023066	Phvul.004G023066	PF00005,PF00
1	Phvul.004G023066.1	Phvul.004G023066	Phvul.004G023066	PF00005,PF00
1	Phvul.004G023066.1	Phvul.004G023066	Phvul.004G023066	PF00005,PF00
1	Phvul.002G097400.1	Phvul.002G097400	Phvul.002G097400	PF01193,PF01
1	Phvul.002G097400.1	Phvul.002G097400	Phvul.002G097400	PF01193,PF01
1	Phvul.002G097400.1	Phvul.002G097400	Phvul.002G097400	PF01193,PF01
1	Phvul.006G008480.2	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.1	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.2	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.1	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.2	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.1	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G029000.1	Phvul.006G029000	Phvul.006G029000	PF08263,PF00
1	Phvul.006G029000.1	Phvul.006G029000	Phvul.006G029000	PF08263,PF00
1	Phvul.006G029000.1	Phvul.006G029000	Phvul.006G029000	PF08263,PF00
1	Phvul.006G110300.1	Phvul.006G110300	Phvul.006G110300	PF00153
1	Phvul.006G110300.1	Phvul.006G110300	Phvul.006G110300	PF00153
1	Phvul.006G110300.1	Phvul.006G110300	Phvul.006G110300	PF00153
1	Phvul.007G191600.1	Phvul.007G191600	Phvul.007G191600	PF00271,PF00
1	Phvul.007G191600.1	Phvul.007G191600	Phvul.007G191600	PF00271,PF00
1	Phvul.007G191600.1	Phvul.007G191600	Phvul.007G191600	PF00271,PF00
1	Phvul.001G070000.1	Phvul.001G070000	Phvul.001G070000	PF07714
1	Phvul.001G070000.1	Phvul.001G070000	Phvul.001G070000	PF07714
1	Phvul.001G070000.1	Phvul.001G070000	Phvul.001G070000	PF07714
1	Phvul.001G264600.2	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.1	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.2	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.1	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.2	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.1	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.003G092500.1	Phvul.003G092500	Phvul.003G092500	PF00403
1	Phvul.003G092500.1	Phvul.003G092500	Phvul.003G092500	PF00403
1	Phvul.004G000300.1	Phvul.004G000300	Phvul.004G000300	PF13180,PF13
1	Phvul.004G000300.1	Phvul.004G000300	Phvul.004G000300	PF13180,PF13
1	Phvul.004G000300.1	Phvul.004G000300	Phvul.004G000300	PF13180,PF13
1	Phvul.004G126100.1	Phvul.004G126100	Phvul.004G126100	PF08263,PF00
1	Phvul.004G126100.1	Phvul.004G126100	Phvul.004G126100	PF08263,PF00
1	Phvul.004G126100.1	Phvul.004G126100	Phvul.004G126100	PF08263,PF00
1	Phvul.005G063700.2	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.1	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.2	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.1	Phvul.005G063700	Phvul.005G063700	PF07714

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2	1 Phvul.005G063700.2	Phvul.005G063700	Phvul.005G063700	PF07714
3	1 Phvul.005G063700.1	Phvul.005G063700	Phvul.005G063700	PF07714
4	1 Phvul.007G020600.1	Phvul.007G020600	Phvul.007G020600	PF00201
5				
6	1 Phvul.007G020600.1	Phvul.007G020600	Phvul.007G020600	PF00201
7	1 Phvul.007G020700.1	Phvul.007G020700	Phvul.007G020700	PF00201
8	1 Phvul.007G020700.1	Phvul.007G020700	Phvul.007G020700	PF00201
9				
10	1 Phvul.007G080800.1	Phvul.007G080800	Phvul.007G080800	PF03033
11	1 Phvul.007G080800.1	Phvul.007G080800	Phvul.007G080800	PF03033
12	1 Phvul.007G080800.1	Phvul.007G080800	Phvul.007G080800	PF03033
13				
14	1 Phvul.007G254000.2	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
15	1 Phvul.007G254000.1	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
16	1 Phvul.007G254000.2	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
17				
18	1 Phvul.007G254000.1	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
19	1 Phvul.007G254000.2	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
20	1 Phvul.007G254000.1	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
21				
22	1 Phvul.008G212500.1	Phvul.008G212500	Phvul.008G212500	PF01476,PF00
23	1 Phvul.008G212500.1	Phvul.008G212500	Phvul.008G212500	PF01476,PF00
24	1 Phvul.008G212500.1	Phvul.008G212500	Phvul.008G212500	PF01476,PF00
25				
26	1 Phvul.008G266300.1	Phvul.008G266300	Phvul.008G266300	PF16656,PF14
27	1 Phvul.008G266300.1	Phvul.008G266300	Phvul.008G266300	PF16656,PF14
28	1 Phvul.008G266300.1	Phvul.008G266300	Phvul.008G266300	PF16656,PF14
29				
30	1 Phvul.011G002600.1	Phvul.011G002600	Phvul.011G002600	0
31	1 Phvul.011G002600.1	Phvul.011G002600	Phvul.011G002600	0
32	1 Phvul.011G002600.1	Phvul.011G002600	Phvul.011G002600	0
33				
34	1 Phvul.011G194501.1	Phvul.011G194501	Phvul.011G194501	PF01657
35	1 Phvul.011G194501.1	Phvul.011G194501	Phvul.011G194501	PF01657
36	1 Phvul.011G194501.1	Phvul.011G194501	Phvul.011G194501	PF01657
37				
38	1 Phvul.L000308.2	Phvul.L000308	Phvul.L000308	PF00847
39	1 Phvul.L000308.1	Phvul.L000308	Phvul.L000308	PF00847
40	1 Phvul.L000308.2	Phvul.L000308	Phvul.L000308	PF00847
41	1 Phvul.L000308.1	Phvul.L000308	Phvul.L000308	PF00847
42				
43	1 Phvul.L000308.2	Phvul.L000308	Phvul.L000308	PF00847
44	1 Phvul.L000308.1	Phvul.L000308	Phvul.L000308	PF00847
45				
46	1 Phvul.001G021750.1	Phvul.001G021750	Phvul.001G021750	PF00036
47	1 Phvul.001G021750.1	Phvul.001G021750	Phvul.001G021750	PF00036
48	1 Phvul.001G021750.1	Phvul.001G021750	Phvul.001G021750	PF00036
49	1 Phvul.001G168600.1	Phvul.001G168600	Phvul.001G168600	PF12776
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51	1 Phvul.001G168600.1	Phvul.001G168600	Phvul.001G168600	PF12776
52	1 Phvul.002G010100.1	Phvul.002G010100	Phvul.002G010100	PF10225
53	1 Phvul.002G010100.1	Phvul.002G010100	Phvul.002G010100	PF10225
54				
55	1 Phvul.002G010100.1	Phvul.002G010100	Phvul.002G010100	PF10225
56	1 Phvul.002G149100.1	Phvul.002G149100	Phvul.002G149100	PF12776
57	1 Phvul.002G149100.1	Phvul.002G149100	Phvul.002G149100	PF12776
58				
59	1 Phvul.002G155200.1	Phvul.002G155200	Phvul.002G155200	PF02214
60	1 Phvul.002G155200.1	Phvul.002G155200	Phvul.002G155200	PF02214
	1 Phvul.002G211400.1	Phvul.002G211400	Phvul.002G211400	PF03000



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2	1 Phvul.002G211400.1	Phvul.002G211400	Phvul.002G211400	PF03000
3	1 Phvul.002G211400.1	Phvul.002G211400	Phvul.002G211400	PF03000
4	1 Phvul.003G069400.1	Phvul.003G069400	Phvul.003G069400	PF12776
5	1 Phvul.003G069400.1	Phvul.003G069400	Phvul.003G069400	PF12776
6	1 Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
7	1 Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
8	1 Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
9	1 Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
10	1 Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
11	1 Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
12	1 Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
13	1 Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
14	1 Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
15	1 Phvul.004G053900.1	Phvul.004G053900	Phvul.004G053900	PF12776
16	1 Phvul.004G053900.1	Phvul.004G053900	Phvul.004G053900	PF12776
17	1 Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
18	1 Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
19	1 Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
20	1 Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
21	1 Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
22	1 Phvul.004G177000.3	Phvul.004G177000	Phvul.004G177000	0
23	1 Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
24	1 Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
25	1 Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
26	1 Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
27	1 Phvul.004G177000.3	Phvul.004G177000	Phvul.004G177000	0
28	1 Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
29	1 Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
30	1 Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
31	1 Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
32	1 Phvul.004G177000.3	Phvul.004G177000	Phvul.004G177000	0
33	1 Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
34	1 Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
35	1 Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
36	1 Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
37	1 Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
38	1 Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
39	1 Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
40	1 Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
41	1 Phvul.006G158500.2	Phvul.006G158500	Phvul.006G158500	PF13920
42	1 Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
43	1 Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
44	1 Phvul.006G158500.2	Phvul.006G158500	Phvul.006G158500	PF13920
45	1 Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
46	1 Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
47	1 Phvul.006G158500.2	Phvul.006G158500	Phvul.006G158500	PF13920
48	1 Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
49	1 Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
50	1 Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
51	1 Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
52	1 Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
53	1 Phvul.007G154900.2	Phvul.007G154900	Phvul.007G154900	PF13921
54	1 Phvul.007G154900.3	Phvul.007G154900	Phvul.007G154900	PF13921
55	1 Phvul.007G154900.3	Phvul.007G154900	Phvul.007G154900	PF13921
56	1 Phvul.007G154900.9	Phvul.007G154900	Phvul.007G154900	PF13921
57	1 Phvul.007G154900.7	Phvul.007G154900	Phvul.007G154900	PF13921
58	1 Phvul.007G154900.6	Phvul.007G154900	Phvul.007G154900	PF13921
59	1 Phvul.007G154900.6	Phvul.007G154900	Phvul.007G154900	PF13921
60	1 Phvul.007G154900.5	Phvul.007G154900	Phvul.007G154900	PF13921
	1 Phvul.007G154900.8	Phvul.007G154900	Phvul.007G154900	PF13921



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2	1	Phvul.007G154900.4	Phvul.007G154900	Phvul.007G154900 PF13921
3	1	Phvul.007G154900.1	Phvul.007G154900	Phvul.007G154900 PF13921
4	1	Phvul.007G154900.2	Phvul.007G154900	Phvul.007G154900 PF13921
5	1	Phvul.007G154900.3	Phvul.007G154900	Phvul.007G154900 PF13921
6	1	Phvul.007G154900.9	Phvul.007G154900	Phvul.007G154900 PF13921
7	1	Phvul.007G154900.7	Phvul.007G154900	Phvul.007G154900 PF13921
8	1	Phvul.007G154900.6	Phvul.007G154900	Phvul.007G154900 PF13921
9	1	Phvul.007G154900.5	Phvul.007G154900	Phvul.007G154900 PF13921
10	1	Phvul.007G154900.8	Phvul.007G154900	Phvul.007G154900 PF13921
11	1	Phvul.007G154900.4	Phvul.007G154900	Phvul.007G154900 PF13921
12	1	Phvul.007G154900.1	Phvul.007G154900	Phvul.007G154900 PF13921
13	1	Phvul.007G154900.15	Phvul.007G154900.	Phvul.007G154900 PF13921
14	1	Phvul.007G154900.13	Phvul.007G154900.	Phvul.007G154900 PF13921
15	1	Phvul.007G154900.14	Phvul.007G154900.	Phvul.007G154900 PF13921
16	1	Phvul.007G154900.11	Phvul.007G154900.	Phvul.007G154900 PF13921
17	1	Phvul.007G154900.12	Phvul.007G154900.	Phvul.007G154900 PF13921
18	1	Phvul.007G154900.10	Phvul.007G154900.	Phvul.007G154900 PF13921
19	1	Phvul.007G154900.15	Phvul.007G154900.	Phvul.007G154900 PF13921
20	1	Phvul.007G154900.13	Phvul.007G154900.	Phvul.007G154900 PF13921
21	1	Phvul.007G154900.14	Phvul.007G154900.	Phvul.007G154900 PF13921
22	1	Phvul.007G154900.11	Phvul.007G154900.	Phvul.007G154900 PF13921
23	1	Phvul.007G154900.12	Phvul.007G154900.	Phvul.007G154900 PF13921
24	1	Phvul.007G154900.10	Phvul.007G154900.	Phvul.007G154900 PF13921
25	1	Phvul.007G154900.15	Phvul.007G154900.	Phvul.007G154900 PF13921
26	1	Phvul.007G154900.13	Phvul.007G154900.	Phvul.007G154900 PF13921
27	1	Phvul.007G154900.14	Phvul.007G154900.	Phvul.007G154900 PF13921
28	1	Phvul.007G154900.11	Phvul.007G154900.	Phvul.007G154900 PF13921
29	1	Phvul.007G154900.12	Phvul.007G154900.	Phvul.007G154900 PF13921
30	1	Phvul.007G154900.10	Phvul.007G154900.	Phvul.007G154900 PF13921
31	1	Phvul.008G106500.1	Phvul.008G106500	Phvul.008G106500 PF08263,PF13
32	1	Phvul.008G106500.1	Phvul.008G106500	Phvul.008G106500 PF08263,PF13
33	1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300 PF01490
34	1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300 PF01490
35	1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300 PF01490
36	1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300 PF01490
37	1	Phvul.009G097000.1	Phvul.009G097000	Phvul.009G097000 PF09762
38	1	Phvul.009G097000.2	Phvul.009G097000	Phvul.009G097000 PF09762
39	1	Phvul.009G097000.1	Phvul.009G097000	Phvul.009G097000 PF09762
40	1	Phvul.009G097000.2	Phvul.009G097000	Phvul.009G097000 PF09762
41	1	Phvul.009G122000.1	Phvul.009G122000	Phvul.009G122000 PF12776
42	1	Phvul.009G122000.1	Phvul.009G122000	Phvul.009G122000 PF12776
43	1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
44	1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
45	1	Phvul.009G227900.1	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
46	1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
47	1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
48	1	Phvul.009G227900.1	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
49	1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
50	1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
51	1	Phvul.009G227900.1	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
52	1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
53	1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900 PF03456,PF02
54	1	Phvul.010G159600.1	Phvul.010G159600	Phvul.010G159600 PF03556
55	1	Phvul.010G159600.1	Phvul.010G159600	Phvul.010G159600 PF03556
56	1	Phvul.011G084000.1	Phvul.011G084000	Phvul.011G084000 PF12848,PF00
57				
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59				
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2	1 Phvul.011G084000.1	Phvul.011G084000	Phvul.011G084000	PF12848,PF00
3	1 Phvul.011G084000.1	Phvul.011G084000	Phvul.011G084000	PF12848,PF00
4	1 Phvul.011G130500.1	Phvul.011G130500	Phvul.011G130500	0
5				
6	1 Phvul.011G130500.1	Phvul.011G130500	Phvul.011G130500	0
7	1 Phvul.011G130500.1	Phvul.011G130500	Phvul.011G130500	0
8	1 Phvul.011G158500.1	Phvul.011G158500	Phvul.011G158500	PF00201
9				
10	1 Phvul.011G158500.1	Phvul.011G158500	Phvul.011G158500	PF00201
11	1 Phvul.011G158500.1	Phvul.011G158500	Phvul.011G158500	PF00201
12	1 Phvul.011G198100.1	Phvul.011G198100	Phvul.011G198100	PF00931
13				
14	1 Phvul.011G198100.1	Phvul.011G198100	Phvul.011G198100	PF00931
15	1 Phvul.011G198100.1	Phvul.011G198100	Phvul.011G198100	PF00931
16	1 Phvul.001G199500.1	Phvul.001G199500	Phvul.001G199500	PF01805,PF04
17				
18	1 Phvul.001G199500.1	Phvul.001G199500	Phvul.001G199500	PF01805,PF04
19	1 Phvul.001G199500.1	Phvul.001G199500	Phvul.001G199500	PF01805,PF04
20	1 Phvul.002G005300.2	Phvul.002G005300	Phvul.002G005300	PF03372
21				
22	1 Phvul.002G005300.1	Phvul.002G005300	Phvul.002G005300	PF03372
23	1 Phvul.002G005300.2	Phvul.002G005300	Phvul.002G005300	PF03372
24	1 Phvul.002G005300.1	Phvul.002G005300	Phvul.002G005300	PF03372
25				
26	1 Phvul.002G005300.2	Phvul.002G005300	Phvul.002G005300	PF03372
27	1 Phvul.002G005300.1	Phvul.002G005300	Phvul.002G005300	PF03372
28	1 Phvul.002G119100.1	Phvul.002G119100	Phvul.002G119100	0
29				
30	1 Phvul.002G119100.1	Phvul.002G119100	Phvul.002G119100	0
31	1 Phvul.002G119100.1	Phvul.002G119100	Phvul.002G119100	0
32	1 Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
33	1 Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
34	1 Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
35	1 Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
36	1 Phvul.002G141000.2	Phvul.002G141000	Phvul.002G141000	0
37	1 Phvul.002G141000.1	Phvul.002G141000	Phvul.002G141000	0
38				
39	1 Phvul.002G141000.2	Phvul.002G141000	Phvul.002G141000	0
40	1 Phvul.002G141000.1	Phvul.002G141000	Phvul.002G141000	0
41				
42	1 Phvul.003G131900.1	Phvul.003G131900	Phvul.003G131900	PF08612
43	1 Phvul.003G131900.1	Phvul.003G131900	Phvul.003G131900	PF08612
44	1 Phvul.003G131900.1	Phvul.003G131900	Phvul.003G131900	PF08612
45	1 Phvul.003G225700.1	Phvul.003G225700	Phvul.003G225700	PF00324
46				
47	1 Phvul.003G238000.1	Phvul.003G238000	Phvul.003G238000	PF13371,PF13
48	1 Phvul.003G238000.1	Phvul.003G238000	Phvul.003G238000	PF13371,PF13
49	1 Phvul.003G259300.1	Phvul.003G259300	Phvul.003G259300	PF07798
50				
51	1 Phvul.003G259300.1	Phvul.003G259300	Phvul.003G259300	PF07798
52	1 Phvul.003G259300.1	Phvul.003G259300	Phvul.003G259300	PF07798
53	1 Phvul.004G037700.1	Phvul.004G037700	Phvul.004G037700	PF03634
54				
55	1 Phvul.004G037700.3	Phvul.004G037700	Phvul.004G037700	PF03634
56	1 Phvul.004G037700.2	Phvul.004G037700	Phvul.004G037700	PF03634
57	1 Phvul.004G037700.1	Phvul.004G037700	Phvul.004G037700	PF03634
58				
59	1 Phvul.004G037700.3	Phvul.004G037700	Phvul.004G037700	PF03634
60	1 Phvul.004G037700.2	Phvul.004G037700	Phvul.004G037700	PF03634
	1 Phvul.004G037700.1	Phvul.004G037700	Phvul.004G037700	PF03634

1				
2	1 Phvul.004G037700.3	Phvul.004G037700	Phvul.004G037700	PF03634
3	1 Phvul.004G037700.2	Phvul.004G037700	Phvul.004G037700	PF03634
4	1 Phvul.004G089300.2	Phvul.004G089300	Phvul.004G089300	PF03372
5				
6	1 Phvul.004G089300.4	Phvul.004G089300	Phvul.004G089300	PF03372
7	1 Phvul.004G089300.2	Phvul.004G089300	Phvul.004G089300	PF03372
8	1 Phvul.004G089300.4	Phvul.004G089300	Phvul.004G089300	PF03372
9				
10	1 Phvul.004G089300.2	Phvul.004G089300	Phvul.004G089300	PF03372
11	1 Phvul.004G089300.4	Phvul.004G089300	Phvul.004G089300	PF03372
12	1 Phvul.004G174700.1	Phvul.004G174700	Phvul.004G174700	PF03485,PF05
13				
14	1 Phvul.004G174700.1	Phvul.004G174700	Phvul.004G174700	PF03485,PF05
15	1 Phvul.004G174700.1	Phvul.004G174700	Phvul.004G174700	PF03485,PF05
16	1 Phvul.005G125500.1	Phvul.005G125500	Phvul.005G125500	PF03015,PF07
17				
18	1 Phvul.005G125500.1	Phvul.005G125500	Phvul.005G125500	PF03015,PF07
19	1 Phvul.006G044400.1	Phvul.006G044400	Phvul.006G044400	PF05739,PF09
20	1 Phvul.006G044400.1	Phvul.006G044400	Phvul.006G044400	PF05739,PF09
21				
22	1 Phvul.006G044400.1	Phvul.006G044400	Phvul.006G044400	PF05739,PF09
23	1 Phvul.007G072700.3	Phvul.007G072700	Phvul.007G072700	PF02902
24	1 Phvul.007G072700.9	Phvul.007G072700	Phvul.007G072700	PF02902
25				
26	1 Phvul.007G072700.8	Phvul.007G072700	Phvul.007G072700	PF02902
27	1 Phvul.007G072700.6	Phvul.007G072700	Phvul.007G072700	PF02902
28	1 Phvul.007G072700.7	Phvul.007G072700	Phvul.007G072700	PF02902
29				
30	1 Phvul.007G072700.2	Phvul.007G072700	Phvul.007G072700	PF02902
31	1 Phvul.007G072700.5	Phvul.007G072700	Phvul.007G072700	PF02902
32	1 Phvul.007G072700.3	Phvul.007G072700	Phvul.007G072700	PF02902
33	1 Phvul.007G072700.9	Phvul.007G072700	Phvul.007G072700	PF02902
34				
35	1 Phvul.007G072700.8	Phvul.007G072700	Phvul.007G072700	PF02902
36	1 Phvul.007G072700.6	Phvul.007G072700	Phvul.007G072700	PF02902
37	1 Phvul.007G072700.7	Phvul.007G072700	Phvul.007G072700	PF02902
38				
39	1 Phvul.007G072700.2	Phvul.007G072700	Phvul.007G072700	PF02902
40	1 Phvul.007G072700.5	Phvul.007G072700	Phvul.007G072700	PF02902
41	1 Phvul.007G072700.12	Phvul.007G072700.	Phvul.007G072700	PF02902
42	1 Phvul.007G072700.13	Phvul.007G072700.	Phvul.007G072700	PF02902
43	1 Phvul.007G072700.10	Phvul.007G072700.	Phvul.007G072700	PF02902
44	1 Phvul.007G072700.11	Phvul.007G072700.	Phvul.007G072700	PF02902
45	1 Phvul.007G072700.12	Phvul.007G072700.	Phvul.007G072700	PF02902
46	1 Phvul.007G072700.13	Phvul.007G072700.	Phvul.007G072700	PF02902
47				
48	1 Phvul.007G072700.10	Phvul.007G072700.	Phvul.007G072700	PF02902
49	1 Phvul.007G072700.11	Phvul.007G072700.	Phvul.007G072700	PF02902
50	1 Phvul.007G215400.1	Phvul.007G215400	Phvul.007G215400	PF13664
51	1 Phvul.007G215400.1	Phvul.007G215400	Phvul.007G215400	PF13664
52	1 Phvul.007G215400.1	Phvul.007G215400	Phvul.007G215400	PF13664
53	1 Phvul.007G249800.1	Phvul.007G249800	Phvul.007G249800	PF00149
54	1 Phvul.007G249800.1	Phvul.007G249800	Phvul.007G249800	PF00149
55	1 Phvul.007G249800.1	Phvul.007G249800	Phvul.007G249800	PF00149
56	1 Phvul.008G074600.3	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
57	1 Phvul.008G074600.2	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
58				
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2	1 Phvul.008G074600.4	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
3	1 Phvul.008G074600.1	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
4	1 Phvul.008G074600.3	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
5	1 Phvul.008G074600.2	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
6	1 Phvul.008G074600.4	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
7	1 Phvul.008G074600.1	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
8	1 Phvul.008G074600.1	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
9	1 Phvul.008G123400.1	Phvul.008G123400	Phvul.008G123400	PF00646
10	1 Phvul.008G123400.1	Phvul.008G123400	Phvul.008G123400	PF00646
11	1 Phvul.008G129500.1	Phvul.008G129500	Phvul.008G129500	PF04851,PF02
12	1 Phvul.008G129500.1	Phvul.008G129500	Phvul.008G129500	PF04851,PF02
13	1 Phvul.008G129500.1	Phvul.008G129500	Phvul.008G129500	PF04851,PF02
14	1 Phvul.008G164600.1	Phvul.008G164600	Phvul.008G164600	PF13855,PF12
15	1 Phvul.008G164600.1	Phvul.008G164600	Phvul.008G164600	PF13855,PF12
16	1 Phvul.008G164600.1	Phvul.008G164600	Phvul.008G164600	PF13855,PF12
17	1 Phvul.008G225300.1	Phvul.008G225300	Phvul.008G225300	PF01490
18	1 Phvul.008G230200.1	Phvul.008G230200	Phvul.008G230200	PF04893
19	1 Phvul.009G030500.1	Phvul.009G030500	Phvul.009G030500	PF07690
20	1 Phvul.009G030500.1	Phvul.009G030500	Phvul.009G030500	PF07690
21	1 Phvul.009G030500.1	Phvul.009G030500	Phvul.009G030500	PF07690
22	1 Phvul.009G099700.1	Phvul.009G099700	Phvul.009G099700	0
23	1 Phvul.009G099700.1	Phvul.009G099700	Phvul.009G099700	0
24	1 Phvul.009G099700.1	Phvul.009G099700	Phvul.009G099700	0
25	1 Phvul.009G233000.1	Phvul.009G233000	Phvul.009G233000	PF04178
26	1 Phvul.009G233000.1	Phvul.009G233000	Phvul.009G233000	PF04178
27	1 Phvul.009G233000.1	Phvul.009G233000	Phvul.009G233000	PF04178
28	1 Phvul.010G021700.1	Phvul.010G021700	Phvul.010G021700	0
29	1 Phvul.010G021700.1	Phvul.010G021700	Phvul.010G021700	0
30	1 Phvul.010G021700.1	Phvul.010G021700	Phvul.010G021700	0
31	1 Phvul.010G104900.2	Phvul.010G104900	Phvul.010G104900	PF02548
32	1 Phvul.010G104900.2	Phvul.010G104900	Phvul.010G104900	PF02548
33	1 Phvul.010G104900.2	Phvul.010G104900	Phvul.010G104900	PF02548
34	1 Phvul.010G129400.1	Phvul.010G129400	Phvul.010G129400	PF03514
35	1 Phvul.010G129400.1	Phvul.010G129400	Phvul.010G129400	PF03514
36	1 Phvul.010G129400.1	Phvul.010G129400	Phvul.010G129400	PF03514
37	1 Phvul.010G157900.4	Phvul.010G157900	Phvul.010G157900	PF16987
38	1 Phvul.010G157900.3	Phvul.010G157900	Phvul.010G157900	PF16987
39	1 Phvul.010G157900.2	Phvul.010G157900	Phvul.010G157900	PF16987
40	1 Phvul.010G157900.4	Phvul.010G157900	Phvul.010G157900	PF16987
41	1 Phvul.010G157900.3	Phvul.010G157900	Phvul.010G157900	PF16987
42	1 Phvul.010G157900.2	Phvul.010G157900	Phvul.010G157900	PF16987
43	1 Phvul.010G157900.4	Phvul.010G157900	Phvul.010G157900	PF16987
44	1 Phvul.010G157900.3	Phvul.010G157900	Phvul.010G157900	PF16987
45	1 Phvul.010G157900.2	Phvul.010G157900	Phvul.010G157900	PF16987
46	1 Phvul.011G006200.1	Phvul.011G006200	Phvul.011G006200	PF01399
47	1 Phvul.011G006200.1	Phvul.011G006200	Phvul.011G006200	PF01399
48	1 Phvul.011G006200.1	Phvul.011G006200	Phvul.011G006200	PF01399

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1 Phvul.011G161100.1	Phvul.011G161100	Phvul.011G161100	PF00067
1 Phvul.011G161100.1	Phvul.011G161100	Phvul.011G161100	PF00067
1 Phvul.011G161100.1	Phvul.011G161100	Phvul.011G161100	PF00067
1 Phvul.011G161900.1	Phvul.011G161900	Phvul.011G161900	PF00067
1 Phvul.011G161900.1	Phvul.011G161900	Phvul.011G161900	PF00067

Do not distribute

1	Panther	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol
2	PTHR24221,P <sup>-</sup>	KOG0058	3.6.3.44		0 GO:0016887,(	AT3G28345.1 0
3	PTHR24221,P <sup>-</sup>	KOG0058	3.6.3.44		0 GO:0016887,(	AT3G28345.1 0
4	PTHR24221,P <sup>-</sup>	KOG0058	3.6.3.44		0 GO:0016887,(	AT3G28345.1 0
5	PTHR11800	KOG1522	2.7.7.6	K03011	GO:0046983,(	AT2G15430.1 NRPB3,NRPD3
6	PTHR11800	KOG1522	2.7.7.6	K03011	GO:0046983,(	AT2G15430.1 NRPB3,NRPD3
7	PTHR11800	KOG1522	2.7.7.6	K03011	GO:0046983,(	AT2G15430.1 NRPB3,NRPD3
8	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
9	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
10	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
11	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
12	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
13	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
14	PTHR24006,P <sup>-</sup>		0 3.4.19.12	K11838	GO:0005515	AT5G06600.2 UBP12
15	PTHR27000,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,(	AT4G20270.1 BAM3
16	PTHR27000,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,(	AT4G20270.1 BAM3
17	PTHR27000,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,(	AT4G20270.1 BAM3
18	PTHR24089,P <sup>-</sup>	KOG0761		0 K15119		0 AT2G46320.1 0
19	PTHR24089,P <sup>-</sup>	KOG0761		0 K15119		0 AT2G46320.1 0
20	PTHR24089,P <sup>-</sup>	KOG0761		0 K15119		0 AT2G46320.1 0
21	PTHR10799,P <sup>-</sup>		0 3.6.4.12	K10841	GO:0005524	AT2G18760.1 CHR8
22	PTHR10799,P <sup>-</sup>		0 3.6.4.12	K10841	GO:0005524	AT2G18760.1 CHR8
23	PTHR10799,P <sup>-</sup>		0 3.6.4.12	K10841	GO:0005524	AT2G18760.1 CHR8
24	PTHR27009,P <sup>-</sup>	KOG1187	3.1.4.46		0 GO:0006468,(	AT5G38260.1 0
25	PTHR27009,P <sup>-</sup>	KOG1187	3.1.4.46		0 GO:0006468,(	AT5G38260.1 0
26	PTHR27009,P <sup>-</sup>	KOG1187	3.1.4.46		0 GO:0006468,(	AT5G38260.1 0
27	PTHR35744,P <sup>-</sup>		0	0	0	0 AT4G12240.1 0
28	PTHR35744,P <sup>-</sup>		0	0	0	0 AT4G12240.1 0
29	PTHR35744,P <sup>-</sup>		0	0	0	0 AT4G12240.1 0
30	PTHR35744,P <sup>-</sup>		0	0	0	0 AT4G12240.1 0
31	PTHR35744,P <sup>-</sup>		0	0	0	0 AT4G12240.1 0
32	PTHR35744,P <sup>-</sup>		0	0	0	0 AT4G12240.1 0
33	PTHR10366,P <sup>-</sup>		0 1.1.1.133	K12451		0 AT1G63000.1 NRS/ER,UER1
34	PTHR10366,P <sup>-</sup>		0 1.1.1.133	K12451		0 AT1G63000.1 NRS/ER,UER1
35	PTHR10366,P <sup>-</sup>		0 1.1.1.133	K12451		0 AT1G63000.1 NRS/ER,UER1
36	PTHR22814,P <sup>-</sup>	KOG1603		0	0 GO:0046872,(	AT5G19090.2 0
37	PTHR22814,P <sup>-</sup>	KOG1603		0	0 GO:0046872,(	AT5G19090.2 0
38	PTHR22939,P <sup>-</sup>	KOG1320	3.4.21.107		0 GO:0005515	AT5G36950.1 DegP10
39	PTHR22939,P <sup>-</sup>	KOG1320	3.4.21.107		0 GO:0005515	AT5G36950.1 DegP10
40	PTHR22939,P <sup>-</sup>	KOG1320	3.4.21.107		0 GO:0005515	AT5G36950.1 DegP10
41	PTHR27000,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,(	AT5G62230.1 ERL1
42	PTHR27000,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,(	AT5G62230.1 ERL1
43	PTHR27000,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,(	AT5G62230.1 ERL1
44	PTHR22967,P <sup>-</sup>	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2 0
45	PTHR22967,P <sup>-</sup>	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2 0
46	PTHR22967,P <sup>-</sup>	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2 0
47	PTHR22967,P <sup>-</sup>	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2 0

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2	PTHR22967,P <sup>-</sup> KOG1989	2.7.11.1	K08853	GO:0006468,C	AT2G32850.2	0
3	PTHR22967,P <sup>-</sup> KOG1989	2.7.11.1	K08853	GO:0006468,C	AT2G32850.2	0
4	PTHR11926,P <sup>-</sup> KOG1192	2.4.1.272		0 GO:0016758,C	AT2G15480.2 UGT73B5	
5						
6	PTHR11926,P <sup>-</sup> KOG1192	2.4.1.272		0 GO:0016758,C	AT2G15480.2 UGT73B5	
7	PTHR11926,P <sup>-</sup> KOG1192	2.4.1.272		0 GO:0016758,C	AT2G15480.2 UGT73B5	
8	PTHR11926,P <sup>-</sup> KOG1192	2.4.1.272		0 GO:0016758,C	AT2G15480.2 UGT73B5	
9						
10	PTHR11926,P <sup>-</sup>	0 2.4.1.173		0 GO:0030259,C	AT1G43620.2 TT15,UGT80B	
11	PTHR11926,P <sup>-</sup>	0 2.4.1.173		0 GO:0030259,C	AT1G43620.2 TT15,UGT80B	
12	PTHR11926,P <sup>-</sup>	0 2.4.1.173		0 GO:0030259,C	AT1G43620.2 TT15,UGT80B	
13						
14	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0048544,C	AT2G41890.1	0
15	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0048544,C	AT2G41890.1	0
16	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0048544,C	AT2G41890.1	0
17						
18	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0048544,C	AT2G41890.1	0
19	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0048544,C	AT2G41890.1	0
20	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0048544,C	AT2G41890.1	0
21						
22	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,C	AT2G33580.1	0
23	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,C	AT2G33580.1	0
24	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,C	AT2G33580.1	0
25						
26	PTHR22953,P <sup>-</sup> KOG1378	3.1.3.2		0 GO:0016787	AT3G20500.1 ATPAP18,PAP	
27	PTHR22953,P <sup>-</sup> KOG1378	3.1.3.2		0 GO:0016787	AT3G20500.1 ATPAP18,PAP	
28	PTHR22953,P <sup>-</sup> KOG1378	3.1.3.2		0 GO:0016787	AT3G20500.1 ATPAP18,PAP	
29						
30	PTHR36356,P <sup>-</sup>	0	0	0	AT2G44870.1	0
31	PTHR36356,P <sup>-</sup>	0	0	0	AT2G44870.1	0
32	PTHR36356,P <sup>-</sup>	0	0	0	AT2G44870.1	0
33						
34	PTHR32411	0	0	0	AT4G05200.1 CRK25	
35	PTHR32411	0	0	0	AT4G05200.1 CRK25	
36	PTHR32411	0	0	0	AT4G05200.1 CRK25	
37						
38	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
39	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
40	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
41	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
42	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
43	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
44	PTHR32467,P <sup>-</sup>	0	0 K09284	GO:0006355,C	AT2G28550.1 RAP2.7,TOE1	
45						
46	0	0	0	0 GO:0005509	0	0
47	0	0	0	0 GO:0005509	0	0
48	0	0	0	0 GO:0005509	0	0
49						
50	PTHR31704,P <sup>-</sup>	0	0	0	AT4G02550.1	0
51	PTHR31704,P <sup>-</sup>	0	0	0	AT4G02550.1	0
52	PTHR31587,P <sup>-</sup>	0	0	0	AT5G67610.1	0
53	PTHR31587,P <sup>-</sup>	0	0	0	AT5G67610.1	0
54	PTHR31587,P <sup>-</sup>	0	0	0	AT5G67610.1	0
55	PTHR31587,P <sup>-</sup>	0	0	0	AT5G67610.1	0
56	PTHR31704,P <sup>-</sup>	0	0	0	AT4G02210.2	0
57	PTHR31704,P <sup>-</sup>	0	0	0	AT4G02210.2	0
58						
59	PTHR11145 KOG2714		0	0 GO:0051260	AT3G09030.1	0
60	PTHR11145 KOG2714		0	0 GO:0051260	AT3G09030.1	0
	PTHR32370,P <sup>-</sup>	0	0	0 GO:0016567	AT5G64330.1 JK218,NPH3,R	



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2	PTHR32370,P <sup>-</sup>	0	0	0 GO:0016567 AT5G64330.1 JK218,NPH3,R	
3	PTHR32370,P <sup>-</sup>	0	0	0 GO:0016567 AT5G64330.1 JK218,NPH3,R	
4	PTHR31704,P <sup>-</sup>	0	0	0	0 AT4G02550.1
5	PTHR31704,P <sup>-</sup>	0	0	0	0 AT4G02550.1
6	PTHR31704,P <sup>-</sup>	0	0	0	0 AT4G02550.1
7	PTHR10795,P <sup>-</sup>	0 3.4.21.25		0 GO:0016020,C AT2G19170.1 SLP3	
8	PTHR10795,P <sup>-</sup>	0 3.4.21.25		0 GO:0016020,C AT2G19170.1 SLP3	
9	PTHR10795,P <sup>-</sup>	0 3.4.21.25		0 GO:0016020,C AT2G19170.1 SLP3	
10	PTHR10795,P <sup>-</sup>	0 3.4.21.25		0 GO:0016020,C AT2G19170.1 SLP3	
11	PTHR34663,P <sup>-</sup>	0	0	0	0 AT2G23270.1
12	PTHR34663,P <sup>-</sup>	0	0	0	0 AT2G23270.1
13	PTHR34663,P <sup>-</sup>	0	0	0	0 AT2G23270.1
14	PTHR34663,P <sup>-</sup>	0	0	0	0 AT2G23270.1
15	PTHR31704,P <sup>-</sup>	0	0	0	0 AT4G02550.1
16	PTHR31704,P <sup>-</sup>	0	0	0	0 AT4G02550.1
17	PTHR31704,P <sup>-</sup>	0	0	0	0 AT4G02550.1
18	PTHR15959,P <sup>-</sup> KOG3894		0 K08492	0 AT1G51740.1 ATSYP81,ATUI	
19	PTHR15959,P <sup>-</sup> KOG3894		0 K08492	0 AT1G51740.1 ATSYP81,ATUI	
20	PTHR15959,P <sup>-</sup> KOG3894		0 K08492	0 AT1G51740.1 ATSYP81,ATUI	
21	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
22	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
23	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
24	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
25	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
26	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
27	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
28	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
29	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
30	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
31	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
32	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
33	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
34	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
35	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
36	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
37	PTHR10302,P <sup>-</sup>	0	0	0 GO:0006260,C AT4G20010.1 OSB2,PTAC9	
38	PTHR13140,P <sup>-</sup>	0 3.6.4.1	K10357	GO:0016459,C AT1G54560.1 ATXIE,XIE	
39	PTHR13140,P <sup>-</sup>	0 3.6.4.1	K10357	GO:0016459,C AT1G54560.1 ATXIE,XIE	
40	PTHR13140,P <sup>-</sup>	0 3.6.4.1	K10357	GO:0016459,C AT1G54560.1 ATXIE,XIE	
41	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
42	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
43	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
44	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
45	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
46	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
47	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
48	PTHR10044,P <sup>-</sup> KOG4172		0	0	0 AT4G03000.2
49	PTHR10799,P <sup>-</sup>	0 3.6.4.12	K11647	GO:0016787,C AT3G06010.1 ATCHR12	
50	PTHR10799,P <sup>-</sup>	0 3.6.4.12	K11647	GO:0016787,C AT3G06010.1 ATCHR12	
51	PTHR10799,P <sup>-</sup>	0 3.6.4.12	K11647	GO:0016787,C AT3G06010.1 ATCHR12	
52	PTHR10799,P <sup>-</sup>	0 3.6.4.12	K11647	GO:0016787,C AT3G06010.1 ATCHR12	
53	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
54	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
55	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
56	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
57	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
58	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
59	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
60	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1
	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1

1						
2	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
3	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
4	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
5	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
6	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
7	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
8	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
9	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
10	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
11	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
12	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
13	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
14	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
15	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
16	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
17	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
18	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
19	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
20	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
21	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
22	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
23	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
24	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
25	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
26	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
27	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
28	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
29	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
30	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
31	PTHR10641,P <sup>-</sup>	0	0	0	0 AT5G41020.1	0
32	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(AT4G08850.1	0
33	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0005515,(AT4G08850.1	0
34						
35	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G47670.1	0
36	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G47670.1	0
37	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G47670.1	0
38						
39	PTHR16441	0	0	0	0 AT4G32560.1	0
40	PTHR16441	0	0	0	0 AT4G32560.1	0
41	PTHR16441	0	0	0	0 AT4G32560.1	0
42	PTHR16441	0	0	0	0 AT4G32560.1	0
43	PTHR16441	0	0	0	0 AT4G32560.1	0
44	PTHR31704,P <sup>-</sup>	0	0	0	0 AT2G24960.2	0
45	PTHR31704,P <sup>-</sup>	0	0	0	0 AT2G24960.2	0
46						
47	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
48	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
49	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
50	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
51	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
52	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
53	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
54	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
55	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
56	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
57	PTHR15288,P <sup>-</sup>	0	0	0	0 AT5G35560.1	0
58						
59	PTHR12281,P <sup>-</sup>	0	0 K17824		0 AT1G15860.2	0
60	PTHR12281,P <sup>-</sup>	0	0 K17824		0 AT1G15860.2	0
	PTHR19211,P <sup>-</sup>	0 3.6.1.3	K06185		GO:0016887,(AT5G60790.1 ATGCN1,GCN:	

1								
2	PTHR19211,P <sup>-</sup>	0 3.6.1.3	K06185	GO:0016887,C	AT5G60790.1	ATGCN1,GCN:		
3	PTHR19211,P <sup>-</sup>	0 3.6.1.3	K06185	GO:0016887,C	AT5G60790.1	ATGCN1,GCN:		
4	PTHR34118,P <sup>-</sup>	0	0 K02116		0 AT2G31040.1		0	
5								
6	PTHR34118,P <sup>-</sup>	0	0 K02116		0 AT2G31040.1		0	
7	PTHR34118,P <sup>-</sup>	0	0 K02116		0 AT2G31040.1		0	
8								
9	PTHR11926,P <sup>-</sup>	0 2.4.1.324		0 GO:0016758,C	AT1G22380.1	AtUGT85A3,U		
10	PTHR11926,P <sup>-</sup>	0 2.4.1.324		0 GO:0016758,C	AT1G22380.1	AtUGT85A3,U		
11	PTHR11926,P <sup>-</sup>	0 2.4.1.324		0 GO:0016758,C	AT1G22380.1	AtUGT85A3,U		
12								
13	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1		0	
14	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1		0	
15	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1		0	
16	PTHR12323 KOG0007		0	0 GO:0006396,C	AT4G31200.3		0	
17								
18	PTHR12323 KOG0007		0	0 GO:0006396,C	AT4G31200.3		0	
19	PTHR12323 KOG0007		0	0 GO:0006396,C	AT4G31200.3		0	
20								
21	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
22	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
23	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
24	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
25	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
26	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
27	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0 AT4G18010.2	5PTASE2,AT5F		
28								
29	PTHR34996,P <sup>-</sup>	0	0	0	0	0	0	
30	PTHR34996,P <sup>-</sup>	0	0	0	0	0	0	
31	PTHR34996,P <sup>-</sup>	0	0	0	0	0	0	
32								
33	PTHR36400	0	0	0 GO:0006412,C	AT5G45590.1		0	
34	PTHR36400	0	0	0 GO:0006412,C	AT5G45590.1		0	
35	PTHR36400	0	0	0 GO:0006412,C	AT5G45590.1		0	
36		0	0	0	0	0	0	
37		0	0	0	0	0	0	
38		0	0	0	0	0	0	
39		0	0	0	0	0	0	
40		0	0	0	0	0	0	
41								
42	PTHR12465	0	0 K13528	GO:0016592,C	AT2G28230.1		0	
43	PTHR12465	0	0 K13528	GO:0016592,C	AT2G28230.1		0	
44	PTHR12465	0	0 K13528	GO:0016592,C	AT2G28230.1		0	
45								
46	PTHR11785,P <sup>-</sup> KOG1286		0	0 GO:0055085,C	AT5G04770.1	ATCAT6,CAT6		
47	PTHR23083,P <sup>-</sup> KOG0548		0	0	0 AT4G37460.1	SRFR1		
48	PTHR23083,P <sup>-</sup> KOG0548		0	0	0 AT4G37460.1	SRFR1		
49	PTHR14360,P <sup>-</sup> KOG3156		0	0	0 AT2G16460.1		0	
50								
51	PTHR14360,P <sup>-</sup> KOG3156		0	0	0 AT2G16460.1		0	
52	PTHR14360,P <sup>-</sup> KOG3156		0	0	0 AT2G16460.1		0	
53								
54	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		
55	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		
56	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		
57	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		
58								
59	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		
60	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		
	PTHR31072,P <sup>-</sup>	0	0	0	0 AT3G02150.2	PTF1,TCP13,TI		

1						
2	PTHR31072,P <sup>-</sup>	0	0	0	0	AT3G02150.2 PTF1,TCP13,TI
3	PTHR31072,P <sup>-</sup>	0	0	0	0	AT3G02150.2 PTF1,TCP13,TI
4	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0	AT1G71710.1
5						
6	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0	AT1G71710.1
7	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0	AT1G71710.1
8	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0	AT1G71710.1
9						
10	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0	AT1G71710.1
11	PTHR11200,P <sup>-</sup> KOG0565	3.1.3.56		0	0	AT1G71710.1
12	PTHR11956,P <sup>-</sup>	0 6.1.1.19	K01887			GO:0006420,(AT4G26300.1 emb1027
13						
14	PTHR11956,P <sup>-</sup>	0 6.1.1.19	K01887			GO:0006420,(AT4G26300.1 emb1027
15	PTHR11956,P <sup>-</sup>	0 6.1.1.19	K01887			GO:0006420,(AT4G26300.1 emb1027
16	PTHR11011,P <sup>-</sup> KOG1221	1.2.1.50,1.2.1	K13356			GO:0080019 AT4G33790.1 CER4,FAR3,G7
17						
18	PTHR11011,P <sup>-</sup> KOG1221	1.2.1.50,1.2.1	K13356			GO:0080019 AT4G33790.1 CER4,FAR3,G7
19	PTHR19957,P <sup>-</sup> KOG3202		0 K08498			GO:0005515,(AT1G28490.1 ATSYP61,OSM
20	PTHR19957,P <sup>-</sup> KOG3202		0 K08498			GO:0005515,(AT1G28490.1 ATSYP61,OSM
21						
22	PTHR19957,P <sup>-</sup> KOG3202		0 K08498			GO:0005515,(AT1G28490.1 ATSYP61,OSM
23	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
24	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
25	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
26	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
27	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
28	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
29	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
30	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
31	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
32	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
33	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
34	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
35	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
36	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
37	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
38	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
39	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
40	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
41	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
42	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
43	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
44	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
45	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
46	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
47	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
48	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
49	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
50	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
51	PTHR12606,P <sup>-</sup> KOG3246	3.4.22.68		0	0	GO:0008234,(AT4G00690.1 ULP1B
52	PTHR23241,P <sup>-</sup> KOG2886		0	0	0	AT3G62580.1
53	PTHR23241,P <sup>-</sup> KOG2886		0	0	0	AT3G62580.1
54	PTHR23241,P <sup>-</sup> KOG2886		0	0	0	AT3G62580.1
55	PTHR32440,P <sup>-</sup> KOG1432		0	0	0	GO:0016787 AT3G10150.1 ATPAP16,PAP
56	PTHR32440,P <sup>-</sup> KOG1432		0	0	0	GO:0016787 AT3G10150.1 ATPAP16,PAP
57	PTHR32440,P <sup>-</sup> KOG1432		0	0	0	GO:0016787 AT3G10150.1 ATPAP16,PAP
58	PTHR32440,P <sup>-</sup> KOG1432		0	0	0	GO:0016787 AT3G10150.1 ATPAP16,PAP
59	PTHR13743,P <sup>-</sup>	0	0	0	0	GO:0005515 AT2G45540.1
60	PTHR13743,P <sup>-</sup>	0	0	0	0	GO:0005515 AT2G45540.1

1							
2	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
3	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
4	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
5	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
6	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
7	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
8	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT2G45540.1	0	
9	PTHR32133,P <sup>-</sup>	0	0	0	GO:0005515 AT3G24760.1	0	
10	PTHR32133,P <sup>-</sup>	0	0	0	GO:0005515 AT3G24760.1	0	
11	PTHR32133,P <sup>-</sup>	0	0	0	GO:0005515 AT3G24760.1	0	
12	PTHR14950,P <sup>-</sup> KOG0701	3.1.26.3	K11592	GO:0016787,(	AT3G03300.3 ATDCL2,DCL2		
13	PTHR14950,P <sup>-</sup> KOG0701	3.1.26.3	K11592	GO:0016787,(	AT3G03300.3 ATDCL2,DCL2		
14	PTHR14950,P <sup>-</sup> KOG0701	3.1.26.3	K11592	GO:0016787,(	AT3G03300.3 ATDCL2,DCL2		
15	PTHR14950,P <sup>-</sup> KOG0701	3.1.26.3	K11592	GO:0016787,(	AT3G03300.3 ATDCL2,DCL2		
16	PTHR27003,P <sup>-</sup>	0 2.7.11.1		0	GO:0005515 AT1G05700.1	0	
17	PTHR27003,P <sup>-</sup>	0 2.7.11.1		0	GO:0005515 AT1G05700.1	0	
18	PTHR27003,P <sup>-</sup>	0 2.7.11.1		0	GO:0005515 AT1G05700.1	0	
19	PTHR27003,P <sup>-</sup>	0 2.7.11.1		0	GO:0005515 AT1G05700.1	0	
20	PTHR22950,P <sup>-</sup> KOG1303		0 K13946		0 AT2G38120.1 AUX1,MAP1,P		
21	PTHR12822,P <sup>-</sup> KOG3114		0	0	GO:0016020 AT2G39805.1	0	
22	PTHR12822,P <sup>-</sup> KOG3114		0	0	GO:0016020 AT2G39805.1	0	
23	PTHR23500,P <sup>-</sup> KOG0254		0	0	GO:0055085,(	AT1G34580.1	0
24	PTHR23500,P <sup>-</sup> KOG0254		0	0	GO:0055085,(	AT1G34580.1	0
25	PTHR23500,P <sup>-</sup> KOG0254		0	0	GO:0055085,(	AT1G34580.1	0
26	PTHR23500,P <sup>-</sup> KOG0254		0	0	GO:0055085,(	AT1G34580.1	0
27	PTHR13129,P <sup>-</sup>	0	0 K11789		0 AT4G31160.1 DCAF1		
28	PTHR13129,P <sup>-</sup>	0	0 K11789		0 AT4G31160.1 DCAF1		
29	PTHR13129,P <sup>-</sup>	0	0 K11789		0 AT4G31160.1 DCAF1		
30	PTHR13129,P <sup>-</sup>	0	0 K11789		0 AT4G31160.1 DCAF1		
31	PTHR21493,P <sup>-</sup> KOG1743		0	0	GO:0016192 AT3G49420.1	0	
32	PTHR21493,P <sup>-</sup> KOG1743		0	0	GO:0016192 AT3G49420.1	0	
33	PTHR21493,P <sup>-</sup> KOG1743		0	0	GO:0016192 AT3G49420.1	0	
34	PTHR21493,P <sup>-</sup> KOG1743		0	0	GO:0016192 AT3G49420.1	0	
35	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1	0	
36	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1	0	
37	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1	0	
38	PTHR31851,P <sup>-</sup>	0	0	0	0 AT4G27860.1	0	
39	PTHR20881 KOG2949	2.1.2.11	K00606	GO:0015940,(	AT3G61530.1 PANB2		
40	PTHR20881 KOG2949	2.1.2.11	K00606	GO:0015940,(	AT3G61530.1 PANB2		
41	PTHR20881 KOG2949	2.1.2.11	K00606	GO:0015940,(	AT3G61530.1 PANB2		
42	PTHR20881 KOG2949	2.1.2.11	K00606	GO:0015940,(	AT3G61530.1 PANB2		
43	PTHR31636,P <sup>-</sup>	0	0	0	0 AT3G13840.1	0	
44	PTHR31636,P <sup>-</sup>	0	0	0	0 AT3G13840.1	0	
45	PTHR31636,P <sup>-</sup>	0	0	0	0 AT3G13840.1	0	
46	PTHR31636,P <sup>-</sup>	0	0	0	0 AT3G13840.1	0	
47	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
48	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
49	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
50	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
51	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
52	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
53	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
54	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
55	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
56	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
57	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
58	PTHR33137,P <sup>-</sup>	0	0 K14972		0 AT1G15780.1	0	
59	PTHR10855 KOG1497		0 K12178	GO:0005515	AT5G42970.1 ATS4,COP14,C		
60	PTHR10855 KOG1497		0 K12178	GO:0005515	AT5G42970.1 ATS4,COP14,C		
	PTHR10855 KOG1497		0 K12178	GO:0005515	AT5G42970.1 ATS4,COP14,C		

1			
2	PTHR24282,P <sup>-</sup> KOG0157	1.14.13.173	0 GO:0055114,C AT3G14690.1 CYP72A15
3	PTHR24282,P <sup>-</sup> KOG0157	1.14.13.173	0 GO:0055114,C AT3G14690.1 CYP72A15
4	PTHR24282,P <sup>-</sup> KOG0157	1.14.13.173	0 GO:0055114,C AT3G14690.1 CYP72A15
5			
6	PTHR24282,P <sup>-</sup> KOG0159	1.14.13.173	0 GO:0055114,C AT3G14690.1 CYP72A15
7	PTHR24282,P <sup>-</sup> KOG0159	1.14.13.173	0 GO:0055114,C AT3G14690.1 CYP72A15
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arabi-defline	ID	Annot_defline	IDENTIFIER	NAME	DESCRIPTION
ABC transporter family protein	Phvul.004G02	PTHR24221:SF	Phvul.004G02	Solute transp	subfamily ABC
ABC transporter family protein	Phvul.004G02	PTHR24221:SF	Phvul.004G02	Solute transp	subfamily ABC
ABC transporter family protein	Phvul.004G02	PTHR24221:SF	Phvul.004G02	Solute transp	subfamily ABC
DNA-directed RNA polymerase	Phvul.002G09	K03011 - DNA	Phvul.002G09	RNA biosynth	subunit 3 of R
DNA-directed RNA polymerase	Phvul.002G09	K03011 - DNA	Phvul.002G09	RNA biosynth	subunit 3 of R
DNA-directed RNA polymerase	Phvul.002G09	K03011 - DNA	Phvul.002G09	RNA biosynth	subunit 3 of R
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
Leucine-rich receptor-like prot	Phvul.006G02	PTHR27000:SF	Phvul.006G02	Protein modif	protein kinase
Leucine-rich receptor-like prot	Phvul.006G02	PTHR27000:SF	Phvul.006G02	Protein modif	protein kinase
Leucine-rich receptor-like prot	Phvul.006G02	PTHR27000:SF	Phvul.006G02	Protein modif	protein kinase
Mitochondrial substrate carrie	Phvul.006G11	K15119 - solut	Phvul.006G11	Solute transp	solute transp
Mitochondrial substrate carrie	Phvul.006G11	K15119 - solut	Phvul.006G11	Solute transp	solute transp
Mitochondrial substrate carrie	Phvul.006G11	K15119 - solut	Phvul.006G11	Solute transp	solute transp
chromatin remodeling 8	Phvul.007G19	K10841 - DNA	Phvul.007G19	DNA damage	DNA repair pr
chromatin remodeling 8	Phvul.007G19	K10841 - DNA	Phvul.007G19	DNA damage	DNA repair pr
chromatin remodeling 8	Phvul.007G19	K10841 - DNA	Phvul.007G19	DNA damage	DNA repair pr
Protein kinase superfamily prc	Phvul.001G07	PTHR27009:SF	Phvul.001G07	Enzyme classi	Rust resistanc
Protein kinase superfamily prc	Phvul.001G07	PTHR27009:SF	Phvul.001G07	Enzyme classi	Rust resistanc
Protein kinase superfamily prc	Phvul.001G07	PTHR27009:SF	Phvul.001G07	Enzyme classi	Rust resistanc
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:SF	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:SF	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:SF	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:SF	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:SF	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:SF	Phvul.001G26	RNA biosynth	C2H2 zinc fing
nucleotide-rhamnose synthas	Phvul.002G15	1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamn
nucleotide-rhamnose synthas	Phvul.002G15	1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamn
nucleotide-rhamnose synthas	Phvul.002G15	1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamn
Heavy metal transport/detoxif	Phvul.003G09	PTHR22814:SF	Phvul.003G09	not assigned.	α (original desc
Heavy metal transport/detoxif	Phvul.003G09	PTHR22814:SF	Phvul.003G09	not assigned.	α (original desc
DegP protease 10	Phvul.004G00	PTHR22939:SF	Phvul.004G00	Protein home	protease (Deg
DegP protease 10	Phvul.004G00	PTHR22939:SF	Phvul.004G00	Protein home	protease (Deg
DegP protease 10	Phvul.004G00	PTHR22939:SF	Phvul.004G00	Protein home	protease (Deg
ERECTA-like 1	Phvul.004G12	PTHR27000:SF	Phvul.004G12	Protein modif	protein kinase
ERECTA-like 1	Phvul.004G12	PTHR27000:SF	Phvul.004G12	Protein modif	protein kinase
ERECTA-like 1	Phvul.004G12	PTHR27000:SF	Phvul.004G12	Protein modif	protein kinase
Protein kinase superfamily prc	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily prc	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily prc	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily prc	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase



1 Protein kinase superfamily prcPhvul.005G06K08853 - AP2-Phvul.005G06Protein modif protein kinase  
2 Protein kinase superfamily prcPhvul.005G06K08853 - AP2-Phvul.005G06Protein modif protein kinase  
3 UDP-glucosyl transferase 73B<sup>5</sup>Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc  
4 UDP-glucosyl transferase 73B<sup>5</sup>Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc  
5 UDP-glucosyl transferase 73B<sup>5</sup>Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc  
6 UDP-glucosyl transferase 73B<sup>5</sup>Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc  
7 UDP-Glycosyltransferase supe Phvul.007G08PTHR11926:SIPhvul.007G08Lipid metaboli UDP-glucose:s  
8 UDP-Glycosyltransferase supe Phvul.007G08PTHR11926:SIPhvul.007G08Lipid metaboli UDP-glucose:s  
9 UDP-Glycosyltransferase supe Phvul.007G08PTHR11926:SIPhvul.007G08Lipid metaboli UDP-glucose:s  
10 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
11 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
12 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
13 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
14 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
15 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
16 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
17 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
18 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase  
19 Protein kinase superfamily prcPhvul.008G21PTHR27001:SIPhvul.008G21External stimu LysM receptor  
20 Protein kinase superfamily prcPhvul.008G21PTHR27001:SIPhvul.008G21External stimu LysM receptor  
21 Protein kinase superfamily prcPhvul.008G21PTHR27001:SIPhvul.008G21External stimu LysM receptor  
22 purple acid phosphatase 18 Phvul.008G26PTHR22953:SIPhvul.008G26not assigned.a (original desc  
23 purple acid phosphatase 18 Phvul.008G26PTHR22953:SIPhvul.008G26not assigned.a (original desc  
24 purple acid phosphatase 18 Phvul.008G26PTHR22953:SIPhvul.008G26not assigned.a (original desc  
25 0 Phvul.011G00PTHR36356:SIPhvul.011G00not assigned.r no hits & (orig  
26 0 Phvul.011G00PTHR36356:SIPhvul.011G00not assigned.r no hits & (orig  
27 0 Phvul.011G00PTHR36356:SIPhvul.011G00not assigned.r no hits & (orig  
28 cysteine-rich RLK (RECEPTOR-IPhvul.011G19PF01657 - SaltPhvul.011G19not assigned.a (original desc  
29 cysteine-rich RLK (RECEPTOR-IPhvul.011G19PF01657 - SaltPhvul.011G19not assigned.a (original desc  
30 cysteine-rich RLK (RECEPTOR-IPhvul.011G19PF01657 - SaltPhvul.011G19not assigned.a (original desc  
31 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f  
32 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f  
33 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f  
34 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f  
35 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f  
36 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f  
37 0 Phvul.001G02PF00036 - EF IPhvul.001G02not assigned.r no hits & (orig  
38 0 Phvul.001G02PF00036 - EF IPhvul.001G02not assigned.r no hits & (orig  
39 0 Phvul.001G02PF00036 - EF IPhvul.001G02not assigned.r no hits & (orig  
40 0 Phvul.001G16PF12776 - MyPhvul.001G16not assigned.r no hits & (orig  
41 0 Phvul.001G16PF12776 - MyPhvul.001G16not assigned.r no hits & (orig  
42 Uncharacterized conserved prPhvul.002G01PF10225 - UncPhvul.002G01not assigned.r no hits & (orig  
43 Uncharacterized conserved prPhvul.002G01PF10225 - UncPhvul.002G01not assigned.r no hits & (orig  
44 Uncharacterized conserved prPhvul.002G01PF10225 - UncPhvul.002G01not assigned.r no hits & (orig  
45 0 Phvul.002G14PF12776 - MyPhvul.002G14not assigned.r no hits & (orig  
46 0 Phvul.002G14PF12776 - MyPhvul.002G14not assigned.r no hits & (orig  
47 BTB/POZ domain-containing pPhvul.002G15PTHR11145 - Phvul.002G15not assigned.a (original desc  
48 BTB/POZ domain-containing pPhvul.002G15PTHR11145 - Phvul.002G15not assigned.a (original desc  
49 Phototropic-responsive NPH3 Phvul.002G21PTHR32370:SIPhvul.002G21Protein home component NI

1 Phototropic-responsive NPH3 Phvul.002G21 PTHR32370:SlPhvul.002G21 Protein home component N  
2 Phototropic-responsive NPH3 Phvul.002G21 PTHR32370:SlPhvul.002G21 Protein home component N  
3  
4 0 Phvul.003G06 PF12776 - MyPhvul.003G06 not assigned.r no hits & (orig  
5 0 Phvul.003G06 PF12776 - MyPhvul.003G06 not assigned.r no hits & (orig  
6 subtilisin-like serine protease :Phvul.003G14 PTHR10795:SlPhvul.003G14 Protein home protease (SBT  
7 subtilisin-like serine protease :Phvul.003G14 PTHR10795:SlPhvul.003G14 Protein home protease (SBT  
8 subtilisin-like serine protease :Phvul.003G14 PTHR10795:SlPhvul.003G14 Protein home protease (SBT  
9  
10 0 0 0 Phvul.003G23 Phytohormon PIP/PIPL precu  
11 0 0 0 Phvul.003G23 Phytohormon PIP/PIPL precu  
12 0 0 0 Phvul.003G23 Phytohormon PIP/PIPL precu  
13 0 Phvul.004G05 PF12776 - MyPhvul.004G05 not assigned.r no hits & (orig  
14 0 Phvul.004G05 PF12776 - MyPhvul.004G05 not assigned.r no hits & (orig  
15  
16 syntaxin of plants 81 Phvul.004G15 K08492 - synt:Phvul.004G15 Vesicle trafficl SYP8-group Q  
17 syntaxin of plants 81 Phvul.004G15 K08492 - synt:Phvul.004G15 Vesicle trafficl SYP8-group Q  
18 syntaxin of plants 81 Phvul.004G15 K08492 - synt:Phvul.004G15 Vesicle trafficl SYP8-group Q  
19  
20 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
21 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
22 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
23 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
24 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
25 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
26 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
27 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
28 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
29 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
30 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
31 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
32 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
33 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
34 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
35 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
36 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynthe TAC9 cofactor  
37 Myosin family protein with DilPhvul.006G10 PTHR13140:SlPhvul.006G10 Cytoskeleton (class XI myosin  
38 Myosin family protein with DilPhvul.006G10 PTHR13140:SlPhvul.006G10 Cytoskeleton (class XI myosin  
39 Myosin family protein with DilPhvul.006G10 PTHR13140:SlPhvul.006G10 Cytoskeleton (class XI myosin  
40 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
41 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
42 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
43 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
44 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
45 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
46 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
47 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc  
48 Homeotic gene regulator Phvul.007G05 PTHR10799:SlPhvul.007G05 Chromatin org chromatin ren  
49 Homeotic gene regulator Phvul.007G05 PTHR10799:SlPhvul.007G05 Chromatin org chromatin ren  
50 Homeotic gene regulator Phvul.007G05 PTHR10799:SlPhvul.007G05 Chromatin org chromatin ren  
51 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynthe transcription f  
52 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynthe transcription f  
53 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynthe transcription f  
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58 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynthe transcription f  
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60 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynthe transcription f

1 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f  
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3 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f  
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12 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f  
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31 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f  
32 Leucine-rich repeat receptor-liPhvul.008G10 PF00069//PF0Phvul.008G10 Protein modif protein kinase  
33 Leucine-rich repeat receptor-liPhvul.008G10 PF00069//PF0Phvul.008G10 Protein modif protein kinase  
34 Transmembrane amino acid trPhvul.009G02 PTHR22950//IPhvu.009G02 Solute transp amino acid tra  
35 Transmembrane amino acid trPhvul.009G02 PTHR22950//IPhvu.009G02 Solute transp amino acid tra  
36 Transmembrane amino acid trPhvul.009G02 PTHR22950//IPhvu.009G02 Solute transp amino acid tra  
37 paramyosin-related Phvul.009G09 PTHR16441 - IPhvu.009G09 not assigned.r no hits & (orig  
38 paramyosin-related Phvul.009G09 PTHR16441 - IPhvu.009G09 not assigned.r no hits & (orig  
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41 0 Phvul.009G12 PF12776 - MyPhvul.009G12 not assigned.r no hits & (orig  
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56 Domain of unknown function iPhvul.010G15 PTHR12281:SlPhvul.010G15 not assigned.r no hits & (orig  
57 ABC transporter family proteirPhvul.011G08 K06185 - ATP-Phvul.011G08 not assigned.r (original desc  
58  
59  
60

1 ABC transporter family proteiPhvul.011G08K06185 - ATP-Phvul.011G08not assigned.a (original desc  
 2 ABC transporter family proteiPhvul.011G08K06185 - ATP-Phvul.011G08not assigned.a (original desc  
 3 ABC transporter family proteiPhvul.011G08K06185 - ATP-Phvul.011G08not assigned.a (original desc  
 4 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor  
 5 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor  
 6 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor  
 7 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor  
 8 UDP-glucosyl transferase 85A:Phvul.011G15PTHR11926:SFPhvul.011G15Enzyme classii Linamarin syn  
 9 UDP-glucosyl transferase 85A:Phvul.011G15PTHR11926:SFPhvul.011G15Enzyme classii Linamarin syn  
 10 UDP-glucosyl transferase 85A:Phvul.011G15PTHR11926:SFPhvul.011G15Enzyme classii Linamarin syn  
 11 LRR and NB-ARC domains-coniPhvul.011G19PTHR23155//IPhvu.011G19not assigned.a (original desc  
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 13 LRR and NB-ARC domains-coniPhvul.011G19PTHR23155//IPhvu.011G19not assigned.a (original desc  
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 15 SWAP (Suppressor-of-White-APhvul.001G19PTHR12323 - (Phvul.001G19not assigned.r no hits & (orig  
 16 SWAP (Suppressor-of-White-APhvul.001G19PTHR12323 - (Phvul.001G19not assigned.r no hits & (orig  
 17 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
 18 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
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 22 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
 23 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
 24 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
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 26 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
 27 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol  
 28 0 0 0 Phvul.002G11not assigned.r no hits & (orig  
 29 0 0 0 Phvul.002G11not assigned.r no hits & (orig  
 30 0 0 0 Phvul.002G11not assigned.r no hits & (orig  
 31 0 0 0 Phvul.002G11not assigned.r no hits & (orig  
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 33 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig  
 34 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig  
 35 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig  
 36 0 0 0 Phvul.002G14not assigned.r no hits & (orig  
 37 0 0 0 Phvul.002G14not assigned.r no hits & (orig  
 38 0 0 0 Phvul.002G14not assigned.r no hits & (orig  
 39 0 0 0 Phvul.002G14not assigned.r no hits & (orig  
 40 0 0 0 Phvul.002G14not assigned.r no hits & (orig  
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 43 TATA-binding related factor (TPhvul.003G13K13528 - medPhvul.003G13RNA biosynthe component M  
 44 cationic amino acid transportePhvul.003G22PTHR11785//IPhvu.003G22Solute transpccationic aminc  
 45 Tetratricopeptide repeat (TPRPhvul.003G23PF13371//PF1Phvul.003G23not assigned.a (original desc  
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 48 Protein of unknown function (Phvul.003G25PTHR14360:SFPhvul.003G25not assigned.r no hits & (orig  
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 53 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f  
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 55 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f  
 56 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f  
 57 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f  
 58 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f  
 59 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f  
 60 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f



1  
2 plastid transcription factor 1 Phvul.004G03 PTHR31072:SlPhvul.004G03 RNA biosynth transcription f  
3 plastid transcription factor 1 Phvul.004G03 PTHR31072:SlPhvul.004G03 RNA biosynth transcription f  
4 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol  
5 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol  
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8 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol  
9 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol  
10 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol  
11 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol  
12 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA  
13 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA  
14 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA  
15 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA  
16 Jojoba acyl CoA reductase-rel Phvul.005G121.2.1.50//1.2. Phvul.005G12 Cell wall orgar acyl CoA redu  
17 Jojoba acyl CoA reductase-rel Phvul.005G121.2.1.50//1.2. Phvul.005G12 Cell wall orgar acyl CoA redu  
18 Jojoba acyl CoA reductase-rel Phvul.005G121.2.1.50//1.2. Phvul.005G12 Cell wall orgar acyl CoA redu  
19 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc  
20 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc  
21 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc  
22 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc  
23 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig  
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28 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig  
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53 Late embryogenesis abundant Phvul.007G21 PTHR23241//I Phvul.007G21 not assigned.r no hits & (orig  
54 Late embryogenesis abundant Phvul.007G21 PTHR23241//I Phvul.007G21 not assigned.r no hits & (orig  
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56 purple acid phosphatase 16 Phvul.007G24 PTHR32440:SlPhvul.007G24 not assigned.a (original desc  
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60 WD-40 repeat family protein /Phvul.008G07 PF00400//PF0 Phvul.008G07 not assigned.a (original desc  
WD-40 repeat family protein /Phvul.008G07 PF00400//PF0 Phvul.008G07 not assigned.a (original desc

1 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.ã (original desc  
 2 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.ã (original desc  
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 14 Leucine-rich repeat transmemPhvul.008G16PF12819//PF1Phvul.008G16not assigned.ã (original desc  
 15 Leucine-rich repeat transmemPhvul.008G16PF12819//PF1Phvul.008G16not assigned.ã (original desc  
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 17 Transmembrane amino acid trPhvul.008G22PTHR22950//IPhvu.008G22Solute transpcauxin transpo  
 18 Integral membrane Yip1 familPhvul.008G23PTHR12822:SIPhvul.008G23not assigned.r no hits & (orig  
 19 Major facilitator superfamily pPhvul.009G03PTHR23500:SIPhvul.009G03Solute transpmonosacchari  
 20 Major facilitator superfamily pPhvul.009G03PTHR23500:SIPhvul.009G03Solute transpmonosacchari  
 21 Major facilitator superfamily pPhvul.009G03PTHR23500:SIPhvul.009G03Solute transpmonosacchari  
 22 DDB1-CUL4 associated factor :Phvul.009G09K11789 - HIV- Phvul.009G09not assigned.ã (original desc  
 23 DDB1-CUL4 associated factor :Phvul.009G09K11789 - HIV- Phvul.009G09not assigned.ã (original desc  
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 25 Got1/Sft2-like vescicle transpcPhvul.009G23PTHR21493:SIPhvul.009G23not assigned.ã (original desc  
 26 Got1/Sft2-like vescicle transpcPhvul.009G23PTHR21493:SIPhvul.009G23not assigned.ã (original desc  
 27 Got1/Sft2-like vescicle transpcPhvul.009G23PTHR21493:SIPhvul.009G23not assigned.ã (original desc  
 28 vacuolar iron transporter (VIT)Phvul.010G02PTHR31851:SIPhvul.010G02Solute transpmetal cation t  
 29 vacuolar iron transporter (VIT)Phvul.010G02PTHR31851:SIPhvul.010G02Solute transpmetal cation t  
 30 vacuolar iron transporter (VIT)Phvul.010G02PTHR31851:SIPhvul.010G02Solute transpmetal cation t  
 31 Phosphoenolpyruvate carboxyPhvul.010G102.1.2.11 - 3-mPhvul.010G10Coenzyme me ketopantoate  
 32 Phosphoenolpyruvate carboxyPhvul.010G102.1.2.11 - 3-mPhvul.010G10Coenzyme me ketopantoate  
 33 Phosphoenolpyruvate carboxyPhvul.010G102.1.2.11 - 3-mPhvul.010G10Coenzyme me ketopantoate  
 34 GRAS family transcription factPhvul.010G12PTHR31636:SIPhvul.010G12External stim component N:  
 35 GRAS family transcription factPhvul.010G12PTHR31636:SIPhvul.010G12External stim component N:  
 36 GRAS family transcription factPhvul.010G12PTHR31636:SIPhvul.010G12External stim component N:  
 37 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 38 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 39 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 40 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 41 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 42 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 43 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 44 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 45 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 46 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M  
 47 Proteasome component (PCI) Phvul.011G00K12178 - COPiPhvul.011G00Protein home component C:  
 48 Proteasome component (PCI) Phvul.011G00K12178 - COPiPhvul.011G00Protein home component C:  
 49 Proteasome component (PCI) Phvul.011G00K12178 - COPiPhvul.011G00Protein home component C:

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cytochrome P450, family 72, sPhvul.011G161.14.13.173 - Phvul.011G16Enzyme classif 11-oxo-beta-a  
cytochrome P450, family 72, sPhvul.011G161.14.13.173 - Phvul.011G16Enzyme classif 11-oxo-beta-a  
cytochrome P450, family 72, sPhvul.011G161.14.13.173 - Phvul.011G16Enzyme classif 11-oxo-beta-a  
cytochrome P450, family 72, sPhvul.011G16KOG0159 - CyPhvul.011G16Enzyme classif 11-oxo-beta-a  
cytochrome P450, family 72, sPhvul.011G16KOG0159 - CyPhvul.011G16Enzyme classif 11-oxo-beta-a

Do not distribute



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2  
3 CB transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0  
4 CB transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0  
5 CB transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0  
6 NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.  
7 NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.  
8 NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.  
9 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
10 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
11 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
12 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
13 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
14 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
15 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
16 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
17 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C  
18 e (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0  
19 e (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0  
20 e (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0  
21 rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00  
22 rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00  
23 rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00  
24 rotein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007G  
25 rotein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007G  
26 rotein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007G  
27 e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10\_wheat : 383.0) & Enzyme classification.EC\_2  
28 e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10\_wheat : 383.0) & Enzyme classification.EC\_2  
29 e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10\_wheat : 383.0) & Enzyme classification.EC\_2  
30 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:  
31 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:  
32 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:  
33 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:  
34 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:  
35 ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00  
36 ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00  
37 ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00  
38 rription: pacid=37144799 transcript=Phvul.003G092500.1 locus=Phvul.003G092500 ID=Phvul.003GC  
39 rription: pacid=37144799 transcript=Phvul.003G092500.1 locus=Phvul.003G092500 ID=Phvul.003GC  
40 r) (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 I  
41 r) (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 I  
42 r) (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 I  
43 e (LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004  
44 e (LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004  
45 e (LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004  
46 e (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063  
47 e (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063  
48 e (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063  
49 e (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063

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2    ε (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063700.2  
3    ε (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063700.2  
4    α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2\_soybn : 540.0) & Enzyme C  
5    α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2\_soybn : 540.0) & Enzyme C  
6    α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2\_soybn : 554.0) & Enzyme C  
7    α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2\_soybn : 554.0) & Enzyme C  
8  
9  
10   sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800.2  
11   sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800.2  
12   sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800.2  
13  
14   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
15   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
16   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
17   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
18   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
19   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
20   ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2  
21  
22   r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=Phvul.008G212500.1  
23   r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=Phvul.008G212500.1  
24   r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=Phvul.008G212500.1  
25  
26   ription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G266300  
27   ription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G266300  
28   ription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G266300  
29  
30   ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Phvul.011G002600  
31   ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Phvul.011G002600  
32   ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Phvul.011G002600  
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34   ription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G194501  
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37  
38   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
39   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
40   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
41   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
42   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
43   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
44   factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2  
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46   ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Phvul.001G021750  
47   ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Phvul.001G021750  
48   ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Phvul.001G021750  
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50   ginal description: pacid=37169040 transcript=Phvul.001G168600.1 locus=Phvul.001G168600 ID=Phvul.001G168600  
51   ginal description: pacid=37169040 transcript=Phvul.001G168600.1 locus=Phvul.001G168600 ID=Phvul.001G168600  
52   ginal description: pacid=37176961 transcript=Phvul.002G010100.1 locus=Phvul.002G010100 ID=Phvul.002G010100  
53   ginal description: pacid=37176961 transcript=Phvul.002G010100.1 locus=Phvul.002G010100 ID=Phvul.002G010100  
54   ginal description: pacid=37176961 transcript=Phvul.002G010100.1 locus=Phvul.002G010100 ID=Phvul.002G010100  
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56   ginal description: pacid=37174417 transcript=Phvul.002G149100.1 locus=Phvul.002G149100 ID=Phvul.002G149100  
57   ginal description: pacid=37174417 transcript=Phvul.002G149100.1 locus=Phvul.002G149100 ID=Phvul.002G149100  
58  
59   ription: pacid=37174540 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G155200  
60   ription: pacid=37174540 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G155200  
PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G155200













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2 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
3 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
4 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
5 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
6 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
7 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
8 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC  
9  
10 BX of SCF E3 ubiquitin ligase complex (original description: pacid=37159322 transcript=Phvul.008G1  
11 BX of SCF E3 ubiquitin ligase complex (original description: pacid=37159322 transcript=Phvul.008G1  
12 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1  
13 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1  
14 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1  
15 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1  
16 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1  
17 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1  
18 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1  
19 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1  
20 rter (AUX/LAX) (original description: pacid=37160317 transcript=Phvul.008G225300.1 locus=Phvul.(  
21 ginal description: pacid=37159379 transcript=Phvul.008G230200.1 locus=Phvul.008G230200 ID=Ph  
22 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P  
23 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P  
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25 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P  
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28 :ription: pacid=37148543 transcript=Phvul.009G099700.1 locus=Phvul.009G099700 ID=Phvul.009GC  
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30 :ription: pacid=37151970 transcript=Phvul.009G233000.1 locus=Phvul.009G233000 ID=Phvul.009G2  
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35 ransporter (MEB) (original description: pacid=37143191 transcript=Phvul.010G021700.1 locus=Phv  
36 ransporter (MEB) (original description: pacid=37143191 transcript=Phvul.010G021700.1 locus=Phv  
37 ransporter (MEB) (original description: pacid=37143191 transcript=Phvul.010G021700.1 locus=Phv  
38 hydroxymethyltransferase (original description: pacid=37143671 transcript=Phvul.010G104900.2 l  
39 hydroxymethyltransferase (original description: pacid=37143671 transcript=Phvul.010G104900.2 l  
40 hydroxymethyltransferase (original description: pacid=37143671 transcript=Phvul.010G104900.2 l  
41 SP1 of NSP1-NSP2 nodulation initiation complex (original description: pacid=37144086 transcript=P  
42 SP1 of NSP1-NSP2 nodulation initiation complex (original description: pacid=37144086 transcript=P  
43 SP1 of NSP1-NSP2 nodulation initiation complex (original description: pacid=37144086 transcript=P  
44 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
45 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
46 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
47 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
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49 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
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56 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
57 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**  
58 SN4 of COP9 signalosome complex (original description: pacid=37156177 transcript=Phvul.011G006  
59 SN4 of COP9 signalosome complex (original description: pacid=37156177 transcript=Phvul.011G006  
60 SN4 of COP9 signalosome complex (original description: pacid=37156177 transcript=Phvul.011G006



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αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254\_glyur : 671.0) & Enzyme classificatio  
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254\_glyur : 671.0) & Enzyme classificatio  
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254\_glyur : 671.0) & Enzyme classificatio  
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254\_glyur : 483.0) & Enzyme classificatio  
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254\_glyur : 483.0) & Enzyme classificatio

Do not distribute

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3 I04G023066 ID=Phvul.004G023066.1.v2.1 annot-version=v2.1) &  
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32 ? transferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 125.6) (original  
33 ? transferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 125.6) (original  
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35 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &  
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46 I92500.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant protein 33 OS=Ar  
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48 I92500.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant protein 33 OS=Ar  
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6 :lassification.EC\_2 transferases.EC\_2.4 glycosyltransferase(50.2.4 : 144.7) (original description: pacic  
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23 Phvul.008G212500 ID=Phvul.008G212500.1.v2.1 annot-version=v2.1) &  
24 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju  
25 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju  
26 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju  
27 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju  
28 Phvul.011G002600.1.v2.1 annot-version=v2.1)  
29 Phvul.011G002600.1.v2.1 annot-version=v2.1)  
30 Phvul.011G002600.1.v2.1 annot-version=v2.1)  
31 194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t  
32 194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t  
33 194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t  
34 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &  
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37 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &  
38 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &  
39 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &  
40 Phvul.001G021750.1.v2.1 annot-version=v2.1)  
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42 Phvul.001G021750.1.v2.1 annot-version=v2.1)  
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45 Phvul.002G010100.1.v2.1 annot-version=v2.1)  
46 Phvul.002G010100.1.v2.1 annot-version=v2.1)  
47 Phvul.002G010100.1.v2.1 annot-version=v2.1)  
48 Phvul.002G149100.1.v2.1 annot-version=v2.1)  
49 Phvul.002G149100.1.v2.1 annot-version=v2.1)  
50 155200.1.v2.1 annot-version=v2.1) & BTB/POZ domain-containing protein At3g09030 OS=Arabidops  
51 155200.1.v2.1 annot-version=v2.1) & BTB/POZ domain-containing protein At3g09030 OS=Arabidops  
52 Phvul.002G211400.1 locus=Phvul.002G211400 ID=Phvul.002G211400.1.v2.1 annot-version=v2.1) &  
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40 vul.009G097000.2.v2.1 annot-version=v2.1)  
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42 vul.009G097000.2.v2.1 annot-version=v2.1)  
43 vul.009G122000.1.v2.1 annot-version=v2.1)  
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57 vul.009G227900.3.v2.1 annot-version=v2.1)  
58 vul.010G159600.1.v2.1 annot-version=v2.1)  
59 vul.010G159600.1.v2.1 annot-version=v2.1)  
60 J84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (:

1  
2 J84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (;  
3 J84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (;  
4 vl.011G130500.1 locus=Phvul.011G130500 ID=Phvul.011G130500.1.v2.1 annot-version=v2.1) &  
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6 vl.011G130500.1 locus=Phvul.011G130500 ID=Phvul.011G130500.1.v2.1 annot-version=v2.1) &  
7 sferases.EC\_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript  
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9 sferases.EC\_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript  
10 198100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidop:  
11 198100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidop:  
12 198100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidop:  
13 vl.001G199500.1.v2.1 annot-version=v2.1)  
14 vl.001G199500.1.v2.1 annot-version=v2.1)  
15 vl.001G199500.1.v2.1 annot-version=v2.1)  
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26 vl.002G132700.1.v2.1 annot-version=v2.1)  
27 vl.002G141000.2.v2.1 annot-version=v2.1)  
28 vl.002G141000.2.v2.1 annot-version=v2.1)  
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31 =37144465 transcript=Phvul.003G131900.1 locus=Phvul.003G131900 ID=Phvul.003G131900.1.v2.1  
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34 is=Phvul.003G225700 ID=Phvul.003G225700.1.v2.1 annot-version=v2.1) &  
35 238000.1.v2.1 annot-version=v2.1) & Suppressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|  
36 238000.1.v2.1 annot-version=v2.1) & Suppressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|  
37 vl.003G259300.1.v2.1 annot-version=v2.1)  
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41 vl.003G259300.1.v2.1 annot-version=v2.1)  
42 vl.003G259300.1.v2.1 annot-version=v2.1)  
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47 vl.003G259300.1.v2.1 annot-version=v2.1)  
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49 vl.003G259300.1.v2.1 annot-version=v2.1)  
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56 vl.003G259300.1.v2.1 annot-version=v2.1)  
57 vl.003G259300.1.v2.1 annot-version=v2.1)  
58 vl.003G259300.1.v2.1 annot-version=v2.1)  
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1 :G037700 ID=Phvul.004G037700.3.v2.1 annot-version=v2.1) &  
2 :G037700 ID=Phvul.004G037700.3.v2.1 annot-version=v2.1) &  
3 :G037700 ID=Phvul.004G037700.3.v2.1 annot-version=v2.1) &  
4 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &  
5 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &  
6 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &  
7 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &  
8 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &  
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11 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &  
12 1700 ID=Phvul.004G174700.1.v2.1 annot-version=v2.1) &  
13 1700 ID=Phvul.004G174700.1.v2.1 annot-version=v2.1) &  
14 1700 ID=Phvul.004G174700.1.v2.1 annot-version=v2.1) &  
15 500 ID=Phvul.005G125500.1.v2.1 annot-version=v2.1) &  
16 500 ID=Phvul.005G125500.1.v2.1 annot-version=v2.1) &  
17 500 ID=Phvul.005G125500.1.v2.1 annot-version=v2.1) &  
18 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &  
19 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &  
20 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &  
21 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &  
22 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &  
23 vul.007G072700.9.v2.1 annot-version=v2.1)  
24 vul.007G072700.9.v2.1 annot-version=v2.1)  
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51 vul.007G072700.9.v2.1 annot-version=v2.1)  
52 vul.007G215400.1.v2.1 annot-version=v2.1)  
53 vul.007G215400.1.v2.1 annot-version=v2.1)  
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55 vul.007G215400.1.v2.1 annot-version=v2.1)  
56 249800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis  
57 249800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis  
58 249800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis  
59 J74600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana  
60 J74600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana



1 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana  
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10 123400.1 locus=Phvul.008G123400 ID=Phvul.008G123400.1.v2.1 annot-version=v2.1) &  
11 123400.1 locus=Phvul.008G123400 ID=Phvul.008G123400.1.v2.1 annot-version=v2.1) &  
12 129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s  
13 129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s  
14 129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s  
15 164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At  
16 164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At  
17 164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At  
18 008G225300 ID=Phvul.008G225300.1.v2.1 annot-version=v2.1) &  
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23 Phvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &  
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25 Phvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &  
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27 099700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis  
28 099700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis  
29 099700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis  
30 233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q  
31 233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q  
32 233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q  
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35 ul.010G021700 ID=Phvul.010G021700.1.v2.1 annot-version=v2.1) &  
36 ul.010G021700 ID=Phvul.010G021700.1.v2.1 annot-version=v2.1) &  
37 ul.010G021700 ID=Phvul.010G021700.1.v2.1 annot-version=v2.1) &  
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39 locus=Phvul.010G104900 ID=Phvul.010G104900.2.v2.1 annot-version=v2.1) &  
40 locus=Phvul.010G104900 ID=Phvul.010G104900.2.v2.1 annot-version=v2.1) &  
41 locus=Phvul.010G104900 ID=Phvul.010G104900.2.v2.1 annot-version=v2.1) &  
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43 Phvul.010G129400.1 locus=Phvul.010G129400 ID=Phvul.010G129400.1.v2.1 annot-version=v2.1) &  
44 Phvul.010G129400.1 locus=Phvul.010G129400 ID=Phvul.010G129400.1.v2.1 annot-version=v2.1) &  
45 Phvul.010G129400.1 locus=Phvul.010G129400 ID=Phvul.010G129400.1.v2.1 annot-version=v2.1) &  
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47 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar  
48 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar  
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59 5200.1 locus=Phvul.011G006200 ID=Phvul.011G006200.1.v2.1 annot-version=v2.1) &  
60 5200.1 locus=Phvul.011G006200 ID=Phvul.011G006200.1.v2.1 annot-version=v2.1) &  
5200.1 locus=Phvul.011G006200 ID=Phvul.011G006200.1.v2.1 annot-version=v2.1) &

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I description: pacid=37168185 transcript=Phvul.001G070000.1 locus=Phvul.001G070000 ID=Phvul.C  
I description: pacid=37168185 transcript=Phvul.001G070000.1 locus=Phvul.001G070000 ID=Phvul.C  
I description: pacid=37168185 transcript=Phvul.001G070000.1 locus=Phvul.001G070000 ID=Phvul.C

abidopsis thaliana (sp|f4jzl7|hip33\_arath : 120.0)  
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4 d=37166010 transcript=Phvul.007G020600.1 locus=Phvul.007G020600 ID=Phvul.007G020600.1.v2.:  
5 d=37166010 transcript=Phvul.007G020600.1 locus=Phvul.007G020600 ID=Phvul.007G020600.1.v2.:  
6 d=37164227 transcript=Phvul.007G020700.1 locus=Phvul.007G020700 ID=Phvul.007G020700.1.v2.:  
7 d=37164227 transcript=Phvul.007G020700.1 locus=Phvul.007G020700 ID=Phvul.007G020700.1.v2.:  
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26 i7|ppa18\_arath : 655.0)  
27 i7|ppa18\_arath : 655.0)  
28 i7|ppa18\_arath : 655.0)  
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33 :haliana (sp|q9m0x5|crk25\_arath : 142.0)  
34 :haliana (sp|q9m0x5|crk25\_arath : 142.0)  
35 :haliana (sp|q9m0x5|crk25\_arath : 142.0)  
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58 sis thaliana (sp|q9s7r7|y3903\_arath : 505.0)  
59 sis thaliana (sp|q9s7r7|y3903\_arath : 505.0)  
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2 sp|q9fjh6|ab1f\_arath : 941.0)

3 sp|q9fjh6|ab1f\_arath : 941.0)  
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8 :=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

9 :=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

10 :=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

11 sis thaliana (sp|q9lrr4|r13l1\_arath : 526.0)

12 sis thaliana (sp|q9lrr4|r13l1\_arath : 526.0)

13 sis thaliana (sp|q9lrr4|r13l1\_arath : 526.0)  
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41 annot-version=v2.1) &

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43 annot-version=v2.1) &

44 |srfr1\_arath : 1278.0)

45 |srfr1\_arath : 1278.0)  
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thaliana (sp|q9sr79|ppa16\_arath : 484.0)  
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 (sp|f4ig73|bchc2\_arath : 2405.0)  
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2 1 (sp|f4ig73|bchc2\_arath : 2405.0)  
3 1 (sp|f4ig73|bchc2\_arath : 2405.0)  
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12 sp|q3ebc8|dcl2\_arath : 1293.0)  
13 sp|q3ebc8|dcl2\_arath : 1293.0)  
14 sp|q3ebc8|dcl2\_arath : 1293.0)  
15 t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570\_arath : 285.0)  
16 t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570\_arath : 285.0)  
17 t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570\_arath : 285.0)  
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27 . thaliana (sp|q9m086|dcf1\_arath : 1457.0)  
28 . thaliana (sp|q9m086|dcf1\_arath : 1457.0)  
29 . thaliana (sp|q9m086|dcf1\_arath : 1457.0)  
30 |6nmm1|got1\_arath : 139.0)  
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action of molecular oxygen(50.1.13 : 128.5) (original description: pacid=37155695 transcript=Phvul.  
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8	uaaucugcaucc	Phvul.001G094400.1	1	-1	1	21
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26	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
27	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
28	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
29	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
30	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
31	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
32	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
33	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
34	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
35	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
36	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
37	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
38	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
39	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
40	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
41	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
42	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
43	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
44	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
45	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
46	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
47	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
48	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
49	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
50	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
51	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
52	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
53	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
54	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
55	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
56	uaaucugcaucc Phvul.009G207500.2	5	-1	1	21
57	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
58	uaaucugcaucc Phvul.009G207500.1	5	-1	1	21
59	uaaucugcaucc Phvul.009G219300.1	5	-1	1	21
60	uaaucugcaucc Phvul.009G219300.1	5	-1	1	21
	uaaucugcaucc Phvul.009G219300.1	5	-1	1	21



1					
2	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
3	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
4	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
5	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
6	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
7	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
8	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
9	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
10	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
11	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
12	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
13	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
14	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
15	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
16	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
17	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
18	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
19	uaaucugcaucc Phvul.011G091400.1	5	-1	1	21
20	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
21	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
22	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
23	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
24	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
25	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
26	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
27	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
28	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
29	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
30	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
31	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
32	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
33	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
34	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
35	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
36	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
37	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
38	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
39	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
40	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
41	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
42	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
43	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
44	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
45	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
46	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
47	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
48	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
49	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
50	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
51	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
52	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
53	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
54	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
55	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
56	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
57	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
58	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
59	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
60	uaaucugcaucc Phvul.L002060.2	5	-1	1	21



1					
2	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
3	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
4	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
5					
6	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
7	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
8	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
9					
10	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
11	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
12	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
13					
14	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
15	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
16	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
17					
18	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
19	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
20	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
21					
22	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
23	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
24	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
25					
26	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
27	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
28	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
29					
30	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
31	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
32	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
33					
34	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
35	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
36	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
37					
38	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
39	uaaucugcaucc Phvul.L002060.3	5	-1	1	21
40	uaaucugcaucc Phvul.L002060.2	5	-1	1	21
41					
42	uaaucugcaucc Phvul.L002060.1	5	-1	1	21
43					
44					
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48					
49					
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51					
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57					
58					
59					
60					





















1				
2	427	447 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
3	352	372 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
4	427	447 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
5				
6	352	372 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
7	427	447 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
8				
9	352	372 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
10	427	447 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
11	352	372 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
12	427	447 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
13				
14	352	372 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
15	427	447 UAAUCUGCAL	::: : : ::::::::::: UGAAAUUAG(Cleavage	pacid=371452
16	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
17				
18	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
19				
20	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
21				
22	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
23				
24	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
25				
26	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
27				
28	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
29				
30	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
31				
32	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
33				
34	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
35				
36	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
37				
38	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
39				
40	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
41				
42	26	46 UAAUCUGCAL	::: .. ::::::::::: GUAACGUUG(Cleavage	pacid=371445
43				
44	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
45				
46	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
47				
48	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
49				
50	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
51				
52	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
53				
54	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
55				
56	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
57				
58	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
59				
60	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534
	222	242 UAAUCUGCAL	::::::::::::::: GUUGC UUCA(Cleavage	pacid=371534









1					
2	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
3	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
4	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
5	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
6	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
7	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
8	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
9					
10	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
11	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
12	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
13	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
14	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
15	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
16	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
17					
18	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
19	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
20	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
21					
22	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
23	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
24	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
25					
26	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
27	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
28	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
29					
30	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
31	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
32	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
33					
34	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
35	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
36	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
37					
38	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
39	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
40	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
41					
42	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
43	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
44	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
45	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
46					
47	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
48	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
49					
50	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
51	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
52	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
53	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
54					
55	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
56	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
57	575	595 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
58	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
59					
60	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	
	742	762 UAAUCUGCAL	.....: GUUGCUUCA(Cleavage	pacid=371658	

































































1				
2	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
3	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
4	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
5				
6	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
7	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
8	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
9				
10	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
11	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
12	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
13				
14	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
15	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
16	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
17				
18	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
19	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
20	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
21				
22	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
23	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
24	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
25	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
26	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
27				
28	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
29	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
30	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
31	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
32	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
33				
34	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
35	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
36	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
37				
38	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
39	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
40	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
41	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
42	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
43				
44	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
45	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
46	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
47				
48	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
49	1868	1888 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
50	1214	1234 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
51	1684	1704 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
52	1681	1701 UAAUCUGCAL :..... : .....	UGGGCUUGG Cleavage	pacid=371651
53	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
54	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
55	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
56	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
57	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
58	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
59	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
60	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594
	259	279 UAAUCUGCAL :..... : .....	GAAACUUCAC Translation	pacid=371594



































1				
2	970	990 UAAUCUGCAL :::: : .....	UAAAUUUUG (Cleavage	pacid=371744
3	970	990 UAAUCUGCAL :::: : .....	UAAAUUUUG (Cleavage	pacid=371744
4	970	990 UAAUCUGCAL :::: : .....	UAAAUUUUG (Cleavage	pacid=371744
5				
6	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
7	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
8	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
9				
10	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
11	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
12	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
13				
14	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
15	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
16	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
17				
18	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
19	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
20	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
21				
22	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
23	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
24	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
25				
26	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
27	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
28	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
29				
30	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
31	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
32	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
33				
34	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
35	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
36	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
37	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
38				
39	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
40	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
41	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
42				
43	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
44	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
45	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
46				
47	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
48	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
49	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
50				
51	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
52	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
53	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
54				
55	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
56	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
57	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
58				
59	2673	2697 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
60	2728	2752 UAAUCUGCAL :::: : .....	UAAGCUUUG (Cleavage	pacid=371756
	377	397 UAAUCUGCAL :::: : .....	UAAACCAGAC (Cleavage	pacid=371772



































1				
2	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
3	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
4	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
5	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
6	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
7	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
8	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
9	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
10	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
11	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
12	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
13	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
14	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
15	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
16	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
17	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
18	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
19	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
20	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
21	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
22	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
23	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
24	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
25	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
26	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
27	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
28	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
29	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
30	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
31	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
32	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
33	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
34	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
35	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
36	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
37	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
38	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
39	754	774 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
40	798	818 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
41	861	881 UAAUCUGCAL	:::::::::: :... : AAAACCUUAC	Cleavage pacid=371574
42				
43				
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1				
2	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
3	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
4	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
5				
6	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
7	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
8	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
9				
10	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
11	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
12	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
13				
14	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
15	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
16	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
17				
18	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
19	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
20	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
21				
22	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
23	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
24	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
25				
26	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
27	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
28	1 Phvul.L002946.2	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
29				
30	1 Phvul.L002946.3	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
31	1 Phvul.L002946.1	Phvul.L002946	Phvul.L00294(PF01833,PF13PTHR23335,P	
32	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
33	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
34				
35	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
36	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
37				
38	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
39	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
40				
41	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
42	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
43				
44	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
45	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
46				
47	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
48	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
49				
50	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
51	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
52				
53	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
54	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
55				
56	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
57	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
58				
59	1 Phvul.002G141800.1	Phvul.002G141800	Phvul.002G14 PF05678	PTHR33783,P
60	1 Phvul.001G062700.2	Phvul.001G062700	Phvul.001G06 PF00566	PTHR22957,P
	1 Phvul.001G062700.2	Phvul.001G062700	Phvul.001G06 PF00566	PTHR22957,P

















































1				
2	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
3	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
4	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
5				
6	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
7	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
8	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
9				
10	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
11	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
12	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
13				
14	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
15	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
16	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
17				
18	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
19	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
20	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
21				
22	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
23	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
24	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
25				
26	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
27	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
28	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
29				
30	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
31	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
32	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
33				
34	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
35	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
36	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
37				
38	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
39	1 Phvul.L002060.3	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
40	1 Phvul.L002060.2	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
41				
42	1 Phvul.L002060.1	Phvul.L002060	Phvul.L002060(PF00155	PTHR10289,P
43				
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60				

1	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol	
2						
3		0	0	0 GO:0005515	AT3G27150.1	0
4		0	0	0 GO:0005515	AT3G27150.1	0
5		0	0	0 GO:0005515	AT3G27150.1	0
6		0	0	0 GO:0005515	AT3G27150.1	0
7		0	0	0 GO:0005515	AT3G27150.1	0
8		0	0	0 GO:0005515	AT3G27150.1	0
9		0	0	0 GO:0005515	AT3G27150.1	0
10		0	0	0 GO:0005515	AT3G27150.1	0
11		0	0	0 GO:0005515	AT3G27150.1	0
12		0	0	0 GO:0005515	AT3G27150.1	0
13		0	0	0 GO:0005515	AT3G27150.1	0
14		0	0	0 GO:0005515	AT3G27150.1	0
15		0	0	0 GO:0005515	AT3G27150.1	0
16		0	0	0 GO:0005515	AT3G27150.1	0
17		0	0	0 GO:0005515	AT3G27150.1	0
18		0	0	0 GO:0005515	AT3G27150.1	0
19		0	0	0 GO:0005515	AT3G27150.1	0
20		0	0	0 GO:0005515	AT3G27150.1	0
21		0	0	0 GO:0005515	AT3G27150.1	0
22		0	0	0 GO:0005515	AT3G27150.1	0
23		0	0	0 GO:0005515	AT3G27150.1	0
24		0	0	0 GO:0005515	AT3G27150.1	0
25		0	0	0 GO:0005515	AT3G27150.1	0
26		0	0	0 GO:0005515	AT3G27150.1	0
27		0	0	0 GO:0005515	AT3G27150.1	0
28		0	0	0 GO:0005515	AT3G27150.1	0
29		0	0	0 GO:0005515	AT3G27150.1	0
30		0	0	0 GO:0005515	AT3G27150.1	0
31	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
32	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
33	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
34	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
35	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
36	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
37	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
38	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
39	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
40	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
41	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
42	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
43	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
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45	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
46	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
47	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
48	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
49	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
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51	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
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53	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
54	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
55	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
56	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
57	KOG1558		0 K14709	GO:0055085,(AT1G10970.1	ATZIP4,ZIP4	
58						
59		0 2.7.11.1		0 GO:0005515	AT3G28890.1 AtRLP43,RLP43	
60		0 2.7.11.1		0 GO:0005515	AT3G28890.1 AtRLP43,RLP43	
		0 2.7.11.1		0 GO:0005515	AT3G28890.1 AtRLP43,RLP43	

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2	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
3	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
4	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
5	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
6	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
7	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
8	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
9	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
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17	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
18	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
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22	0	2.7.11.1	0 GO:0005515 AT3G28890.1 AtRLP43,RLP43	
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25	0			
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27	0	0	0 GO:0005515 AT5G12300.1	0
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29	0	0	0 GO:0005515 AT5G12300.1	0
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32	0	0	0 GO:0005515 AT5G12300.1	0
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34	0	0	0 GO:0005515 AT5G12300.1	0
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36	0	0	0 GO:0005515 AT5G12300.1	0
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47	0	0	0 GO:0005515 AT5G12300.1	0
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49	0	0	0 GO:0005515 AT5G12300.1	0
50	0	0	0 GO:0005515 AT5G12300.1	0
51	0	0	0 GO:0005515 AT5G12300.1	0
52	0	0	0 GO:0005515 AT5G12300.1	0
53	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
54	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
55	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
56	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
57	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
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59	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
60	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	

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3	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
4	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
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13				
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17	KOG0907	3.5.1.52	0 GO:0045454,(AT1G08570.1 ACHT4	
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25		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
26		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
27		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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37		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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39		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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41		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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43		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
44		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
45		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
46		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
47		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
48		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
49		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
50		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
51		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
52		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
53		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
54		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
55		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
56		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
57		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
58		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
59		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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		0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0

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2	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
3	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
4	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
5			
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7	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
8	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
9			
10	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
11	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
12	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
13			
14	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
15	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
16	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
17	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
18	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
19	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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23	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
24	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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26	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
27	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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36	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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38	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
39	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
40	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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42	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
43	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
44	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
45	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
46			
47	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
48	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
49	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
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51	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
52	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
53	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
54			
55	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
56	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
57	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
58			
59	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
60	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0
	0 3.2.1.39	0 GO:0005975,(AT4G31140.1	0

1				
2	0 3.2.1.39		0 GO:0005975,(AT4G31140.1	0
3	0 3.2.1.39		0 GO:0005975,(AT4G31140.1	0
4	0 3.2.1.39		0 GO:0005975,(AT4G31140.1	0
5	0 3.2.1.39		0 GO:0005975,(AT4G31140.1	0
6	0 3.2.1.39		0 GO:0005975,(AT4G31140.1	0
7	0 3.2.1.39		0 GO:0005975,(AT4G31140.1	0
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9	0		0 GO:0003676,(AT3G53500.2 RSZ32	0
10	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
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12	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
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31	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
32	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
33	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
34	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
35	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
36	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
37	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
38	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
39	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
40	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
41	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
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43	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
44	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
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58	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
59	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
60	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	
	0	0	0 GO:0003676,(AT3G53500.2 RSZ32	



1			
2	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
3	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
4	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
5	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
6	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
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22	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
23	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
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25	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
26	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
27	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
28	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
29	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
30	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
31	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
32	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
33	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
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46	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
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53	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
54	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
55	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
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57	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
58	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
59	0	0	0 GO:0003676,(AT3G53500.2 RSZ32
60	KOG1448	2.7.6.1	0 GO:0009116 AT1G10700.1 PRS3
	KOG1448	2.7.6.1	0 GO:0009116 AT1G10700.1 PRS3



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2	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
3	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
4	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
5	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
6	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
7	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
8	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
9	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
10	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
11	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
12	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
13	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
14	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
15	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
16	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
17	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
18	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
19	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
20	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
21	KOG2095	2.7.7.7	K03509	GO:0006281,(AT5G44740.2	POLH	
22	KOG1853,KOC		0	0	0 AT4G03000.1	0
23	KOG1853,KOC		0	0	0 AT4G03000.1	0
24	KOG1853,KOC		0	0	0 AT4G03000.1	0
25	KOG1853,KOC		0	0	0 AT4G03000.1	0
26	KOG1853,KOC		0	0	0 AT4G03000.1	0
27	KOG1853,KOC		0	0	0 AT4G03000.1	0
28	KOG1853,KOC		0	0	0 AT4G03000.1	0
29	KOG1853,KOC		0	0	0 AT4G03000.1	0
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31	KOG1853,KOC		0	0	0 AT4G03000.1	0
32	KOG1853,KOC		0	0	0 AT4G03000.1	0
33	KOG1853,KOC		0	0	0 AT4G03000.1	0
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35	KOG1853,KOC		0	0	0 AT4G03000.1	0
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38	KOG1853,KOC		0	0	0 AT4G03000.1	0
39	KOG1853,KOC		0	0	0 AT4G03000.1	0
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41	KOG1853,KOC		0	0	0 AT4G03000.1	0
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45	KOG1853,KOC		0	0	0 AT4G03000.1	0
46	KOG1853,KOC		0	0	0 AT4G03000.1	0
47	KOG1853,KOC		0	0	0 AT4G03000.1	0
48	KOG1853,KOC		0	0	0 AT4G03000.1	0
49	KOG1853,KOC		0	0	0 AT4G03000.1	0
50	KOG1853,KOC		0	0	0 AT4G03000.1	0
51	KOG1853,KOC		0	0	0 AT4G03000.1	0
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53	KOG1853,KOC		0	0	0 AT4G03000.1	0
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59	KOG1853,KOC		0	0	0 AT4G03000.1	0
60	KOG1853,KOC		0	0	0 AT4G03000.1	0
	KOG1853,KOC		0	0	0 AT4G03000.1	0

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2	KOG1853,KOC	0	0	0 AT4G03000.1	0
3	KOG1853,KOC	0	0	0 AT4G03000.1	0
4	KOG1853,KOC	0	0	0 AT4G03000.1	0
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6	KOG1853,KOC	0	0	0 AT4G03000.1	0
7	KOG1853,KOC	0	0	0 AT4G03000.1	0
8	KOG1853,KOC	0	0	0 AT4G03000.1	0
9	KOG1853,KOC	0	0	0 AT4G03000.1	0
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15	KOG1853,KOC	0	0	0 AT4G03000.1	0
16	0	0	0	0 AT4G16695.1	0
17	0	0	0	0 AT4G16695.1	0
18	0	0	0	0 AT4G16695.1	0
19	0	0	0	0 AT4G16695.1	0
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21	0	0	0	0 AT4G16695.1	0
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27	0	0	0	0 AT4G16695.1	0
28	0	0	0	0 AT4G16695.1	0
29	0	0	0	0 AT4G16695.1	0
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33	0	0	0	0 AT4G16695.1	0
34	0	0	0	0 AT4G16695.1	0
35	0	0	0	0 AT4G16695.1	0
36	0	0	0	0 AT4G16695.1	0
37	0	0	0	0 AT4G16695.1	0
38	0	0	0	0 AT4G16695.1	0
39	0	0	0	0 AT4G16695.1	0
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41	0	0	0	0 AT4G16695.1	0
42	0	0	0	0 AT4G16695.1	0
43	0	0	0	0 AT4G16695.1	0
44	0	0	0	0 GO:0019901,(AT5G48630.2	0
45	0	0	0	0 GO:0019901,(AT5G48630.2	0
46	0	0	0	0 GO:0019901,(AT5G48630.2	0
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48	0	0	0	0 GO:0019901,(AT5G48630.2	0
49	0	0	0	0 GO:0019901,(AT5G48630.2	0
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52	0	0	0	0 GO:0019901,(AT5G48630.2	0
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60	0	0	0	0 GO:0019901,(AT5G48630.2	0
	0	0	0	0 GO:0019901,(AT5G48630.2	0

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2	0	0	0	GO:0019901,AT5G48630.2	0
3	0	0	0	GO:0019901,AT5G48630.2	0
4	0	0	0	GO:0019901,AT5G48630.2	0
5	0	0	0	GO:0019901,AT5G48630.2	0
6	0	0	0	GO:0019901,AT5G48630.2	0
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39	0	0	0	AT3G10420.2	0
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7	0	0	0	0 AT1G25550.1	0
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12	0	0	0	0 AT1G25550.1	0
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19	0	0	0	0 AT1G25550.1	0
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26	0	0	0	0 AT1G25550.1	0
27	0	0	0	0 AT1G25550.1	0
28	0	0	0	0 AT1G25550.1	0
29	0	0	0	0 AT1G25550.1	0
30	0	0	0	0 AT1G25550.1	0
31	0	0	0	0 AT1G25550.1	0
32	0	0	0	0 AT1G25550.1	0
33	0	0	0	0 GO:0019901,(AT5G48630.1	0
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49	0	0	0	0 GO:0019901,(AT5G48630.1	0
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57	0	0	0	0 GO:0019901,(AT5G48630.1	0
58	0	0	0	0 GO:0019901,(AT5G48630.1	0
59	0	0	0	0 GO:0019901,(AT5G48630.1	0
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2	0	0	0 GO:0019901,(AT5G48630.1	0
3	0	0	0 GO:0019901,(AT5G48630.1	0
4	0	0	0 GO:0019901,(AT5G48630.1	0
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33	0	0	0 GO:0019901,(AT5G48630.1	0
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60	0	0	0 GO:0019901,(AT5G48630.1	0
	0	0	0 GO:0019901,(AT5G48630.1	0



1				
2	0	0	0 GO:0019901,(AT5G48630.1	0
3	0	0	0 GO:0019901,(AT5G48630.1	0
4	0	0	0 GO:0019901,(AT5G48630.1	0
5	0	0	0 GO:0019901,(AT5G48630.1	0
6	0	0	0 GO:0019901,(AT5G48630.1	0
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7	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
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9	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
10	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
11	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
12	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
13	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
14	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
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16	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
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23	KOG1187	2.7.11.1	0	GO:0005515,(AT3G56370.1	0
24		0	0	0 AT4G37460.1 SRFR1	
25		0	0	0 AT4G37460.1 SRFR1	
26		0	0	0 AT4G37460.1 SRFR1	
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52	KOG2521		0	0 AT2G18245.1	0
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	KOG2521		0	0 AT2G18245.1	0

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2	KOG2521	0	0	0 AT2G18245.1	0
3	KOG2521	0	0	0 AT2G18245.1	0
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45	KOG2521	0	0	0 AT2G18245.1	0
46					
47	0	0	0	0 GO:0019901,(AT5G45190.1	0
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	0	0	0 GO:0019901,(AT5G45190.1	0

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2	0	0	0 GO:0019901,(AT5G45190.1	0
3	0	0	0 GO:0019901,(AT5G45190.1	0
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5	0	0	0 GO:0019901,(AT5G45190.1	0
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57	0	0	0 GO:0019901,(AT5G45190.1	0
58	0	0	0 GO:0019901,(AT5G45190.1	0
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60	0	0	0 GO:0019901,(AT5G45190.1	0
	0	0	0 GO:0019901,(AT5G45190.1	0



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2	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
3	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
4	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
5	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
6	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
7	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
8	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
9	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
10	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
11	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
12	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
13	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
14	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
15	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
16	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
17	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
18	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
19	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
20	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
21	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
22	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
23	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
24	KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1 ATGSTU18,GST29,GSTL	
25	KOG1650		0	0	GO:0006813,(AT4G04850.2 ATKEA3,KEA3	
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52	KOG1650		0	0	GO:0006813,(AT4G04850.2 ATKEA3,KEA3	
53		0	0	0	0 AT5G42655.1	0
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57		0	0	0	0 AT5G42655.1	0
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		0	0	0	0 AT5G42655.1	0

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2	0	0	0	0 AT5G42655.1	0
3	0	0	0	0 AT5G42655.1	0
4	0	0	0	0 AT5G42655.1	0
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19	0	0	0	0 AT5G42655.1	0
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36	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
37	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
38	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
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41	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
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43	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
44	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
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46	0 3.6.4.4	K10395	GO:0008017,(AT5G47820.2 FRA1		
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15	KOG4529	0	0	0 AT1G73380.1	0
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17	KOG4529	0	0	0 AT1G73380.1	0
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23	KOG4529	0	0	0 AT1G73380.1	0
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41	KOG4529	0	0	0 AT1G73380.1	0
42	KOG4529	0	0	0 AT1G73380.1	0
43		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
44		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
45		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
46		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
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52		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
53		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
54		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
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56		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
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59		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
60		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	
		0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA	



1					
2		0	0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA
3		0	0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA
4		0	0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA
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6		0	0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA
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9		0	0	0	0 AT1G65680.1 ATEXPB2,ATHEXP BETA
10	KOG4495		0	0	GO:0005515 AT5G57860.3 0
11	KOG4495		0	0	GO:0005515 AT5G57860.3 0
12	KOG4495		0	0	GO:0005515 AT5G57860.3 0
13	KOG4495		0	0	GO:0005515 AT5G57860.3 0
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15	KOG4495		0	0	GO:0005515 AT5G57860.3 0
16	KOG4495		0	0	GO:0005515 AT5G57860.3 0
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22	KOG4495		0	0	GO:0005515 AT5G57860.3 0
23	KOG4495		0	0	GO:0005515 AT5G57860.3 0
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25	KOG4495		0	0	GO:0005515 AT5G57860.3 0
26	KOG4495		0	0	GO:0005515 AT5G57860.3 0
27	KOG4495		0	0	GO:0005515 AT5G57860.3 0
28	KOG4495		0	0	GO:0005515 AT5G57860.3 0
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37		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
38		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
39		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
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41		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
42		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
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45		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
46		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
47		0	2.7.11.22,2.7.	0	GO:0006468,(AT5G39420.1 cdc2cAt
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3	KOG4696	0	0	0 AT5G24680.1	0
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56	0 3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1	
57	0 3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1	
58	0 3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1	
59	0 3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1	
60	0 3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1	
	0 3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1	

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37	KOG0257	2.6.1.78,2.6.1	K15849
38	KOG0257	2.6.1.78,2.6.1	K15849
39	KOG0257	2.6.1.78,2.6.1	K15849
40	KOG0257	2.6.1.78,2.6.1	K15849
41	KOG0257	2.6.1.78,2.6.1	K15849
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45	KOG0257	2.6.1.78,2.6.1	K15849
46	KOG0257	2.6.1.78,2.6.1	K15849
47	KOG0257	2.6.1.78,2.6.1	K15849
48	KOG0257	2.6.1.78,2.6.1	K15849
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3	0	0 K15164	GO:0016592,(AT1G55325.2 GCT		
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14	0	0 K15164	GO:0016592,(AT1G55325.2 GCT		
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19	0	0	0 AT2G22560.1		0
20	0	0	0 AT2G22560.1		0
21	0	0	0 AT2G22560.1		0
22	0	0	0 AT2G22560.1		0
23	0	0	0 AT2G22560.1		0
24	0	0	0 AT2G22560.1		0
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37	0	0	0 AT2G22560.1		0
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44	0	0	0 AT1G34370.2 STOP1		
45	0	0	0 AT1G34370.2 STOP1		
46	0	0	0 AT1G34370.2 STOP1		
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57	0	0	0 AT1G34370.2 STOP1		
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59	0	0	0 AT1G34370.2 STOP1		
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2	0	0	0	0	AT1G34370.2 STOP1	
3	0	0	0	0	AT1G34370.2 STOP1	
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12	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
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21	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
22	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
23	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
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25	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
26	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
27	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
28	0 2.3.1.12			0	GO:0016746,(AT3G25860.1 LTA2,PLE2	
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1						
2	0	0	0	0	0	0
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4	0	0	0	0	0	0
5						
6	0 1.2.1.3		0	GO:0055114,(AT3G66658.2	ALDH22A1	
7	0 1.2.1.3		0	GO:0055114,(AT3G66658.2	ALDH22A1	
8	0 1.2.1.3		0	GO:0055114,(AT3G66658.2	ALDH22A1	
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10	0 1.2.1.3		0	GO:0055114,(AT3G66658.2	ALDH22A1	
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19	0 1.2.1.3		0	GO:0055114,(AT3G66658.2	ALDH22A1	
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53	0	0 K13462	0	GO:0032012,(AT3G43300.1	ATMIN7,BEN1	
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55	0	0 K13462	0	GO:0032012,(AT3G43300.1	ATMIN7,BEN1	
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57	0	0 K13462	0	GO:0032012,(AT3G43300.1	ATMIN7,BEN1	
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	0	0 K17086	0	GO:0016021	AT5G35160.2	0

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2	0	0 K17086	GO:0016021 AT5G35160.2		0
3	0	0 K17086	GO:0016021 AT5G35160.2		0
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5	0	0 K17086	GO:0016021 AT5G35160.2		0
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7	0	0 K17086	GO:0016021 AT5G35160.2		0
8	0	0 K17086	GO:0016021 AT5G35160.2		0
9	0	0 K17086	GO:0016021 AT5G35160.2		0
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23	0	0 K17086	GO:0016021 AT5G35160.2		0
24	0	0 K17086	GO:0016021 AT5G35160.2		0
25	0	0 K17086	GO:0016021 AT5G35160.2		0
26	0	0 K17086	GO:0016021 AT5G35160.2		0
27	0	0 K17086	GO:0016021 AT5G35160.2		0
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29	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
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35	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
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37	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
38	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
39	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
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41	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
42	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
43	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
44	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
45	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
46	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
47	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
48	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
49	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
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55	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
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59	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		
60	0	0	0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H		



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2	0	0	0	GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H	
3	0	0	0	GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H	
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9	0	0	0	GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H	
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21	0	0	0	GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H	
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23	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
24	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
25	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
26	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
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28	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
29	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
30	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
31	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
32	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
33	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
34	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
35	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
36	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
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38	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
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42	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
43	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
44	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
45	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
46	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
47	KOG4208	0 K14838	GO:0003676	AT5G04600.1	0
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56	0	0	0	AT5G54970.1	0
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5	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26330.1 CYP71B37		
6	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26330.1 CYP71B37		
7	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26330.1 CYP71B37		
8	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26330.1 CYP71B37		
9	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26330.1 CYP71B37		
10	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26330.1 CYP71B37		
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16	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26300.1 CYP71B34		
17	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26300.1 CYP71B34		
18	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26300.1 CYP71B34		
19	KOG0156	1.14.13.121	0	GO:0055114,(AT3G26300.1 CYP71B34		
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47		0	0	0	AT5G47380.1	0
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		0	0	0	AT5G47380.1	0

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4		0	0	0	0 AT5G47380.1
5		0	0	0	0 AT5G47380.1
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6	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
7	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
8	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
9					
10	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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19	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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23	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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29					
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37					
38	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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41					
42	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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46					
47	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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49					
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54	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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57					
58	KOG0265	0	K16240	GO:0005515 AT4G11110.1 SPA2	
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29	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
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41	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
42	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
43	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
44	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
45	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
46	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
47	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
48	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
49	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
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54	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
55	KOG0001	0 K08770		0 AT4G05320.2 UBQ10	
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46	0	0	0 GO:0046983 AT5G56960.1	0
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3	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
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6	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
7	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
8	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
9	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
10	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
11	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
12	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
13	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
14	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
15	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
16	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
17	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
18	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
19	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
20	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
21	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
22	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
23	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
24	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
25	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
26	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
27	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
28	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
29	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
30	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
31	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
32	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
33	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
34	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
35	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
36	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
37	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
38	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
39	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
40	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
41	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
42	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
43	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
44	0	0	0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE
45	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
46	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
47	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
48	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
49	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
50	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
51	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
52	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
53	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
54	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
55	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
56	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
57	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
58	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
59	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
60	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5
	0 1.10.3.3		0 GO:0055114,(AT4G12420.2 SKU5



1				
2	0 3.1.3.48		0 GO:0004725 AT2G35320.1 ATEYA,EYA	
3	0 3.1.3.48		0 GO:0004725 AT2G35320.1 ATEYA,EYA	
4	0 3.1.3.48		0 GO:0004725 AT2G35320.1 ATEYA,EYA	
5	0 3.1.3.48		0 GO:0004725 AT2G35320.1 ATEYA,EYA	
6	0 3.1.3.48		0 GO:0004725 AT2G35320.1 ATEYA,EYA	
7	0 1.14.11.27		0 AT5G46910.1	0
8	0 1.14.11.27		0 AT5G46910.1	0
9	0 1.14.11.27		0 AT5G46910.1	0
10	0 1.14.11.27		0 AT5G46910.1	0
11	0 1.14.11.27		0 AT5G46910.1	0
12	0 1.14.11.27		0 AT5G46910.1	0
13	0 1.14.11.27		0 AT5G46910.1	0
14	0 1.14.11.27		0 AT5G46910.1	0
15	0 1.14.11.27		0 AT5G46910.1	0
16	0 1.14.11.27		0 AT5G46910.1	0
17	0 1.14.11.27		0 AT5G46910.1	0
18	0 1.14.11.27		0 AT5G46910.1	0
19	0 1.14.11.27		0 AT5G46910.1	0
20	0 1.14.11.27		0 AT5G46910.1	0
21	0 1.14.11.27		0 AT5G46910.1	0
22	0 1.14.11.27		0 AT5G46910.1	0
23	0 1.14.11.27		0 AT5G46910.1	0
24	0 1.14.11.27		0 AT5G46910.1	0
25	0 1.14.11.27		0 AT5G46910.1	0
26	0 1.14.11.27		0 AT5G46910.1	0
27	0 1.14.11.27		0 AT5G46910.1	0
28	0 1.14.11.27		0 AT5G46910.1	0
29	0 1.14.11.27		0 AT5G46910.1	0
30	0 1.14.11.27		0 AT5G46910.1	0
31	0 1.14.11.27		0 AT5G46910.1	0
32	0 1.14.11.27		0 AT5G46910.1	0
33	0 1.14.11.27		0 AT5G46910.1	0
34	0 1.14.11.27		0 AT5G46910.1	0
35	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
36	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
37	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
38	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
39	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
40	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
41	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
42	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
43	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
44	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
45	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
46	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
47	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
48	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
49	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
50	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
51	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
52	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
53	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
54	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
55	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
56	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
57	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
58	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
59	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
60	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	
	KOG0498	0 K05391	GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG	

1							
2	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
3	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
4	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
5	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
6	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
7	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
8	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
9	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
10	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
11	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
12	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
13	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
14	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
15	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
16	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
17	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
18	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
19	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
20	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
21	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
22	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
23	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
24	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
25	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
26	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
27	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
28	KOG0541	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1		
29							
30		0	0	0	0	0	0
31		0	0	0	0	0	0
32		0	0	0	0	0	0
33		0	0	0	0	0	0
34		0	0	0	0	0	0
35		0	0	0	0	0	0
36		0	0	0	0	0	0
37		0	0	0	0	0	0
38		0	0	0	0	0	0
39		0	0	0	0	0	0
40		0	0	0	0	0	0
41		0	0	0	0	0	0
42		0	0	0	0	0	0
43		0	0	0	0	0	0
44		0	0	0	0	0	0
45		0	0	0	0	0	0
46		0	0	0	0	0	0
47		0	0	0	0	0	0
48		0	0	0	0	0	0
49		0	0	0	0	0	0
50		0	0	0	0	0	0
51		0	0	0	0	0	0
52		0	0	0	0	0	0
53		0	0	0	0	0	0
54		0	0	0	0	0	0
55		0	0	0	0	0	0
56		0	0	0	0	0	0
57	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1			
58	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1			
59	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1			
60	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1			

1					
2	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
3	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
4	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
5					
6	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
7	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
8	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
9					
10	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
11	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
12	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
13					
14	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
15	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
16	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
17					
18	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
19	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
20	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
21					
22	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
23	KOG0806	3.5.1.53	K12251	GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1	
24		0	0	0 AT5G45480.1	0
25		0	0	0 AT5G45480.1	0
26		0	0	0 AT5G45480.1	0
27		0	0	0 AT5G45480.1	0
28		0	0	0 AT5G45480.1	0
29		0	0	0 AT5G45480.1	0
30		0	0	0 AT5G45480.1	0
31		0	0	0 AT5G45480.1	0
32		0	0	0 AT5G45480.1	0
33		0	0	0 AT5G45480.1	0
34		0	0	0 AT5G45480.1	0
35		0	0	0 AT5G45480.1	0
36		0	0	0 AT5G45480.1	0
37		0	0	0 AT5G45480.1	0
38		0	0	0 AT5G45480.1	0
39		0	0	0 AT5G45480.1	0
40		0	0	0 AT5G45480.1	0
41		0	0	0 AT5G45480.1	0
42		0	0	0 AT5G45480.1	0
43		0	0	0 AT5G45480.1	0
44		0	0	0 AT5G45480.1	0
45		0	0	0 AT5G45480.1	0
46		0	0	0 AT5G45480.1	0
47		0	0	0 AT5G45480.1	0
48		0	0	0 AT5G45480.1	0
49		0	0	0 AT5G45480.1	0
50		0	0	0 AT5G45480.1	0
51		0	0	0 AT5G45480.1	0
52	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
53	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
54					
55	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
56	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
57	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
58					
59	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
60	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0



1					
2	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
3	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
4	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
5	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
6	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
7	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
8	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
9	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
10	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
11	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
12	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
13	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
14	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
15	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
16	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
17	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
18	KOG2915	2.1.1.220	K07442	GO:0031515,(AT5G14600.1	0
19		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
20		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
21		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
22		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
23		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
24		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
25		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
26		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
27		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
28		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
29		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
30		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
31		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
32		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
33		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
34		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
35		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
36		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
37		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
38		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
39		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
40		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
41		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
42		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
43		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
44		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
45		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
46		0 1.8.1.9	K00384	GO:0045454,(AT2G41680.1 NTRC	
47		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
48		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
49		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
50		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
51		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
52		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
53		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
54		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
55		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
56		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
57		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
58		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
59		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
60		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
		0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0



1				
2	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
3	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
4	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
5	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
6	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
7	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
8	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
9	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
10	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
11	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
12	0 3.6.4.4	K10395	GO:0008017,(AT5G60930.1	0
13	0	0	0 GO:0010468,(AT5G64710.1	0
14	0	0	0 GO:0010468,(AT5G64710.1	0
15	0	0	0 GO:0010468,(AT5G64710.1	0
16	0	0	0 GO:0010468,(AT5G64710.1	0
17	0	0	0 GO:0010468,(AT5G64710.1	0
18	0	0	0 GO:0010468,(AT5G64710.1	0
19	0	0	0 GO:0010468,(AT5G64710.1	0
20	0	0	0 GO:0010468,(AT5G64710.1	0
21	0	0	0 GO:0010468,(AT5G64710.1	0
22	0	0	0 GO:0010468,(AT5G64710.1	0
23	0	0	0 GO:0010468,(AT5G64710.1	0
24	0	0	0 GO:0010468,(AT5G64710.1	0
25	0	0	0 GO:0010468,(AT5G64710.1	0
26	0	0	0 GO:0010468,(AT5G64710.1	0
27	0	0	0 GO:0010468,(AT5G64710.1	0
28	0	0	0 GO:0010468,(AT5G64710.1	0
29	0	0	0 GO:0010468,(AT5G64710.1	0
30	0	0	0 GO:0010468,(AT5G64710.1	0
31	0	0	0 GO:0010468,(AT5G64710.1	0
32	0	0	0 GO:0010468,(AT5G64710.1	0
33	0	0	0 GO:0010468,(AT5G64710.1	0
34	0	0	0 GO:0010468,(AT5G64710.1	0
35	0	0	0 GO:0010468,(AT5G64710.1	0
36	0	0	0 GO:0010468,(AT5G64710.1	0
37	0	0	0 GO:0010468,(AT5G64710.1	0
38	0	0	0 GO:0010468,(AT5G64710.1	0
39	0	0	0 GO:0010468,(AT5G64710.1	0
40	0	0	0 GO:0010468,(AT5G64710.1	0
41	0	0	0 GO:0010468,(AT5G64710.1	0
42	0	0	0 GO:0010468,(AT5G64710.1	0
43	0	0	0 GO:0010468,(AT5G64710.1	0
44	0	0	0 GO:0010468,(AT5G64710.1	0
45	0	0	0 GO:0010468,(AT5G64710.1	0
46	0	0	0 GO:0010468,(AT5G64710.1	0
47	0	0	0 GO:0010468,(AT5G64710.1	0
48	0	0	0 GO:0010468,(AT5G64710.1	0
49	0	0	0 GO:0010468,(AT5G64710.1	0
50	0	0	0 GO:0010468,(AT5G64710.1	0
51	0	0	0 GO:0010468,(AT5G64710.1	0
52	0	0	0 GO:0010468,(AT5G64710.1	0
53	0	0	0 GO:0010468,(AT5G64710.1	0
54	0	0	0 GO:0010468,(AT5G64710.1	0
55	0	0	0 GO:0010468,(AT5G64710.1	0
56	0	0	0 GO:0010468,(AT5G64710.1	0
57	0	0	0 GO:0010468,(AT5G64710.1	0
58	0	0	0 GO:0010468,(AT5G64710.1	0
59	0	0	0 GO:0010468,(AT5G64710.1	0
60	0	0	0 GO:0010468,(AT5G64710.1	0

1					
2		0	0	0 GO:0010468,(AT5G64710.1	0
3		0	0	0 GO:0010468,(AT5G64710.1	0
4		0	0	0 GO:0010468,(AT5G64710.1	0
5		0	0	0 GO:0010468,(AT5G64710.1	0
6		0	0	0 GO:0010468,(AT5G64710.1	0
7		0	0	0 GO:0010468,(AT5G64710.1	0
8	KOG2131		0	0 AT5G63080.1	0
9	KOG2131		0	0 AT5G63080.1	0
10	KOG2131		0	0 AT5G63080.1	0
11	KOG2131		0	0 AT5G63080.1	0
12	KOG2131		0	0 AT5G63080.1	0
13	KOG2131		0	0 AT5G63080.1	0
14	KOG2131		0	0 AT5G63080.1	0
15	KOG2131		0	0 AT5G63080.1	0
16	KOG2131		0	0 AT5G63080.1	0
17	KOG2131		0	0 AT5G63080.1	0
18	KOG2131		0	0 AT5G63080.1	0
19	KOG2131		0	0 AT5G63080.1	0
20	KOG2131		0	0 AT5G63080.1	0
21	KOG2131		0	0 AT5G63080.1	0
22	KOG2131		0	0 AT5G63080.1	0
23	KOG2131		0	0 AT5G63080.1	0
24	KOG2131		0	0 AT5G63080.1	0
25	KOG2131		0	0 AT5G63080.1	0
26	KOG2131		0	0 AT5G63080.1	0
27	KOG2131		0	0 AT5G63080.1	0
28	KOG2131		0	0 AT5G63080.1	0
29	KOG2131		0	0 AT5G63080.1	0
30	KOG2131		0	0 AT5G63080.1	0
31	KOG2131		0	0 AT5G63080.1	0
32	KOG2131		0	0 AT5G63080.1	0
33	KOG2131		0	0 AT5G63080.1	0
34	KOG2131		0	0 AT5G63080.1	0
35	KOG2131		0	0 AT5G63080.1	0
36	KOG2131		0	0 AT5G63080.1	0
37	KOG2131		0	0 AT5G63080.1	0
38	KOG2131		0	0 AT5G63080.1	0
39	KOG2131		0	0 AT5G63080.1	0
40	KOG2131		0	0 AT5G63080.1	0
41	KOG2131		0	0 AT5G63080.1	0
42	KOG2131		0	0 AT5G63080.1	0
43	KOG2131		0	0 AT5G63080.1	0
44	KOG2131		0	0 AT5G63080.1	0
45	KOG2131		0	0 AT5G63080.1	0
46	KOG2131		0	0 AT5G63080.1	0
47	KOG2131		0	0 AT5G63080.1	0
48	KOG2131		0	0 AT5G63080.1	0
49	KOG2131		0	0 AT5G63080.1	0
50	KOG2131		0	0 AT5G63080.1	0
51	KOG2131		0	0 AT5G63080.1	0
52	KOG2131		0	0 AT5G63080.1	0
53	KOG2131		0	0 AT5G63080.1	0
54	KOG2131		0	0 AT5G63080.1	0
55	KOG2131		0	0 AT5G63080.1	0
56	KOG2131		0	0 AT5G63080.1	0
57	KOG2131		0	0 AT5G63080.1	0
58	KOG2131		0	0 AT5G63080.1	0
59	KOG2131		0	0 AT5G63080.1	0
60	KOG2131		0	0 AT5G63080.1	0
	KOG2131		0	0 AT5G63080.1	0

1					
2	KOG2131		0	0	0 AT5G63080.1
3	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
4	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
5	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
6	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
7	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
8	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
9	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
10	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
11	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
12	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
13	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
14	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
15	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
16	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
17	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
18	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
19	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
20	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
21	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
22	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
23	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
24	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
25	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
26	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
27	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
28	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
29	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
30	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
31	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
32	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
33	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
34	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
35	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
36	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
37	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
38	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
39	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
40	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
41	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
42	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
43	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
44	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
45	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
46	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
47	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
48	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
49	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
50	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
51	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
52	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
53	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
54	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
55	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
56	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
57	KOG3882		0	0	GO:0016021 AT4G28050.1 TET7
58	KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.3
59	KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.3
60	KOG1187	2.7.11.1		0	GO:0006468,(AT1G56720.3

1				
2	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
3	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
4	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
5	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
6	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
7	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
8	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
9	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
10	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
11	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
12	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
13	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
14	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
15	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
16	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
17	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
18	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
19	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
20	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
21	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
22	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
23	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
24	KOG1187	2.7.11.1	0 GO:0006468,(AT1G56720.3	0
25				
26	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
27	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
28	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
29	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
30	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
31	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
32	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
33	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
34	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
35	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
36	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
37	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
38	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
39	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
40	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
41	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
42	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
43	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
44	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
45	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
46	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
47	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
48	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
49	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
50	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
51	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
52	0	0 K14832	0 AT1G72440.1 EDA25,SWA2	
53	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
54	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
55	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
56	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
57	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
58	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
59	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
60	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	
	0	0	0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F	



1			
2	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
3	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
4	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
5	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
6	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
7	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
8	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
9	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
10	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
11	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
12	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
13	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
14	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
15	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
16	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
17	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
18	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
19	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
20	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
21	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
22	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
23	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
24	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
25	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
26	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
27	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
28	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
29	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
30	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
31	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
32	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
33	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
34	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
35	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
36	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
37	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
38	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
39	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
40	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
41	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
42	KOG1368	4.1.2.5,4.1.2.4	0 GO:0030170,(AT1G08630.4 THA1
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25		0	0
26		0	0
27		0	0
28	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
29	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
30	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
31	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
32	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
33	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
34	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
35	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
36	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
37	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
38	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
39	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
40	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
41	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
42	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
43	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
44	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
45	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
46	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
47	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
48	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
49	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
50	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
51	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
52	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
53	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
54	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
55	polyubiquitin 10	Phvul.003G12K08770 - ubiq	Phvul.003G12Protein home ubiquitin-fold
56	ARM repeat superfamily prot	Phvul.003G12PTHR21576:SI	Phvul.003G12not assigned.r no hits & (ori
57	ARM repeat superfamily prot	Phvul.003G12PTHR21576:SI	Phvul.003G12not assigned.r no hits & (ori
58	ARM repeat superfamily prot	Phvul.003G12PTHR21576:SI	Phvul.003G12not assigned.r no hits & (ori
59	ARM repeat superfamily prot	Phvul.003G12PTHR21576:SI	Phvul.003G12not assigned.r no hits & (ori
60	ARM repeat superfamily prot	Phvul.003G12PTHR21576:SI	Phvul.003G12not assigned.r no hits & (ori



























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2	2-oxoglutarate (2OG) and Fe(	Phvul.009G17PTHR12480:SI
3	tetraspanin7	Phvul.009G20PTHR32191:SI
4	tetraspanin7	Phvul.009G20PTHR32191:SI
5	tetraspanin7	Phvul.009G20PTHR32191:SI
6	tetraspanin7	Phvul.009G20PTHR32191:SI
7	tetraspanin7	Phvul.009G20PTHR32191:SI
8	tetraspanin7	Phvul.009G20PTHR32191:SI
9	tetraspanin7	Phvul.009G20PTHR32191:SI
10	tetraspanin7	Phvul.009G20PTHR32191:SI
11	tetraspanin7	Phvul.009G20PTHR32191:SI
12	tetraspanin7	Phvul.009G20PTHR32191:SI
13	tetraspanin7	Phvul.009G20PTHR32191:SI
14	tetraspanin7	Phvul.009G20PTHR32191:SI
15	tetraspanin7	Phvul.009G20PTHR32191:SI
16	tetraspanin7	Phvul.009G20PTHR32191:SI
17	tetraspanin7	Phvul.009G20PTHR32191:SI
18	tetraspanin7	Phvul.009G20PTHR32191:SI
19	tetraspanin7	Phvul.009G20PTHR32191:SI
20	tetraspanin7	Phvul.009G20PTHR32191:SI
21	tetraspanin7	Phvul.009G20PTHR32191:SI
22	tetraspanin7	Phvul.009G20PTHR32191:SI
23	tetraspanin7	Phvul.009G20PTHR32191:SI
24	tetraspanin7	Phvul.009G20PTHR32191:SI
25	tetraspanin7	Phvul.009G20PTHR32191:SI
26	tetraspanin7	Phvul.009G20PTHR32191:SI
27	tetraspanin7	Phvul.009G20PTHR32191:SI
28	tetraspanin7	Phvul.009G20PTHR32191:SI
29	tetraspanin7	Phvul.009G20PTHR32191:SI
30	tetraspanin7	Phvul.009G20PTHR32191:SI
31	tetraspanin7	Phvul.009G20PTHR32191:SI
32	tetraspanin7	Phvul.009G20PTHR32191:SI
33	tetraspanin7	Phvul.009G20PTHR32191:SI
34	tetraspanin7	Phvul.009G20PTHR32191:SI
35	tetraspanin7	Phvul.009G20PTHR32191:SI
36	tetraspanin7	Phvul.009G20PTHR32191:SI
37	tetraspanin7	Phvul.009G20PTHR32191:SI
38	tetraspanin7	Phvul.009G20PTHR32191:SI
39	tetraspanin7	Phvul.009G20PTHR32191:SI
40	tetraspanin7	Phvul.009G20PTHR32191:SI
41	tetraspanin7	Phvul.009G20PTHR32191:SI
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43	tetraspanin7	Phvul.009G20PTHR32191:SI
44	tetraspanin7	Phvul.009G20PTHR32191:SI
45	tetraspanin7	Phvul.009G20PTHR32191:SI
46	tetraspanin7	Phvul.009G20PTHR32191:SI
47	tetraspanin7	Phvul.009G20PTHR32191:SI
48	tetraspanin7	Phvul.009G20PTHR32191:SI
49	tetraspanin7	Phvul.009G20PTHR32191:SI
50	tetraspanin7	Phvul.009G20PTHR32191:SI
51	tetraspanin7	Phvul.009G20PTHR32191:SI
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53	tetraspanin7	Phvul.009G20PTHR32191:SI
54	tetraspanin7	Phvul.009G20PTHR32191:SI
55	tetraspanin7	Phvul.009G20PTHR32191:SI
56	tetraspanin7	Phvul.009G20PTHR32191:SI
57	tetraspanin7	Phvul.009G20PTHR32191:SI
58		
59	Protein kinase superfamily pr	Phvul.009G21PTHR27001:SI
60	Protein kinase superfamily pr	Phvul.009G21PTHR27001:SI
	Protein kinase superfamily pr	Phvul.009G21PTHR27001:SI







1		
2	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
3	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
4	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
5	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
6	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
7	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
8	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
9	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
10	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
11	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
12	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
13	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
14	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
15	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
16	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
17	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
18	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
19	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
20	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
21	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
22	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
23	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
24	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
25	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
26	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
27	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
28	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
29	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
30	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
31	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
32	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
33	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
34	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
35	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
36	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
37	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
38	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
39	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
40	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
41	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
42	threonine aldolase 1	Phvul.L00206(4.1.2.5 - L-thr
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2 vul.004G099600.1.v2.1 annot-version=v2.1)  
3 vul.004G099600.1.v2.1 annot-version=v2.1)  
4 vul.004G099600.1.v2.1 annot-version=v2.1)  
5 vul.004G099600.1.v2.1 annot-version=v2.1)  
6 vul.004G099600.1.v2.1 annot-version=v2.1)  
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8 vul.004G099600.1.v2.1 annot-version=v2.1)  
9 vul.004G099600.1.v2.1 annot-version=v2.1)  
10 vul.004G099600.1.v2.1 annot-version=v2.1)  
11 vul.004G099600.1.v2.1 annot-version=v2.1)  
12 vul.004G099600.1.v2.1 annot-version=v2.1)  
13 vul.004G099600.1.v2.1 annot-version=v2.1)  
14 vul.004G099600.1.v2.1 annot-version=v2.1)  
15 vul.004G099600.1.v2.1 annot-version=v2.1)  
16 vul.004G099600.1.v2.1 annot-version=v2.1)  
17 vul.004G099600.1.v2.1 annot-version=v2.1)  
18 vul.004G099600.1.v2.1 annot-version=v2.1)  
19 vul.004G099600.1.v2.1 annot-version=v2.1)  
20 vul.004G099600.1.v2.1 annot-version=v2.1)  
21 vul.004G099600.1.v2.1 annot-version=v2.1)  
22 vul.004G099600.1.v2.1 annot-version=v2.1)  
23 vul.004G099600.1.v2.1 annot-version=v2.1)  
24 vul.004G099600.1.v2.1 annot-version=v2.1)  
25 vul.006G030900.1.v2.1 annot-version=v2.1)  
26 vul.006G030900.1.v2.1 annot-version=v2.1)  
27 vul.006G030900.1.v2.1 annot-version=v2.1)  
28 vul.006G030900.1.v2.1 annot-version=v2.1)  
29 vul.006G030900.1.v2.1 annot-version=v2.1)  
30 vul.006G030900.1.v2.1 annot-version=v2.1)  
31 vul.006G030900.1.v2.1 annot-version=v2.1)  
32 vul.006G030900.1.v2.1 annot-version=v2.1)  
33 vul.006G030900.1.v2.1 annot-version=v2.1)  
34 vul.006G030900.1.v2.1 annot-version=v2.1)  
35 vul.006G030900.1.v2.1 annot-version=v2.1)  
36 vul.006G030900.1.v2.1 annot-version=v2.1)  
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38 vul.006G030900.1.v2.1 annot-version=v2.1)  
39 vul.006G030900.1.v2.1 annot-version=v2.1)  
40 vul.006G030900.1.v2.1 annot-version=v2.1)  
41 vul.006G030900.1.v2.1 annot-version=v2.1)  
42 vul.006G030900.1.v2.1 annot-version=v2.1)  
43 vul.006G030900.1.v2.1 annot-version=v2.1)  
44 vul.006G030900.1.v2.1 annot-version=v2.1)  
45 vul.006G030900.1.v2.1 annot-version=v2.1)  
46 vul.006G030900.1.v2.1 annot-version=v2.1)  
47 vul.006G030900.1.v2.1 annot-version=v2.1)  
48 vul.006G030900.1.v2.1 annot-version=v2.1)  
49 vul.006G030900.1.v2.1 annot-version=v2.1)  
50 vul.006G030900.1.v2.1 annot-version=v2.1)  
51 vul.006G030900.1.v2.1 annot-version=v2.1)  
52 vul.006G030900.1.v2.1 annot-version=v2.1)  
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56 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &  
57 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &  
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60 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &







































1 vul.010G014800.2.v2.1 annot-version=v2.1)  
2 vul.010G014800.2.v2.1 annot-version=v2.1)  
3 vul.010G014800.2.v2.1 annot-version=v2.1)  
4 vul.010G014800.2.v2.1 annot-version=v2.1)  
5 vul.010G014800.2.v2.1 annot-version=v2.1)  
6 vul.010G014800.2.v2.1 annot-version=v2.1)  
7 vul.010G014800.2.v2.1 annot-version=v2.1)  
8 vul.010G014800.2.v2.1 annot-version=v2.1)  
9 vul.010G014800.2.v2.1 annot-version=v2.1)  
10 vul.010G014800.2.v2.1 annot-version=v2.1)  
11 vul.010G014800.2.v2.1 annot-version=v2.1)  
12 vul.010G014800.2.v2.1 annot-version=v2.1)  
13 vul.010G014800.2.v2.1 annot-version=v2.1)  
14 vul.010G014800.2.v2.1 annot-version=v2.1)  
15 vul.010G014800.2.v2.1 annot-version=v2.1)  
16 vul.010G014800.2.v2.1 annot-version=v2.1)  
17 vul.010G014800.2.v2.1 annot-version=v2.1)  
18 vul.010G014800.2.v2.1 annot-version=v2.1)  
19 vul.010G014800.2.v2.1 annot-version=v2.1)  
20 vul.010G014800.2.v2.1 annot-version=v2.1)  
21 vul.010G014800.2.v2.1 annot-version=v2.1)  
22 vul.010G014800.2.v2.1 annot-version=v2.1)  
23 vul.010G014800.2.v2.1 annot-version=v2.1)  
24 vul.010G014800.2.v2.1 annot-version=v2.1)  
25 vul.010G014800.2.v2.1 annot-version=v2.1)  
26 vul.010G014800.2.v2.1 annot-version=v2.1)  
27 vul.010G014800.2.v2.1 annot-version=v2.1)  
28 vul.010G014800.2.v2.1 annot-version=v2.1)  
29 vul.010G014800.2.v2.1 annot-version=v2.1)  
30 vul.010G014800.2.v2.1 annot-version=v2.1)  
31 vul.010G014800.2.v2.1 annot-version=v2.1)  
32 vul.010G014800.2.v2.1 annot-version=v2.1)  
33 vul.010G014800.2.v2.1 annot-version=v2.1)  
34 vul.010G014800.2.v2.1 annot-version=v2.1)  
35 vul.010G014800.2.v2.1 annot-version=v2.1)  
36 vul.010G014800.2.v2.1 annot-version=v2.1)  
37 vul.010G014800.2.v2.1 annot-version=v2.1)  
38 vul.010G014800.2.v2.1 annot-version=v2.1)  
39 vul.010G014800.2.v2.1 annot-version=v2.1)  
40 vul.010G014800.2.v2.1 annot-version=v2.1)  
41 vul.010G014800.2.v2.1 annot-version=v2.1)  
42 vul.010G014800.2.v2.1 annot-version=v2.1)  
43 vul.010G014800.2.v2.1 annot-version=v2.1)  
44 vul.010G014800.2.v2.1 annot-version=v2.1)  
45 vul.010G014800.2.v2.1 annot-version=v2.1)  
46 vul.010G014800.2.v2.1 annot-version=v2.1)  
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49 vul.010G014800.2.v2.1 annot-version=v2.1)  
50 vul.010G014800.2.v2.1 annot-version=v2.1)  
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1 )09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &  
2 )09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &  
3 )09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &  
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1 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &  
2 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &  
3 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &  
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7 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &  
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9 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &  
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Do not distribute

	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
1						
2						
3	ggaau	Phvul.008G004800.1	2.5	-1	1	22
4	ggaau	Phvul.009G006000.1	2.5	-1	1	22
5	ggaau	Phvul.009G006000.2	2.5	-1	1	22
6	ggaau	Phvul.002G315000.1	3	-1	1	22
7	ggaau	Phvul.002G315000.2	3	-1	1	22
8	ggaau	Phvul.004G164800.1	3	-1	1	22
9	ggaau	Phvul.005G049000.1	3	-1	1	22
10	ggaau	Phvul.010G108200.1	3	-1	1	22
11	ggaau	Phvul.L008143.1	3	-1	1	22
12	ggaau	Phvul.002G189700.1	3.5	-1	1	22
13	ggaau	Phvul.002G189700.2	3.5	-1	1	22
14	ggaau	Phvul.002G189700.3	3.5	-1	1	22
15	ggaau	Phvul.002G189700.4	3.5	-1	1	22
16	ggaau	Phvul.002G258800.1	3.5	-1	1	22
17	ggaau	Phvul.003G202100.1	3.5	-1	1	22
18	ggaau	Phvul.003G282800.1	3.5	-1	1	22
19	ggaau	Phvul.004G083900.1	3.5	-1	1	22
20	ggaau	Phvul.006G110000.1	3.5	-1	1	22
21	ggaau	Phvul.007G031800.1	3.5	-1	1	22
22	ggaau	Phvul.007G031800.2	3.5	-1	1	22
23	ggaau	Phvul.007G094100.1	3.5	-1	1	22
24	ggaau	Phvul.008G081700.2	3.5	-1	1	22
25	ggaau	Phvul.009G201900.1	3.5	-1	1	22
26	ggaau	Phvul.009G233100.2	3.5	-1	1	22
27	ggaau	Phvul.009G246200.2	3.5	-1	1	22
28	ggaau	Phvul.010G125200.1	3.5	-1	1	22
29	ggaau	Phvul.011G073400.1	3.5	-1	1	22
30	ggaau	Phvul.001G001700.1	4	-1	1	22
31	ggaau	Phvul.001G160000.1	4	-1	1	22
32	ggaau	Phvul.002G011900.1	4	-1	1	22
33	ggaau	Phvul.002G028700.1	4	-1	1	22
34	ggaau	Phvul.002G185800.1	4	-1	1	22
35	ggaau	Phvul.002G206900.1	4	-1	1	22
36	ggaau	Phvul.002G206900.2	4	-1	1	22
37	ggaau	Phvul.003G078900.1	4	-1	1	22
38	ggaau	Phvul.003G210500.1	4	-1	1	22
39	ggaau	Phvul.003G262300.3	4	-1	1	22
40	ggaau	Phvul.003G262300.1	4	-1	1	22
41	ggaau	Phvul.003G262300.2	4	-1	1	22
42	ggaau	Phvul.003G262300.4	4	-1	1	22
43	ggaau	Phvul.004G093900.4	4	-1	1	22
44	ggaau	Phvul.004G093900.6	4	-1	1	22
45	ggaau	Phvul.004G093900.5	4	-1	1	22
46	ggaau	Phvul.004G093900.3	4	-1	1	22
47	ggaau	Phvul.004G093900.1	4	-1	1	22
48	ggaau	Phvul.004G093900.1	4	-1	1	22
49	ggaau	Phvul.004G093900.1	4	-1	1	22
50	ggaau	Phvul.004G093900.1	4	-1	1	22
51	ggaau	Phvul.004G093900.1	4	-1	1	22
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53	ggaau	Phvul.004G093900.1	4	-1	1	22
54	ggaau	Phvul.004G093900.1	4	-1	1	22
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56	ggaau	Phvul.004G093900.1	4	-1	1	22
57	ggaau	Phvul.004G093900.1	4	-1	1	22
58	ggaau	Phvul.004G093900.1	4	-1	1	22
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60	ggaau	Phvul.004G093900.1	4	-1	1	22



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3	ggaaugggcuga Phvul.004G093900.7	4	-1	1	22
4	ggaaugggcuga Phvul.004G105600.1	4	-1	1	22
5	ggaaugggcuga Phvul.004G135400.1	4	-1	1	22
6	ggaaugggcuga Phvul.004G159500.1	4	-1	1	22
7	ggaaugggcuga Phvul.004G159500.1	4	-1	1	22
8	ggaaugggcuga Phvul.004G170000.1	4	-1	1	22
9	ggaaugggcuga Phvul.005G001000.1	4	-1	1	22
10	ggaaugggcuga Phvul.005G022800.1	4	-1	1	22
11	ggaaugggcuga Phvul.005G022800.1	4	-1	1	22
12	ggaaugggcuga Phvul.005G072300.1	4	-1	1	22
13	ggaaugggcuga Phvul.007G034000.1	4	-1	1	22
14	ggaaugggcuga Phvul.007G034000.2	4	-1	1	22
15	ggaaugggcuga Phvul.007G034000.2	4	-1	1	22
16	ggaaugggcuga Phvul.007G244033.1	4	-1	1	22
17	ggaaugggcuga Phvul.007G244033.1	4	-1	1	22
18	ggaaugggcuga Phvul.007G244033.1	4	-1	1	22
19	ggaaugggcuga Phvul.007G244066.1	4	-1	1	22
20	ggaaugggcuga Phvul.008G079000.1	4	-1	1	22
21	ggaaugggcuga Phvul.008G267400.5	4	-1	1	22
22	ggaaugggcuga Phvul.008G267400.2	4	-1	1	22
23	ggaaugggcuga Phvul.008G267400.2	4	-1	1	22
24	ggaaugggcuga Phvul.008G267400.3	4	-1	1	22
25	ggaaugggcuga Phvul.008G267400.3	4	-1	1	22
26	ggaaugggcuga Phvul.008G267400.4	4	-1	1	22
27	ggaaugggcuga Phvul.009G053900.2	4	-1	1	22
28	ggaaugggcuga Phvul.009G081900.1	4	-1	1	22
29	ggaaugggcuga Phvul.009G081900.1	4	-1	1	22
30	ggaaugggcuga Phvul.009G213000.1	4	-1	1	22
31	ggaaugggcuga Phvul.011G065200.2	4	-1	1	22
32	ggaaugggcuga Phvul.001G079400.1	4.5	-1	1	22
33	ggaaugggcuga Phvul.001G079400.1	4.5	-1	1	22
34	ggaaugggcuga Phvul.001G087700.1	4.5	-1	1	22
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36	ggaaugggcuga Phvul.002G007100.1	4.5	-1	1	22
37	ggaaugggcuga Phvul.002G115800.1	4.5	-1	1	22
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39	ggaaugggcuga Phvul.002G115800.3	4.5	-1	1	22
40	ggaaugggcuga Phvul.002G163600.1	4.5	-1	1	22
41	ggaaugggcuga Phvul.002G168500.1	4.5	-1	1	22
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43	ggaaugggcuga Phvul.002G168500.2	4.5	-1	1	22
44	ggaaugggcuga Phvul.002G177500.1	4.5	-1	1	22
45	ggaaugggcuga Phvul.002G315000.1	4.5	-1	1	22
46	ggaaugggcuga Phvul.002G315000.1	4.5	-1	1	22
47	ggaaugggcuga Phvul.002G315000.2	4.5	-1	1	22
48	ggaaugggcuga Phvul.003G185300.1	4.5	-1	1	22
49	ggaaugggcuga Phvul.003G212800.2	4.5	-1	1	22
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51	ggaaugggcuga Phvul.004G121900.1	4.5	-1	1	22
52	ggaaugggcuga Phvul.006G033600.1	4.5	-1	1	22
53	ggaaugggcuga Phvul.006G033600.2	4.5	-1	1	22
54	ggaaugggcuga Phvul.006G033600.2	4.5	-1	1	22
55	ggaaugggcuga Phvul.006G219000.1	4.5	-1	1	22
56	ggaaugggcuga Phvul.007G008100.2	4.5	-1	1	22
57	ggaaugggcuga Phvul.007G086600.1	4.5	-1	1	22
58	ggaaugggcuga Phvul.007G086600.1	4.5	-1	1	22
59	ggaaugggcuga Phvul.007G168600.1	4.5	-1	1	22
60	ggaaugggcuga Phvul.008G002700.1	4.5	-1	1	22
	ggaaugggcuga Phvul.009G062500.1	4.5	-1	1	22

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2	ggaaugggcuga Phvul.001G186500.1	5	-1	1	22
3	ggaaugggcuga Phvul.002G028700.1	5	-1	1	22
4	ggaaugggcuga Phvul.003G202300.1	5	-1	1	22
5	ggaaugggcuga Phvul.003G202300.2	5	-1	1	22
6	ggaaugggcuga Phvul.003G248400.1	5	-1	1	22
7	ggaaugggcuga Phvul.003G248400.2	5	-1	1	22
8	ggaaugggcuga Phvul.003G248400.3	5	-1	1	22
9	ggaaugggcuga Phvul.004G024400.1	5	-1	1	22
10	ggaaugggcuga Phvul.004G071800.1	5	-1	1	22
11	ggaaugggcuga Phvul.004G178500.1	5	-1	1	22
12	ggaaugggcuga Phvul.004G178500.1	5	-1	1	22
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18	ggaaugggcuga Phvul.007G204100.1	5	-1	1	22
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20	ggaaugggcuga Phvul.008G034200.2	5	-1	1	22
21	ggaaugggcuga Phvul.009G184400.1	5	-1	1	22
22	ggaaugggcuga Phvul.009G184400.2	5	-1	1	22
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1				
2	96	117 GGAAUGGGCI	.....CAUUUCUCA	Cleavage pacid=371628
3	69	90 GGAAUGGGCI	.....CAUUUCUCA	Cleavage pacid=371628
4	212	233 GGAAUGGGCI	.....GCCUUCCG	Cleavage pacid=371629
5	357	378 GGAAUGGGCI	.....AACUCCCAA	Cleavage pacid=371629
6	1475	1496 GGAAUGGGCI	.....UCUUUCUCA	Cleavage pacid=371632
7				
8	273	294 GGAAUGGGCI	.....GCCUUCUCG	Translation pacid=371616
9				
10	2164	2185 GGAAUGGGCI	.....UGCUUCUCA	Cleavage pacid=371530
11	1223	1244 GGAAUGGGCI	.....AUCUUCUCA	Cleavage pacid=371540
12	885	906 GGAAUGGGCI	.....AUUUUCUCA	Translation pacid=371543
13				
14	1650	1671 GGAAUGGGCI	.....UGAUUCGUA	Cleavage pacid=371676
15	1160	1181 GGAAUGGGCI	.....UGAUUCGUA	Cleavage pacid=371676
16	311	332 GGAAUGGGCI	.....CUCUCCCAA	Translation pacid=371653
17	497	518 GGAAUGGGCI	.....CUCUCCCAA	Translation pacid=371653
18				
19	497	518 GGAAUGGGCI	.....CUCUCCCAA	Translation pacid=371643
20	1570	1591 GGAAUGGGCI	.....AUCUUCCA	Cleavage pacid=371607
21	1521	1542 GGAAUGGGCI	.....UGCUUCACA	Cleavage pacid=371602
22	1517	1538 GGAAUGGGCI	.....UGCUUCACA	Cleavage pacid=371602
23	1636	1657 GGAAUGGGCI	.....UGCUUCACA	Cleavage pacid=371602
24	1630	1651 GGAAUGGGCI	.....UGCUUCACA	Cleavage pacid=371602
25				
26	5313	5334 GGAAUGGGCI	.....GAAAACCAA	Cleavage pacid=371507
27	3042	3063 GGAAUGGGCI	.....UUUUUCUA	Cleavage pacid=371520
28				
29	21	42 GGAAUGGGCI	.....CCUCCUAG	Cleavage pacid=371495
30	114	135 GGAAUGGGCI	.....GGCUACGCA	Cleavage pacid=371555
31	154	175 GGAAUGGGCI	.....GACUCCCA	Cleavage pacid=371688
32	537	558 GGAAUGGGCI	.....CGCUCCCAA	Cleavage pacid=371681
33	179	200 GGAAUGGGCI	.....UUCUUCUA	Translation pacid=371685
34	9	30 GGAAUGGGCI	.....AGCUGCUUA	Cleavage pacid=371751
35	39	60 GGAAUGGGCI	.....GGUUUUUA	Cleavage pacid=371771
36	39	60 GGAAUGGGCI	.....GGUUUUUA	Cleavage pacid=371771
37	340	361 GGAAUGGGCI	.....AGUUUCCG	Cleavage pacid=371780
38	745	766 GGAAUGGGCI	.....ACCUUCCAA	Cleavage pacid=371779
39	745	766 GGAAUGGGCI	.....ACCUUCCAA	Cleavage pacid=371779
40	190	211 GGAAUGGGCI	.....UUCUCCAA	Translation pacid=371764
41	296	317 GGAAUGGGCI	.....CCUCUUUA	Cleavage pacid=371747
42	296	317 GGAAUGGGCI	.....CCUCUUUA	Cleavage pacid=371747
43	775	796 GGAAUGGGCI	.....AGUUUCUA	Cleavage pacid=371444
44	3	24 GGAAUGGGCI	.....CGUUUCUA	Cleavage pacid=371453
45	938	959 GGAAUGGGCI	.....CUCUUCUA	Translation pacid=371625
46	2003	2024 GGAAUGGGCI	.....UGCUUCUA	Cleavage pacid=371727
47	1944	1965 GGAAUGGGCI	.....UGCUUCUA	Cleavage pacid=371727
48	2213	2234 GGAAUGGGCI	.....UCCUUCUA	Cleavage pacid=371737
49	610	630 GGAAUGGGCI	.....UGCU-CCUA	Cleavage pacid=371646
50	72	93 GGAAUGGGCI	.....CCCUUCUA	Cleavage pacid=371652
51	428	449 GGAAUGGGCI	.....AUCUUCCA	Cleavage pacid=371667
52	2027	2048 GGAAUGGGCI	.....UGUUUCUA	Cleavage pacid=371597
53	431	452 GGAAUGGGCI	.....CUCUUCUA	Cleavage pacid=371494

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2	356	377 GGAAUGGGCI ::::: . : :::::AGCUUCUGA\ Cleavage	pacid=371681
3	369	390 GGAAUGGGCI : ::::: : :::::UCAGGUCCA\ Cleavage	pacid=371746
4	1365	1386 GGAAUGGGCI ::::: : . :::::GGCUUCCA\ Translation	pacid=371476
5	1353	1374 GGAAUGGGCI ::::: : . :::::GGCUUCCA\ Translation	pacid=371476
6	1808	1829 GGAAUGGGCI ::::: . : :::::UGCUUCUAG\ Cleavage	pacid=371477
7	1808	1829 GGAAUGGGCI ::::: . : :::::UGCUUCUAG\ Cleavage	pacid=371477
8	1753	1774 GGAAUGGGCI ::::: . : :::::UGCUUCUAG\ Cleavage	pacid=371477
9	631	652 GGAAUGGGCI ::::: : . :::::UGUUUCUG Cleavage	pacid=371627
10	1160	1181 GGAAUGGGCI ::: : ::::: : :::::UGCCUUCA\ Cleavage	pacid=371631
11	2494	2515 GGAAUGGGCI ::::: : . :::::UGCUUCCA\ Cleavage	pacid=371625
12	1938	1959 GGAAUGGGCI : ::: : : : :::::UAUUCCAA\ Cleavage	pacid=371625
13	2522	2543 GGAAUGGGCI : ::::: : . :::::GACUUCCA\ Cleavage	pacid=371531
14	2522	2543 GGAAUGGGCI : ::::: : . :::::GACUUCCA\ Cleavage	pacid=371531
15	562	584 GGAAUGGGCI ::::: : . :::::UGCUUCAUC\ Cleavage	pacid=371714
16	207	229 GGAAUGGGCI ::::: : . :::::UGCUUCAUC\ Cleavage	pacid=371714
17	427	448 GGAAUGGGCI : ::: : : : :::::CAAUUUCUC\ Cleavage	pacid=371739
18	2093	2113 GGAAUGGGCI ::::: : : : : :::::AGCUUCCA\ Cleavage	pacid=371675
19	1852	1873 GGAAUGGGCI ::::: . : :::::UGUUCCUU\ Cleavage	pacid=371582
20	553	574 GGAAUGGGCI : : ::::: : . :::::UCCUUCCA\ Cleavage	pacid=371600
21	1626	1646 GGAAUGGGCI ::::: : : . :::::UGCUUCUCA- Cleavage	pacid=371494
22	1620	1640 GGAAUGGGCI ::::: : : . :::::UGCUUCUCA- Cleavage	pacid=371494
23			
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	Multiplicity	Target_Acc.	ID	locusName	Pfam
1					
2					
3	1	Phvul.008G004800.1	Phvul.008G004800	Phvul.008G004800	PF00175,PF00
4	1	Phvul.009G006000.1	Phvul.009G006000	Phvul.009G006000	PF00650
5	1	Phvul.009G006000.2	Phvul.009G006000	Phvul.009G006000	PF00650
6	1	Phvul.009G006000.2	Phvul.009G006000	Phvul.009G006000	PF00650
7	2	Phvul.002G315000.1	Phvul.002G315000	Phvul.002G315000	0
8	2	Phvul.002G315000.2	Phvul.002G315000	Phvul.002G315000	0
9	2	Phvul.002G315000.2	Phvul.002G315000	Phvul.002G315000	0
10	1	Phvul.004G164800.1	Phvul.004G164800	Phvul.004G164800	PF16113,PF00
11	1	Phvul.005G049000.1	Phvul.005G049000	Phvul.005G049000	PF10184
12	1	Phvul.010G108200.1	Phvul.010G108200	Phvul.010G108200	PF07707,PF00
13	1	Phvul.010G108200.1	Phvul.010G108200	Phvul.010G108200	PF07707,PF00
14	1	Phvul.L008143.1	Phvul.L008143	Phvul.L008143	0
15	1	Phvul.002G189700.1	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
16	1	Phvul.002G189700.2	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
17	1	Phvul.002G189700.2	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
18	1	Phvul.002G189700.3	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
19	1	Phvul.002G189700.4	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
20	1	Phvul.002G189700.4	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
21	1	Phvul.002G258800.1	Phvul.002G258800	Phvul.002G258800	0
22	1	Phvul.003G202100.1	Phvul.003G202100	Phvul.003G202100	PF08263,PF00
23	1	Phvul.003G282800.1	Phvul.003G282800	Phvul.003G282800	PF05965
24	1	Phvul.004G083900.1	Phvul.004G083900	Phvul.004G083900	PF00155
25	1	Phvul.004G083900.1	Phvul.004G083900	Phvul.004G083900	PF00155
26	2	Phvul.006G110000.1	Phvul.006G110000	Phvul.006G110000	0
27	1	Phvul.007G031800.1	Phvul.007G031800	Phvul.007G031800	PF02358,PF00
28	1	Phvul.007G031800.2	Phvul.007G031800	Phvul.007G031800	PF02358,PF00
29	1	Phvul.007G031800.2	Phvul.007G031800	Phvul.007G031800	PF02358,PF00
30	1	Phvul.007G094100.1	Phvul.007G094100	Phvul.007G094100	PF04715,PF00
31	1	Phvul.007G094100.1	Phvul.007G094100	Phvul.007G094100	PF04715,PF00
32	1	Phvul.008G081700.2	Phvul.008G081700	Phvul.008G081700	PF00122,PF12
33	1	Phvul.009G201900.1	Phvul.009G201900	Phvul.009G201900	0
34	1	Phvul.009G233100.2	Phvul.009G233100	Phvul.009G233100	0
35	1	Phvul.009G246200.2	Phvul.009G246200	Phvul.009G246200	PF03171,PF14
36	1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G125200	PF03914
37	1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G125200	PF03914
38	1	Phvul.011G073400.1	Phvul.011G073400	Phvul.011G073400	PF09786
39	1	Phvul.001G001700.1	Phvul.001G001700	Phvul.001G001700	PF00326,PF02
40	1	Phvul.001G001700.1	Phvul.001G001700	Phvul.001G001700	PF00326,PF02
41	1	Phvul.001G160000.1	Phvul.001G160000	Phvul.001G160000	PF13639
42	1	Phvul.002G011900.1	Phvul.002G011900	Phvul.002G011900	PF00332,PF07
43	2	Phvul.002G028700.1	Phvul.002G028700	Phvul.002G028700	PF04788
44	1	Phvul.002G028700.1	Phvul.002G028700	Phvul.002G028700	PF04788
45	1	Phvul.002G185800.1	Phvul.002G185800	Phvul.002G185800	PF00282
46	1	Phvul.002G206900.1	Phvul.002G206900	Phvul.002G206900	PF08263,PF00
47	1	Phvul.002G206900.2	Phvul.002G206900	Phvul.002G206900	PF08263,PF00
48	1	Phvul.002G206900.2	Phvul.002G206900	Phvul.002G206900	PF08263,PF00
49	1	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
50	1	Phvul.003G210500.1	Phvul.003G210500	Phvul.003G210500	PF02201
51	1	Phvul.003G262300.3	Phvul.003G262300	Phvul.003G262300	PF00641
52	1	Phvul.003G262300.1	Phvul.003G262300	Phvul.003G262300	PF00641
53	1	Phvul.003G262300.1	Phvul.003G262300	Phvul.003G262300	PF00641
54	1	Phvul.003G262300.2	Phvul.003G262300	Phvul.003G262300	PF00641
55	1	Phvul.003G262300.2	Phvul.003G262300	Phvul.003G262300	PF00641
56	1	Phvul.003G262300.4	Phvul.003G262300	Phvul.003G262300	PF00641
57	1	Phvul.004G093900.4	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
58	1	Phvul.004G093900.6	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
59	1	Phvul.004G093900.5	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
60	1	Phvul.004G093900.3	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
60	1	Phvul.004G093900.1	Phvul.004G093900	Phvul.004G093900	PF00201,PF03



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2	1	Phvul.004G093900.2	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
3	1	Phvul.004G093900.7	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
4	1	Phvul.004G105600.1	Phvul.004G105600	Phvul.004G105600	PF00560
5	1	Phvul.004G135400.1	Phvul.004G135400	Phvul.004G135400	PF00005,PF01
6	1	Phvul.004G159500.1	Phvul.004G159500	Phvul.004G159500	PF00067
7	1	Phvul.004G170000.1	Phvul.004G170000	Phvul.004G170000	PF02516
8	1	Phvul.005G001000.1	Phvul.005G001000	Phvul.005G001000	PF03552
9	1	Phvul.005G022800.1	Phvul.005G022800	Phvul.005G022800	PF00022
10	1	Phvul.005G072300.1	Phvul.005G072300	Phvul.005G072300	PF00179
11	1	Phvul.007G034000.1	Phvul.007G034000	Phvul.007G034000	PF03034
12	1	Phvul.007G034000.2	Phvul.007G034000	Phvul.007G034000	PF03034
13	2	Phvul.007G244033.1	Phvul.007G244033	Phvul.007G244033	0
14	2	Phvul.007G244033.1	Phvul.007G244033	Phvul.007G244033	0
15	1	Phvul.007G244066.1	Phvul.007G244066	Phvul.007G244066	0
16	1	Phvul.008G079000.1	Phvul.008G079000	Phvul.008G079000	PF06697
17	1	Phvul.008G267400.5	Phvul.008G267400	Phvul.008G267400	PF00012
18	1	Phvul.008G267400.2	Phvul.008G267400	Phvul.008G267400	PF00012
19	1	Phvul.008G267400.3	Phvul.008G267400	Phvul.008G267400	PF00012
20	1	Phvul.008G267400.4	Phvul.008G267400	Phvul.008G267400	PF00012
21	1	Phvul.009G053900.2	Phvul.009G053900	Phvul.009G053900	PF14691,PF07
22	1	Phvul.009G081900.1	Phvul.009G081900	Phvul.009G081900	PF12937
23	1	Phvul.009G213000.1	Phvul.009G213000	Phvul.009G213000	PF14531,PF03
24	1	Phvul.011G065200.2	Phvul.011G065200	Phvul.011G065200	0
25	1	Phvul.001G079400.1	Phvul.001G079400	Phvul.001G079400	PF11145
26	1	Phvul.001G087700.1	Phvul.001G087700	Phvul.001G087700	PF03982,PF00
27	1	Phvul.001G117500.1	Phvul.001G117500	Phvul.001G117500	PF02446,PF00
28	1	Phvul.002G007100.1	Phvul.002G007100	Phvul.002G007100	PF13912
29	1	Phvul.002G115800.1	Phvul.002G115800	Phvul.002G115800	PF07714
30	1	Phvul.002G115800.3	Phvul.002G115800	Phvul.002G115800	PF07714
31	1	Phvul.002G163600.1	Phvul.002G163600	Phvul.002G163600	0
32	1	Phvul.002G168500.1	Phvul.002G168500	Phvul.002G168500	PF13912
33	1	Phvul.002G168500.2	Phvul.002G168500	Phvul.002G168500	PF13912
34	1	Phvul.002G177500.1	Phvul.002G177500	Phvul.002G177500	PF01762,PF00
35	2	Phvul.002G315000.1	Phvul.002G315000	Phvul.002G315000	0
36	2	Phvul.002G315000.2	Phvul.002G315000	Phvul.002G315000	0
37	1	Phvul.003G185300.1	Phvul.003G185300	Phvul.003G185300	PF07983
38	1	Phvul.003G212800.2	Phvul.003G212800	Phvul.003G212800	PF00847
39	1	Phvul.004G121900.1	Phvul.004G121900	Phvul.004G121900	PF01554
40	1	Phvul.006G033600.1	Phvul.006G033600	Phvul.006G033600	PF00069
41	1	Phvul.006G033600.2	Phvul.006G033600	Phvul.006G033600	PF00069
42	1	Phvul.006G219000.1	Phvul.006G219000	Phvul.006G219000	PF00439
43	1	Phvul.007G008100.2	Phvul.007G008100	Phvul.007G008100	PF10075
44	1	Phvul.007G086600.1	Phvul.007G086600	Phvul.007G086600	PF00847
45	1	Phvul.007G168600.1	Phvul.007G168600	Phvul.007G168600	PF07883
46	1	Phvul.008G002700.1	Phvul.008G002700	Phvul.008G002700	PF03141
47	1	Phvul.009G062500.1	Phvul.009G062500	Phvul.009G062500	PF04130



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2	1	Phvul.001G186500.1	Phvul.001G186500	Phvul.001G186500	PF15629,PF15
3	2	Phvul.002G028700.1	Phvul.002G028700	Phvul.002G028700	PF04788
4	1	Phvul.003G202300.1	Phvul.003G202300	Phvul.003G202300	0
5					0
6	1	Phvul.003G202300.2	Phvul.003G202300	Phvul.003G202300	0
7	1	Phvul.003G248400.1	Phvul.003G248400	Phvul.003G248400	PF14694,PF14
8	1	Phvul.003G248400.2	Phvul.003G248400	Phvul.003G248400	PF14694,PF14
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10	1	Phvul.003G248400.3	Phvul.003G248400	Phvul.003G248400	PF14694,PF14
11	1	Phvul.004G024400.1	Phvul.004G024400	Phvul.004G024400	0
12	1	Phvul.004G071800.1	Phvul.004G071800	Phvul.004G071800	PF03094
13					
14	2	Phvul.004G178500.1	Phvul.004G178500	Phvul.004G178500	PF00432
15	2	Phvul.004G178500.1	Phvul.004G178500	Phvul.004G178500	PF00432
16	1	Phvul.005G175600.1	Phvul.005G175600	Phvul.005G175600	PF00005,PF00
17	1	Phvul.005G175600.2	Phvul.005G175600	Phvul.005G175600	PF00005,PF00
18	1	Phvul.006G053300.1	Phvul.006G053300	Phvul.006G053300	PF03106
19	1	Phvul.006G053300.2	Phvul.006G053300	Phvul.006G053300	PF03106
20					
21	2	Phvul.006G110000.1	Phvul.006G110000	Phvul.006G110000	0
22	1	Phvul.007G204100.1	Phvul.007G204100	Phvul.007G204100	PF04810,PF08
23	1	Phvul.008G006800.1	Phvul.008G006800	Phvul.008G006800	PF00400,PF12
24					
25	1	Phvul.008G034200.2	Phvul.008G034200	Phvul.008G034200	PF00201
26	1	Phvul.009G184400.1	Phvul.009G184400	Phvul.009G184400	PF05904
27	1	Phvul.009G184400.2	Phvul.009G184400	Phvul.009G184400	PF05904
28					
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	Panther	KOG	KEGG	KOG	GO	Best-hit-arabi
1						
2						
3	PTHR19384,P <sup>-</sup>		0 1.5.1.30		0 GO:0055114,(	AT3G02280.1
4	PTHR23324,P <sup>-</sup>		0	0	0	0 AT4G39170.1
5	PTHR23324,P <sup>-</sup>		0	0	0	0 AT4G39170.1
6	PTHR23324,P <sup>-</sup>		0	0	0	0 AT4G39170.1
7	PTHR11005,P <sup>-</sup>	KOG2624	3.1.1.3		0	0 AT1G73920.1
8	PTHR11005,P <sup>-</sup>	KOG2624	3.1.1.3		0	0 AT1G73920.1
9	PTHR23309,P <sup>-</sup>	KOG1683	5.1.2.3,1.1.1.3	K10527	GO:0055114,(	AT4G29010.1
10	PTHR22750,P <sup>-</sup>	KOG4457		0	0	0 AT1G79510.1
11	PTHR24412,P <sup>-</sup>		0	0	0 GO:0005515	AT3G61600.1
12	PTHR24412,P <sup>-</sup>		0	0	0	0
13	PTHR33912,P <sup>-</sup>		0	0	0	0
14	PTHR33912,P <sup>-</sup>		0	0	0	0
15	PTHR11254,P <sup>-</sup>		0 6.3.2.19	K10592	GO:0004842	AT1G55860.2
16	PTHR11254,P <sup>-</sup>		0 6.3.2.19	K10592	GO:0004842	AT1G55860.2
17	PTHR11254,P <sup>-</sup>		0 6.3.2.19	K10592	GO:0004842	AT1G55860.2
18	PTHR11254,P <sup>-</sup>		0 6.3.2.19	K10592	GO:0004842	AT1G55860.2
19	PTHR11254,P <sup>-</sup>		0 6.3.2.19	K10592	GO:0004842	AT1G55860.2
20	PTHR31852,P <sup>-</sup>		0	0	0	0 AT3G26350.1
21	PTHR27000,P <sup>-</sup>	KOG0472	2.7.11.1		0 GO:0005515	AT4G20140.1
22	PTHR22715,P <sup>-</sup>		0 2.1.1.43		0 GO:0005634	AT1G26330.1
23	PTHR22715,P <sup>-</sup>		0 2.1.1.43		0 GO:0005634	AT1G26330.1
24	PTHR11751,P <sup>-</sup>	KOG0633	2.6.1.9	K00817	GO:0030170,(	AT1G71920.2
25	PTHR11751,P <sup>-</sup>	KOG0633	2.6.1.9	K00817	GO:0030170,(	AT1G71920.2
26	PTHR31234,P <sup>-</sup>		0	0	0	0 AT4G01110.1
27	PTHR10788,P <sup>-</sup>		0 2.4.1.15,3.1.3	K16055	GO:0005992,(	AT4G17770.1
28	PTHR10788,P <sup>-</sup>		0 2.4.1.15,3.1.3	K16055	GO:0005992,(	AT4G17770.1
29	PTHR10788,P <sup>-</sup>		0 2.4.1.15,3.1.3	K16055	GO:0005992,(	AT4G17770.1
30	PTHR11236,P <sup>-</sup>		0 2.6.1.85	K13950	GO:0016833,(	AT2G28880.1
31	PTHR11236,P <sup>-</sup>		0 2.6.1.85	K13950	GO:0016833,(	AT2G28880.1
32	PTHR24092,P <sup>-</sup>		0 3.6.3.1	K14802	GO:0046872,(	AT5G04930.1
33	PTHR24092,P <sup>-</sup>		0 3.6.3.1	K14802	GO:0046872,(	AT5G04930.1
34	PTHR33673,P <sup>-</sup>		0	0	0	0 AT1G74220.1
35	PTHR33673,P <sup>-</sup>		0	0	0	0 AT1G74220.1
36	PTHR33977,P <sup>-</sup>		0	0	0	0 AT4G13970.1
37	PTHR33977,P <sup>-</sup>		0	0	0	0 AT4G13970.1
38	PTHR10209,P <sup>-</sup>	KOG0143	1.14.11.32		0 GO:0055114,(	AT3G21420.1
39	PTHR10209,P <sup>-</sup>	KOG0143	1.14.11.32		0 GO:0055114,(	AT3G21420.1
40	PTHR12048		0	0 K14832	GO:0008236,(	AT1G72440.1
41	PTHR12048		0	0 K14832	GO:0008236,(	AT1G72440.1
42	PTHR21780,P <sup>-</sup>	KOG4670		0	0	0 AT1G07970.1
43	PTHR21780,P <sup>-</sup>	KOG4670		0	0	0 AT1G07970.1
44	PTHR11757,P <sup>-</sup>		0 3.4.21.26	K01322	GO:0008236,(	AT1G76140.1
45	PTHR11757,P <sup>-</sup>		0 3.4.21.26	K01322	GO:0008236,(	AT1G76140.1
46	PTHR14155,P <sup>-</sup>		0	0	0 GO:0008270,(	AT5G43420.1
47	PTHR14155,P <sup>-</sup>		0	0	0 GO:0008270,(	AT5G43420.1
48	PTHR32227,P <sup>-</sup>		0 3.2.1.39		0 GO:0005975,(	AT5G67460.1
49	PTHR32227,P <sup>-</sup>		0 3.2.1.39		0 GO:0005975,(	AT5G67460.1
50	PTHR31300,P <sup>-</sup>		0	0	0	0 AT5G66740.1
51	PTHR31300,P <sup>-</sup>		0	0	0	0 AT5G66740.1
52	PTHR11999,P <sup>-</sup>		0 4.1.1.15	K01580	GO:0030170,(	AT5G17330.1
53	PTHR11999,P <sup>-</sup>		0 4.1.1.15	K01580	GO:0030170,(	AT5G17330.1
54	PTHR27001,P <sup>-</sup>	KOG1187	2.7.11.1,2.7.11.1		0 GO:0006468,(	AT4G33430.1
55	PTHR27001,P <sup>-</sup>	KOG1187	2.7.11.1,2.7.11.1		0 GO:0006468,(	AT4G33430.1
56	PTHR27001,P <sup>-</sup>	KOG1187	2.7.11.1,2.7.11.1		0 GO:0006468,(	AT4G33430.1
57	PTHR27001,P <sup>-</sup>	KOG1187	2.7.11.1,2.7.11.1		0 GO:0006468,(	AT4G33430.1
58	PTHR34775,P <sup>-</sup>		0	0	0	0 AT2G16270.1
59	PTHR34775,P <sup>-</sup>		0	0	0	0 AT2G16270.1
60	PTHR13844,P <sup>-</sup>	KOG2570		0 K11650	GO:0005515	AT5G14170.1
61	PTHR13844,P <sup>-</sup>	KOG2570		0 K11650	GO:0005515	AT5G14170.1
62	PTHR23111,P <sup>-</sup>		0	0	0 GO:0008270	AT2G17975.1
63	PTHR23111,P <sup>-</sup>		0	0	0 GO:0008270	AT2G17975.1
64	PTHR23111,P <sup>-</sup>		0	0	0 GO:0008270	AT2G17975.1
65	PTHR23111,P <sup>-</sup>		0	0	0 GO:0008270	AT2G17975.1
66	PTHR23111,P <sup>-</sup>		0	0	0 GO:0008270	AT2G17975.1
67	PTHR11926,P <sup>-</sup>		0 2.4.1.173		0 GO:0016758,(	AT1G43620.3
68	PTHR11926,P <sup>-</sup>		0 2.4.1.173		0 GO:0016758,(	AT1G43620.3
69	PTHR11926,P <sup>-</sup>		0 2.4.1.173		0 GO:0016758,(	AT1G43620.3
70	PTHR11926,P <sup>-</sup>		0 2.4.1.173		0 GO:0016758,(	AT1G43620.3
71	PTHR11926,P <sup>-</sup>		0 2.4.1.173		0 GO:0016758,(	AT1G43620.3

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2	PTHR11926,P <sup>-</sup>	0 2.4.1.173		0 GO:0016758,(	AT1G43620.3	
3	PTHR11926,P <sup>-</sup>	0 2.4.1.173		0 GO:0016758,(	AT1G43620.3	
4	PTHR27004,P <sup>-</sup> KOG0472	2.7.11.1		0 GO:0005515	AT2G34930.1	
5						
6	PTHR19241,P <sup>-</sup>	0 3.6.3.25		0 GO:0016887,(	AT1G17840.1	
7	PTHR24298,P <sup>-</sup>	0 1.14.13.123,1.		0 GO:0055114,(	AT3G26300.1	
8	PTHR13872,P <sup>-</sup>	0 2.4.99.18	K07151	GO:0016020,(	AT5G19690.1	
9						
10	PTHR13301,P <sup>-</sup>	0 2.4.1.12		0 GO:0030244,(	AT4G24010.1	
11	PTHR11937,P <sup>-</sup> KOG0676		0 K16615	0 AT3G60830.1		
12	PTHR24067,P <sup>-</sup> KOG0417	6.3.2.19	K10581	0 AT3G15355.1		
13						
14	PTHR15362,P <sup>-</sup>	0 2.7.8.8	K08730	GO:0006659	AT1G15110.1	
15	PTHR15362,P <sup>-</sup>	0 2.7.8.8	K08730	GO:0006659	AT1G15110.1	
16	0	0	0	0	0	0
17	0	0	0	0	0	0
18	0	0	0	0	0	0
19	0	0	0	0	0	0
20	PTHR33512,P <sup>-</sup>	0	0	0	0 AT3G08600.1	
21	PTHR19375,P <sup>-</sup>	0	0 K09489	0 AT1G11660.1		
22	PTHR19375,P <sup>-</sup>	0	0 K09489	0 AT1G11660.1		
23	PTHR19375,P <sup>-</sup>	0	0 K09489	0 AT1G11660.1		
24	PTHR19375,P <sup>-</sup>	0	0 K09489	0 AT1G11660.1		
25	PTHR19375,P <sup>-</sup>	0	0 K09489	0 AT1G11660.1		
26	PTHR19375,P <sup>-</sup>	0	0 K09489	0 AT1G11660.1		
27	PTHR11938,P <sup>-</sup>	0 1.4.1.14	K00264	GO:0055114,(	AT5G53460.1	
28	PTHR24006,P <sup>-</sup> KOG4341		0	0 GO:0005515	AT4G33210.1	
29	PTHR24343,P <sup>-</sup> KOG0583	2.7.11.1		0 GO:0007165	AT1G30270.1	
30						
31	0	0	0	0	0 AT5G59305.1	
32	PTHR33389,P <sup>-</sup>	0	0	0	0 AT4G21700.1	
33	PTHR22753,P <sup>-</sup>	0	0	0 GO:0016747	AT5G41130.1	
34						
35	PTHR32518,P <sup>-</sup>	0 2.4.1.25	K00705	GO:0005975,(	AT2G40840.1	
36	PTHR26374,P <sup>-</sup>	0	0	0	0 AT4G17810.1	
37	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1,2.7.11.1		0 GO:0006468,(	AT2G17220.1	
38	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1,2.7.11.1		0 GO:0006468,(	AT2G17220.1	
39						
40	0	0	0	0	0	0
41	PTHR26374,P <sup>-</sup>	0	0	0	0 AT1G26610.1	
42	PTHR26374,P <sup>-</sup>	0	0	0	0 AT1G26610.1	
43						
44	PTHR11214,P <sup>-</sup> KOG2287	2.4.1.134		0 GO:0016020,(	AT4G21060.2	
45	PTHR11005,P <sup>-</sup> KOG2624	3.1.1.3		0	0 AT1G73920.1	
46	PTHR11005,P <sup>-</sup> KOG2624	3.1.1.3		0	0 AT1G73920.1	
47						
48	PTHR32227,P <sup>-</sup>	0	0	0	0 AT1G18650.1	
49	PTHR31839,P <sup>-</sup>	0	0	0 GO:0006355,(	AT5G51990.1	
50						
51	PTHR11206,P <sup>-</sup> KOG1347		0 K03327	GO:0055085,(	AT4G23030.1	
52	PTHR24055,P <sup>-</sup> KOG0660	2.7.11.24	K04371	GO:0006468,(	AT2G42880.1	
53	PTHR24055,P <sup>-</sup> KOG0660	2.7.11.24	K04371	GO:0006468,(	AT2G42880.1	
54						
55	PTHR22880,P <sup>-</sup>	0	0	0 GO:0005515	AT1G58025.3	
56	PTHR12436,P <sup>-</sup> KOG1861		0	0	0 AT2G39340.1	
57	PTHR31677,P <sup>-</sup>	0	0	0 GO:0006355,(	AT1G12890.1	
58	PTHR37236,P <sup>-</sup>	0	0	0	0 AT4G02980.1	
59						
60	PTHR10108,P <sup>-</sup>	0 2.1.1.41		0 GO:0008168	AT2G43200.1	
	PTHR19302,P <sup>-</sup>	0	0 K16572	GO:0005815,(	AT1G80260.1	

1					
2	PTHR10359,P <sup>-</sup>	0 4.2.99.18	0	0	AT5G04560.2
3	PTHR31300,P <sup>-</sup>	0	0	0	AT5G66740.1
4	PTHR34805	0	0	0	AT4G24680.1
5	PTHR34805	0	0	0	AT4G24680.1
6	PTHR16057,P <sup>-</sup>	0	0	0	AT3G50430.1
7	PTHR16057,P <sup>-</sup>	0	0	0	AT3G50430.1
8	PTHR16057,P <sup>-</sup>	0	0	0	AT3G50430.1
9	PTHR16057,P <sup>-</sup>	0	0	0	AT3G50430.1
10	PTHR16057,P <sup>-</sup>	0	0	0	AT3G50430.1
11	0	0	0	0	0
12	PTHR31942,P <sup>-</sup>	0	0 K08472	GO:0016021,C	AT2G39200.1
13	PTHR11764,P <sup>-</sup>	0 5.4.99.41		0 GO:0003824	AT2G07050.1
14	PTHR11764,P <sup>-</sup>	0 5.4.99.41		0 GO:0003824	AT2G07050.1
15	PTHR24223,P <sup>-</sup>	0 3.6.3.44	K05674	GO:0016887,C	AT2G07680.1
16	PTHR24223,P <sup>-</sup>	0 3.6.3.44	K05674	GO:0016887,C	AT2G07680.1
17	PTHR24223,P <sup>-</sup>	0 3.6.3.44	K05674	GO:0016887,C	AT2G07680.1
18	PTHR31221,P <sup>-</sup>	0	0	0 GO:0043565,C	AT4G26640.2
19	PTHR31221,P <sup>-</sup>	0	0	0 GO:0043565,C	AT4G26640.2
20	PTHR31221,P <sup>-</sup>	0	0	0 GO:0043565,C	AT4G26640.2
21	PTHR31234,P <sup>-</sup>	0	0	0	AT4G01110.1
22	PTHR31234,P <sup>-</sup>	0	0	0	AT4G01110.1
23	PTHR13803,P <sup>-</sup>	0	0 K14007	GO:0030127,C	AT3G07100.1
24	PTHR22850	0	0 K14848	GO:0005515	AT2G19540.1
25	PTHR11926,P <sup>-</sup>	0 2.4.1.170		0 GO:0016758,C	AT3G02100.1
26	PTHR11926,P <sup>-</sup>	0 2.4.1.170		0 GO:0016758,C	AT3G02100.1
27	PTHR33167,P <sup>-</sup>	0	0	0	AT1G13940.1
28	PTHR33167,P <sup>-</sup>	0	0	0	AT1G13940.1
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1	arabi-symbol	arabi-defline	ID	Annot_defline
2		0 Flavodoxin family protein	Phvul.008G001.5.1.30	- Flav
3		0 Sec14p-like phosphatidylinositol transfer family	Phvul.009G00PTHR23324	:SF
4		0 Sec14p-like phosphatidylinositol transfer family	Phvul.009G00PTHR23324	:SF
5		0 alpha/beta-Hydrolases superfamily protein	Phvul.002G31PTHR11005	:SF
6		0 alpha/beta-Hydrolases superfamily protein	Phvul.002G31PTHR11005	:SF
7	AIM1	Enoyl-CoA hydratase/isomerase family	Phvul.004G161.1.1.35	//4.2.
8		0 Uncharacterized conserved protein (DUF2358)	Phvul.005G04PTHR22750	- (
9	ATPOB1,POB1	POZ/BTB containin G-protein 1	Phvul.010G10PF00651	//PFC
10		0	0 Phvul.L00814	:PTHR33912:SF
11	UPL1	ubiquitin-protein ligase 1	Phvul.002G18PTHR11254	:SF
12	UPL1	ubiquitin-protein ligase 1	Phvul.002G18PTHR11254	:SF
13	UPL1	ubiquitin-protein ligase 1	Phvul.002G18PTHR11254	:SF
14	UPL1	ubiquitin-protein ligase 1	Phvul.002G18PTHR11254	:SF
15		0	0 Phvul.002G25PTHR31852	:SF
16	GSO1	Leucine-rich repeat transmembrane protein kin	Phvul.003G20PF00560	//PFC
17		0 DNA binding	Phvul.003G28PTHR22715	-
18	HISN6B	HISTIDINE BIOSYNTHESIS 6B	Phvul.004G082.6.1.9	- Histic
19		0	0 Phvul.006G11PTHR31234	:SF
20	ATPS5,TPS5	trehalose phosphatase/synthase 5	Phvul.007G03PTHR10788	:SF
21	ATPS5,TPS5	trehalose phosphatase/synthase 5	Phvul.007G03PTHR10788	:SF
22	ADCS,emb1997	para-aminobenzoate (PABA) synthase family pr	Phvul.007G092.6.1.85	- Ami
23	ALA1	aminophospholipid ATPase 1	Phvul.008G08K14802	- phos
24		0	0	0
25		0 zinc ion binding	Phvul.009G23PTHR33977	:SF
26		0 2-oxoglutarate (2OG) and Fe(II)-dependent oxy	Phvul.009G24PTHR10209	//I
27	EDA25,SWA2	CCAAT-binding factor	Phvul.010G12K14832	- ribos
28		0	0 Phvul.011G07PTHR21780	:SF
29		0 Prolyl oligopeptidase family protein	Phvul.001G003.4.21.26	- Pro
30		0 RING/U-box superfamily protein	Phvul.001G16PTHR14155	//I
31		0 O-Glycosyl hydrolases family 17 protein	Phvul.002G01PTHR32227	:SF
32		0 Protein of unknown function (DUF620)	Phvul.002G02PF04788	- Pro
33	GAD,GAD1	glutamate decarboxylase	Phvul.002G18PTHR11999	//I
34	ATBAK1,ATSERK3,BAK	:BRI1-associated receptor kinase	Phvul.002G20K13416	- bras
35	ATBAK1,ATSERK3,BAK	:BRI1-associated receptor kinase	Phvul.002G20K13416	- bras
36		0	0	0
37	CHC1	SWIB/MDM2 domain superfamily protein	Phvul.003G21K11650	- SWI/
38		0 zinc finger (Ran-binding) family protein	Phvul.003G26PTHR23111	//I
39		0 zinc finger (Ran-binding) family protein	Phvul.003G26PTHR23111	//I
40		0 zinc finger (Ran-binding) family protein	Phvul.003G26PTHR23111	//I
41		0 zinc finger (Ran-binding) family protein	Phvul.003G26PTHR23111	//I
42	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926	:SF
43	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926	:SF
44	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926	:SF
45	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926	:SF
46	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926	:SF

1					
2	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926:SI		
3	TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09PTHR11926:SI		
4		0 disease resistance family protein / LRR family protein	Phvul.004G10KOG0472 - Lei		
5					
6	ABCG11,ATWBC11,CO	white-brown complex homolog protein 11	Phvul.004G13PTHR19241://I		
7	CYP71B34	cytochrome P450, family 71, subfamily B, polyp	Phvul.004G15PF00067 - Cyt		
8	<b>STT3A</b>	<b>staurosporin and temperature sensitive 3-like</b>	<b>A</b> Phvul.004G17PTHR13872:SI		
9					
10	ATCSLG1,CSLG1	cellulose synthase like G1	Phvul.005G00PTHR13301://I		
11	ARP7,ATARP7	actin-related protein 7	Phvul.005G02K16615 - actir		
12	PFU1,UBC25	ubiquitin-conjugating enzyme 25	Phvul.005G07PTHR24067:SI		
13					
14		0 phosphatidyl serine synthase family protein	Phvul.007G032.7.8.8 - CDP-		
15		0 phosphatidyl serine synthase family protein	Phvul.007G032.7.8.8 - CDP-		
16		0	0	0	0
17		0	0	0	0
18		0	0	0	0
19		<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>
20		0 Protein of unknown function (DUF1191)	Phvul.008G07PF06697 - Pro		
21		0 heat shock protein 70 (Hsp 70) family protein	Phvul.008G26PTHR19375://I		
22		0 heat shock protein 70 (Hsp 70) family protein	Phvul.008G26PTHR19375://I		
23		0 heat shock protein 70 (Hsp 70) family protein	Phvul.008G26PTHR19375://I		
24		0 heat shock protein 70 (Hsp 70) family protein	Phvul.008G26PTHR19375://I		
25		0 heat shock protein 70 (Hsp 70) family protein	Phvul.008G26PTHR19375://I		
26					
27	GLT1	NADH-dependent glutamate synthase 1	Phvul.009G051.4.1.14 - Glut		
28	SLOMO	F-box family protein	Phvul.009G08PTHR24006:SI		
29					
30	ATCIPK23,CIPK23,LKS1	CBL-interacting protein kinase 23	Phvul.009G21PTHR24343:SI		
31		0	0	0	0
32		0 Protein of unknown function (DUF2921)	Phvul.001G07PF11145 - Pro		
33		0 Esterase/lipase/thioesterase family protein	Phvul.001G08PTHR22753:SI		
34					
35	DPE2	disproportionating enzyme 2	Phvul.001G112.4.1.25 - 4-al		
36		0 C2H2 and C2HC zinc fingers superfamily protein	Phvul.002G00PF13912 - C2f		
37		0 Protein kinase superfamily protein	Phvul.002G11PTHR27001:SI		
38		0 Protein kinase superfamily protein	Phvul.002G11PTHR27001:SI		
39		0	0	0	0
40		0 C2H2-like zinc finger protein	Phvul.002G16PTHR26374:SI		
41		0 C2H2-like zinc finger protein	Phvul.002G16PTHR26374:SI		
42		0 Galactosyltransferase family protein	Phvul.002G17PTHR11214:SI		
43		0 alpha/beta-Hydrolases superfamily protein	Phvul.002G31PTHR11005:SI		
44		0 alpha/beta-Hydrolases superfamily protein	Phvul.002G31PTHR11005:SI		
45					
46	PDCB3	plasmodesmata callose-binding protein 3	Phvul.003G18PTHR32227:SI		
47					
48	CBF4,DREB1D	C-repeat-binding factor 4	Phvul.003G21PTHR31839:SI		
49					
50		0 MATE efflux family protein	Phvul.004G12PTHR11206:SI		
51					
52	ATMPK20,MPK20	MAP kinase 20	Phvul.006G03PTHR24055:SI		
53	ATMPK20,MPK20	MAP kinase 20	Phvul.006G03PTHR24055:SI		
54					
55		0 DNA-binding bromodomain-containing protein	Phvul.006G21PTHR22880:SI		
56		0 SAC3/GANP/Nin1/mts3/eIF-3 p25 family	Phvul.007G00PTHR12436:SI		
57		0 Integrase-type DNA-binding superfamily protein	Phvul.007G08PF00847 - APz		
58					
59	ABP,ABP1	endoplasmic reticulum auxin binding protein 1	Phvul.007G16PTHR37236:SI		
60		0 S-adenosyl-L-methionine-dependent methyltra	Phvul.008G00PTHR10108://I		
	emb1427	Spc97 / Spc98 family of spindle pole body (SBP)	Phvul.009G06K16572 - gam		

1			
2	DME	HhH-GPD base excision DNA repair family prote	Phvul.001G18PTHR10359:SI
3		0 Protein of unknown function (DUF620)	Phvul.002G02PF04788 - Pro
4	MOS1	modifier of snc1	Phvul.003G20PF07001 - BA1
5	MOS1	modifier of snc1	Phvul.003G20PF07001 - BA1
6		0	0 Phvul.003G24PTHR16057 - \
7		0	0 Phvul.003G24PTHR16057 - \
8		0	0 Phvul.003G24PTHR16057 - \
9		0	0 Phvul.003G24PTHR16057 - \
10		0	0 Phvul.003G24PTHR16057 - \
11		0	0 0 0
12	ATMLO12,MLO12	Seven transmembrane MLO family protein	Phvul.004G07PTHR31942:SI
13	CAS1	cycloartenol synthase 1	Phvul.004G17PTHR11764//I
14	CAS1	cycloartenol synthase 1	Phvul.004G17PTHR11764//I
15	ATMRP11,MRP11	multidrug resistance-associated protein 11	Phvul.005G17K05674 - ATP-
16	ATMRP11,MRP11	multidrug resistance-associated protein 11	Phvul.005G17K05674 - ATP-
17	AtWRKY20,WRKY20	WRKY family transcription factor family protein	Phvul.006G05PTHR31221:SI
18	AtWRKY20,WRKY20	WRKY family transcription factor family protein	Phvul.006G05PTHR31221:SI
19		0	0 Phvul.006G11PTHR31234:SI
20	ERMO2,SEC24A	Sec23/Sec24 protein transport family protein	Phvul.007G20K14007 - prot
21		0 Transducin family protein / WD-40 repeat famil	Phvul.008G00K14848 - ribos
22		0 UDP-Glycosyltransferase superfamily protein	Phvul.008G03PTHR11926//I
23		0 Plant protein of unknown function (DUF863)	Phvul.009G18PTHR33167:SI
24		0 Plant protein of unknown function (DUF863)	Phvul.009G18PTHR33167:SI
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IDENTIFIER	NAME	DESCRIPTION
Phvul.008G00	Coenzyme me component TAH18 of cytosolic CIA system assembly phase (original de	
Phvul.009G00	not assigned.ε (original description: pacid=37150821 transcript=Phvul.009G006000.3	
Phvul.009G00	not assigned.ε (original description: pacid=37150821 transcript=Phvul.009G006000.3	
Phvul.002G31	not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G	
Phvul.002G31	not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G	
Phvul.004G16	Lipid metaboli multifunctional enzyme (MFP) (original description: pacid=37162576 tr	
Phvul.005G04	not assigned.r no hits & (original description: pacid=37153695 transcript=Phvul.005G	
Phvul.010G10	Protein home component LRB of CUL3-BTB E3 ubiquitin ligase complex (original desc	
Phvul.L00814	:not assigned.r no hits & (original description: pacid=37178968 transcript=Phvul.L008	
Phvul.002G18	Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717	
Phvul.002G18	Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717	
Phvul.002G18	Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717	
Phvul.002G18	Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717	
Phvul.002G25	not assigned.r no hits & (original description: pacid=37175064 transcript=Phvul.002G	
Phvul.003G20	Phytohormon CIF-peptide receptor (GSO) (original description: pacid=37147649 tran:	
Phvul.003G28	not assigned.r no hits & (original description: pacid=37147414 transcript=Phvul.003G	
Phvul.004G08	Amino acid m histidinol-phosphate aminotransferase (original description: pacid=371	
Phvul.006G11	not assigned.r no hits & (original description: pacid=37173968 transcript=Phvul.006G	
Phvul.007G03	Enzyme classii Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabic	
Phvul.007G03	Enzyme classii Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabic	
Phvul.007G09	Coenzyme me aminodeoxychorismate synthase (original description: pacid=3716718(	
Phvul.008G08	Solute transp P4-type ATPase component ALA of phospholipid flippase complex (orig	
Phvul.009G20	not assigned.r no hits & (original description: pacid=37150792 transcript=Phvul.009G	
Phvul.009G23	not assigned.r no hits & (original description: pacid=37149731 transcript=Phvul.009G	
Phvul.009G24	Phytohormon oxidoreductase (LBO) (original description: pacid=37151443 transcript:	
Phvul.010G12	Protein biosyr component NOC1 of ribosomal subunit nuclear export complex (origin	
Phvul.011G07	not assigned.r no hits & (original description: pacid=37154989 transcript=Phvul.011G	
Phvul.001G00	Enzyme classii Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting on pepi	
Phvul.001G16	Protein home RING-H2-class E3 ligase (original description: pacid=37168057 transcrip	
Phvul.002G01	Enzyme classii Glucan endo-1,3-beta-glucosidase 13 OS=Arabidopsis thaliana (sp q9fj	
Phvul.002G02	Multi-process GTPase effector (BDR) (original description: pacid=37174686 transcript	
Phvul.002G18	Amino acid m glutamate decarboxylase (original description: pacid=37174418 transcr	
Phvul.002G20	Protein modif protein kinase (LRR-II) (original description: pacid=37176803 transcript	
Phvul.002G20	Protein modif protein kinase (LRR-II) (original description: pacid=37176803 transcript	
Phvul.003G07	not assigned.r no hits & (original description: pacid=37147041 transcript=Phvul.003G	
Phvul.003G21	Chromatin orç component BAF60 of chromatin remodeling complex (original descript	
Phvul.003G26	not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G	
Phvul.003G26	not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G	
Phvul.003G26	not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G	
Phvul.003G26	not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G	
Phvul.004G09	Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371	
Phvul.004G09	Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371	
Phvul.004G09	Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371	
Phvul.004G09	Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371	
Phvul.004G09	Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371	

1 Phvul.004G09Lipid metabolite UDP-glucose:sterol glucosyltransferase (original description: pacid=371  
2 Phvul.004G09Lipid metabolite UDP-glucose:sterol glucosyltransferase (original description: pacid=371  
3 Phvul.004G10not assigned.ε (original description: pacid=37162970 transcript=Phvul.004G105600.1  
4 Phvul.004G13Solute transport subfamily ABCG transporter (original description: pacid=37162910 tra  
5 Phvul.004G15Enzyme class II Cytochrome P450 CYP736A12 OS=Panax ginseng (sp|h2dh18|c7a12\_p  
6 **Phvul.004G17Protein modification component STT3 of oligosaccharyl transferase (OST) complex (original**  
7 **Phvul.005G00not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1**  
8 Phvul.005G02Chromatin organization component ARP7 of chromatin remodeling complex (original descriptio  
9 Phvul.005G07not assigned.ε (original description: pacid=37154333 transcript=Phvul.005G072300.1  
10 Phvul.007G03Lipid metabolite base-exchange-type phosphatidylserine synthase (original description:  
11 Phvul.007G03Lipid metabolite base-exchange-type phosphatidylserine synthase (original description:  
12 Phvul.007G24not assigned.r no hits & (original description: pacid=37165375 transcript=Phvul.007G  
13 Phvul.007G24not assigned.r no hits & (original description: pacid=37165375 transcript=Phvul.007G  
14 **Phvul.007G24not assigned.r no hits & (original description: pacid=37164381 transcript=Phvul.007G**  
15 Phvul.008G07not assigned.r no hits & (original description: pacid=37160757 transcript=Phvul.008G  
16 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=  
17 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=  
18 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=  
19 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=  
20 Phvul.009G05Nutrient uptake NADH-dependent glutamate synthase (original description: pacid=371  
21 Phvul.009G08not assigned.ε (original description: pacid=37152092 transcript=Phvul.009G081900.1  
22 Phvul.009G21Protein modification SNF1-related protein kinase (SnRK3) (original description: pacid=37149  
23 Phvul.011G06Phytohormone CLE precursor polypeptide (original description: pacid=37155545 trans  
24 Phvul.001G07not assigned.r no hits & (original description: pacid=37168871 transcript=Phvul.001G  
25 Phvul.001G08not assigned.ε (original description: pacid=37168110 transcript=Phvul.001G087700.1  
26 Phvul.001G11not assigned.ε (original description: pacid=37168578 transcript=Phvul.001G117500.1  
27 Phvul.002G00RNA biosynthesis C2H2 zinc finger transcription factor (original description: pacid=37175  
28 Phvul.002G11Protein modification receptor-like protein kinase (RLCK-VIIa) (original description: pacid=37  
29 Phvul.002G11Protein modification receptor-like protein kinase (RLCK-VIIa) (original description: pacid=37  
30 Phvul.002G16not assigned.r no hits & (original description: pacid=37178055 transcript=Phvul.002G  
31 Phvul.002G16RNA biosynthesis C2H2 zinc finger transcription factor (original description: pacid=37177  
32 Phvul.002G16RNA biosynthesis C2H2 zinc finger transcription factor (original description: pacid=37177  
33 Phvul.002G17Cell wall organization AGP hydroxyproline O-galactosyltransferase (original description: pacid  
34 Phvul.002G31not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G  
35 Phvul.002G31not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G  
36 Phvul.003G18not assigned.ε (original description: pacid=37144453 transcript=Phvul.003G185300.1  
37 Phvul.003G21RNA biosynthesis transcription factor (DREB) (original description: pacid=37145319 trans  
38 Phvul.004G12Solute transport metabolite transporter (DTX) (original description: pacid=37162548 tra  
39 Phvul.006G03Protein modification protein kinase (MAPK) (original description: pacid=37172750 transcrip  
40 Phvul.006G03Protein modification protein kinase (MAPK) (original description: pacid=37172750 transcrip  
41 Phvul.006G21not assigned.r no hits & (original description: pacid=37173703 transcript=Phvul.006G  
42 Phvul.007G00RNA processing scaffold component GANP/SAC3 of TREX-2 mRNP trafficking complex (o  
43 Phvul.007G08RNA biosynthesis transcription factor (ERF) (original description: pacid=37165267 transcri  
44 Phvul.007G16not assigned.ε (original description: pacid=37166775 transcript=Phvul.007G168600.1  
45 Phvul.008G00not assigned.ε (original description: pacid=37159786 transcript=Phvul.008G002700.1  
46 Phvul.009G06Cytoskeleton organization component GCP5 of gamma-Tubulin ring complex (gamma-TuRC) (orig

1 Phvul.001G18DNA damage bifunctional DNA glycosylase/lyase (ROS1) (original description: pacid=  
2 Phvul.002G02Multi-process GTPase effector (BDR) (original description: pacid=37174686 transcript=  
3 Phvul.003G20not assigned.ε (original description: pacid=37147665 transcript=Phvul.003G202300.2  
4 Phvul.003G20not assigned.ε (original description: pacid=37147665 transcript=Phvul.003G202300.2  
5 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C  
6 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C  
7 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C  
8 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C  
9 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C  
10 Phvul.004G02not assigned.r no hits & (original description: pacid=37162719 transcript=Phvul.004C  
11 Phvul.004G02not assigned.r no hits & (original description: pacid=37162719 transcript=Phvul.004C  
12 Phvul.004G07not assigned.ε (original description: pacid=37163131 transcript=Phvul.004G071800.1  
13 Phvul.004G17Secondary me triterpenoid synthase (original description: pacid=37162519 transcript:  
14 Phvul.004G17Secondary me triterpenoid synthase (original description: pacid=37162519 transcript:  
15 Phvul.005G17Solute transpεsubfamily ABCC transporter (original description: pacid=37153148 tran  
16 Phvul.005G17Solute transpεsubfamily ABCC transporter (original description: pacid=37153148 tran  
17 Phvul.005G17Solute transpεsubfamily ABCC transporter (original description: pacid=37153148 tran  
18 Phvul.006G05RNA biosynthεtranscription factor (WRKY) (original description: pacid=37171441 tran  
19 Phvul.006G05RNA biosynthεtranscription factor (WRKY) (original description: pacid=37171441 tran  
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21 Phvul.006G11not assigned.r no hits & (original description: pacid=37173968 transcript=Phvul.006C  
22 Phvul.007G20Vesicle traffiεcomponent Sec24 of Sec23/24 cargo adaptor subcomplex (original des  
23 Phvul.008G00not assigned.ε (original description: pacid=37158292 transcript=Phvul.008G006800.1  
24 Phvul.008G03Enzyme classii UDP-glycosyltransferase 83A1 OS=Arabidopsis thaliana (sp|q9sga8|u8  
25 Phvul.009G18not assigned.r no hits & (original description: pacid=37149447 transcript=Phvul.009C  
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28 Phvul.009G18not assigned.r no hits & (original description: pacid=37149447 transcript=Phvul.009C  
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2 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann  
3 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann  
4 l locus=Phvul.004G105600 ID=Phvul.004G105600.1.v2.1 annot-version=v2.1) & Receptor-like protei  
5 nscript=Phvul.004G135400.1 locus=Phvul.004G135400 ID=Phvul.004G135400.1.v2.1 annot-version=  
6 ang : 559.0) & Enzyme classification.EC\_1 oxidoreductases.EC\_1.14 oxidoreductase acting on paire  
7 **description: pacid=37161693 transcript=Phvul.004G170000.1 locus=Phvul.004G170000 ID=Phvul.004G170000.1.v2.1**  
8 **l locus=Phvul.005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-l**  
9 **on: pacid=37154025 transcript=Phvul.005G022800.1 locus=Phvul.005G022800 ID=Phvul.005G022800.1.v2.1**  
10 **l locus=Phvul.005G072300 ID=Phvul.005G072300.1.v2.1 annot-version=v2.1) & Probable ubiquitin-**  
11 **: pacid=37167617 transcript=Phvul.007G034000.2 locus=Phvul.007G034000 ID=Phvul.007G034000.**  
12 **: pacid=37167617 transcript=Phvul.007G034000.2 locus=Phvul.007G034000 ID=Phvul.007G034000.**  
13 **5244033.1 locus=Phvul.007G244033 ID=Phvul.007G244033.1.v2.1 annot-version=v2.1)**  
14 **5244033.1 locus=Phvul.007G244033 ID=Phvul.007G244033.1.v2.1 annot-version=v2.1)**  
15 **5244066.1 locus=Phvul.007G244066 ID=Phvul.007G244066.1.v2.1 annot-version=v2.1)**  
16 **5079000.1 locus=Phvul.008G079000 ID=Phvul.008G079000.1.v2.1 annot-version=v2.1)**  
17 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &  
18 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &  
19 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &  
20 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &  
21 50765 transcript=Phvul.009G053900.2 locus=Phvul.009G053900 ID=Phvul.009G053900.2.v2.1 ann  
22 l locus=Phvul.009G081900 ID=Phvul.009G081900.1.v2.1 annot-version=v2.1) & F-box/LRR-repeat p  
23 50546 transcript=Phvul.009G213000.1 locus=Phvul.009G213000 ID=Phvul.009G213000.1.v2.1 annot-  
24 script=Phvul.011G065200.2 locus=Phvul.011G065200 ID=Phvul.011G065200.2.v2.1 annot-version=v  
25 5079400.1 locus=Phvul.001G079400 ID=Phvul.001G079400.1.v2.1 annot-version=v2.1)  
26 l locus=Phvul.001G087700 ID=Phvul.001G087700.1.v2.1 annot-version=v2.1) & Acyltransferase-like  
27 l locus=Phvul.001G117500 ID=Phvul.001G117500.1.v2.1 annot-version=v2.1) & 4-alpha-glucanotrar  
28 5159 transcript=Phvul.002G007100.1 locus=Phvul.002G007100 ID=Phvul.002G007100.1.v2.1 annot-  
29 177142 transcript=Phvul.002G115800.3 locus=Phvul.002G115800 ID=Phvul.002G115800.3.v2.1 an  
30 177142 transcript=Phvul.002G115800.3 locus=Phvul.002G115800 ID=Phvul.002G115800.3.v2.1 an  
31 5163600.1 locus=Phvul.002G163600 ID=Phvul.002G163600.1.v2.1 annot-version=v2.1)  
32 7986 transcript=Phvul.002G168500.2 locus=Phvul.002G168500 ID=Phvul.002G168500.2.v2.1 annot-  
33 7986 transcript=Phvul.002G168500.2 locus=Phvul.002G168500 ID=Phvul.002G168500.2.v2.1 annot-  
34 d=37176445 transcript=Phvul.002G177500.1 locus=Phvul.002G177500 ID=Phvul.002G177500.1.v2.1  
35 5315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)  
36 5315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)  
37 l locus=Phvul.003G185300 ID=Phvul.003G185300.1.v2.1 annot-version=v2.1) & PLASMODESMATA (  
38 script=Phvul.003G212800.2 locus=Phvul.003G212800 ID=Phvul.003G212800.2.v2.1 annot-version=v  
39 50546 transcript=Phvul.004G121900.1 locus=Phvul.004G121900 ID=Phvul.004G121900.1.v2.1 annot-versior  
40 t=Phvul.006G033600.2 locus=Phvul.006G033600 ID=Phvul.006G033600.2.v2.1 annot-version=v2.1)  
41 t=Phvul.006G033600.2 locus=Phvul.006G033600 ID=Phvul.006G033600.2.v2.1 annot-version=v2.1)  
42 5219000.1 locus=Phvul.006G219000 ID=Phvul.006G219000.1.v2.1 annot-version=v2.1)  
43 original description: pacid=37164656 transcript=Phvul.007G008100.2 locus=Phvul.007G008100 ID=  
44 ript=Phvul.007G086600.1 locus=Phvul.007G086600 ID=Phvul.007G086600.1.v2.1 annot-version=v2  
45 l locus=Phvul.007G168600 ID=Phvul.007G168600.1.v2.1 annot-version=v2.1) & Auxin-binding prote  
46 l locus=Phvul.008G002700 ID=Phvul.008G002700.1.v2.1 annot-version=v2.1) & Probable methyltra  
47 jinal description: pacid=37149462 transcript=Phvul.009G062500.1 locus=Phvul.009G062500 ID=Phv

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2 =37168174 transcript=Phvul.001G186500.1 locus=Phvul.001G186500 ID=Phvul.001G186500.1.v2.1 ;  
3 t=Phvul.002G028700.1 locus=Phvul.002G028700 ID=Phvul.002G028700.1.v2.1 annot-version=v2.1)  
4 ? locus=Phvul.003G202300 ID=Phvul.003G202300.2.v2.1 annot-version=v2.1) & Protein MODIFIER C  
5 ? locus=Phvul.003G202300 ID=Phvul.003G202300.2.v2.1 annot-version=v2.1) & Protein MODIFIER C  
6 5248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)  
7 5248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)  
8 5248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)  
9 5024400.1 locus=Phvul.004G024400 ID=Phvul.004G024400.1.v2.1 annot-version=v2.1)  
10 l locus=Phvul.004G071800 ID=Phvul.004G071800.1.v2.1 annot-version=v2.1) & MLO-like protein 12  
11 =Phvul.004G178500.1 locus=Phvul.004G178500 ID=Phvul.004G178500.1.v2.1 annot-version=v2.1) ;  
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13 rscript=Phvul.005G175600.2 locus=Phvul.005G175600 ID=Phvul.005G175600.2.v2.1 annot-version=  
14 rscript=Phvul.005G175600.2 locus=Phvul.005G175600 ID=Phvul.005G175600.2.v2.1 annot-version=  
15 rscript=Phvul.006G053300.2 locus=Phvul.006G053300 ID=Phvul.006G053300.2.v2.1 annot-version=  
16 rscript=Phvul.006G053300.2 locus=Phvul.006G053300 ID=Phvul.006G053300.2.v2.1 annot-version=  
17 5110000.1 locus=Phvul.006G110000 ID=Phvul.006G110000.1.v2.1 annot-version=v2.1)  
18 ;cription: pacid=37167521 transcript=Phvul.007G204100.1 locus=Phvul.007G204100 ID=Phvul.007G  
19 l locus=Phvul.008G006800 ID=Phvul.008G006800.1.v2.1 annot-version=v2.1) & Histone-binding pro  
20 3a1\_arath : 307.0) & Enzyme classification.EC\_2 transferases.EC\_2.4 glycosyltransferase(50.2.4 : 19  
21 5184400.2 locus=Phvul.009G184400 ID=Phvul.009G184400.2.v2.1 annot-version=v2.1)  
22 5184400.2 locus=Phvul.009G184400 ID=Phvul.009G184400.2.v2.1 annot-version=v2.1)  
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3 G004800.1.v2.1 annot-version=v2.1) &

4 |/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8\_arath : 681.0

5 |/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8\_arath : 681.0

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10 n=v2.1) &

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12 108200.1.v2.1 annot-version=v2.1) &

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24 ot-version=v2.1) &

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27 glycosyltransferase(50.2.4 : 545.4) (original description: pacid=37165866 transcript=Phvul.007G031

28 glycosyltransferase(50.2.4 : 545.4) (original description: pacid=37165866 transcript=Phvul.007G031

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31 vul.008G081700.2.v2.1 annot-version=v2.1) &

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36 l.010G125200.1.v2.1 annot-version=v2.1) &

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39 01700.1 locus=Phvul.001G001700 ID=Phvul.001G001700.1.v2.1 annot-version=v2.1) &

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41 (original description: pacid=37175571 transcript=Phvul.002G011900.1 locus=Phvul.002G011900 ID

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 2 not-version=v2.1) &  
 3 not-version=v2.1) &  
 4 in EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 345.0)  
 5 =v2.1) &  
 6 ed donor with incorporation or reduction of molecular oxygen(50.1.13 : 407.0) (original description:  
 7 **04G170000.1.v2.1 annot-version=v2.1) &**  
 8 like protein G1 OS=Arabidopsis thaliana (sp|q570s7|cslg1\_arath : 409.0)  
 9 00.1.v2.1 annot-version=v2.1) &  
 10 conjugating enzyme E2 26 OS=Arabidopsis thaliana (sp|q8gy87|ubc26\_arath : 359.0)  
 11 .2.v2.1 annot-version=v2.1) &  
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 27 ot-version=v2.1) &  
 28 rotein 15 OS=Arabidopsis thaliana (sp|q9smy8|fbl15\_arath : 1013.0)  
 29 -version=v2.1) &  
 30 /2.1) &  
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 33 e protein At3g26840, chloroplastic OS=Arabidopsis thaliana (sp|q9lw26|y3684\_arath : 661.0)  
 34 nsferase DPE2 OS=Oryza sativa subsp. japonica (sp|q69q02|dpe2\_orysj : 394.0)  
 35 -version=v2.1) &  
 36 not-version=v2.1) &  
 37 not-version=v2.1) &  
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 41 -version=v2.1) &  
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 43 1 annot-version=v2.1) &  
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 48 CALLOSE-BINDING PROTEIN 3 OS=Arabidopsis thaliana (sp|q9fz86|pdcb3\_arath : 138.0)  
 49 v2.1) &  
 50 r=v2.1) &  
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 56 =Phvul.007G008100.2.v2.1 annot-version=v2.1) &  
 57 !.1) &  
 58 ein T85 OS=Nicotiana tabacum (sp|p33490|abp1\_tobac : 271.0)  
 59 nsferase PMT19 OS=Arabidopsis thaliana (sp|q9zw75|pmtj\_arath : 639.0)  
 60 /ul.009G062500.1.v2.1 annot-version=v2.1) &

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2 annot-version=v2.1) &

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4 JF SNC1 1 OS=Arabidopsis thaliana (sp|q9sb63|mos1\_arath : 429.0)

5 JF SNC1 1 OS=Arabidopsis thaliana (sp|q9sb63|mos1\_arath : 429.0)

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12 2 OS=Arabidopsis thaliana (sp|o80961|mlo12\_arath : 669.0)

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23 i204100.1.v2.1 annot-version=v2.1) &

24 rotein MSI1 homolog OS=Oryza sativa subsp. japonica (sp|q10g81|msi1\_orysj : 130.0)

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26 5.8) (original description: pacid=37160064 transcript=Phvul.008G034200.2 locus=Phvul.008G034200.2)

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7 : pacid=37163295 transcript=Phvul.004G159500.1 locus=Phvul.004G159500 ID=Phvul.004G159500.  
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00 ID=Phvul.008G034200.2.v2.1 annot-version=v2.1) &

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	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
1						
2						
3	ucgauaaaccuc	Phvul.002G040800.1	2.5	-1	1	21
4	uggaggcagcgg	Phvul.002G112900.2	2.5	-1	1	22
5	uggaggcagcgg	Phvul.002G112900.1	2.5	-1	1	22
6	uggaggcagcgg	Phvul.002G112900.2	2.5	-1	1	22
7	uggaggcagcgg	Phvul.002G112900.1	2.5	-1	1	22
8	uggaggcagcgg	Phvul.002G112900.1	2.5	-1	1	22
9	uggaggcagcgg	Phvul.001G016450.1	3	-1	1	22
10	uggaggcagcgg	Phvul.001G016450.1	3	-1	1	22
11	uggaggcagcgg	Phvul.002G255100.1	3	-1	1	22
12	uggaggcagcgg	Phvul.002G255100.1	3	-1	1	22
13	uggaggcagcgg	Phvul.002G332500.1	3	-1	1	21
14	uggaggcagcgg	Phvul.005G022900.2	3	-1	1	22
15	uggaggcagcgg	Phvul.005G022900.2	3	-1	1	22
16	uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
17	uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
18	uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
19	uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
20	uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
21	uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
22	ucgauaaaccuc	Phvul.006G176000.1	3	-1	1	21
23	ucgauaaaccuc	Phvul.007G172400.1	3	-1	1	21
24	uggaggcagcgg	Phvul.009G109200.2	3	-1	1	22
25	uggaggcagcgg	Phvul.009G109200.3	3	-1	1	22
26	uggaggcagcgg	Phvul.009G109200.1	3	-1	1	22
27	uggaggcagcgg	Phvul.009G109200.2	3	-1	1	22
28	uggaggcagcgg	Phvul.009G109200.3	3	-1	1	22
29	uggaggcagcgg	Phvul.009G109200.1	3	-1	1	22
30	uggaggcagcgg	Phvul.009G109200.1	3	-1	1	22
31	uggaggcagcgg	Phvul.009G260000.1	3	-1	1	21
32	ucgauaaaccuc	Phvul.003G050000.1	3.5	-1	1	22
33	uggaggcagcgg	Phvul.003G050000.1	3.5	-1	1	22
34	uggaggcagcgg	Phvul.004G050550.1	3.5	-1	1	22
35	uggaggcagcgg	Phvul.004G050550.1	3.5	-1	1	22
36	uggaggcagcgg	Phvul.004G050550.1	3.5	-1	1	22
37	uggaggcagcgg	Phvul.005G136500.1	3.5	-1	1	21
38	uggaggcagcgg	Phvul.006G105000.1	3.5	-1	1	22
39	uggaggcagcgg	Phvul.006G105000.1	3.5	-1	1	22
40	uggaggcagcgg	Phvul.007G006700.1	3.5	-1	1	22
41	uggaggcagcgg	Phvul.007G006700.1	3.5	-1	1	22
42	uggaggcagcgg	Phvul.007G216500.4	3.5	-1	1	22
43	uggaggcagcgg	Phvul.007G216500.3	3.5	-1	1	22
44	uggaggcagcgg	Phvul.007G216500.1	3.5	-1	1	22
45	uggaggcagcgg	Phvul.007G216500.4	3.5	-1	1	22
46	uggaggcagcgg	Phvul.007G216500.3	3.5	-1	1	22
47	uggaggcagcgg	Phvul.007G216500.1	3.5	-1	1	22
48	uggaggcagcgg	Phvul.007G216500.4	3.5	-1	1	22
49	uggaggcagcgg	Phvul.007G216500.3	3.5	-1	1	22
50	uggaggcagcgg	Phvul.007G216500.1	3.5	-1	1	22
51	uggaggcagcgg	Phvul.007G216500.1	3.5	-1	1	22
52	ucgauaaaccuc	Phvul.008G055300.1	3.5	-1	1	21
53	uggaggcagcgg	Phvul.008G173900.2	3.5	-1	1	22
54	uggaggcagcgg	Phvul.008G173900.1	3.5	-1	1	22
55	uggaggcagcgg	Phvul.008G173900.2	3.5	-1	1	22
56	uggaggcagcgg	Phvul.008G173900.1	3.5	-1	1	22
57	uggaggcagcgg	Phvul.008G173900.2	3.5	-1	1	22
58	uggaggcagcgg	Phvul.008G173900.1	3.5	-1	1	22
59	uggaggcagcgg	Phvul.011G132801.1	3.5	-1	1	22
60	uggaggcagcgg	Phvul.011G132801.1	3.5	-1	1	22

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2	uggaggcagcgg Phvul.011G157600.3	3.5	-1	1	22
3	uggaggcagcgg Phvul.011G157600.4	3.5	-1	1	22
4	uggaggcagcgg Phvul.011G157600.2	3.5	-1	1	22
5					
6	uggaggcagcgg Phvul.011G157600.3	3.5	-1	1	22
7	uggaggcagcgg Phvul.011G157600.4	3.5	-1	1	22
8					
9	uggaggcagcgg Phvul.011G157600.2	3.5	-1	1	22
10	uggaggcagcgg Phvul.001G026200.1	4	-1	1	22
11	uggaggcagcgg Phvul.001G026200.1	4	-1	1	22
12	uggaggcagcgg Phvul.001G141300.1	4	-1	1	22
13					
14	uggaggcagcgg Phvul.001G141300.1	4	-1	1	22
15	uggaggcagcgg Phvul.001G256400.1	4	-1	1	22
16	uggaggcagcgg Phvul.001G256400.1	4	-1	1	22
17					
18	uggaggcagcgg Phvul.001G256600.1	4	-1	1	22
19	uggaggcagcgg Phvul.001G256600.1	4	-1	1	22
20	uggaggcagcgg Phvul.002G003600.1	4	-1	1	22
21					
22	uggaggcagcgg Phvul.002G003600.1	4	-1	1	22
23	uggaggcagcgg Phvul.002G075900.1	4	-1	1	22
24	uggaggcagcgg Phvul.002G075900.1	4	-1	1	22
25					
26	uggaggcagcgg Phvul.002G102800.2	4	-1	1	22
27	uggaggcagcgg Phvul.002G102800.2	4	-1	1	22
28	uggaggcagcgg Phvul.002G146600.2	4	-1	1	22
29					
30	uggaggcagcgg Phvul.002G146600.1	4	-1	1	22
31	uggaggcagcgg Phvul.002G146600.2	4	-1	1	22
32	uggaggcagcgg Phvul.002G146600.1	4	-1	1	22
33					
34	uggaggcagcgg Phvul.002G158200.1	4	-1	1	22
35	uggaggcagcgg Phvul.002G158200.1	4	-1	1	22
36	ucgauaaaccuc Phvul.003G013200.2	4	-1	1	21
37	uggaggcagcgg Phvul.003G156333.1	4	-1	1	22
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40	ucgauaaaccuc Phvul.003G179800.1	4	-1	1	21
41	uggaggcagcgg Phvul.003G179800.1	4	-1	1	22
42					
43	uggaggcagcgg Phvul.003G179800.1	4	-1	1	22
44	uggaggcagcgg Phvul.003G261400.2	4	-1	1	22
45	uggaggcagcgg Phvul.003G261400.1	4	-1	1	22
46					
47	uggaggcagcgg Phvul.003G261400.2	4	-1	1	22
48	uggaggcagcgg Phvul.003G261400.1	4	-1	1	22
49					
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52	uggaggcagcgg Phvul.003G291600.1	4	-1	1	22
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54					
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56	uggaggcagcgg Phvul.004G068900.2	4	-1	1	22
57	ucgauaaaccuc Phvul.005G069600.1	4	-1	1	21
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59	ucgauaaaccuc Phvul.007G249600.1	4	-1	1	21
60	uggaggcagcgg Phvul.008G111200.1	4	-1	1	22

1					
2	uggaggcagcgg Phvul.008G111200.1	4	-1	1	22
3	ucgauaaaccuc Phvul.008G230800.1	4	-1	1	21
4	uggaggcagcgg Phvul.009G080800.1	4	-1	1	22
5	uggaggcagcgg Phvul.009G080800.1	4	-1	1	22
6	uggaggcagcgg Phvul.009G119700.1	4	-1	1	22
7	uggaggcagcgg Phvul.009G119700.1	4	-1	1	22
8	uggaggcagcgg Phvul.009G119700.1	4	-1	1	22
9	uggaggcagcgg Phvul.009G119700.1	4	-1	1	22
10	ucgauaaaccuc Phvul.010G119500.1	4	-1	1	21
11	uggaggcagcgg Phvul.011G008600.1	4	-1	1	22
12	uggaggcagcgg Phvul.011G008600.1	4	-1	1	22
13	uggaggcagcgg Phvul.011G140900.1	4	-1	1	22
14	uggaggcagcgg Phvul.011G140900.1	4	-1	1	22
15	uggaggcagcgg Phvul.011G140900.1	4	-1	1	22
16	ucgauaaaccuc Phvul.011G169222.1	4	-1	1	21
17	uggaggcagcgg Phvul.011G215900.1	4	-1	1	22
18	uggaggcagcgg Phvul.011G215900.1	4	-1	1	22
19	uggaggcagcgg Phvul.011G215900.1	4	-1	1	22
20	ucgauaaaccuc Phvul.001G096200.1	4.5	-1	1	21
21	uggaggcagcgg Phvul.001G104700.2	4.5	-1	1	22
22	uggaggcagcgg Phvul.001G104700.1	4.5	-1	1	22
23	uggaggcagcgg Phvul.001G104700.1	4.5	-1	1	22
24	uggaggcagcgg Phvul.001G104700.2	4.5	-1	1	22
25	uggaggcagcgg Phvul.001G104700.1	4.5	-1	1	22
26	uggaggcagcgg Phvul.001G104700.1	4.5	-1	1	22
27	uggaggcagcgg Phvul.001G211000.1	4.5	-1	1	22
28	uggaggcagcgg Phvul.001G211000.1	4.5	-1	1	22
29	uggaggcagcgg Phvul.001G211000.1	4.5	-1	1	22
30	uggaggcagcgg Phvul.002G147900.2	4.5	-1	1	22
31	uggaggcagcgg Phvul.002G147900.1	4.5	-1	1	22
32	uggaggcagcgg Phvul.002G147900.2	4.5	-1	1	22
33	uggaggcagcgg Phvul.002G147900.1	4.5	-1	1	22
34	uggaggcagcgg Phvul.002G147900.1	4.5	-1	1	22
35	ucgauaaaccuc Phvul.002G182700.2	4.5	-1	1	21
36	ucgauaaaccuc Phvul.002G182700.1	4.5	-1	1	21
37	ucgauaaaccuc Phvul.002G202300.1	4.5	-1	1	21
38	ucgauaaaccuc Phvul.002G202300.1	4.5	-1	1	21
39	ucgauaaaccuc Phvul.002G238000.1	4.5	-1	1	21
40	uggaggcagcgg Phvul.002G267100.1	4.5	-1	1	22
41	uggaggcagcgg Phvul.002G267100.1	4.5	-1	1	22
42	uggaggcagcgg Phvul.002G267100.1	4.5	-1	1	22
43	uggaggcagcgg Phvul.002G274400.2	4.5	-1	1	22
44	uggaggcagcgg Phvul.002G274400.1	4.5	-1	1	22
45	uggaggcagcgg Phvul.002G274400.2	4.5	-1	1	22
46	uggaggcagcgg Phvul.002G274400.2	4.5	-1	1	22
47	uggaggcagcgg Phvul.002G274400.1	4.5	-1	1	22
48	ucgauaaaccuc Phvul.002G304500.1	4.5	-1	1	21
49	uggaggcagcgg Phvul.002G327900.1	4.5	-1	1	22
50	uggaggcagcgg Phvul.002G327900.1	4.5	-1	1	22
51	uggaggcagcgg Phvul.002G327900.1	4.5	-1	1	22
52	ucgauaaaccuc Phvul.003G010700.1	4.5	-1	1	21
53	ucgauaaaccuc Phvul.003G023101.2	4.5	-1	1	21
54	ucgauaaaccuc Phvul.003G023101.2	4.5	-1	1	21
55	ucgauaaaccuc Phvul.003G023101.1	4.5	-1	1	21
56	uggaggcagcgg Phvul.003G044200.1	4.5	-1	1	22
57	uggaggcagcgg Phvul.003G044200.1	4.5	-1	1	22
58	uggaggcagcgg Phvul.003G044200.1	4.5	-1	1	22
59	ucgauaaaccuc Phvul.003G080700.1	4.5	-1	1	21
60	uggaggcagcgg Phvul.003G090000.2	4.5	-1	1	22
	uggaggcagcgg Phvul.003G090000.2	4.5	-1	1	22

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2	ucgauaaaccuc	Phvul.003G096500.1	4.5	-1	1	21
3	uggaggcagcgg	Phvul.003G113900.1	4.5	-1	1	22
4	uggaggcagcgg	Phvul.003G113900.1	4.5	-1	1	22
5	uggaggcagcgg	Phvul.003G154900.1	4.5	-1	1	22
6	uggaggcagcgg	Phvul.003G154900.1	4.5	-1	1	22
7	uggaggcagcgg	Phvul.003G154900.1	4.5	-1	1	22
8	uggaggcagcgg	Phvul.003G209900.1	4.5	-1	1	22
9	uggaggcagcgg	Phvul.003G209900.1	4.5	-1	1	22
10	uggaggcagcgg	Phvul.003G209900.1	4.5	-1	1	22
11	uggaggcagcgg	Phvul.003G254900.2	4.5	-1	1	22
12	uggaggcagcgg	Phvul.003G254900.1	4.5	-1	1	22
13	uggaggcagcgg	Phvul.003G254900.2	4.5	-1	1	22
14	uggaggcagcgg	Phvul.003G254900.2	4.5	-1	1	22
15	uggaggcagcgg	Phvul.003G254900.1	4.5	-1	1	22
16	ucgauaaaccuc	Phvul.003G295700.2	4.5	-1	1	21
17	ucgauaaaccuc	Phvul.003G295700.1	4.5	-1	1	21
18	uggaggcagcgg	Phvul.005G088636.1	4.5	-1	1	22
19	uggaggcagcgg	Phvul.005G088636.1	4.5	-1	1	22
20	uggaggcagcgg	Phvul.005G088636.1	4.5	-1	1	22
21	uggaggcagcgg	Phvul.005G088636.1	4.5	-1	1	22
22	ucgauaaaccuc	Phvul.006G112000.1	4.5	-1	1	21
23	ucgauaaaccuc	Phvul.006G112000.2	4.5	-1	1	21
24	ucgauaaaccuc	Phvul.007G015000.1	4.5	-1	1	21
25	ucgauaaaccuc	Phvul.007G028800.1	4.5	-1	1	21
26	ucgauaaaccuc	Phvul.007G028800.1	4.5	-1	1	21
27	uggaggcagcgg	Phvul.007G038000.1	4.5	-1	1	22
28	uggaggcagcgg	Phvul.007G038000.1	4.5	-1	1	22
29	uggaggcagcgg	Phvul.007G038000.1	4.5	-1	1	22
30	uggaggcagcgg	Phvul.007G062900.1	4.5	-1	1	22
31	uggaggcagcgg	Phvul.007G062900.1	4.5	-1	1	22
32	uggaggcagcgg	Phvul.007G100700.1	4.5	-1	1	22
33	uggaggcagcgg	Phvul.007G100700.1	4.5	-1	1	22
34	uggaggcagcgg	Phvul.007G100700.1	4.5	-1	1	22
35	ucgauaaaccuc	Phvul.007G149300.1	4.5	-1	1	21
36	ucgauaaaccuc	Phvul.007G230450.1	4.5	-1	1	21
37	ucgauaaaccuc	Phvul.007G230450.1	4.5	-1	1	21
38	ucgauaaaccuc	Phvul.008G046100.1	4.5	-1	1	21
39	ucgauaaaccuc	Phvul.008G177200.1	4.5	-1	1	21
40	ucgauaaaccuc	Phvul.008G177200.2	4.5	-1	1	21
41	ucgauaaaccuc	Phvul.008G181900.2	4.5	-1	1	21
42	ucgauaaaccuc	Phvul.008G181900.1	4.5	-1	1	21
43	ucgauaaaccuc	Phvul.008G181900.1	4.5	-1	1	21
44	uggaggcagcgg	Phvul.008G260900.2	4.5	-1	1	22
45	uggaggcagcgg	Phvul.008G260900.1	4.5	-1	1	22
46	uggaggcagcgg	Phvul.008G260900.1	4.5	-1	1	22
47	uggaggcagcgg	Phvul.008G260900.2	4.5	-1	1	22
48	uggaggcagcgg	Phvul.008G260900.1	4.5	-1	1	22
49	uggaggcagcgg	Phvul.008G260900.1	4.5	-1	1	22
50	uggaggcagcgg	Phvul.009G041100.2	4.5	-1	1	22
51	uggaggcagcgg	Phvul.009G041100.1	4.5	-1	1	22
52	uggaggcagcgg	Phvul.009G041100.2	4.5	-1	1	22
53	uggaggcagcgg	Phvul.009G041100.1	4.5	-1	1	22
54	uggaggcagcgg	Phvul.009G041100.1	4.5	-1	1	22
55	ucgauaaaccuc	Phvul.009G175100.3	4.5	-1	1	21
56	ucgauaaaccuc	Phvul.009G175100.2	4.5	-1	1	21
57	ucgauaaaccuc	Phvul.009G175100.1	4.5	-1	1	21
58	ucgauaaaccuc	Phvul.009G175100.1	4.5	-1	1	21
59	uggaggcagcgg	Phvul.009G200500.3	4.5	-1	1	22
60	uggaggcagcgg	Phvul.009G200500.2	4.5	-1	1	22
	uggaggcagcgg	Phvul.009G200500.3	4.5	-1	1	22

1					
2	uggaggcagcgg Phvul.009G200500.2	4.5	-1	1	22
3	uggaggcagcgg Phvul.011G080200.1	4.5	-1	1	22
4	uggaggcagcgg Phvul.011G080200.1	4.5	-1	1	22
5					
6	uggaggcagcgg Phvul.011G174000.1	4.5	-1	1	22
7	uggaggcagcgg Phvul.011G174000.1	4.5	-1	1	22
8	ucgauaaaccuc Phvul.001G110400.1	5	-1	1	21
9					
10	uggaggcagcgg Phvul.001G123400.1	5	-1	1	22
11	uggaggcagcgg Phvul.001G123400.1	5	-1	1	22
12	ucgauaaaccuc Phvul.001G154700.1	5	-1	1	21
13					
14	uggaggcagcgg Phvul.001G179800.1	5	-1	1	22
15	uggaggcagcgg Phvul.001G179800.1	5	-1	1	22
16	ucgauaaaccuc Phvul.001G184000.1	5	-1	1	21
17					
18	uggaggcagcgg Phvul.001G259000.1	5	-1	1	22
19	uggaggcagcgg Phvul.001G259000.1	5	-1	1	22
20	uggaggcagcgg Phvul.002G028100.1	5	-1	1	22
21					
22	uggaggcagcgg Phvul.002G028100.1	5	-1	1	22
23	ucgauaaaccuc Phvul.002G092900.2	5	-1	1	21
24	ucgauaaaccuc Phvul.002G092900.1	5	-1	1	21
25					
26	ucgauaaaccuc Phvul.002G137100.1	5	-1	1	21
27	uggaggcagcgg Phvul.002G137200.1	5	-1	1	22
28	uggaggcagcgg Phvul.002G137200.1	5	-1	1	22
29					
30	ucgauaaaccuc Phvul.002G139900.2	5	-1	1	21
31	ucgauaaaccuc Phvul.002G139900.1	5	-1	1	21
32	ucgauaaaccuc Phvul.002G156300.1	5	-1	1	21
33					
34	uggaggcagcgg Phvul.003G032500.1	5	-1	1	22
35	uggaggcagcgg Phvul.003G032500.1	5	-1	1	22
36	uggaggcagcgg Phvul.003G252400.1	5	-1	1	22
37					
38	uggaggcagcgg Phvul.003G252400.1	5	-1	1	22
39	ucgauaaaccuc Phvul.003G265700.1	5	-1	1	21
40	uggaggcagcgg Phvul.003G291600.1	5	-1	1	22
41	uggaggcagcgg Phvul.003G291600.2	5	-1	1	22
42					
43	uggaggcagcgg Phvul.003G291600.1	5	-1	1	22
44	uggaggcagcgg Phvul.003G291600.2	5	-1	1	22
45	ucgauaaaccuc Phvul.004G176100.1	5	-1	1	21
46					
47	ucgauaaaccuc Phvul.005G001500.2	5	-1	1	21
48	ucgauaaaccuc Phvul.005G001500.1	5	-1	1	21
49	uggaggcagcgg Phvul.005G043500.1	5	-1	1	22
50					
51	uggaggcagcgg Phvul.005G043500.1	5	-1	1	22
52	ucgauaaaccuc Phvul.005G093400.1	5	-1	1	21
53	ucgauaaaccuc Phvul.005G131700.1	5	-1	1	21
54					
55	ucgauaaaccuc Phvul.005G183800.1	5	-1	1	21
56	ucgauaaaccuc Phvul.005G183800.2	5	-1	1	21
57	ucgauaaaccuc Phvul.006G098700.1	5	-1	1	21
58					
59	uggaggcagcgg Phvul.006G131400.1	5	-1	1	22
60	uggaggcagcgg Phvul.006G131400.1	5	-1	1	22
	uggaggcagcgg Phvul.006G208400.1	5	-1	1	22

1					
2	uggaggcagcgg Phvul.006G208400.1	5	-1	1	22
3	uggaggcagcgg Phvul.007G043900.2	5	-1	1	22
4	uggaggcagcgg Phvul.007G043900.1	5	-1	1	22
5	uggaggcagcgg Phvul.007G043900.2	5	-1	1	22
6	uggaggcagcgg Phvul.007G043900.1	5	-1	1	22
7	uggaggcagcgg Phvul.007G043900.2	5	-1	1	22
8	uggaggcagcgg Phvul.007G043900.1	5	-1	1	22
9	ucgauaaaccuc Phvul.007G062100.1	5	-1	1	21
10	ucgauaaaccuc Phvul.007G067800.1	5	-1	1	21
11	uggaggcagcgg Phvul.007G080900.2	5	-1	1	22
12	uggaggcagcgg Phvul.007G080900.1	5	-1	1	22
13	uggaggcagcgg Phvul.007G080900.2	5	-1	1	22
14	uggaggcagcgg Phvul.007G080900.1	5	-1	1	22
15	uggaggcagcgg Phvul.007G139300.1	5	-1	1	22
16	uggaggcagcgg Phvul.007G139300.1	5	-1	1	22
17	uggaggcagcgg Phvul.007G139300.1	5	-1	1	22
18	ucgauaaaccuc Phvul.007G173400.1	5	-1	1	21
19	ucgauaaaccuc Phvul.007G246700.1	5	-1	1	21
20	uggaggcagcgg Phvul.007G274200.1	5	-1	1	22
21	uggaggcagcgg Phvul.007G274200.1	5	-1	1	22
22	uggaggcagcgg Phvul.007G274200.1	5	-1	1	22
23	ucgauaaaccuc Phvul.008G019000.1	5	-1	1	21
24	uggaggcagcgg Phvul.008G055500.1	5	-1	1	22
25	uggaggcagcgg Phvul.008G055500.1	5	-1	1	22
26	ucgauaaaccuc Phvul.008G077000.1	5	-1	1	21
27	uggaggcagcgg Phvul.008G114700.1	5	-1	1	22
28	uggaggcagcgg Phvul.008G114700.1	5	-1	1	22
29	ucgauaaaccuc Phvul.008G211500.4	5	-1	1	21
30	ucgauaaaccuc Phvul.008G211500.3	5	-1	1	21
31	ucgauaaaccuc Phvul.008G211500.1	5	-1	1	21
32	ucgauaaaccuc Phvul.008G211500.2	5	-1	1	21
33	uggaggcagcgg Phvul.008G250000.1	5	-1	1	22
34	uggaggcagcgg Phvul.008G250000.1	5	-1	1	22
35	uggaggcagcgg Phvul.009G086300.2	5	-1	1	22
36	uggaggcagcgg Phvul.009G086300.1	5	-1	1	22
37	uggaggcagcgg Phvul.009G086300.2	5	-1	1	22
38	uggaggcagcgg Phvul.009G086300.1	5	-1	1	22
39	ucgauaaaccuc Phvul.009G149800.1	5	-1	1	21
40	uggaggcagcgg Phvul.009G154300.6	5	-1	1	22
41	uggaggcagcgg Phvul.009G154300.5	5	-1	1	22
42	uggaggcagcgg Phvul.009G154300.3	5	-1	1	22
43	uggaggcagcgg Phvul.009G154300.4	5	-1	1	22
44	uggaggcagcgg Phvul.009G154300.1	5	-1	1	22
45	uggaggcagcgg Phvul.009G154300.6	5	-1	1	22
46	uggaggcagcgg Phvul.009G154300.5	5	-1	1	22
47	uggaggcagcgg Phvul.009G154300.3	5	-1	1	22
48	uggaggcagcgg Phvul.009G154300.4	5	-1	1	22
49	uggaggcagcgg Phvul.009G154300.1	5	-1	1	22
50	ucgauaaaccuc Phvul.009G240100.1	5	-1	1	21
51	uggaggcagcgg Phvul.011G017800.1	5	-1	1	22



1					
2	uggaggcagcgg Phvul.011G017800.1	5	-1	1	22
3	ucgauaaaccuc Phvul.011G100200.2	5	-1	1	21
4	ucgauaaaccuc Phvul.011G100200.1	5	-1	1	21
5					
6	ucgauaaaccuc Phvul.011G108300.1	5	-1	1	21
7	uggaggcagcgg Phvul.011G129700.1	5	-1	1	22
8	uggaggcagcgg Phvul.011G129700.1	5	-1	1	22
9					
10	ucgauaaaccuc Phvul.011G140050.2	5	-1	1	21
11	ucgauaaaccuc Phvul.011G140050.1	5	-1	1	21
12					
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	Target_start	Target_end	miRNA_alignment	Target_alignment	Inhibition	Target_Desc.
1						
2						
3	2888	2907	UCGAUAAACC	::: ::::: GGGGAUG-AC	Cleavage	pacid=371763
4	400	421	UGGAGGCAG	: ::::: AACCGAUGG/	Cleavage	pacid=371750
5	400	421	UGGAGGCAG	: ::::: AACCGAUGG/	Cleavage	pacid=371750
6	400	421	UGGAGGCAG	: ::::: AACCGAUGG/	Cleavage	pacid=371750
7	400	421	UGGAGGCAG	: ::::: AACCGAUGG/	Cleavage	pacid=371750
8	400	421	UGGAGGCAG	: ::::: AACCGAUGG/	Cleavage	pacid=371750
9	187	207	UGGAGGCAG	: : ::::: CCACGA-GAA	Cleavage	pacid=371691
10	187	207	UGGAGGCAG	: : ::::: CCACGA-GAA	Cleavage	pacid=371691
11	246	267	UGGAGGCAG	: ::::: AGCAGAUGA	Cleavage	pacid=371771
12	246	267	UGGAGGCAG	: ::::: AGCAGAUGA	Cleavage	pacid=371771
13	1000	1020	UCGAUAAACC	::: : : AAGGGUGGA	Cleavage	pacid=371778
14	220	241	UGGAGGCAG	: ::::: GUUUGAUGG	Cleavage	pacid=371541
15	220	241	UGGAGGCAG	: ::::: GUUUGAUGG	Cleavage	pacid=371541
16	282	303	UGGAGGCAG	: : ::::: CUAUGAGGA	Translation	pacid=371526
17	282	303	UGGAGGCAG	: : ::::: CUAUGAGGA	Translation	pacid=371526
18	1116	1136	UCGAUAAACC	: ::::: : : GAGGAUGCA	Translation	pacid=371738
19	473	493	UCGAUAAACC	: ::::: : : CAGGAUGGA	Cleavage	pacid=371646
20	315	336	UGGAGGCAG	: : ::::: UGUUGACCA/	Cleavage	pacid=371495
21	315	336	UGGAGGCAG	: : ::::: UGUUGACCA/	Cleavage	pacid=371495
22	315	336	UGGAGGCAG	: : ::::: UGUUGACCA/	Cleavage	pacid=371495
23	315	336	UGGAGGCAG	: : ::::: UGUUGACCA/	Cleavage	pacid=371495
24	315	336	UGGAGGCAG	: : ::::: UGUUGACCA/	Cleavage	pacid=371495
25	315	336	UGGAGGCAG	: : ::::: UGUUGACCA/	Cleavage	pacid=371495
26	3637	3658	UCGAUAA-AC	: ::::: : : CUGGAUGCA	Cleavage	pacid=371490
27	1587	1608	UGGAGGCAG	: ::::: : : AAAAGGUGA/	Cleavage	pacid=371459
28	1587	1608	UGGAGGCAG	: ::::: : : AAAAGGUGA/	Cleavage	pacid=371459
29	3823	3844	UGGAGGCAG	: : ::::: UGUUUUAUGG	Translation	pacid=371632
30	3823	3844	UGGAGGCAG	: : ::::: UGUUUUAUGG	Translation	pacid=371632
31	427	447	UCGAUAAACC	: : ::::: : : UUGAAUGCG	Cleavage	pacid=371525
32	2271	2292	UGGAGGCAG	: ::::: : : AACUGAUGA	Translation	pacid=371719
33	2271	2292	UGGAGGCAG	: ::::: : : AACUGAUGA	Translation	pacid=371719
34	694	715	UGGAGGCAG	: ::::: : : UUGGGAUGG	Cleavage	pacid=371667
35	694	715	UGGAGGCAG	: ::::: : : UUGGGAUGG	Cleavage	pacid=371667
36	1058	1079	UGGAGGCAG	: ::::: : : UGACUAUGG/	Translation	pacid=371659
37	1056	1077	UGGAGGCAG	: ::::: : : UGACUAUGG/	Translation	pacid=371659
38	1058	1079	UGGAGGCAG	: ::::: : : UGACUAUGG/	Translation	pacid=371659
39	1058	1079	UGGAGGCAG	: ::::: : : UGACUAUGG/	Translation	pacid=371659
40	1056	1077	UGGAGGCAG	: ::::: : : UGACUAUGG/	Translation	pacid=371659
41	1058	1079	UGGAGGCAG	: ::::: : : UGACUAUGG/	Translation	pacid=371659
42	747	767	UCGAUAAACC	: : ::::: : : GAGGCAGCA	Cleavage	pacid=371602
43	1646	1667	UGGAGGCAG	: ::::: : : GACCGAUGG/	Cleavage	pacid=371611
44	1736	1757	UGGAGGCAG	: ::::: : : GACCGAUGG/	Cleavage	pacid=371611
45	1646	1667	UGGAGGCAG	: ::::: : : GACCGAUGG/	Cleavage	pacid=371611
46	1736	1757	UGGAGGCAG	: ::::: : : GACCGAUGG/	Cleavage	pacid=371611
47	2079	2101	UGGAGGCAG	: : ::::: : : GGACGACUG/	Cleavage	pacid=371551
48	2079	2101	UGGAGGCAG	: : ::::: : : GGACGACUG/	Cleavage	pacid=371551



1				
2	240	261 UGGAGGCAG(	..... : : : : : GCGUGGUGG	Translation pacid=371603
3	759	779 UCGAUAAACC	..... : : : : : GUGGGUGGA	Cleavage pacid=371577
4	1095	1116 UGGAGGCAG(	..... : : : : : UCUUGAUGA	Cleavage pacid=371489
5	1095	1116 UGGAGGCAG(	..... : : : : : UCUUGAUGA	Cleavage pacid=371489
6	1778	1799 UGGAGGCAG(	..... : : : : : CGCAAUGA	Translation pacid=371487
7	1778	1799 UGGAGGCAG(	..... : : : : : CGCAAUGA	Translation pacid=371487
8				
9				
10	421	441 UCGAUAAACC	..... : : : : : CUAGCUGUG	Cleavage pacid=371439
11	78	99 UGGAGGCAG(	..... : : : : : UAACAAUGA	Translation pacid=371574
12	78	99 UGGAGGCAG(	..... : : : : : UAACAAUGA	Translation pacid=371574
13				
14	719	740 UGGAGGCAG(	..... : : : : : GCUCGGUCA	Cleavage pacid=371549
15	719	740 UGGAGGCAG(	..... : : : : : GCUCGGUCA	Cleavage pacid=371549
16	844	864 UCGAUAAACC	..... : : : : : GAAGAUGCA	Translation pacid=371550
17				
18	2952	2973 UGGAGGCAG(	..... : : : : : AAUCGAGCA	Cleavage pacid=371569
19	2952	2973 UGGAGGCAG(	..... : : : : : AAUCGAGCA	Cleavage pacid=371569
20	2488	2508 UCGAUAAACC	..... : : : : : UAGGAUGUA	Cleavage pacid=371678
21				
22	1245	1266 UGGAGGCAG(	..... : : : : : AAGGGAUGG	Cleavage pacid=371677
23	1269	1290 UGGAGGCAG(	..... : : : : : AAGGGAUGG	Cleavage pacid=371677
24	1245	1266 UGGAGGCAG(	..... : : : : : AAGGGAUGG	Cleavage pacid=371677
25	1269	1290 UGGAGGCAG(	..... : : : : : AAGGGAUGG	Cleavage pacid=371677
26				
27	902	923 UGGAGGCAG(	..... : : : : : UGAUGAUCA	Translation pacid=371686
28	902	923 UGGAGGCAG(	..... : : : : : UGAUGAUCA	Translation pacid=371686
29				
30	252	273 UGGAGGCAG(	..... : : : : : GAGCGAUGC	Translation pacid=371759
31	252	273 UGGAGGCAG(	..... : : : : : GAGCGAUGC	Translation pacid=371759
32	252	273 UGGAGGCAG(	..... : : : : : GAGCGAUGC	Translation pacid=371759
33	252	273 UGGAGGCAG(	..... : : : : : GAGCGAUGC	Translation pacid=371759
34				
35	405	425 UCGAUAAACC	..... : : : : : UUGGAUUCA	Translation pacid=371779
36	405	425 UCGAUAAACC	..... : : : : : UUGGAUUCA	Translation pacid=371779
37				
38	1306	1326 UCGAUAAACC	..... : : : : : GUGGUGGCA	Cleavage pacid=371780
39	819	839 UCGAUAAACC	..... : : : : : UUGGAUGCA	Translation pacid=371752
40	521	542 UGGAGGCAG(	..... : : : : : GGAACAUGG	Cleavage pacid=371777
41	521	542 UGGAGGCAG(	..... : : : : : GGAACAUGG	Cleavage pacid=371777
42				
43	1039	1060 UGGAGGCAG(	..... : : : : : GGACGAUGG	Translation pacid=371754
44	1132	1153 UGGAGGCAG(	..... : : : : : GGACGAUGG	Translation pacid=371754
45	1039	1060 UGGAGGCAG(	..... : : : : : GGACGAUGG	Translation pacid=371754
46	1132	1153 UGGAGGCAG(	..... : : : : : GGACGAUGG	Translation pacid=371754
47				
48	2338	2358 UCGAUAAACC	..... : : : : : GUUGAUGAA	Cleavage pacid=371749
49	518	539 UGGAGGCAG(	..... : : : : : UGUUGAUGG	Translation pacid=371782
50	518	539 UGGAGGCAG(	..... : : : : : UGUUGAUGG	Translation pacid=371782
51				
52	1259	1278 UCGAUAAACC	..... : : : : : GAGGAUGCG	Cleavage pacid=371466
53	1050	1069 UCGAUAAACC	..... : : : : : UUUGAUGCA	Cleavage pacid=371447
54	1169	1188 UCGAUAAACC	..... : : : : : UUUGAUGCA	Cleavage pacid=371447
55	1729	1750 UGGAGGCAG(	..... : : : : : UUGUUAUGA	Cleavage pacid=371481
56	1729	1750 UGGAGGCAG(	..... : : : : : UUGUUAUGA	Cleavage pacid=371481
57				
58	940	960 UCGAUAAACC	..... : : : : : AUCGAUGAA	Cleavage pacid=371474
59	1008	1029 UGGAGGCAG(	..... : : : : : AUUAGAUGG	Translation pacid=371481
60	1008	1029 UGGAGGCAG(	..... : : : : : AUUAGAUGG	Translation pacid=371481











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372	393 UGGAGGCAG(:.: :.: :.: :GGUUCUUGA.Cleavage	pacid=371562
1076	1096 UCGAUAAACC.: :.: :.: : UUUGAUCCG(Cleavage	pacid=371558
1076	1096 UCGAUAAACC.: :.: :.: : UUUGAUCCG(Cleavage	pacid=371558
110	130 UCGAUAAACC :.: :.: : : UGAGAUGCA(Cleavage	pacid=371546
1572	1593 UGGAGGCAG( :.: :.: : : :AGUUGGUGA Cleavage	pacid=371553
1572	1593 UGGAGGCAG( :.: :.: : : :AGUUGGUGA Cleavage	pacid=371553
2490	2510 UCGAUAAACC :.: :.: : : GACGAUGCG(Cleavage	pacid=371551
2586	2606 UCGAUAAACC :.: :.: : : GACGAUGCG(Cleavage	pacid=371551

Do not distribute

Multiplicity	Target_Acc.	ID	locusName	Pfam	Panther
1	Phvul.002G040800.1	Phvul.002G040800	Phvul.002G04	PF00675,PF05	PTHR11851,P
1	Phvul.002G112900.2	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.002G112900.1	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.002G112900.2	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.002G112900.1	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.001G016450.1	Phvul.001G016450	Phvul.001G01	PF13656	PTHR13946,P
1	Phvul.001G016450.1	Phvul.001G016450	Phvul.001G01	PF13656	PTHR13946,P
1	Phvul.002G255100.1	Phvul.002G255100	Phvul.002G25	PF00083	PTHR23505,P
1	Phvul.002G255100.1	Phvul.002G255100	Phvul.002G25	PF00083	PTHR23505,P
1	Phvul.002G332500.1	Phvul.002G332500	Phvul.002G33		0 PTHR10593,P
1	Phvul.005G022900.2	Phvul.005G022900	Phvul.005G02	PF02775,PF13	PTHR18968,P
1	Phvul.005G022900.2	Phvul.005G022900	Phvul.005G02	PF02775,PF13	PTHR18968,P
1	Phvul.005G165300.1	Phvul.005G165300	Phvul.005G16	PF00235	PTHR11604,P
1	Phvul.005G165300.1	Phvul.005G165300	Phvul.005G16	PF00235	PTHR11604,P
1	Phvul.006G176000.1	Phvul.006G176000	Phvul.006G17	PF13837	PTHR31307,P
1	Phvul.007G172400.1	Phvul.007G172400	Phvul.007G17	PF01765	PTHR20982,P
1	Phvul.009G109200.2	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.3	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.1	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.2	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.3	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.1	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G260000.1	Phvul.009G260000	Phvul.009G26	PF04851,PF14	PTHR14950,P
1	Phvul.003G050000.1	Phvul.003G050000	Phvul.003G05	PF08241	PTHR12176,P
1	Phvul.003G050000.1	Phvul.003G050000	Phvul.003G05	PF08241	PTHR12176,P
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G05	PF13650	PTHR34482,P
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G05	PF13650	PTHR34482,P
1	Phvul.005G136500.1	Phvul.005G136500	Phvul.005G13	PF05739	PTHR19957,P
1	Phvul.006G105000.1	Phvul.006G105000	Phvul.006G10	PF13857,PF11	PTHR12447,P
1	Phvul.006G105000.1	Phvul.006G105000	Phvul.006G10	PF13857,PF11	PTHR12447,P
1	Phvul.007G006700.1	Phvul.007G006700	Phvul.007G00	PF01040	PTHR11048,P
1	Phvul.007G006700.1	Phvul.007G006700	Phvul.007G00	PF01040	PTHR11048,P
1	Phvul.007G216500.4	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.3	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.1	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.4	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.3	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.1	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.008G055300.1	Phvul.008G055300	Phvul.008G05	PF00571	PTHR13780,P
1	Phvul.008G173900.2	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.008G173900.1	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.008G173900.2	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.008G173900.1	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.011G132801.1	Phvul.011G132801	Phvul.011G13		0 0
1	Phvul.011G132801.1	Phvul.011G132801	Phvul.011G13		0 0

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2	1	Phvul.011G157600.3	Phvul.011G157600	Phvul.011G15	0 PTHR24067,P
3	1	Phvul.011G157600.4	Phvul.011G157600	Phvul.011G15	0 PTHR24067,P
4	1	Phvul.011G157600.2	Phvul.011G157600	Phvul.011G15	0 PTHR24067,P
5	1	Phvul.011G157600.3	Phvul.011G157600	Phvul.011G15	0 PTHR24067,P
6	1	Phvul.011G157600.4	Phvul.011G157600	Phvul.011G15	0 PTHR24067,P
7	1	Phvul.011G157600.2	Phvul.011G157600	Phvul.011G15	0 PTHR24067,P
8	1	Phvul.001G026200.1	Phvul.001G026200	Phvul.001G02 PF00887	PTHR23310,P
9	1	Phvul.001G026200.1	Phvul.001G026200	Phvul.001G02 PF00887	PTHR23310,P
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12	1	Phvul.001G256400.1	Phvul.001G256400	Phvul.001G25	0 PTHR10314,P
13	1	Phvul.001G256400.1	Phvul.001G256400	Phvul.001G25	0 PTHR10314,P
14	1	Phvul.001G256600.1	Phvul.001G256600	Phvul.001G25 PF15413,PF01	PTHR10972,P
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16	1	Phvul.002G003600.1	Phvul.002G003600	Phvul.002G00 PF02880,PF00	PTHR22573,P
17	1	Phvul.002G003600.1	Phvul.002G003600	Phvul.002G00 PF02880,PF00	PTHR22573,P
18	1	Phvul.002G075900.1	Phvul.002G075900	Phvul.002G07	0 0
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20	1	Phvul.002G102800.2	Phvul.002G102800	Phvul.002G10 PF00232	PTHR10353,P
21	1	Phvul.002G102800.2	Phvul.002G102800	Phvul.002G10 PF00232	PTHR10353,P
22	1	Phvul.002G146600.2	Phvul.002G146600	Phvul.002G14 PF04564	PTHR27003
23	1	Phvul.002G146600.1	Phvul.002G146600	Phvul.002G14 PF04564	PTHR27003
24	1	Phvul.002G146600.2	Phvul.002G146600	Phvul.002G14 PF04564	PTHR27003
25	1	Phvul.002G146600.1	Phvul.002G146600	Phvul.002G14 PF04564	PTHR27003
26	1	Phvul.002G158200.1	Phvul.002G158200	Phvul.002G15	0 PTHR31798,P
27	1	Phvul.002G158200.1	Phvul.002G158200	Phvul.002G15	0 PTHR31798,P
28	1	Phvul.003G013200.2	Phvul.003G013200	Phvul.003G01 PF03171	PTHR10209,P
29	1	Phvul.003G156333.1	Phvul.003G156333	Phvul.003G15 PF01287	PTHR11673,P
30	1	Phvul.003G156333.1	Phvul.003G156333	Phvul.003G15 PF01287	PTHR11673,P
31	1	Phvul.003G179800.1	Phvul.003G179800	Phvul.003G17	0 0
32	1	Phvul.003G179800.1	Phvul.003G179800	Phvul.003G17	0 0
33	1	Phvul.003G179800.1	Phvul.003G179800	Phvul.003G17	0 0
34	1	Phvul.003G261400.2	Phvul.003G261400	Phvul.003G26 PF10018	PTHR13208,P
35	1	Phvul.003G261400.1	Phvul.003G261400	Phvul.003G26 PF10018	PTHR13208,P
36	1	Phvul.003G261400.2	Phvul.003G261400	Phvul.003G26 PF10018	PTHR13208,P
37	1	Phvul.003G261400.1	Phvul.003G261400	Phvul.003G26 PF10018	PTHR13208,P
38	2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
39	2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
40	2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
41	2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
42	1	Phvul.004G068900.2	Phvul.004G068900	Phvul.004G06 PF00847	PTHR31677,P
43	1	Phvul.004G068900.2	Phvul.004G068900	Phvul.004G06 PF00847	PTHR31677,P
44	1	Phvul.005G069600.1	Phvul.005G069600	Phvul.005G06 PF13771,PF00	PTHR23069,P
45	1	Phvul.007G157700.1	Phvul.007G157700	Phvul.007G15 PF13041	PTHR24015,P
46	1	Phvul.007G249600.1	Phvul.007G249600	Phvul.007G24 PF08799,PF00	PTHR19846
47	1	Phvul.008G111200.1	Phvul.008G111200	Phvul.008G11 PF01612	PTHR13620

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2	1	Phvul.008G111200.1	Phvul.008G111200	Phvul.008G11 PF01612	PTHR13620
3	1	Phvul.008G230800.1	Phvul.008G230800	Phvul.008G23 PF01535,PF13	PTHR24015
4	1	Phvul.009G080800.1	Phvul.009G080800	Phvul.009G08 PF02042	PTHR32002
5	1	Phvul.009G080800.1	Phvul.009G080800	Phvul.009G08 PF02042	PTHR32002
6	1	Phvul.009G119700.1	Phvul.009G119700	Phvul.009G11 PF00632	PTHR11254,P
7	1	Phvul.009G119700.1	Phvul.009G119700	Phvul.009G11 PF00632	PTHR11254,P
8	1	Phvul.010G119500.1	Phvul.010G119500	Phvul.010G11 PF00076	PTHR24012
9	1	Phvul.011G008600.1	Phvul.011G008600	Phvul.011G00	0 0
10	1	Phvul.011G008600.1	Phvul.011G008600	Phvul.011G00	0 0
11	1	Phvul.011G140900.1	Phvul.011G140900	Phvul.011G14 PF12490	PTHR13268,P
12	1	Phvul.011G140900.1	Phvul.011G140900	Phvul.011G14 PF12490	PTHR13268,P
13	1	Phvul.011G169222.1	Phvul.011G169222	Phvul.011G16 PF13639	PTHR14155,P
14	1	Phvul.011G215900.1	Phvul.011G215900	Phvul.011G21 PF01926,PF00	PTHR11566,P
15	1	Phvul.011G215900.1	Phvul.011G215900	Phvul.011G21 PF01926,PF00	PTHR11566,P
16	1	Phvul.001G096200.1	Phvul.001G096200	Phvul.001G09 PF12796	PTHR24158,P
17	1	Phvul.001G104700.2	Phvul.001G104700	Phvul.001G10 PF13906,PF13	PTHR11785,P
18	1	Phvul.001G104700.1	Phvul.001G104700	Phvul.001G10 PF13906,PF13	PTHR11785,P
19	1	Phvul.001G104700.2	Phvul.001G104700	Phvul.001G10 PF13906,PF13	PTHR11785,P
20	1	Phvul.001G104700.1	Phvul.001G104700	Phvul.001G10 PF13906,PF13	PTHR11785,P
21	1	Phvul.001G211000.1	Phvul.001G211000	Phvul.001G21 PF13632	PTHR13301,P
22	1	Phvul.001G211000.1	Phvul.001G211000	Phvul.001G21 PF13632	PTHR13301,P
23	1	Phvul.002G147900.2	Phvul.002G147900	Phvul.002G14 PF01663	PTHR23072,P
24	1	Phvul.002G147900.1	Phvul.002G147900	Phvul.002G14 PF01663	PTHR23072,P
25	1	Phvul.002G147900.2	Phvul.002G147900	Phvul.002G14 PF01663	PTHR23072,P
26	1	Phvul.002G147900.1	Phvul.002G147900	Phvul.002G14 PF01663	PTHR23072,P
27	1	Phvul.002G182700.2	Phvul.002G182700	Phvul.002G18 PF02746,PF13	PTHR13794,P
28	1	Phvul.002G182700.1	Phvul.002G182700	Phvul.002G18 PF02746,PF13	PTHR13794,P
29	1	Phvul.002G202300.1	Phvul.002G202300	Phvul.002G20 PF07800	PTHR31197,P
30	1	Phvul.002G238000.1	Phvul.002G238000	Phvul.002G23	0 PTHR34669,P
31	1	Phvul.002G267100.1	Phvul.002G267100	Phvul.002G26	0 PTHR33828,P
32	1	Phvul.002G267100.1	Phvul.002G267100	Phvul.002G26	0 PTHR33828,P
33	1	Phvul.002G274400.2	Phvul.002G274400	Phvul.002G27 PF00646	PTHR31370,P
34	1	Phvul.002G274400.1	Phvul.002G274400	Phvul.002G27 PF00646	PTHR31370,P
35	1	Phvul.002G274400.2	Phvul.002G274400	Phvul.002G27 PF00646	PTHR31370,P
36	1	Phvul.002G274400.1	Phvul.002G274400	Phvul.002G27 PF00646	PTHR31370,P
37	1	Phvul.002G304500.1	Phvul.002G304500	Phvul.002G30 PF07714	PTHR27001,P
38	1	Phvul.002G327900.1	Phvul.002G327900	Phvul.002G32 PF00462	PTHR10168,P
39	1	Phvul.002G327900.1	Phvul.002G327900	Phvul.002G32 PF00462	PTHR10168,P
40	1	Phvul.003G010700.1	Phvul.003G010700	Phvul.003G01 PF00067	PTHR24286,P
41	1	Phvul.003G023101.2	Phvul.003G023101	Phvul.003G02 PF13906,PF13	PTHR11785,P
42	1	Phvul.003G023101.1	Phvul.003G023101	Phvul.003G02 PF13906,PF13	PTHR11785,P
43	1	Phvul.003G044200.1	Phvul.003G044200	Phvul.003G04 PF01536	PTHR11570,P
44	1	Phvul.003G044200.1	Phvul.003G044200	Phvul.003G04 PF01536	PTHR11570,P
45	1	Phvul.003G080700.1	Phvul.003G080700	Phvul.003G08 PF03595	PTHR31269,P
46	1	Phvul.003G090000.2	Phvul.003G090000	Phvul.003G09 PF07714	PTHR27003,P
47	1	Phvul.003G090000.2	Phvul.003G090000	Phvul.003G09 PF07714	PTHR27003,P

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2	1	Phvul.003G096500.1	Phvul.003G096500	Phvul.003G09PF161113,PF00PTHR23309,P
3	1	Phvul.003G113900.1	Phvul.003G113900	Phvul.003G11 0 PTHR36033,P
4	1	Phvul.003G113900.1	Phvul.003G113900	Phvul.003G11 0 PTHR36033,P
5	1	Phvul.003G154900.1	Phvul.003G154900	Phvul.003G15PF02847,PF02PTHR23253,P
6	1	Phvul.003G154900.1	Phvul.003G154900	Phvul.003G15PF02847,PF02PTHR23253,P
7	1	Phvul.003G209900.1	Phvul.003G209900	Phvul.003G20 PF08387 PTHR32212,P
8	1	Phvul.003G209900.1	Phvul.003G209900	Phvul.003G20 PF08387 PTHR32212,P
9	1	Phvul.003G254900.2	Phvul.003G254900	Phvul.003G25PF00646,PF01PTHR16517,P
10	1	Phvul.003G254900.1	Phvul.003G254900	Phvul.003G25PF00646,PF01PTHR16517,P
11	1	Phvul.003G254900.2	Phvul.003G254900	Phvul.003G25PF00646,PF01PTHR16517,P
12	1	Phvul.003G254900.1	Phvul.003G254900	Phvul.003G25PF00646,PF01PTHR16517,P
13	1	Phvul.003G254900.1	Phvul.003G254900	Phvul.003G25PF00646,PF01PTHR16517,P
14	1	Phvul.003G295700.2	Phvul.003G295700	Phvul.003G29PF01535,PF13PTHR24015,P
15	1	Phvul.003G295700.1	Phvul.003G295700	Phvul.003G29PF01535,PF13PTHR24015,P
16	1	Phvul.005G088636.1	Phvul.005G088636	Phvul.005G08 0 0
17	1	Phvul.005G088636.1	Phvul.005G088636	Phvul.005G08 0 0
18	1	Phvul.006G112000.1	Phvul.006G112000	Phvul.006G11 PF01764 PTHR21493,P
19	1	Phvul.006G112000.2	Phvul.006G112000	Phvul.006G11 PF01764 PTHR21493,P
20	1	Phvul.007G015000.1	Phvul.007G015000	Phvul.007G01 PF03634 PTHR31072,P
21	1	Phvul.007G028800.1	Phvul.007G028800	Phvul.007G02PF04557,PF03PTHR11451,P
22	1	Phvul.007G038000.1	Phvul.007G038000	Phvul.007G03 PF00403 PTHR22814,P
23	1	Phvul.007G038000.1	Phvul.007G038000	Phvul.007G03 PF00403 PTHR22814,P
24	1	Phvul.007G062900.1	Phvul.007G062900	Phvul.007G06PF14306,PF01PTHR11055,P
25	1	Phvul.007G062900.1	Phvul.007G062900	Phvul.007G06PF14306,PF01PTHR11055,P
26	1	Phvul.007G100700.1	Phvul.007G100700	Phvul.007G10 PF05512 PTHR33294,P
27	1	Phvul.007G100700.1	Phvul.007G100700	Phvul.007G10 PF05512 PTHR33294,P
28	1	Phvul.007G149300.1	Phvul.007G149300	Phvul.007G14 PF10270 PTHR21181
29	1	Phvul.007G230450.1	Phvul.007G230450	Phvul.007G23 PF07766 PTHR14009,P
30	1	Phvul.008G046100.1	Phvul.008G046100	Phvul.008G04PF12854,PF13PTHR24015,P
31	1	Phvul.008G177200.1	Phvul.008G177200	Phvul.008G17 0 PTHR35689,P
32	1	Phvul.008G177200.2	Phvul.008G177200	Phvul.008G17 0 PTHR35689,P
33	1	Phvul.008G181900.2	Phvul.008G181900	Phvul.008G18 0 PTHR34464
34	1	Phvul.008G181900.1	Phvul.008G181900	Phvul.008G18 0 PTHR34464
35	1	Phvul.008G260900.2	Phvul.008G260900	Phvul.008G26PF00642,PF12PTHR14493,P
36	1	Phvul.008G260900.1	Phvul.008G260900	Phvul.008G26PF00642,PF12PTHR14493,P
37	1	Phvul.008G260900.2	Phvul.008G260900	Phvul.008G26PF00642,PF12PTHR14493,P
38	1	Phvul.008G260900.1	Phvul.008G260900	Phvul.008G26PF00642,PF12PTHR14493,P
39	1	Phvul.009G041100.2	Phvul.009G041100	Phvul.009G04 0 PTHR31789,P
40	1	Phvul.009G041100.1	Phvul.009G041100	Phvul.009G04 0 PTHR31789,P
41	1	Phvul.009G041100.2	Phvul.009G041100	Phvul.009G04 0 PTHR31789,P
42	1	Phvul.009G041100.1	Phvul.009G041100	Phvul.009G04 0 PTHR31789,P
43	1	Phvul.009G175100.3	Phvul.009G175100	Phvul.009G17PF01535,PF13PTHR24015,P
44	1	Phvul.009G175100.2	Phvul.009G175100	Phvul.009G17PF01535,PF13PTHR24015,P
45	1	Phvul.009G175100.1	Phvul.009G175100	Phvul.009G17PF01535,PF13PTHR24015,P
46	1	Phvul.009G200500.3	Phvul.009G200500	Phvul.009G20 PF08616 PTHR13677,P
47	1	Phvul.009G200500.2	Phvul.009G200500	Phvul.009G20 PF08616 PTHR13677,P
48	1	Phvul.009G200500.3	Phvul.009G200500	Phvul.009G20 PF08616 PTHR13677,P

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2	1	Phvul.009G200500.2	Phvul.009G200500	Phvul.009G20 PF08616	PTHR13677,P
3	1	Phvul.011G080200.1	Phvul.011G080200	Phvul.011G08 PF00320	PTHR10071,P
4	1	Phvul.011G080200.1	Phvul.011G080200	Phvul.011G08 PF00320	PTHR10071,P
5	1	Phvul.011G174000.1	Phvul.011G174000	Phvul.011G17PF13906,PF13	PTHR11785,P
6	1	Phvul.011G174000.1	Phvul.011G174000	Phvul.011G17PF13906,PF13	PTHR11785,P
7	1	Phvul.001G110400.1	Phvul.001G110400	Phvul.001G11 PF04410	PTHR23237
8	1	Phvul.001G123400.1	Phvul.001G123400	Phvul.001G12 PF05678	PTHR33624,P
9	1	Phvul.001G123400.1	Phvul.001G123400	Phvul.001G12 PF05678	PTHR33624,P
10	1	Phvul.001G154700.1	Phvul.001G154700	Phvul.001G15 PF00447	PTHR10015,P
11	1	Phvul.001G179800.1	Phvul.001G179800	Phvul.001G17PF01535,PF13	PTHR24015,P
12	1	Phvul.001G179800.1	Phvul.001G179800	Phvul.001G17PF01535,PF13	PTHR24015,P
13	1	Phvul.001G184000.1	Phvul.001G184000	Phvul.001G18PF10312,PF09	PTHR21737,P
14	1	Phvul.001G259000.1	Phvul.001G259000	Phvul.001G25 PF00044,PF02	PTHR10836,P
15	1	Phvul.001G259000.1	Phvul.001G259000	Phvul.001G25 PF00044,PF02	PTHR10836,P
16	1	Phvul.002G028100.1	Phvul.002G028100	Phvul.002G02 PF12171	PTHR10593,P
17	1	Phvul.002G028100.1	Phvul.002G028100	Phvul.002G02 PF12171	PTHR10593,P
18	1	Phvul.002G092900.2	Phvul.002G092900	Phvul.002G09PF00118,PF01	PTHR11353,P
19	1	Phvul.002G092900.1	Phvul.002G092900	Phvul.002G09PF00118,PF01	PTHR11353,P
20	1	Phvul.002G137100.1	Phvul.002G137100	Phvul.002G13PF02928,PF02	PTHR10694,P
21	1	Phvul.002G137200.1	Phvul.002G137200	Phvul.002G13 PF00076	PTHR24012,P
22	1	Phvul.002G137200.1	Phvul.002G137200	Phvul.002G13 PF00076	PTHR24012,P
23	1	Phvul.002G139900.2	Phvul.002G139900	Phvul.002G13 PF00076	PTHR24012,P
24	1	Phvul.002G139900.1	Phvul.002G139900	Phvul.002G13 PF00076	PTHR24012,P
25	1	Phvul.002G156300.1	Phvul.002G156300	Phvul.002G15 PF14111	PTHR24012,P
26	1	Phvul.003G032500.1	Phvul.003G032500	Phvul.003G03 PF03547	PTHR31752,P
27	1	Phvul.003G032500.1	Phvul.003G032500	Phvul.003G03 PF03547	PTHR31752,P
28	1	Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25 PF12171	PTHR10593,P
29	1	Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25 PF12171	PTHR10593,P
30	1	Phvul.003G265700.1	Phvul.003G265700	Phvul.003G26	0 PTHR34049,P
31	2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
32	2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
33	2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
34	2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29 PF01039	PTHR22855,P
35	1	Phvul.004G176100.1	Phvul.004G176100	Phvul.004G17PF01426,PF00	PTHR10629,P
36	1	Phvul.005G001500.2	Phvul.005G001500	Phvul.005G00 PF13417	PTHR11260,P
37	1	Phvul.005G001500.1	Phvul.005G001500	Phvul.005G00 PF13417	PTHR11260,P
38	1	Phvul.005G043500.1	Phvul.005G043500	Phvul.005G04PF08442,PF16	PTHR23118,P
39	1	Phvul.005G043500.1	Phvul.005G043500	Phvul.005G04PF08442,PF16	PTHR23118,P
40	1	Phvul.005G093400.1	Phvul.005G093400	Phvul.005G09	0 PTHR11017,P
41	1	Phvul.005G131700.1	Phvul.005G131700	Phvul.005G13PF00076,PF14	PTHR24012,P
42	1	Phvul.005G183800.1	Phvul.005G183800	Phvul.005G18 PF01167	PTHR16517,P
43	1	Phvul.005G183800.2	Phvul.005G183800	Phvul.005G18 PF01167	PTHR16517,P
44	1	Phvul.006G098700.1	Phvul.006G098700	Phvul.006G09 PF02458	PTHR31642,P
45	1	Phvul.006G131400.1	Phvul.006G131400	Phvul.006G13PF11900,PF00	PTHR24413,P
46	1	Phvul.006G131400.1	Phvul.006G131400	Phvul.006G13PF11900,PF00	PTHR24413,P
47	1	Phvul.006G208400.1	Phvul.006G208400	Phvul.006G20 PF00201	PTHR11926,P



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2	1	Phvul.006G208400.1	Phvul.006G208400	Phvul.006G20 PF00201	PTHR11926,P
3	1	Phvul.007G043900.2	Phvul.007G043900	Phvul.007G04 PF04484	PTHR31807,P
4	1	Phvul.007G043900.1	Phvul.007G043900	Phvul.007G04 PF04484	PTHR31807,P
5	1	Phvul.007G043900.2	Phvul.007G043900	Phvul.007G04 PF04484	PTHR31807,P
6	1	Phvul.007G043900.1	Phvul.007G043900	Phvul.007G04 PF04484	PTHR31807,P
7	1	Phvul.007G062100.1	Phvul.007G062100	Phvul.007G06 PF00248	PTHR11732,P
8	1	Phvul.007G062100.1	Phvul.007G062100	Phvul.007G06 PF00248	PTHR11732,P
9	1	Phvul.007G062100.1	Phvul.007G062100	Phvul.007G06 PF00248	PTHR11732,P
10	1	Phvul.007G067800.1	Phvul.007G067800	Phvul.007G06 PF00447	PTHR10015,P
11	1	Phvul.007G080900.2	Phvul.007G080900	Phvul.007G08 PF05055	PTHR31113,P
12	1	Phvul.007G080900.1	Phvul.007G080900	Phvul.007G08 PF05055	PTHR31113,P
13	1	Phvul.007G080900.2	Phvul.007G080900	Phvul.007G08 PF05055	PTHR31113,P
14	1	Phvul.007G080900.2	Phvul.007G080900	Phvul.007G08 PF05055	PTHR31113,P
15	1	Phvul.007G080900.1	Phvul.007G080900	Phvul.007G08 PF05055	PTHR31113,P
16	1	Phvul.007G139300.1	Phvul.007G139300	Phvul.007G13 PF00249,PF14	PTHR31499,P
17	1	Phvul.007G139300.1	Phvul.007G139300	Phvul.007G13 PF00249,PF14	PTHR31499,P
18	1	Phvul.007G139300.1	Phvul.007G139300	Phvul.007G13 PF00249,PF14	PTHR31499,P
19	1	Phvul.007G173400.1	Phvul.007G173400	Phvul.007G17 PF04570	PTHR33059,P
20	1	Phvul.007G246700.1	Phvul.007G246700	Phvul.007G24 PF04043,PF01	PTHR31707,P
21	1	Phvul.007G246700.1	Phvul.007G246700	Phvul.007G24 PF04043,PF01	PTHR31707,P
22	1	Phvul.007G274200.1	Phvul.007G274200	Phvul.007G27 PF01248	PTHR23105,P
23	1	Phvul.007G274200.1	Phvul.007G274200	Phvul.007G27 PF01248	PTHR23105,P
24	1	Phvul.007G274200.1	Phvul.007G274200	Phvul.007G27 PF01248	PTHR23105,P
25	1	Phvul.008G019000.1	Phvul.008G019000	Phvul.008G01 PF00533,PF03	PTHR23081,P
26	1	Phvul.008G055500.1	Phvul.008G055500	Phvul.008G05 PF00005	PTHR24220,P
27	1	Phvul.008G055500.1	Phvul.008G055500	Phvul.008G05 PF00005	PTHR24220,P
28	1	Phvul.008G077000.1	Phvul.008G077000	Phvul.008G07 PF03514	PTHR31636,P
29	1	Phvul.008G114700.1	Phvul.008G114700	Phvul.008G11 PF03208	PTHR12859
30	1	Phvul.008G114700.1	Phvul.008G114700	Phvul.008G11 PF03208	PTHR12859
31	1	Phvul.008G114700.1	Phvul.008G114700	Phvul.008G11 PF03208	PTHR12859
32	1	Phvul.008G211500.4	Phvul.008G211500	Phvul.008G21	0 PTHR32098,P
33	1	Phvul.008G211500.3	Phvul.008G211500	Phvul.008G21	0 PTHR32098,P
34	1	Phvul.008G211500.1	Phvul.008G211500	Phvul.008G21	0 PTHR32098,P
35	1	Phvul.008G211500.1	Phvul.008G211500	Phvul.008G21	0 PTHR32098,P
36	1	Phvul.008G211500.2	Phvul.008G211500	Phvul.008G21	0 PTHR32098,P
37	1	Phvul.008G250000.1	Phvul.008G250000	Phvul.008G25 PF16940	PTHR34935
38	1	Phvul.008G250000.1	Phvul.008G250000	Phvul.008G25 PF16940	PTHR34935
39	1	Phvul.008G250000.1	Phvul.008G250000	Phvul.008G25 PF16940	PTHR34935
40	1	Phvul.009G086300.2	Phvul.009G086300	Phvul.009G08 PF12776	PTHR31704,P
41	1	Phvul.009G086300.1	Phvul.009G086300	Phvul.009G08 PF12776	PTHR31704,P
42	1	Phvul.009G086300.1	Phvul.009G086300	Phvul.009G08 PF12776	PTHR31704,P
43	1	Phvul.009G086300.2	Phvul.009G086300	Phvul.009G08 PF12776	PTHR31704,P
44	1	Phvul.009G086300.1	Phvul.009G086300	Phvul.009G08 PF12776	PTHR31704,P
45	1	Phvul.009G149800.1	Phvul.009G149800	Phvul.009G14 PF00454	PTHR10048,P
46	1	Phvul.009G154300.6	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
47	1	Phvul.009G154300.5	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
48	1	Phvul.009G154300.3	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
49	1	Phvul.009G154300.3	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
50	1	Phvul.009G154300.4	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
51	1	Phvul.009G154300.4	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
52	1	Phvul.009G154300.1	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
53	1	Phvul.009G154300.6	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
54	1	Phvul.009G154300.6	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
55	1	Phvul.009G154300.5	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
56	1	Phvul.009G154300.3	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
57	1	Phvul.009G154300.4	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
58	1	Phvul.009G154300.1	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
59	1	Phvul.009G154300.1	Phvul.009G154300	Phvul.009G15 PF02146	PTHR11085,P
60	1	Phvul.009G240100.1	Phvul.009G240100	Phvul.009G24 PF07714	PTHR27001,P
	1	Phvul.011G017800.1	Phvul.011G017800	Phvul.011G01 PF12537,PF12	PTHR15948



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2	1 Phvul.011G017800.1	Phvul.011G017800	Phvul.011G01PF12537,PF12	PTHR15948
3	1 Phvul.011G100200.2	Phvul.011G100200	Phvul.011G10	0 PTHR34210,P
4	1 Phvul.011G100200.1	Phvul.011G100200	Phvul.011G10	0 PTHR34210,P
5				
6	1 Phvul.011G108300.1	Phvul.011G108300	Phvul.011G10 PF14111	0
7	1 Phvul.011G129700.1	Phvul.011G129700	Phvul.011G12	0 PTHR24006,P
8	1 Phvul.011G129700.1	Phvul.011G129700	Phvul.011G12	0 PTHR24006,P
9				
10	1 Phvul.011G140050.2	Phvul.011G140050	Phvul.011G14 PF13041	PTHR24015,P
11	1 Phvul.011G140050.1	Phvul.011G140050	Phvul.011G14 PF13041	PTHR24015,P
12				
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Do not distribute

1	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol	
2	KOG0959	3.4.21.102		0	0 AT5G42390.1	0
3		0 2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
4		0 2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
5		0 2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
6		0 2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
7		0 2.7.7.6		0	0 AT2G29540.1 ATRPAC14,AT	
8		0 2.7.7.6		0	0 AT2G29540.1 ATRPAC14,AT	
9	KOG1330		0	0 GO:0055085,(	AT5G10190.1	0
10	KOG1330		0	0 GO:0055085,(	AT5G10190.1	0
11	KOG2462		0	0	0 AT2G01940.1 ATIDD15,SGR5	
12	KOG1223	2.2.1.9,4.2.99	K14759	GO:0030976,(	AT1G68890.1	0
13	KOG1223	2.2.1.9,4.2.99	K14759	GO:0030976,(	AT1G68890.1	0
14	KOG1755		0 K05759		0 AT5G56600.1 PFN3,PRF3	
15	KOG1755		0 K05759		0 AT5G56600.1 PFN3,PRF3	
16	<b>KOG4282</b>		<b>0</b>	<b>0</b>	<b>0 AT3G58630.1</b>	<b>0</b>
17	KOG4759		0 K02838	GO:0006412	AT3G63190.1 AtcpRRF,cpRR	
18	KOG1285	1.13.11.51		0	0 AT3G63520.1 ATCCD1,ATNC	
19	KOG1285	1.13.11.51		0	0 AT3G63520.1 ATCCD1,ATNC	
20	KOG1285	1.13.11.51		0	0 AT3G63520.1 ATCCD1,ATNC	
21	KOG1285	1.13.11.51		0	0 AT3G63520.1 ATCCD1,ATNC	
22	KOG1285	1.13.11.51		0	0 AT3G63520.1 ATCCD1,ATNC	
23	KOG1285	1.13.11.51		0	0 AT3G63520.1 ATCCD1,ATNC	
24		0 3.1.26.3	K11592	GO:0016787,(	AT1G01040.1 ASU1,ATDCL1	
25	KOG2352	3.4.24.71		0 GO:0008168,(	AT2G31740.1	0
26	KOG2352	3.4.24.71		0 GO:0008168,(	AT2G31740.1	0
27		0	0	0	0 AT3G29750.1	0
28		0	0	0	0 AT3G29750.1	0
29		0	0 K08506	GO:0005515	AT3G09740.1 ATSYP71,SYP7	
30		0	0	0	0 AT3G04470.1	0
31		0	0	0	0 AT3G04470.1	0
32	KOG1380		0 K02257	GO:0016021,(	AT2G44520.1 COX10	
33	KOG1380		0 K02257	GO:0016021,(	AT2G44520.1 COX10	
34	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
35	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
36	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
37	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
38	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
39	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
40	KOG4683	2.3.1.78	K10532		0 AT5G47900.1	0
41	KOG1764		0	0	0 AT1G65320.1	0
42		0	0	0 GO:0005515	AT1G78230.1	0
43		0	0	0 GO:0005515	AT1G78230.1	0
44		0	0	0 GO:0005515	AT1G78230.1	0
45		0	0	0 GO:0005515	AT1G78230.1	0
46		0	0	0	0	0
47		0	0	0	0	0

1					
2	0	0	0	0 AT1G53025.1	0
3	0	0	0	0 AT1G53025.1	0
4	0	0	0	0 AT1G53025.1	0
5	0	0	0	0 AT1G53025.1	0
6	0	0	0	0 AT1G53025.1	0
7	0	0	0	0 AT1G53025.1	0
8	0	0	0	0 AT1G53025.1	0
9					
10	KOG0817	0	0	GO:0000062 AT4G24230.6 ACBP3	
11	KOG0817	0	0	GO:0000062 AT4G24230.6 ACBP3	
12	KOG0148,KOC	0 K12741		GO:0003676 AT3G15010.2	0
13	KOG0148,KOC	0 K12741		GO:0003676 AT3G15010.2	0
14					
15	0 4.4.1.15		0	0 AT3G26115.1	0
16	0 4.4.1.15		0	0 AT3G26115.1	0
17					
18	0	0	0	0 AT1G13170.1 ORP1D	
19	0	0	0	0 AT1G13170.1 ORP1D	
20	0 5.4.2.3	K01836		GO:0016868,(AT5G18070.1 DRT101	
21	0 5.4.2.3	K01836		GO:0016868,(AT5G18070.1 DRT101	
22					
23	0	0	0	0 AT5G06650.1 GIS2	
24	0	0	0	0 AT5G06650.1 GIS2	
25					
26	0 3.2.1.21	K01188		GO:0005975,(AT1G26560.1 BGLU40	
27	0 3.2.1.21	K01188		GO:0005975,(AT1G26560.1 BGLU40	
28	0 6.3.2.19			0 GO:0016567,(AT5G65500.1	0
29	0 6.3.2.19			0 GO:0016567,(AT5G65500.1	0
30	0 6.3.2.19			0 GO:0016567,(AT5G65500.1	0
31	0 6.3.2.19			0 GO:0016567,(AT5G65500.1	0
32	0 6.3.2.19			0 GO:0016567,(AT5G65500.1	0
33	0	0	0	0 AT5G52430.1	0
34	0	0	0	0 AT5G52430.1	0
35					
36	KOG0143 1.14.11.31			0 GO:0055114,(AT4G25310.1	0
37	KOG3271	0 K03263		GO:0045905,(AT1G13950.1 ATELF5A-1,EIF	
38	KOG3271	0 K03263		GO:0045905,(AT1G13950.1 ATELF5A-1,EIF	
39					
40	0	0	0	0 0	0
41	0	0	0	0 0	0
42	0	0	0	0 0	0
43	0	0	0	0 0	0
44	0	0		0 GO:0016592,(AT5G02850.1	0
45	0	0		0 GO:0016592,(AT5G02850.1	0
46	0	0		0 GO:0016592,(AT5G02850.1	0
47	0	0		0 GO:0016592,(AT5G02850.1	0
48	0	0		0 GO:0016592,(AT5G02850.1	0
49	0 6.4.1.4	K01969		0 AT4G34030.1 MCCB	
50	0 6.4.1.4	K01969		0 AT4G34030.1 MCCB	
51	0 6.4.1.4	K01969		0 AT4G34030.1 MCCB	
52	0 6.4.1.4	K01969		0 AT4G34030.1 MCCB	
53	0	0 K09286		GO:0006355,(AT5G13910.1 LEP	
54	0	0 K09286		GO:0006355,(AT5G13910.1 LEP	
55	0	0		0 GO:0005524 AT3G15120.1	0
56	0	0		0 AT3G53700.1 MEE40	
57	0	0 K12662		GO:0005515 AT2G41500.1 EMB2776,LIS	
58	0			0 GO:0008408,(AT4G13870.1 ATWEX,ATWR	
59	0 3.6.4.12				
60					

1					
2	0	3.6.4.12		0	GO:0008408,(AT4G13870.1 ATWEX,ATWR
3	0		0	0	0 AT2G34400.1
4	0		0	0	0 AT5G16100.1
5	0		0	0	0 AT5G16100.1
6	0		0	0	0 AT5G16100.1
7	0	6.3.2.19	K10590	GO:0004842	AT4G38600.1 KAK,UPL3
8	0	6.3.2.19	K10590	GO:0004842	AT4G38600.1 KAK,UPL3
9					
10	KOG0131,KOC		0 K13126	GO:0003676	AT1G01080.1
11	0		0	0	0 0
12	0		0	0	0 0
13					
14	KOG2109		0	0	0 AT1G03380.1 ATATG18G,AT
15	KOG2109		0	0	0 AT1G03380.1 ATATG18G,AT
16	0		0	0	0 GO:0008270,(AT3G05200.1 ATL6
17					
18	KOG0446	3.6.5.5	K01528	GO:0005525,(AT1G59610.1 ADL3,CF1,DL3	
19	KOG0446	3.6.5.5	K01528	GO:0005525,(AT1G59610.1 ADL3,CF1,DL3	
20	KOG0508,KOC		0	0	0 AT5G14230.1
21					
22	KOG1286		0 K13863	GO:0016020,(AT1G58030.1 CAT2	
23	KOG1286		0 K13863	GO:0016020,(AT1G58030.1 CAT2	
24	KOG1286		0 K13863	GO:0016020,(AT1G58030.1 CAT2	
25	KOG1286		0 K13863	GO:0016020,(AT1G58030.1 CAT2	
26					
27	0	2.4.2.24	K00770	0	AT1G02730.1 ATCSLD5,CSLL
28	0	2.4.2.24	K00770	0	AT1G02730.1 ATCSLD5,CSLL
29					
30	KOG2125		0	0	GO:0003824 AT2G22530.1
31	KOG2125		0	0	GO:0003824 AT2G22530.1
32	KOG2125		0	0	GO:0003824 AT2G22530.1
33	KOG2125		0	0	GO:0003824 AT2G22530.1
34					
35	0		0	0	GO:0008152,(AT3G18270.1 CYP77A5P
36	0		0	0	GO:0008152,(AT3G18270.1 CYP77A5P
37	0		0	0	0 AT1G68140.3
38	0		0	0	0 AT4G28590.1
39	0		0	0	0 AT5G11600.1
40	0		0	0	0 AT5G11600.1
41	0		0	0	0 AT5G11600.1
42	0		0	0	0 GO:0005515 AT5G39450.1
43	0		0	0	0 GO:0005515 AT5G39450.1
44	0		0	0	0 GO:0005515 AT5G39450.1
45	0		0	0	0 GO:0005515 AT5G39450.1
46	0		0	0	0 GO:0005515 AT5G39450.1
47	0		0	0	0 GO:0005515 AT5G39450.1
48	KOG1187	2.7.11.1		0	GO:0006468,(AT3G13690.1
49	KOG2824		0 K17479	GO:0045454,(AT4G10630.1	
50	KOG2824		0 K17479	GO:0045454,(AT4G10630.1	
51					
52	0		0 K01723	GO:0055114,(AT5G42650.1 AOS,CYP74A,[	
53	KOG1286		0	0	GO:0016020,(AT4G21120.1 AAT1,CAT1
54	KOG1286		0	0	GO:0016020,(AT4G21120.1 AAT1,CAT1
55					
56	KOG0788	4.1.1.50	K01611	GO:0008295,(AT3G25570.2	0
57	KOG0788	4.1.1.50	K01611	GO:0008295,(AT3G25570.2	0
58					
59	0		0	0	GO:0055085,(AT1G62280.1 SLAH1
60	KOG0472	2.7.11.1		0	GO:0006468,(AT5G49760.1
	KOG0472	2.7.11.1		0	GO:0006468,(AT5G49760.1

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2	KOG1683	5.1.2.3,1.1.1.3	K10527	GO:0055114,(AT3G06860.1	ATMFP2,MFP:	
3		0	0	0	0 AT3G17030.1	0
4		0	0	0	0 AT3G17030.1	0
5						
6	KOG0401		0 K03260	GO:0005515,(AT5G57870.2	elFiso4G1	
7	KOG0401		0 K03260	GO:0005515,(AT5G57870.2	elFiso4G1	
8		0	0	0	0 AT4G14096.1	0
9		0	0	0	0 AT4G14096.1	0
10						
11	KOG2502		0	0 GO:0005515	AT2G18280.2 AtTLP2,TLP2	
12	KOG2502		0	0 GO:0005515	AT2G18280.2 AtTLP2,TLP2	
13	KOG2502		0	0 GO:0005515	AT2G18280.2 AtTLP2,TLP2	
14	KOG2502		0	0 GO:0005515	AT2G18280.2 AtTLP2,TLP2	
15						
16		0	0	0	0 AT4G04790.1	0
17		0	0	0	0 AT4G04790.1	0
18		0	0	0	0	0
19		0	0	0	0	0
20		0	0	0	0	0
21		0	0	0	0	0
22		0	0	0	GO:0006629 AT1G02660.1	0
23		0	0	0	GO:0006629 AT1G02660.1	0
24		0	0	0	0 AT5G23280.1	0
25						
26		0 6.1.1.18	K01886	GO:0006425,(AT1G25350.1	OVA9	
27	KOG1603		0	0 GO:0046872,(AT1G23000.1		0
28	KOG1603		0	0 GO:0046872,(AT1G23000.1		0
29						
30		0 2.7.7.4	K13811	GO:0004781	AT3G22890.1 APS1	
31		0 2.7.7.4	K13811	GO:0004781	AT3G22890.1 APS1	
32		0	0	0	0 AT1G04560.1	0
33		0	0	0	0 AT1G04560.1	0
34						
35		0	0	0	0 AT5G03345.1	0
36	KOG1043		0	0	0 AT3G11560.4	0
37		0	0	0	0 AT2G44880.1	0
38						
39		0	0	0	0 AT4G09060.1	0
40		0	0	0	0 AT4G09060.1	0
41		0	0	0	0 AT4G38060.2	0
42		0	0	0	0 AT4G38060.2	0
43						
44	KOG1595		0	0 GO:0046872	AT5G58620.1	0
45	KOG1595		0	0 GO:0046872	AT5G58620.1	0
46	KOG1595		0	0 GO:0046872	AT5G58620.1	0
47	KOG1595		0	0 GO:0046872	AT5G58620.1	0
48	KOG1595		0	0 GO:0046872	AT5G58620.1	0
49		0	0	0	0 AT3G54190.1	0
50		0	0	0	0 AT3G54190.1	0
51		0	0	0	0 AT3G54190.1	0
52		0	0	0	0 AT3G54190.1	0
53		0	0	0	0 AT3G54190.1	0
54		0	0	0	0 AT1G64310.1	0
55		0	0	0	0 AT1G64310.1	0
56		0	0	0	0 AT1G64310.1	0
57		0	0	0	0 AT1G64310.1	0
58		0	0	0	0 AT1G73930.2	0
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60		0	0	0	0 AT1G73930.2	0

1					
2		0	0	0	0 AT1G73930.2
3		0	0	0	0 GO:0043565,(AT1G08000.2 GATA10
4		0	0	0	0 GO:0043565,(AT1G08000.2 GATA10
5		0	0	0	0 GO:0043565,(AT1G08000.2 GATA10
6	KOG1286		0 K03294		GO:0016020,(AT1G17120.1 CAT8
7	KOG1286		0 K03294		GO:0016020,(AT1G17120.1 CAT8
8		0	0 K11128		GO:0042254,(AT3G03920.1
9		0	0	0	0 AT2G41180.1
10		0	0	0	0 AT2G41180.1
11		0	0	0	0 AT2G41180.1
12	KOG0627		0 K09419		GO:0043565,(AT3G22830.1 AT-HSFA6B,HS
13		0	0	0	0 AT5G37570.1
14		0	0	0	0 AT5G37570.1
15		0	0	0	0 AT5G37570.1
16		0	0	0	0 GO:0005515 AT1G03910.1
17		0	0	0	0 AT5G66730.1
18	KOG0657	1.2.1.12	K00134		GO:0055114,(AT3G04120.1 GAPC,GAPC-1,
19	KOG0657	1.2.1.12	K00134		GO:0055114,(AT3G04120.1 GAPC,GAPC-1,
20		0	0	0	0 AT5G66730.1
21		0	0	0	0 AT5G66730.1
22		0	0	0	0 AT5G66730.1
23		0 2.7.1.150	K00921		GO:0005524,(AT1G71010.1 FAB1C
24		0 2.7.1.150	K00921		GO:0005524,(AT1G71010.1 FAB1C
25		0 1.14.11.27		0	0 AT5G46910.1
26		0	0	0	0 GO:0003676
27		0	0	0	0 GO:0003676
28		0	0	0	0 GO:0003676
29		0	0	0	0 GO:0003676 AT5G46840.1
30		0	0	0	0 GO:0003676 AT5G46840.1
31		0	0	0	0 GO:0003676 AT5G46840.1
32		0	0	0	0
33		0	0 K13947		GO:0055085,(AT1G70940.1 ATPIN3,PIN3
34		0	0 K13947		GO:0055085,(AT1G70940.1 ATPIN3,PIN3
35		0	0	0	0 AT5G66730.1
36		0	0	0	0 AT5G66730.1
37		0	0	0	0 AT5G66730.1
38		0	0	0	0 AT4G35930.1
39		0	0	0	0 AT4G35930.1
40		0 6.4.1.4	K01969		0 AT4G34030.1 MCCB
41		0 6.4.1.4	K01969		0 AT4G34030.1 MCCB
42		0 6.4.1.4	K01969		0 AT4G34030.1 MCCB
43		0 6.4.1.4	K01969		0 AT4G34030.1 MCCB
44		0 6.4.1.4	K01969		0 AT4G34030.1 MCCB
45		0 2.1.1.37	K00558		GO:0003682 AT1G69770.1 CMT3
46		0	0	0	0 GO:0005515 AT4G10000.1
47		0	0	0	0 GO:0005515 AT4G10000.1
48		0	0	0	0 GO:0005515 AT4G10000.1
49	KOG1254	2.3.3.8	K01648		0 AT1G60810.1 ACLA-2
50	KOG1254	2.3.3.8	K01648		0 AT1G60810.1 ACLA-2
51	KOG4579		0	0	0 AT1G69550.1
52		0	0	0	0 GO:0003676
53		0	0	0	0 GO:0003676
54	KOG2502		0	0	0 AT1G16070.1 AtTLP8,TLP8
55	KOG2502		0	0	0 AT1G16070.1 AtTLP8,TLP8
56		0 2.3.1.196		0	0 GO:0016747 AT5G17540.1
57		0	0 K14508		GO:0005515 AT5G45110.1 ATNPR3,NPR3
58		0	0 K14508		GO:0005515 AT5G45110.1 ATNPR3,NPR3
59		0	0 K14508		GO:0005515 AT5G45110.1 ATNPR3,NPR3
60		0 2.4.1.273		0	0 GO:0016758,(AT2G22590.1

1					
2	0	2.4.1.273		0 GO:0016758,(AT2G22590.1	0
3	0		0	0 AT1G49890.1	0
4	0		0	0 AT1G49890.1	0
5	0		0	0 AT1G49890.1	0
6	0		0	0 AT1G49890.1	0
7	0		0	0 AT1G49890.1	0
8	KOG1575	1.1.1.317		0 AT1G60710.1 ATB2	
9					
10	0		0 K09419	GO:0043565,(AT5G62020.1 AT-HSFB2A,H	
11	0		0	0 AT1G20180.1	0
12	0		0	0 AT1G20180.1	0
13	0		0	0 AT1G20180.1	0
14	0		0	0 AT1G20180.1	0
15	0		0	0 AT1G20180.1	0
16	0		0	0 AT3G24120.1	0
17	0		0	0 AT3G24120.1	0
18	0		0	0 AT3G24120.1	0
19	0		0	0 AT3G22550.1	0
20	0	3.1.1.11	K01051	GO:0004857,(AT4G02330.1 ATPMEPCRB	
21					
22	KOG3166		0 K02936	0 AT3G62870.1	0
23	KOG3166		0 K02936	0 AT3G62870.1	0
24		0 3.1.3.16	K18999	0 AT2G33540.1 ATCPL3,CPL3	
25					
26		0 3.6.3.25		0 GO:0016887,(AT1G65410.1 ATNAP11,NAF	
27		0 3.6.3.25		0 GO:0016887,(AT1G65410.1 ATNAP11,NAF	
28		0	0	0 AT3G54220.1 SCR,SGR1	
29					
30	KOG4050		0	0 AT5G02040.2 PRA1.A1	
31	KOG4050		0	0 AT5G02040.2 PRA1.A1	
32		0 5.5.1.19		0 AT2G32640.1	0
33		0 5.5.1.19		0 AT2G32640.1	0
34		0 5.5.1.19		0 AT2G32640.1	0
35		0 5.5.1.19		0 AT2G32640.1	0
36		0 5.5.1.19		0 AT2G32640.1	0
37		0	0	0 AT1G06950.1 ATTIC110,TIC1	
38		0	0	0 AT1G06950.1 ATTIC110,TIC1	
39		0	0	0 AT1G06950.1 ATTIC110,TIC1	
40		0	0	0 AT2G24960.2	0
41		0	0	0 AT2G24960.2	0
42		0	0	0 AT2G24960.2	0
43		0	0	0 AT2G24960.2	0
44		0	0	0 AT2G24960.2	0
45		0 2.7.1.67	K00888	GO:0016773,(AT5G64070.1 PI-4KBETA1,PI	
46					
47	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
48	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
49	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
50	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
51	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
52	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
53	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
54	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
55	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
56	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
57	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
58	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
59	KOG2683	3.5.1.98	K11414	GO:0070403 AT5G09230.7 AtSRT2,SRT2	
60	KOG1187	2.7.11.1		0 GO:0006468,(AT2G18890.1	0
	0	0		0 GO:0016020 AT4G27630.2 GTG2	



1					
2		0	0	0 GO:0016020 AT4G27630.2 GTG2	
3		0	0	0	0 AT5G22040.2
4		0	0	0	0 AT5G22040.2
5					
6		0	0	0	0 0
7	KOG1947		0	0	0 AT2G42620.1 MAX2,ORE9,P
8	KOG1947		0	0	0 AT2G42620.1 MAX2,ORE9,P
9					
10		0	0	0	0 AT4G04790.1
11		0	0	0	0 AT4G04790.1
12					
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arabi-defline	ID	Annot_defline	IDENTIFIER	NAME
Insulinase (Peptidase family M16) family	Phvul.002G04	PTHR11851:Sf	Phvul.002G04	Protein modif
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:Sf	Phvul.002G11	not assigned.a
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:Sf	Phvul.002G11	not assigned.a
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:Sf	Phvul.002G11	not assigned.a
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:Sf	Phvul.002G11	not assigned.a
RNApolymerase 14 kDa subunit	Phvul.001G01	PTHR13946:Sf	Phvul.001G01	RNA biosynthe
RNApolymerase 14 kDa subunit	Phvul.001G01	PTHR13946:Sf	Phvul.001G01	RNA biosynthe
Major facilitator superfamily protein	Phvul.002G25	KOG1330 - Su	Phvul.002G25	Solute transpo
Major facilitator superfamily protein	Phvul.002G25	KOG1330 - Su	Phvul.002G25	Solute transpo
C2H2-like zinc finger protein	Phvul.002G33	PTHR10593:Sf	Phvul.002G33	RNA biosynthe
magnesium ion binding;thiamin pyrophc	Phvul.005G02	K14759 - isoc	Phvul.005G02	Coenzyme me
magnesium ion binding;thiamin pyrophc	Phvul.005G02	K14759 - isoc	Phvul.005G02	Coenzyme me
profilin 3	Phvul.005G16	K05759 - profi	Phvul.005G16	Cytoskeleton
profilin 3	Phvul.005G16	K05759 - profi	Phvul.005G16	Cytoskeleton
sequence-specific DNA binding transcrip	Phvul.006G17	KOG4282 - Tr	Phvul.006G17	RNA biosynthe
ribosome recycling factor, chloroplast pr	Phvul.007G17	PTHR20982:Sf	Phvul.007G17	Protein biosyr
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//I	Phvul.009G10	Enzyme classif
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//I	Phvul.009G10	Enzyme classif
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//I	Phvul.009G10	Enzyme classif
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//I	Phvul.009G10	Enzyme classif
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//I	Phvul.009G10	Enzyme classif
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//I	Phvul.009G10	Enzyme classif
dicer-like 1	Phvul.009G26	PTHR14950:Sf	Phvul.009G26	RNA processir
S-adenosyl-L-methionine-dependent me	Phvul.003G05	PTHR12176:Sf	Phvul.003G05	not assigned.r
S-adenosyl-L-methionine-dependent me	Phvul.003G05	PTHR12176:Sf	Phvul.003G05	not assigned.r
Eukaryotic aspartyl protease family prot	Phvul.004G05	PF13650 - Asp	Phvul.004G05	not assigned.r
Eukaryotic aspartyl protease family prot	Phvul.004G05	PF13650 - Asp	Phvul.004G05	not assigned.r
syntaxin of plants 71	Phvul.005G13	K08506 - synt	Phvul.005G13	Vesicle trafficl
Ankyrin repeat family protein	Phvul.006G10	PTHR12447:Sf	Phvul.006G10	not assigned.r
Ankyrin repeat family protein	Phvul.006G10	PTHR12447:Sf	Phvul.006G10	not assigned.r
cytochrome c oxidase 10	Phvul.007G00	K02257 - prot	Phvul.007G00	not assigned.a
cytochrome c oxidase 10	Phvul.007G00	K02257 - prot	Phvul.007G00	not assigned.a
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.r
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.r
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.r
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.r
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.r
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.r
Cystathionine beta-synthase (CBS) famil	Phvul.008G05	PTHR13780:Sf	Phvul.008G05	not assigned.a
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:Sf	Phvul.008G17	not assigned.r
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:Sf	Phvul.008G17	not assigned.r
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:Sf	Phvul.008G17	not assigned.r
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:Sf	Phvul.008G17	not assigned.r
	0	0	0	Phvul.011G13 not assigned.r
	0	0	0	Phvul.011G13 not assigned.r

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2	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
3	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
4	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
5	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
6	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
7	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
8	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
9	Ubiquitin-conjugating enzyme family prc	Phvul.011G15PTHR24067:Sf	Phvul.011G15	not assigned.r
10	acyl-CoA-binding domain 3	Phvul.001G02PTHR23310:Sf	Phvul.001G02	not assigned.a
11	acyl-CoA-binding domain 3	Phvul.001G02PTHR23310:Sf	Phvul.001G02	not assigned.a
12	RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.001G14KOG0148//KC	Phvul.001G14	not assigned.a
13	RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.001G14KOG0148//KC	Phvul.001G14	not assigned.a
14	RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.001G14KOG0148//KC	Phvul.001G14	not assigned.a
15	Pyridoxal-5'-phosphate-dependent enz	Phvul.001G25PTHR10314//I	Phvul.001G25	not assigned.a
16	Pyridoxal-5'-phosphate-dependent enz	Phvul.001G25PTHR10314//I	Phvul.001G25	not assigned.a
17	Pyridoxal-5'-phosphate-dependent enz	Phvul.001G25PTHR10314//I	Phvul.001G25	not assigned.a
18	OSBP(oxysterol binding protein)-related	Phvul.001G25PTHR10972:Sf	Phvul.001G25	not assigned.a
19	OSBP(oxysterol binding protein)-related	Phvul.001G25PTHR10972:Sf	Phvul.001G25	not assigned.a
20	OSBP(oxysterol binding protein)-related	Phvul.001G25PTHR10972:Sf	Phvul.001G25	not assigned.a
21	phosphoglucosamine mutase-related	Phvul.002G005.4.2.3 - Phos	Phvul.002G00	Carbohydrate
22	phosphoglucosamine mutase-related	Phvul.002G005.4.2.3 - Phos	Phvul.002G00	Carbohydrate
23	C2H2 and C2HC zinc fingers superfamily	0	0	Phvul.002G07RNA biosynthe
24	C2H2 and C2HC zinc fingers superfamily	0	0	Phvul.002G07RNA biosynthe
25	C2H2 and C2HC zinc fingers superfamily	0	0	Phvul.002G07RNA biosynthe
26	beta glucosidase 40	Phvul.002G10PTHR10353:Sf	Phvul.002G10	Enzyme classifi
27	beta glucosidase 40	Phvul.002G10PTHR10353:Sf	Phvul.002G10	Enzyme classifi
28	U-box domain-containing protein kinase	Phvul.002G14PTHR27003:Sf	Phvul.002G14	not assigned.a
29	U-box domain-containing protein kinase	Phvul.002G14PTHR27003:Sf	Phvul.002G14	not assigned.a
30	U-box domain-containing protein kinase	Phvul.002G14PTHR27003:Sf	Phvul.002G14	not assigned.a
31	U-box domain-containing protein kinase	Phvul.002G14PTHR27003:Sf	Phvul.002G14	not assigned.a
32	U-box domain-containing protein kinase	Phvul.002G14PTHR27003:Sf	Phvul.002G14	not assigned.a
33	U-box domain-containing protein kinase	Phvul.002G14PTHR27003:Sf	Phvul.002G14	not assigned.a
34	hydroxyproline-rich glycoprotein family	0	0	Phvul.002G15 not assigned.a
35	hydroxyproline-rich glycoprotein family	0	0	Phvul.002G15 not assigned.a
36	hydroxyproline-rich glycoprotein family	0	0	Phvul.002G15 not assigned.a
37	2-oxoglutarate (2OG) and Fe(II)-depend	Phvul.003G01PTHR10209:Sf	Phvul.003G01	Enzyme classifi
38	eukaryotic elongation factor 5A-1	Phvul.003G15K03263 - tran	Phvul.003G15	Protein biosyr
39	eukaryotic elongation factor 5A-1	Phvul.003G15K03263 - tran	Phvul.003G15	Protein biosyr
40	eukaryotic elongation factor 5A-1	0	0	Phvul.003G17 not assigned.r
41	eukaryotic elongation factor 5A-1	0	0	Phvul.003G17 not assigned.r
42	eukaryotic elongation factor 5A-1	0	0	Phvul.003G17 not assigned.r
43	eukaryotic elongation factor 5A-1	0	0	Phvul.003G17 not assigned.r
44	hydroxyproline-rich glycoprotein family	Phvul.003G26PTHR13208 - I	Phvul.003G26	RNA biosynthe
45	hydroxyproline-rich glycoprotein family	Phvul.003G26PTHR13208 - I	Phvul.003G26	RNA biosynthe
46	hydroxyproline-rich glycoprotein family	Phvul.003G26PTHR13208 - I	Phvul.003G26	RNA biosynthe
47	hydroxyproline-rich glycoprotein family	Phvul.003G26PTHR13208 - I	Phvul.003G26	RNA biosynthe
48	hydroxyproline-rich glycoprotein family	Phvul.003G26PTHR13208 - I	Phvul.003G26	RNA biosynthe
49	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-m	Phvul.003G29	Amino acid m
50	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-m	Phvul.003G29	Amino acid m
51	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-m	Phvul.003G29	Amino acid m
52	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-m	Phvul.003G29	Amino acid m
53	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-m	Phvul.003G29	Amino acid m
54	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-m	Phvul.003G29	Amino acid m
55	Integrase-type DNA-binding superfamily	Phvul.004G06PTHR31677:Sf	Phvul.004G06	RNA biosynthe
56	Integrase-type DNA-binding superfamily	Phvul.004G06PTHR31677:Sf	Phvul.004G06	RNA biosynthe
57	Integrase-type DNA-binding superfamily	Phvul.004G06PTHR31677:Sf	Phvul.004G06	RNA biosynthe
58	P-loop containing nucleoside triphospha	Phvul.005G06PTHR23069//I	Phvul.005G06	DNA damage
59	Pentatricopeptide repeat (PPR) superfar	Phvul.007G15PF13041 - PP	Phvul.007G15	not assigned.a
60	WD-40 repeat family protein / small nuc	Phvul.007G24K12662 - U4/L	Phvul.007G24	RNA processir
	Werner syndrome-like exonuclease	Phvul.008G11PTHR13620 -	Phvul.008G11	not assigned.a

1	Werner syndrome-like exonuclease	Phvul.008G11PTHR13620 -	Phvul.008G11 not assigned.
2	Pentatricopeptide repeat (PPR-like) superfamily protein	Phvul.008G23PF01535//PF1	Phvul.008G23 not assigned.
3		0 Phvul.009G08PF02042 - RW	Phvul.009G08 not assigned.
4		0 Phvul.009G08PF02042 - RW	Phvul.009G08 not assigned.
5	HEAT repeat ;HECT-domain (ubiquitin-tr	Phvul.009G11PTHR11254:SF	Phvul.009G11 Protein home
6	HEAT repeat ;HECT-domain (ubiquitin-tr	Phvul.009G11PTHR11254:SF	Phvul.009G11 Protein home
7	RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.010G11KOG0131//KC	Phvul.010G11 not assigned.
8		0	0 Phvul.011G00 not assigned.
9		0	0 Phvul.011G00 not assigned.
10	homolog of yeast autophagy 18 (ATG18)	Phvul.011G14PTHR13268:SF	Phvul.011G14 Protein home
11	homolog of yeast autophagy 18 (ATG18)	Phvul.011G14PTHR13268:SF	Phvul.011G14 Protein home
12	RING/U-box superfamily protein	Phvul.011G16PTHR14155:SF	Phvul.011G16 not assigned.
13	dynamamin-like 3	Phvul.011G21PTHR11566//I	Phvul.011G21 Vesicle traffi
14	dynamamin-like 3	Phvul.011G21PTHR11566//I	Phvul.011G21 Vesicle traffi
15		0 Phvul.001G09KOG0508//KC	Phvul.001G09 not assigned.
16	cationic amino acid transporter 2	Phvul.001G10K13863 - solu	Phvul.001G10 Solute transp
17	cationic amino acid transporter 2	Phvul.001G10K13863 - solu	Phvul.001G10 Solute transp
18	cationic amino acid transporter 2	Phvul.001G10K13863 - solu	Phvul.001G10 Solute transp
19	cationic amino acid transporter 2	Phvul.001G10K13863 - solu	Phvul.001G10 Solute transp
20	cellulose synthase-like D5	Phvul.001G21K00770 - 1,4- $\beta$	Phvul.001G21 Cell wall organ
21	cellulose synthase-like D5	Phvul.001G21K00770 - 1,4- $\beta$	Phvul.001G21 Cell wall organ
22	Alkaline-phosphatase-like family protein	Phvul.002G14K05310 - etha	Phvul.002G14 not assigned.
23	Alkaline-phosphatase-like family protein	Phvul.002G14K05310 - etha	Phvul.002G14 not assigned.
24	Alkaline-phosphatase-like family protein	Phvul.002G14K05310 - etha	Phvul.002G14 not assigned.
25	Alkaline-phosphatase-like family protein	Phvul.002G14K05310 - etha	Phvul.002G14 not assigned.
26	cytochrome P450, family 77, subfamily A	Phvul.002G18PTHR13794 - I	Phvul.002G18 not assigned.
27	cytochrome P450, family 77, subfamily A	Phvul.002G18PTHR13794 - I	Phvul.002G18 not assigned.
28	Protein of unknown function (DUF1644)	Phvul.002G20PF07800 - Pro	Phvul.002G20 not assigned.
29		0	0 Phvul.002G23 not assigned.
30		0	0 Phvul.002G26 not assigned.
31		0	0 Phvul.002G26 not assigned.
32	F-box family protein	Phvul.002G27PF00646 - F-b	Phvul.002G27 not assigned.
33	F-box family protein	Phvul.002G27PF00646 - F-b	Phvul.002G27 not assigned.
34	F-box family protein	Phvul.002G27PF00646 - F-b	Phvul.002G27 not assigned.
35	F-box family protein	Phvul.002G27PF00646 - F-b	Phvul.002G27 not assigned.
36	Protein kinase protein with adenine nuc	Phvul.002G302.7.11.1 - Non	Phvul.002G30 Protein modif
37	Glutaredoxin family protein	Phvul.002G32PTHR10168:SF	Phvul.002G32 not assigned.
38	Glutaredoxin family protein	Phvul.002G32PTHR10168:SF	Phvul.002G32 not assigned.
39	allene oxide synthase	Phvul.003G01K01723 - hydr	Phvul.003G01 Phytohormon
40	amino acid transporter 1	Phvul.003G02PTHR11785:SF	Phvul.003G02 Solute transp
41	amino acid transporter 1	Phvul.003G02PTHR11785:SF	Phvul.003G02 Solute transp
42	Adenosylmethionine decarboxylase fam	Phvul.003G044.1.1.50 - Ade	Phvul.003G04 Polyamine me
43	Adenosylmethionine decarboxylase fam	Phvul.003G044.1.1.50 - Ade	Phvul.003G04 Polyamine me
44	SLAC1 homologue 1	Phvul.003G08PF03595 - Vol	Phvul.003G08 Solute transp
45	Leucine-rich repeat protein kinase famil	Phvul.003G09PTHR27003:SF	Phvul.003G09 Protein modif
46	Leucine-rich repeat protein kinase famil	Phvul.003G09PTHR27003:SF	Phvul.003G09 Protein modif

1				
2	multifunctional protein 2	Phvul.003G091.1.1.35//4.2.	Phvul.003G09	Lipid metaboli
3	Nucleic acid-binding proteins superfamil	Phvul.003G11PTHR36033:Sf	Phvul.003G11	not assigned.r
4	Nucleic acid-binding proteins superfamil	Phvul.003G11PTHR36033:Sf	Phvul.003G11	not assigned.r
5	MIF4G domain-containing protein / MA	Phvul.003G15PTHR23253//I	Phvul.003G15	Protein biosyr
6	MIF4G domain-containing protein / MA	Phvul.003G15PTHR23253//I	Phvul.003G15	Protein biosyr
7	MIF4G domain-containing protein / MA	Phvul.003G15PTHR23253//I	Phvul.003G15	Protein biosyr
8	F-box/RNI-like superfamily protein	Phvul.003G20PF08387 - FB	Phvul.003G20	not assigned.r
9	F-box/RNI-like superfamily protein	Phvul.003G20PF08387 - FB	Phvul.003G20	not assigned.r
10	tubby like protein 2	Phvul.003G25PTHR16517:Sf	Phvul.003G25	RNA biosynthe
11	tubby like protein 2	Phvul.003G25PTHR16517:Sf	Phvul.003G25	RNA biosynthe
12	tubby like protein 2	Phvul.003G25PTHR16517:Sf	Phvul.003G25	RNA biosynthe
13	tubby like protein 2	Phvul.003G25PTHR16517:Sf	Phvul.003G25	RNA biosynthe
14	Tetratricopeptide repeat (TPR)-like supe	Phvul.003G29PF01535//PF1	Phvul.003G29	not assigned.a
15	Tetratricopeptide repeat (TPR)-like supe	Phvul.003G29PF01535//PF1	Phvul.003G29	not assigned.a
16		0	0	0 Phvul.005G08not assigned.a
17		0	0	0 Phvul.005G08not assigned.a
18				
19	alpha/beta-Hydrolases superfamily prot	Phvul.006G11PTHR21493//I	Phvul.006G11	Lipid metaboli
20	alpha/beta-Hydrolases superfamily prot	Phvul.006G11PTHR21493//I	Phvul.006G11	Lipid metaboli
21	TCP family transcription factor	Phvul.007G01PTHR31072:Sf	Phvul.007G01	Multi-process
22	glutamine-tRNA ligase, putative / glutan	Phvul.007G026.1.1.18 - Glut	Phvul.007G02	Protein biosyr
23	Heavy metal transport/detoxification su	Phvul.007G03PTHR22814//I	Phvul.007G03	not assigned.a
24	Heavy metal transport/detoxification su	Phvul.007G03PTHR22814//I	Phvul.007G03	not assigned.a
25	ATP sulfurylase 1	Phvul.007G062.7.7.4 - Sulfa	Phvul.007G06	Nutrient uptal
26	ATP sulfurylase 1	Phvul.007G062.7.7.4 - Sulfa	Phvul.007G06	Nutrient uptal
27	AWPM-19-like family protein	Phvul.007G10PTHR33294:Sf	Phvul.007G10	not assigned.a
28	AWPM-19-like family protein	Phvul.007G10PTHR33294:Sf	Phvul.007G10	not assigned.a
29		0	Phvul.007G14PF10270 - Me	Phvul.007G14Solute transpc
30	LETM1-like protein	Phvul.007G23PTHR14009:Sf	Phvul.007G23	not assigned.r
31	Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04PF01535//PF1	Phvul.008G04	RNA processir
32		0	Phvul.008G17PTHR35689:Sf	Phvul.008G17not assigned.r
33		0	Phvul.008G17PTHR35689:Sf	Phvul.008G17not assigned.r
34		0	0	0 Phvul.008G18not assigned.r
35		0	0	0 Phvul.008G18not assigned.r
36	zinc finger (CCCH-type) family protein	Phvul.008G26PTHR14493:Sf	Phvul.008G26	RNA processir
37	zinc finger (CCCH-type) family protein	Phvul.008G26PTHR14493:Sf	Phvul.008G26	RNA processir
38	zinc finger (CCCH-type) family protein	Phvul.008G26PTHR14493:Sf	Phvul.008G26	RNA processir
39	zinc finger (CCCH-type) family protein	Phvul.008G26PTHR14493:Sf	Phvul.008G26	RNA processir
40	Transducin/WD40 repeat-like superfami	0	0	0 Phvul.009G04not assigned.r
41	Transducin/WD40 repeat-like superfami	0	0	0 Phvul.009G04not assigned.r
42	Transducin/WD40 repeat-like superfami	0	0	0 Phvul.009G04not assigned.r
43	Transducin/WD40 repeat-like superfami	0	0	0 Phvul.009G04not assigned.r
44	Tetratricopeptide repeat (TPR)-like supe	Phvul.009G17PF01535//PF1	Phvul.009G17	not assigned.a
45	Tetratricopeptide repeat (TPR)-like supe	Phvul.009G17PF01535//PF1	Phvul.009G17	not assigned.a
46	Tetratricopeptide repeat (TPR)-like supe	Phvul.009G17PF01535//PF1	Phvul.009G17	not assigned.a
47		0	Phvul.009G20PTHR13677:Sf	Phvul.009G20not assigned.r
48		0	Phvul.009G20PTHR13677:Sf	Phvul.009G20not assigned.r
49		0	Phvul.009G20PTHR13677:Sf	Phvul.009G20not assigned.r
50				
51				
52				
53				
54				
55				
56				
57				
58				
59				
60				



1		0 Phvul.009G20PTHR13677:SlPhvul.009G20not assigned.r
2		
3	GATA transcription factor 10	Phvul.011G08PTHR10071:SlPhvul.011G08RNA biosynthe
4	GATA transcription factor 10	Phvul.011G08PTHR10071:SlPhvul.011G08RNA biosynthe
5		
6	cationic amino acid transporter 8	Phvul.011G17PTHR11785:SlPhvul.011G17Solute transp
7	cationic amino acid transporter 8	Phvul.011G17PTHR11785:SlPhvul.011G17Solute transp
8	H/ACA ribonucleoprotein complex, subu	Phvul.001G11K11128 - H/A(Phvul.001G11Protein biosyr
9		
10	VQ motif-containing protein	Phvul.001G12PTHR33624:SlPhvul.001G12External stimu
11	VQ motif-containing protein	Phvul.001G12PTHR33624:SlPhvul.001G12External stimu
12	heat shock transcription factor A6B	Phvul.001G15PTHR10015//lPhvul.001G15RNA biosynthe
13		
14	Pentatricopeptide repeat (PPR-like) supε	Phvul.001G17PF01535//PF1Phvul.001G17not assigned.a
15	Pentatricopeptide repeat (PPR-like) supε	Phvul.001G17PF01535//PF1Phvul.001G17not assigned.a
16		0 Phvul.001G18PTHR21737:SlPhvul.001G18not assigned.a
17		
18	glyceraldehyde-3-phosphate dehydroge	Phvul.001G25PTHR10836:SlPhvul.001G25Cellular respir
19	glyceraldehyde-3-phosphate dehydroge	Phvul.001G25PTHR10836:SlPhvul.001G25Cellular respir
20	C2H2-like zinc finger protein	Phvul.002G02PTHR10593:SlPhvul.002G02RNA biosynthe
21	C2H2-like zinc finger protein	Phvul.002G02PTHR10593:SlPhvul.002G02RNA biosynthe
22		
23	FORMS APLOID AND BINUCLEATE CELLS	Phvul.002G09PTHR11353:SlPhvul.002G09Multi-process
24	FORMS APLOID AND BINUCLEATE CELLS	Phvul.002G09PTHR11353:SlPhvul.002G09Multi-process
25		
26	Transcription factor jumonji (jmj) family	Phvul.002G13PTHR10694:SlPhvul.002G13RNA biosynthe
27		0 Phvul.002G13PF00076 - RNlPhvul.002G13not assigned.r
28		0 Phvul.002G13PF00076 - RNlPhvul.002G13not assigned.r
29		
30	RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.002G13K14837 - nuclPhvul.002G13not assigned.r
31	RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.002G13K14837 - nuclPhvul.002G13not assigned.r
32		0 Phvul.002G15PF14111 - DorPhvul.002G15not assigned.r
33		
34	Auxin efflux carrier family protein	Phvul.003G03K13947 - auxilPhvul.003G03Solute transp
35	Auxin efflux carrier family protein	Phvul.003G03K13947 - auxilPhvul.003G03Solute transp
36	C2H2-like zinc finger protein	Phvul.003G25PTHR10593:SlPhvul.003G25RNA biosynthe
37	C2H2-like zinc finger protein	Phvul.003G25PTHR10593:SlPhvul.003G25RNA biosynthe
38		
39	F-box family protein	0 0 Phvul.003G26not assigned.a
40	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m
41	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m
42	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m
43	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m
44	3-methylcrotonyl-CoA carboxylase	Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m
45	chromomethylase 3	Phvul.004G17PTHR10629:SlPhvul.004G17Chromatin org
46		
47	Thioredoxin family protein	Phvul.005G00PTHR11260:SlPhvul.005G00not assigned.r
48	Thioredoxin family protein	Phvul.005G00PTHR11260:SlPhvul.005G00not assigned.r
49	ATP-citrate lyase A-2	Phvul.005G04KOG1254 - ATPPhvul.005G04Lipid metaboli
50	ATP-citrate lyase A-2	Phvul.005G04KOG1254 - ATPPhvul.005G04Lipid metaboli
51		
52	disease resistance protein (TIR-NBS-LRR	Phvul.005G09PTHR11017//lPhvul.005G09not assigned.a
53		0 Phvul.005G13PF00076//PF1Phvul.005G13not assigned.r
54		
55	tubby like protein 8	Phvul.005G18PTHR16517:SlPhvul.005G18RNA biosynthe
56	tubby like protein 8	Phvul.005G18PTHR16517:SlPhvul.005G18RNA biosynthe
57	HXXXD-type acyl-transferase family prot	Phvul.006G09PTHR31642:SlPhvul.006G09Enzyme classif
58		
59	NPR1-like protein 3	Phvul.006G13PTHR24413:SlPhvul.006G13Phytohormon
60	NPR1-like protein 3	Phvul.006G13PTHR24413:SlPhvul.006G13Phytohormon
	UDP-Glycosyltransferase superfamily pr	Phvul.006G20PTHR11926//lPhvul.006G20Enzyme classif

1			
2	UDP-Glycosyltransferase superfamily pr	Phvul.006G20PTHR11926//I	Phvul.006G20Enzyme classifi
3	Family of unknown function (DUF566)	Phvul.007G04PTHR31807:Sf	Phvul.007G04not assigned.a
4	Family of unknown function (DUF566)	Phvul.007G04PTHR31807:Sf	Phvul.007G04not assigned.a
5	Family of unknown function (DUF566)	Phvul.007G04PTHR31807:Sf	Phvul.007G04not assigned.a
6	Family of unknown function (DUF566)	Phvul.007G04PTHR31807:Sf	Phvul.007G04not assigned.a
7	Family of unknown function (DUF566)	Phvul.007G04PTHR31807:Sf	Phvul.007G04not assigned.a
8	NAD(P)-linked oxidoreductase superfam	Phvul.007G06PTHR11732//I	Phvul.007G06Enzyme classifi
9	<b>heat shock transcription factor B2A</b>	<b>Phvul.007G06PTHR10015:Sf</b>	<b>Phvul.007G06RNA biosynthe</b>
10	Protein of unknown function (DUF677)	Phvul.007G08PF05055 - Pro	Phvul.007G08not assigned.a
11	Protein of unknown function (DUF677)	Phvul.007G08PF05055 - Pro	Phvul.007G08not assigned.a
12	Protein of unknown function (DUF677)	Phvul.007G08PF05055 - Pro	Phvul.007G08not assigned.a
13	Protein of unknown function (DUF677)	Phvul.007G08PF05055 - Pro	Phvul.007G08not assigned.a
14	Protein of unknown function (DUF677)	Phvul.007G08PF05055 - Pro	Phvul.007G08not assigned.a
15	Homeodomain-like superfamily protein	Phvul.007G13PTHR31499:Sf	Phvul.007G13RNA biosynthe
16	Homeodomain-like superfamily protein	Phvul.007G13PTHR31499:Sf	Phvul.007G13RNA biosynthe
17	Protein of unknown function (DUF581)	Phvul.007G17PF04570 - zinc	Phvul.007G17Multi-process
18	Plant invertase/pectin methylesterase ir	Phvul.007G24PTHR31707:Sf	Phvul.007G24Cell wall organ
19	Ribosomal protein L7Ae/L30e/S12e/Gad	Phvul.007G27K02936 - large	Phvul.007G27Protein biosyr
20	Ribosomal protein L7Ae/L30e/S12e/Gad	Phvul.007G27K02936 - large	Phvul.007G27Protein biosyr
21	C-terminal domain phosphatase-like 3	Phvul.008G01PTHR23081:Sf	Phvul.008G01Protein modif
22	<b>non-intrinsic ABC protein 11</b>	<b>Phvul.008G05PTHR24220:Sf</b>	<b>Phvul.008G05Lipid metaboli</b>
23	<b>non-intrinsic ABC protein 11</b>	<b>Phvul.008G05PTHR24220:Sf</b>	<b>Phvul.008G05Lipid metaboli</b>
24	GRAS family transcription factor	Phvul.008G07PTHR31636:Sf	Phvul.008G07External stimu
25	<b>prenylated RAB acceptor 1.A1</b>	<b>Phvul.008G11PTHR12859 - I</b>	<b>Phvul.008G11Vesicle trafficl</b>
26	<b>prenylated RAB acceptor 1.A1</b>	<b>Phvul.008G11PTHR12859 - I</b>	<b>Phvul.008G11Vesicle trafficl</b>
27	Lycopene beta/epsilon cyclase protein	Phvul.008G21PTHR32098:Sf	Phvul.008G21not assigned.r
28	Lycopene beta/epsilon cyclase protein	Phvul.008G21PTHR32098:Sf	Phvul.008G21not assigned.r
29	Lycopene beta/epsilon cyclase protein	Phvul.008G21PTHR32098:Sf	Phvul.008G21not assigned.r
30	Lycopene beta/epsilon cyclase protein	Phvul.008G21PTHR32098:Sf	Phvul.008G21not assigned.r
31	translocon at the inner envelope membe	Phvul.008G25PF16940 - Chl	Phvul.008G25Protein transla
32	translocon at the inner envelope membe	Phvul.008G25PF16940 - Chl	Phvul.008G25Protein transla
33		0 Phvul.009G08PF12776 - My	Phvul.009G08not assigned.a
34		0 Phvul.009G08PF12776 - My	Phvul.009G08not assigned.a
35		0 Phvul.009G08PF12776 - My	Phvul.009G08not assigned.a
36		0 Phvul.009G08PF12776 - My	Phvul.009G08not assigned.a
37	phosphatidylinositol 4-OH kinase beta1	Phvul.009G14K00888 - phos	Phvul.009G14Multi-process
38	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
39	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
40	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
41	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
42	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
43	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
44	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
45	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
46	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
47	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
48	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
49	sirtuin 2	Phvul.009G15PTHR11085:Sf	Phvul.009G15Protein modif
50	Protein kinase superfamily protein	Phvul.009G242.7.11.1 - Non	Phvul.009G24Multi-process
51	GPCR-type G protein 2	Phvul.011G01PTHR15948 - (	Phvul.011G01External stimu



1  
2 GPCR-type G protein 2 Phvul.011G01PTHR15948 - (Phvul.011G01External stimu  
3 0 0 0 Phvul.011G10not assigned.r  
4 0 0 0 Phvul.011G10not assigned.r  
5  
6 0 Phvul.011G10PF14111 - DorPhvul.011G10not assigned.r  
7 RNI-like superfamily protein Phvul.011G12PTHR24006:SfPhvul.011G12Phytohormon  
8 RNI-like superfamily protein Phvul.011G12PTHR24006:SfPhvul.011G12Phytohormon  
9  
10 Tetratricopeptide repeat (TPR)-like supePhvul.011G14PF13041 - PPFPhvul.011G14not assigned.a  
11 Tetratricopeptide repeat (TPR)-like supePhvul.011G14PF13041 - PPFPhvul.011G14not assigned.a  
12  
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Do not distribute

## DESCRIPTION

stromal processing peptidase (SPP) (original description: pacid=37176362 transcript=Phvul.002G04  
(original description: pacid=37175092 transcript=Phvul.002G112900.2 locus=Phvul.002G112900 IC  
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C2H2 zinc finger transcription factor (original description: pacid=37177813 transcript=Phvul.002G3  
multifunctional phylloquinone biosynthesis protein (PHYLLO) (original description: pacid=37154118  
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profilin actin nucleation protein (original description: pacid=37152607 transcript=Phvul.005G1653C  
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**transcription factor (Trihelix) (original description: pacid=37173860 transcript=Phvul.006G176000.:**  
RRF translation ribosome recycling factor (original description: pacid=37164667 transcript=Phvul.0  
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Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1\_pea : 232.0) & |  
Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1\_pea : 232.0) & |  
endoribonuclease component DCL1 of DCL1-HYL1 miRNA biogenesis complex (original description:  
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19 N-acetylglucosamine-phosphate mutase (original description: pacid=37177997 transcript=Phvul.00  
20 N-acetylglucosamine-phosphate mutase (original description: pacid=37177997 transcript=Phvul.00  
21 C2H2 zinc finger transcription factor (original description: pacid=37177254 transcript=Phvul.002G0  
22 C2H2 zinc finger transcription factor (original description: pacid=37177254 transcript=Phvul.002G0  
23 Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0|bgl40\_arath : 833.0) & Enzyme classificati  
24 Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0|bgl40\_arath : 833.0) & Enzyme classificati  
25 (original description: pacid=37174585 transcript=Phvul.002G146600.2 locus=Phvul.002G146600 IC  
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31 Probable 2-oxoglutarate/Fe(II)-dependent dioxygenase OS=Papaver somniferum (sp|d4n501|diox2  
32 poly-P/G elongation factor (eEF5/eIF5A) (original description: pacid=37147810 transcript=Phvul.00  
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37 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des  
38 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des  
39 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des  
40 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des  
41 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t  
42 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t  
43 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t  
44 transcription factor (ERF) (original description: pacid=37161639 transcript=Phvul.004G068900.2 loc  
45 transcription factor (ERF) (original description: pacid=37161639 transcript=Phvul.004G068900.2 loc  
46 component BRCA1|BARD1 of BRCA1,ÄBARD1 DNA-damage response heterodimer (original descrip  
47 (original description: pacid=37166946 transcript=Phvul.007G157700.1 locus=Phvul.007G157700 IC  
48 protein factor PRPF4 of U4/U6 small nuclear ribonucleoprotein particle (snRNP) (original descriptio  
49 (original description: pacid=37160389 transcript=Phvul.008G111200.1 locus=Phvul.008G111200 IC  
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5 monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37148701 transcript=Phvul.009G  
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7 (original description: pacid=37143928 transcript=Phvul.010G119500.1 locus=Phvul.010G119500 IC  
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13 DRP2-type clathrin coated vesicle dynamin (original description: pacid=37156922 transcript=Phvul.  
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36 protein kinase (PERK-related) (original description: pacid=37174973 transcript=Phvul.002G304500.  
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39 allene oxidase synthase (AOS) (original description: pacid=37146668 transcript=Phvul.003G010700  
40 cationic amino acid transporter (CAT) (original description: pacid=37144797 transcript=Phvul.003G  
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42 S-adenosyl methionine decarboxylase (original description: pacid=37148102 transcript=Phvul.003G  
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44 anion channel (SLAC) (original description: pacid=37147406 transcript=Phvul.003G080700.1 locus=  
45 protein kinase (LRR-VIII-1) (original description: pacid=37148128 transcript=Phvul.003G090000.2 lc  
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16 phosphatidylglycerol lipase (PLIP1) (original description: pacid=37172685 transcript=Phvul.006G11.  
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18 CHE circadian clock repression factor (original description: pacid=37166457 transcript=Phvul.007G(  
19 glutamine-tRNA ligase (original description: pacid=37166017 transcript=Phvul.007G028800.1 locus  
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27 no hits & (original description: pacid=37164585 transcript=Phvul.007G230450.1 locus=Phvul.007G  
28 RNA editing factor (AHG11) (original description: pacid=37160213 transcript=Phvul.008G046100.1  
29 no hits & (original description: pacid=37160926 transcript=Phvul.008G177200.2 locus=Phvul.008G  
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2 transcription factor (GATA) (original description: pacid=37156368 transcript=Phvul.011G080200.1 l  
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4 cationic amino acid transporter (CAT) (original description: pacid=37155925 transcript=Phvul.011G  
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6 core component Gar1 of H/ACA small nucleolar ribonucleoprotein (snoRNP) RNA pseudouridylation  
7 WRKY33-activating protein (SIB) (original description: pacid=37168270 transcript=Phvul.001G12340  
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9 transcription factor (HSF) (original description: pacid=37170201 transcript=Phvul.001G154700.1 lo  
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13 NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (original description: pacid=3717044;  
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15 C2H2 zinc finger transcription factor (original description: pacid=37177695 transcript=Phvul.002G0  
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17 phosphatidylinositol 3-phosphate 5-kinase (FAB1) (original description: pacid=37176675 transcript:  
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19 transcription factor (JUMONJI) (original description: pacid=37177660 transcript=Phvul.002G137100  
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27 C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript=Phvul.003G2  
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29 (original description: pacid=37144586 transcript=Phvul.003G265700.1 locus=Phvul.003G265700 IC  
30 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 tr  
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34 DNA chromomethylase (CMT) (original description: pacid=37163557 transcript=Phvul.004G176100  
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43 Benzyl alcohol O-benzoyltransferase OS=Nicotiana tabacum (sp|q8gt20|bebt\_tobac : 533.0) & Enz  
44 receptor protein (NPR3|4) (original description: pacid=37172197 transcript=Phvul.006G131400.1 l  
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46 Soyasaponin III rhamnosyltransferase OS=Glycine max (sp|d4q9z5|sgt3\_soybn : 536.0) & Enzyme c

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2 (original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 IC  
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15 SnRK1-interacting factor (FLZ) (original description: pacid=37167409 transcript=Phvul.007G173400  
16 pectin methylesterase (original description: pacid=37164403 transcript=Phvul.007G246700.1 locus  
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19 subcluster H/CPL3-4 phosphatase (original description: pacid=37159302 transcript=Phvul.008G019  
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60 cold sensor (COLD1) (original description: pacid=37156295 transcript=Phvul.011G017800.1 locus=F



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16 D)=Phvul.003G295700.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4  
17 D)=Phvul.003G295700.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4  
18 D)=Phvul.005G088636.1.v2.1 annot-version=v2.1) & Ribosomal protein S1, mitochondrial OS=Marchi  
19 D)=Phvul.005G088636.1.v2.1 annot-version=v2.1) & Ribosomal protein S1, mitochondrial OS=Marchi  
20  
21 2000.2 locus=Phvul.006G112000 ID=Phvul.006G112000.2.v2.1 annot-version=v2.1) &  
22 2000.2 locus=Phvul.006G112000 ID=Phvul.006G112000.2.v2.1 annot-version=v2.1) &  
23 015000.1 locus=Phvul.007G015000 ID=Phvul.007G015000.1.v2.1 annot-version=v2.1) &  
24 i=Phvul.007G028800 ID=Phvul.007G028800.1.v2.1 annot-version=v2.1) &  
25  
26 D)=Phvul.007G038000.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant pro  
27 D)=Phvul.007G038000.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant pro  
28  
29 .007G062900 ID=Phvul.007G062900.1.v2.1 annot-version=v2.1) &  
30 .007G062900 ID=Phvul.007G062900.1.v2.1 annot-version=v2.1) &  
31  
32 D)=Phvul.007G100700.1.v2.1 annot-version=v2.1) & Membrane protein PM19L OS=Oryza sativa subs  
33 D)=Phvul.007G100700.1.v2.1 annot-version=v2.1) & Membrane protein PM19L OS=Oryza sativa subs  
34  
35 'G149300.1 locus=Phvul.007G149300 ID=Phvul.007G149300.1.v2.1 annot-version=v2.1) &  
36 i230450 ID=Phvul.007G230450.1.v2.1 annot-version=v2.1)  
37 locus=Phvul.008G046100 ID=Phvul.008G046100.1.v2.1 annot-version=v2.1) &  
38  
39 i177200 ID=Phvul.008G177200.2.v2.1 annot-version=v2.1)  
40 i177200 ID=Phvul.008G177200.2.v2.1 annot-version=v2.1)  
41 i181900 ID=Phvul.008G181900.2.v2.1 annot-version=v2.1)  
42 i181900 ID=Phvul.008G181900.2.v2.1 annot-version=v2.1)  
43  
44 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &  
45 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &  
46 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &  
47 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &  
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49 i041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)  
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52  
53 D)=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr  
54 D)=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr  
55 D)=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr  
56  
57 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)  
58 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)  
59 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)  
60



1 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)  
2 locus=Phvul.011G080200 ID=Phvul.011G080200.1.v2.1 annot-version=v2.1) &  
3 locus=Phvul.011G080200 ID=Phvul.011G080200.1.v2.1 annot-version=v2.1) &  
4 i174000.1 locus=Phvul.011G174000 ID=Phvul.011G174000.1.v2.1 annot-version=v2.1) &  
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6 n complex (original description: pacid=37171084 transcript=Phvul.001G110400.1 locus=Phvul.001G  
7 00.1 locus=Phvul.001G123400 ID=Phvul.001G123400.1.v2.1 annot-version=v2.1) &  
8 00.1 locus=Phvul.001G123400 ID=Phvul.001G123400.1.v2.1 annot-version=v2.1) &  
9 cus=Phvul.001G154700 ID=Phvul.001G154700.1.v2.1 annot-version=v2.1) &  
10 )=Phvul.001G179800.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr  
11 )=Phvul.001G179800.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr  
12 )=Phvul.001G184000.1.v2.1 annot-version=v2.1) & Cactin OS=Arabidopsis thaliana (sp|f4i2j8|catin\_  
13 2 transcript=Phvul.001G259000.1 locus=Phvul.001G259000 ID=Phvul.001G259000.1.v2.1 annot-ver  
14 2 transcript=Phvul.001G259000.1 locus=Phvul.001G259000 ID=Phvul.001G259000.1.v2.1 annot-ver  
15 )28100.1 locus=Phvul.002G028100 ID=Phvul.002G028100.1.v2.1 annot-version=v2.1) &  
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17 =Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvul.002G092900.2.v2.1 annot-version=v2.1) &  
18 =Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvul.002G092900.2.v2.1 annot-version=v2.1) &  
19 0.1 locus=Phvul.002G137100 ID=Phvul.002G137100.1.v2.1 annot-version=v2.1) &  
20 i137200 ID=Phvul.002G137200.1.v2.1 annot-version=v2.1)  
21 i137200 ID=Phvul.002G137200.1.v2.1 annot-version=v2.1)  
22 i139900 ID=Phvul.002G139900.2.v2.1 annot-version=v2.1)  
23 i139900 ID=Phvul.002G139900.2.v2.1 annot-version=v2.1)  
24 i156300 ID=Phvul.002G156300.1.v2.1 annot-version=v2.1)  
25 .1 locus=Phvul.003G032500 ID=Phvul.003G032500.1.v2.1 annot-version=v2.1) &  
26 .1 locus=Phvul.003G032500 ID=Phvul.003G032500.1.v2.1 annot-version=v2.1) &  
27 !52400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1) &  
28 !52400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1) &  
29 )=Phvul.003G265700.1.v2.1 annot-version=v2.1) & F-box protein At4g35930 OS=Arabidopsis thaliana  
30 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic  
31 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic  
32 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic  
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34 ).1 locus=Phvul.004G176100 ID=Phvul.004G176100.1.v2.1 annot-version=v2.1) &  
35 i001500 ID=Phvul.005G001500.2.v2.1 annot-version=v2.1)  
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37 pt=Phvul.005G043500.1 locus=Phvul.005G043500 ID=Phvul.005G043500.1.v2.1 annot-version=v2.1  
38 pt=Phvul.005G043500.1 locus=Phvul.005G043500 ID=Phvul.005G043500.1.v2.1 annot-version=v2.1  
39 )=Phvul.005G093400.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP5 OS=Arabidopsis  
40 i131700 ID=Phvul.005G131700.1.v2.1 annot-version=v2.1)  
41 locus=Phvul.005G183800 ID=Phvul.005G183800.2.v2.1 annot-version=v2.1) &  
42 locus=Phvul.005G183800 ID=Phvul.005G183800.2.v2.1 annot-version=v2.1) &  
43 yme classification.EC\_2 transferases.EC\_2.3 acyltransferase(50.2.3 : 37.5) (original description: paci  
44 locus=Phvul.006G131400 ID=Phvul.006G131400.1.v2.1 annot-version=v2.1) &  
45 locus=Phvul.006G131400 ID=Phvul.006G131400.1.v2.1 annot-version=v2.1) &  
46 classification.EC\_2 transferases.EC\_2.4 glycosyltransferase(50.2.4 : 134.3) (original description: paci

1 classification.EC\_2 transferases.EC\_2.4 glycosyltransferase(50.2.4 : 134.3) (original description: paci  
2 )=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t  
3 )=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t  
4 )=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t  
5 )=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t  
6 )=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t  
7 on.EC\_1 oxidoreductases.EC\_1.1 oxidoreductase acting on CH-OH group of donor(50.1.1 : 438.7) (or  
8 [cus=Phvul.007G067800 ID=Phvul.007G067800.1.v2.1 annot-version=v2.1](#)) &  
9 )=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th  
10 )=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th  
11 )=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th  
12 )=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th  
13 )=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th  
14 )=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th  
15 300.1 locus=Phvul.007G139300 ID=Phvul.007G139300.1.v2.1 annot-version=v2.1) &  
16 300.1 locus=Phvul.007G139300 ID=Phvul.007G139300.1.v2.1 annot-version=v2.1) &  
17 1.1 locus=Phvul.007G173400 ID=Phvul.007G173400.1.v2.1 annot-version=v2.1) &  
18 is=Phvul.007G246700 ID=Phvul.007G246700.1.v2.1 annot-version=v2.1) &  
19 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &  
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21 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &  
22 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &  
23 1000.1 locus=Phvul.008G019000 ID=Phvul.008G019000.1.v2.1 annot-version=v2.1) &  
24 [nscript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 annot-version=](#)  
25 [nscript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 annot-version=](#)  
26 [08G077000.1 locus=Phvul.008G077000 ID=Phvul.008G077000.1.v2.1 annot-version=v2.1](#)) &  
27 [us=Phvul.008G114700 ID=Phvul.008G114700.1.v2.1 annot-version=v2.1](#)) &  
28 [us=Phvul.008G114700 ID=Phvul.008G114700.1.v2.1 annot-version=v2.1](#)) &  
29 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)  
30 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)  
31 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)  
32 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)  
33 29 transcript=Phvul.008G250000.1 locus=Phvul.008G250000 ID=Phvul.008G250000.1.v2.1 annot-ve  
34 29 transcript=Phvul.008G250000.1 locus=Phvul.008G250000 ID=Phvul.008G250000.1.v2.1 annot-ve  
35 )=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein  
36 )=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein  
37 )=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein  
38 )=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein  
39 09G149800.1 locus=Phvul.009G149800 ID=Phvul.009G149800.1.v2.1 annot-version=v2.1) &  
40 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
41 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
42 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
43 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
44 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
45 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
46 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
47 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
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55 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
56 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
57 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
58 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
59 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &  
60 ul.009G240100.1 locus=Phvul.009G240100 ID=Phvul.009G240100.1.v2.1 annot-version=v2.1) &  
Phvul.011G017800 ID=Phvul.011G017800.1.v2.1 annot-version=v2.1) &



1 Phvul.011G017800 ID=Phvul.011G017800.1.v2.1 annot-version=v2.1) &  
2 i100200 ID=Phvul.011G100200.2.v2.1 annot-version=v2.1)  
3 i100200 ID=Phvul.011G100200.2.v2.1 annot-version=v2.1)  
4 i108300 ID=Phvul.011G108300.1.v2.1 annot-version=v2.1)  
5 i129700.1 locus=Phvul.011G129700 ID=Phvul.011G129700.1.v2.1 annot-version=v2.1) &  
6 i129700.1 locus=Phvul.011G129700 ID=Phvul.011G129700.1.v2.1 annot-version=v2.1) &  
7 O=Phvul.011G140050.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4  
8 O=Phvul.011G140050.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4  
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Do not distribute

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4 *aliana* (sp|q7xa86|zdh11\_arath : 318.0)  
5 *aliana* (sp|q7xa86|zdh11\_arath : 318.0)  
6 *aliana* (sp|q7xa86|zdh11\_arath : 318.0)  
7 *aliana* (sp|q7xa86|zdh11\_arath : 318.0)  
8 *aliana* (sp|q7xa86|zdh11\_arath : 318.0)  
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16 *sion=v2.1*) &  
17 *sion=v2.1*) &  
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23  
24 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575  
25 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575  
26 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575  
27 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575  
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31 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575  
32 .1.v2.1 annot-version=v2.1) &  
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43 *al OS=Arabidopsis thaliana* (sp|o64886|cox10\_arath : 442.0)  
44 *al OS=Arabidopsis thaliana* (sp|o64886|cox10\_arath : 442.0)  
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53 *idopsis thaliana* (sp|q8gza4|cbsx6\_arath : 500.0)  
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OS=Arabidopsis thaliana (sp|q9stx1|acbp3\_arath : 116.0)

OS=Arabidopsis thaliana (sp|q9stx1|acbp3\_arath : 116.0)

thaliana (sp|q9lka4|uba2c\_arath : 175.0)

thaliana (sp|q9lka4|uba2c\_arath : 175.0)

Arabidopsis thaliana (sp|a1l4v7|dcyd2\_arath : 443.0)

Arabidopsis thaliana (sp|a1l4v7|dcyd2\_arath : 443.0)

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S=Arabidopsis thaliana (sp|q9fgd7|pub50\_arath : 342.0)

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Arabidopsis thaliana (sp|q9sre5|y1666\_arath : 119.0)

Arabidopsis thaliana (sp|q9sre5|y1666\_arath : 119.0)

paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 122.3) (original description)

i261400.2.v2.1 annot-version=v2.1) &

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on=v2.1) &

on=v2.1) &

on=v2.1) &

9600.1.v2.1 annot-version=v2.1) &

3g53700, chloroplastic OS=Arabidopsis thaliana (sp|q9lff1|pp281\_arath : 948.0)

0.1.v2.1 annot-version=v2.1) &

Arabidopsis thaliana (sp|q84lh3|wex\_arath : 98.6)

1  
2 *Arabidopsis thaliana* (sp|q84lh3|wex\_arath : 98.6)  
3 2g34400 OS=*Arabidopsis thaliana* (sp|o64705|pp184\_arath : 608.0)  
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10 *Arabidopsis thaliana* (sp|q39061|cp33\_arath : 102.0)  
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14 10.1.v2.1 annot-version=v2.1) &  
15 10.1.v2.1 annot-version=v2.1) &  
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35 *Chocarpa* (sp|b9i2j6|axep\_poptr : 565.0)  
36 *Chocarpa* (sp|b9i2j6|axep\_poptr : 565.0)  
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39 1 MRL7, chloroplastic OS=*Arabidopsis thaliana* (sp|f4jlc1|mrl7\_arath : 334.0)  
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43 *Na* (sp|q8rwd6|fb271\_arath : 511.0)  
44 *Na* (sp|q8rwd6|fb271\_arath : 511.0)  
45 *Na* (sp|q8rwd6|fb271\_arath : 511.0)  
46 *Na* (sp|q8rwd6|fb271\_arath : 511.0)  
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49 *Arabidopsis thaliana* (sp|q9fle8|y5986\_arath : 127.0)  
50 *Arabidopsis thaliana* (sp|q9fle8|y5986\_arath : 127.0)  
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16 4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304\_arath : 449.0)

17 4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304\_arath : 449.0)

18 antia polymorpha (sp|p26863|rt01\_marpo : 94.7)

19 antia polymorpha (sp|p26863|rt01\_marpo : 94.7)  
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27 rtein 37 OS=Arabidopsis thaliana (sp|a2rvm8|hip37\_arath : 113.0)

28 rtein 37 OS=Arabidopsis thaliana (sp|a2rvm8|hip37\_arath : 113.0)  
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32 sp. japonica (sp|q6l4d2|pm19l\_orysj : 166.0)

33 sp. japonica (sp|q6l4d2|pm19l\_orysj : 166.0)  
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54 rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104\_arath : 473.0)

55 rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104\_arath : 473.0)

56 rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104\_arath : 473.0)  
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8 i110400 ID=Phvul.001G110400.1.v2.1 annot-version=v2.1) &  
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14 rotein At5g37570 OS=Arabidopsis thaliana (sp|q9fhr3|pp403\_arath : 574.0)

15 rotein At5g37570 OS=Arabidopsis thaliana (sp|q9fhr3|pp403\_arath : 574.0)

16 \_arath : 759.0)

17 rsion=v2.1) &

18 rsion=v2.1) &  
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39 na (sp|q5xf11|fb248\_arath : 202.0)

40 n=v2.1) &

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51 s thaliana (sp|f4jnb7|rpp5\_arath : 109.0)  
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57 id=37171403 transcript=Phvul.006G098700.1 locus=Phvul.006G098700 ID=Phvul.006G098700.1.v2.  
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d=37173062 transcript=Phvul.006G208400.1 locus=Phvul.006G208400 ID=Phvul.006G208400.1.v2.



1 id=37173062 transcript=Phvul.006G208400.1 locus=Phvul.006G208400 ID=Phvul.006G208400.1.v2.  
2 thaliana (sp|q8gxd9|sco3\_arath : 320.0)  
3 thaliana (sp|q8gxd9|sco3\_arath : 320.0)  
4 thaliana (sp|q8gxd9|sco3\_arath : 320.0)  
5 thaliana (sp|q8gxd9|sco3\_arath : 320.0)  
6 original description: pacid=37166204 transcript=Phvul.007G062100.1 locus=Phvul.007G062100 ID=Phvul.007G062100.1.v2.  
7 aliana (sp|q6dye5|u496k\_arath : 151.0)  
8 aliana (sp|q6dye5|u496k\_arath : 151.0)  
9 aliana (sp|q6dye5|u496k\_arath : 151.0)  
10 aliana (sp|q6dye5|u496k\_arath : 151.0)  
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OS=Arabidopsis thaliana (sp|q9ffj8|limyb\_arath : 115.0)

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4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304\_arath : 558.0)  
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ion: pacid=37145792 transcript=Phvul.003G013200.2 locus=Phvul.003G013200 ID=Phvul.003G0132

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	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
1						
2						
3	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
4	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
5	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
6	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
7	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
8	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
9	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
10	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
11	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
12	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
13	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
14	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
15	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	21
16	ggaaucuugauξ	Phvul.001G174400.1	0.5	-1	1	24
17	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
18	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
19	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
20	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
21	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
22	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
23	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
24	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
25	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
26	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
27	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
28	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
29	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
30	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	21
31	ggaaucuugauξ	Phvul.002G016900.1	0.5	-1	1	24
32	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
33	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
34	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
35	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
36	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
37	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
38	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
39	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
40	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
41	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
42	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
43	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
44	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	21
45	ggaaucuugauξ	Phvul.003G241900.1	0.5	-1	1	24
46	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
47	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
48	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
49	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
50	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
51	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
52	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
53	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
54	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
55	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
56	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
57	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
58	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
59	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21
60	ggaaucuugauξ	Phvul.011G071100.2	1	-1	1	21
	ggaaucuugauξ	Phvul.011G071100.1	1	-1	1	21

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2	ggaaucuugauξPhvul.011G071100.2	1	-1	1	21
3	ggaaucuugauξPhvul.011G071100.1	1	-1	1	21
4	ggaaucuugauξPhvul.011G071100.2	1	-1	1	21
5	ggaaucuugauξPhvul.011G071100.1	1	-1	1	21
6	ggaaucuugauξPhvul.011G071100.2	1	-1	1	21
7	ggaaucuugauξPhvul.011G071100.1	1	-1	1	21
8	ggaaucuugauξPhvul.011G071100.2	1	-1	1	21
9	ggaaucuugauξPhvul.011G071100.1	1	-1	1	21
10	ggaaucuugauξPhvul.011G071100.2	1	-1	1	21
11	ggaaucuugauξPhvul.011G071100.1	1	-1	1	21
12	ggaaucuugauξPhvul.011G071100.2	1	-1	1	24
13	ggaaucuugauξPhvul.011G071100.1	1	-1	1	24
14	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
15	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
16	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
17	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
18	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
19	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
20	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
21	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
22	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
23	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
24	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
25	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
26	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
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29	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
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36	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
37	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
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39	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
40	ggaaucuugauξPhvul.L000308.2	1	-1	1	21
41	ggaaucuugauξPhvul.L000308.1	1	-1	1	21
42	ggaaucuugauξPhvul.L000308.2	1	-1	1	24
43	ggaaucuugauξPhvul.L000308.1	1	-1	1	24
44	uggaaucuugaI Phvul.001G174400.1	1.5	-1	1	22
45	uggaaucuugaI Phvul.002G016900.1	1.5	-1	1	22
46	uggaaucuugaI Phvul.003G241900.1	1.5	-1	1	22
47	ggaaucuugauξPhvul.005G132300.2	1.5	-1	1	21
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54					
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57					
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60					













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7	10	33 GGAAUCUUG	.....	UUUCCUCAG Translation	pacid=371693
8	13	34 UGGAUCUU	.....	CCUCAGCAUC Translation	pacid=371693
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11	725	746 UGGAUCUU	.....	AGUCAGCAG Cleavage	pacid=371678
12	460	480 GGAAUCUUG	.....	GCGCUGCAU Cleavage	pacid=371786
13	460	480 GGAAUCUUG	.....	GCGCUGCAU Cleavage	pacid=371786
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25	460	480 GGAAUCUUG	.....	GCGCUGCAU Cleavage	pacid=371786
26	637	658 UGGAUCUU	.....	GAUCAGCAU Translation	pacid=371757
27	251	272 UGGAUCUU	.....	UUUCGGCGU Translation	pacid=371760
28	446	467 UGGAUCUU	.....	UUCAGCUU Translation	pacid=371756
29	672	693 UGGAUCUU	.....	UUCAGCUU Translation	pacid=371756
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31	186	207 UGGAUCUU	.....	CACCAGCGUC Cleavage	pacid=371456
32	165	186 UGGAUCUU	.....	CACCAGCGUC Cleavage	pacid=371462
33	1854	1874 GGAAUCUUG	.....	AUGUAUCUU Cleavage	pacid=371541
34	1854	1874 GGAAUCUUG	.....	AUGUAUCUU Cleavage	pacid=371541
35	1854	1874 GGAAUCUUG	.....	AUGUAUCUU Cleavage	pacid=371541
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47	1851	1874 GGAAUCUUG	.....	CUUAUGUAU Cleavage	pacid=371541
48	1854	1875 UGGAUCUU	.....	AUGUAUCUU Cleavage	pacid=371541
49	1903	1924 UGGAUCUU	.....	UUUUAUCUU Cleavage	pacid=371531
50	2017	2038 UGGAUCUU	.....	UUUUAUCUU Cleavage	pacid=371531
51	2016	2037 UGGAUCUU	.....	UUUUAUCUU Cleavage	pacid=371531
52	1836	1857 UGGAUCUU	.....	CUCUACCUUC Cleavage	pacid=371538
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54	18	38 GGAAUCUUG	.....	CAUCAUCAUC Cleavage	pacid=371523
55	18	38 GGAAUCUUG	.....	CAUCAUCAUC Cleavage	pacid=371523
56	18	38 GGAAUCUUG	.....	CAUCAUCAUC Cleavage	pacid=371523
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59	18	38 GGAAUCUUG	.....	CAUCAUCAUC Cleavage	pacid=371523
60	18	38 GGAAUCUUG	.....	CAUCAUCAUC Cleavage	pacid=371523

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3	18	38	GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage	pacid=371523
4	18	38	GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage	pacid=371523
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8	18	39	UGGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage	pacid=371523
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10	764	785	UGGAAUCUUG, ::::: AUGUAGCAUC Cleavage	pacid=371539
11	764	785	UGGAAUCUUG, ::::: AUGUAGCAUC Cleavage	pacid=371539
12	604	623	GGAAUCUUG, ::::: GUGCAGU-UC Cleavage	pacid=371730
13	604	623	GGAAUCUUG, ::::: GUGCAGU-UC Cleavage	pacid=371730
14	604	623	GGAAUCUUG, ::::: GUGCAGU-UC Cleavage	pacid=371730
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25	604	623	GGAAUCUUG, ::::: GUGCAGU-UC Cleavage	pacid=371730
26	601	623	GGAAUCUUG, : ::::: AAGGUGCAGI Cleavage	pacid=371730
27	1503	1524	UGGAAUCUUG, ::::: CAGCAGCAUC Cleavage	pacid=371641
28	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
29	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
30	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
31	339	359	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
32	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
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52	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
53	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
54	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
55	339	359	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
56	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
57	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
58	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
59	339	359	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
60	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597
	342	362	GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage	pacid=371597









1					
2	186	206 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371456
3	186	206 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371456
4	186	206 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371456
5	186	206 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371456
6	186	206 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371456
7	186	206 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371456
8	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
9	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
10	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
11	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
12	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
13	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
14	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
15	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
16	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
17	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
18	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
19	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
20	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
21	165	185 GGAAUCUUG,	.....: CACCAGCGUC	Cleavage	pacid=371462
22	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
23	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
24	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
25	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
26	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
27	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
28	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
29	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
30	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
31	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
32	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
33	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
34	1430	1450 GGAAUCUUG,	:: .....: UCUCACCAUC	Cleavage	pacid=371544
35	1096	1117 UGGAUCUU:	:: : .....: CUUCACUACC	Cleavage	pacid=371722
36	1247	1268 UGGAUCUU:	:: : .....: CUUCACUACC	Cleavage	pacid=371722
37	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
38	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
39	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
40	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
41	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
42	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
43	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
44	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
45	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
46	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
47	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
48	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
49	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
50	1203	1223 GGAAUCUUG,	...: .....: GGGUGGCCUI	Cleavage	pacid=371734
51	195	216 UGGAUCUU:	.....:UCAAGACAUC	Cleavage	pacid=371729
52	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
53	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
54	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
55	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
56	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
57	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
58	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
59	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729
60	1892	1912 GGAAUCUUG,	:: : .....: UUGGGGAAU	Cleavage	pacid=371729





1				
2	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
3	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
4	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
5	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
6	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
7	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
8	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
9	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
10	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
11	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
12	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
13	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
14	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
15	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
16	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
17	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
18	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
19	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
20	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
21	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
22	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
23	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
24	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
25	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
26	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
27	1154	1174 GGAAUCUUG, ...	..... AUGCGAAAUC Cleavage	pacid=371505
28	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
29	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
30	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
31	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
32	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
33	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
34	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
35	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
36	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
37	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
38	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
39	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
40	1044	1064 GGAAUCUUG, ....	..... CUGCAAUAU Cleavage	pacid=371487
41	1041	1064 GGAAUCUUG, ....	..... UGCCUGCAAL Cleavage	pacid=371487
42	467	488 UGGAUCUU, .....	..... GAGUGGCAC Cleavage	pacid=371506
43	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
44	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
45	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
46	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
47	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
48	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
49	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
50	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
51	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
52	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
53	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
54	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
55	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
56	286	306 GGAAUCUUG, .....	..... AUGCAGCAU Translation	pacid=371433
57	283	306 GGAAUCUUG, .....	..... AGCAUGCAG Translation	pacid=371433
58	286	307 UGGAUCUU, .....	..... AUGCAGCAU Translation	pacid=371433
59	1306	1327 UGGAUCUU, ....	..... AUGCAGGAC Translation	pacid=371570
60	2984	3004 GGAAUCUUG, .....	..... CUGUGGCAU Cleavage	pacid=371569



1				
2	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
3	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
4	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
5	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
6	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
7	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
8	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
9	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
10	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
11	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
12	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
13	1397	1417 GGAAUCUUG, .....	UUGCACCGU Cleavage	pacid=371485
14	1394	1417 GGAAUCUUG, .....	UUAUUGCAC Cleavage	pacid=371485
15	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
16	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
17	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
18	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
19	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
20	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
21	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
22	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
23	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
24	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
25	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
26	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
27	249	271 GGAAUCUUG- .....	AAGCAGCAUC Cleavage	pacid=371446
28	246	271 GGAAUCUUG- .....	AGAAAGCAG Cleavage	pacid=371446
29	249	272 UGGAUCUUG, .....	AAGCAGCAUC Translation	pacid=371446
30				
31	1104	1125 UGGAUCUUG, .....	AUUUUGUAU Cleavage	pacid=371685
32	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
33	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
34	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
35	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
36	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
37	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
38	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
39	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
40	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
41	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
42	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
43	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
44	311	331 GGAAUCUUG, .....	UCGCGGUGU Translation	pacid=371712
45	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
46	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
47	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
48	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
49	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
50	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
51	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
52	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
53	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
54	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
55	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
56	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
57	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
58	154	174 GGAAUCUUG, .....	CCUCAGCAUC Cleavage	pacid=371703
59	657	677 GGAAUCUUG, .....	AGUCAGCAG Cleavage	pacid=371678
60	725	745 GGAAUCUUG, .....	AGUCAGCAG Cleavage	pacid=371678
	657	677 GGAAUCUUG, .....	AGUCAGCAG Cleavage	pacid=371678







1				
2	248	271 GGAAUCUUG/	:: ::::: ::::UCGUUUCGG	Translation pacid=371760
3	1999	2020 UGGAUCUU(:	:: ::::: ::::CUAGAGUI	Cleavage pacid=371787
4	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
5	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
6	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
7	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
8	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
9	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
10	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
11	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
12	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
13	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
14	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
15	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
16	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
17	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
18	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
19	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
20	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
21	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
22	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
23	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
24	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
25	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
26	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
27	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
28	446	466 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
29	672	692 GGAAUCUUG/	:: ::::: ::::UCCAGCUU	Cleavage pacid=371756
30	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
31	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
32	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
33	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
34	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
35	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
36	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
37	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
38	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
39	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
40	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
41	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
42	261	281 GGAAUCUUG/	:: ::::: ::::CAAAGCAGC	Cleavage pacid=371448
43	12225	12246 UGGAUCUU(:	:: ::::: ::::CAGCGCUU	Translation pacid=371454
44	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
45	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
46	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
47	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
48	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
49	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
50	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
51	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
52	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
53	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
54	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
55	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
56	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
57	2133	2153 GGAAUCUUG/	:: ::::: ::::CGGCAGCAU	Translation pacid=371445
58	2130	2153 GGAAUCUUG/	:: ::::: ::::CCCCGGCAGC	Translation pacid=371445
59	1083	1103 GGAAUCUUG/	:: ::::: ::::GUGUGGCAU	Cleavage pacid=371476
60	1216	1236 GGAAUCUUG/	:: ::::: ::::GUGUGGCAU	Cleavage pacid=371476







1					
2	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
3	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
4	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
5	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
6	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
7	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
8	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
9	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
10	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
11	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
12	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
13	381	401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation			pacid=371633
14	378	401 GGAAUCUUG,::: :::: ::::: CUUUUGCUU(Translation			pacid=371633
15	1146	1167 UGGAUCUU(,::: :::: ::::: UUCCAGUACC Cleavage			pacid=371632
16	1151	1172 UGGAUCUU(,::: :::: ::::: UUCCAGUACC Cleavage			pacid=371631
17	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
18	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
19	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
20	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
21	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
22	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
23	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
24	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
25	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
26	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
27	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
28	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
29	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
30	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
31	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
32	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
33	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
34	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
35	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
36	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
37	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
38	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
39	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
40	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
41	1181	1201 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
42	1262	1282 GGAAUCUUG, ::::: ::::: GUGCAGCAU( Cleavage			pacid=371529
43	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
44	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
45	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
46	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
47	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
48	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
49	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
50	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
51	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
52	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
53	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
54	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
55	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
56	1836	1856 GGAAUCUUG,::: ::: ::::: CUCUACCUUC Cleavage			pacid=371538
57	1833	1856 GGAAUCUUG,::: ::: ::::: CUUCUCUACC Cleavage			pacid=371538
58	888	908 GGAAUCUUG,::: ::: ::::: CUUCGUCAU( Cleavage			pacid=371540
59	899	919 GGAAUCUUG,::: ::: ::::: CUUCGUCAU( Cleavage			pacid=371540
60	888	908 GGAAUCUUG,::: ::: ::::: CUUCGUCAU( Cleavage			pacid=371540











1				
2	1448	1469 GGAAUCUUG):::: : ::::: UUGUAUGUA Cleavage	pacid=371614	
3	1448	1469 GGAAUCUUG):::: : ::::: UUGUAUGUA Cleavage	pacid=371614	
4	1448	1469 GGAAUCUUG):::: : ::::: UUGUAUGUA Cleavage	pacid=371614	
5	1448	1469 GGAAUCUUG):::: : ::::: UUGUAUGUA Cleavage	pacid=371614	
6	1448	1469 GGAAUCUUG):::: : ::::: UUGUAUGUA Cleavage	pacid=371614	
7	1448	1469 GGAAUCUUG):::: : ::::: UUGUAUGUA Cleavage	pacid=371614	
8	1445	1469 GGAAUCUUG):::: : ::::: UACUUGUAU Cleavage	pacid=371614	
9	1044	1065 UGGAUCUU):::: : ::::: CUGCAAUAU Cleavage	pacid=371487	
10				
11	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
12	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
13	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
14	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
15	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
16	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
17	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
18	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
19	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
20	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
21	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
22	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
23	65	85 GGAAUCUUG):::: : ::::: UGAUAGCAU Cleavage	pacid=371423	
24	329	350 UGGAUCUU):::: : ::::: UUGCAGCAG Cleavage	pacid=371436	
25				
26	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
27	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
28	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
29	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
30	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
31	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
32	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
33	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
34	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
35	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
36	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
37	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
38	102	122 GGAAUCUUG):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
39	102	123 UGGAUCUU):::: : ::::: CAGCAGCAGC Cleavage	pacid=371568	
40	695	716 UGGAUCUU):::: : ::::: ACUCCCAUC Cleavage	pacid=371547	
41	695	716 UGGAUCUU):::: : ::::: ACUCCCAUC Cleavage	pacid=371547	
42				
43	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
44	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
45	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
46	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
47	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
48	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
49	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
50	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
51	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
52	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
53	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
54	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
55	1306	1326 GGAAUCUUG):::: : ::::: AUGCAGGACC Translation	pacid=371570	
56	426	446 GGAAUCUUG):::: : ::::: UGACAGUGU Translation	pacid=371553	
57	426	446 GGAAUCUUG):::: : ::::: UGACAGUGU Translation	pacid=371553	
58	426	446 GGAAUCUUG):::: : ::::: UGACAGUGU Translation	pacid=371553	
59	426	446 GGAAUCUUG):::: : ::::: UGACAGUGU Translation	pacid=371553	
60	426	446 GGAAUCUUG):::: : ::::: UGACAGUGU Translation	pacid=371553	























1				
2	836	856 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
3	938	958 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
4	941	961 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371609	
5	833	853 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
6	836	856 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
7	938	958 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
8	941	961 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371609	
9	833	853 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
10	836	856 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
11	938	958 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
12	941	961 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371609	
13	833	853 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
14	836	856 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
15	938	958 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
16	941	961 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371609	
17	833	853 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
18	836	856 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
19	938	958 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371610	
20	941	961 GGAAUCUUG).....: UUGCUGCAG(Cleavage	pacid=371609	
21	830	853 GGAAUCUUG).....:UGGUUGCUG Cleavage	pacid=371610	
22	833	856 GGAAUCUUG).....:UGGUUGCUG Cleavage	pacid=371610	
23	935	958 GGAAUCUUG).....:UGGUUGCUG Cleavage	pacid=371610	
24	938	961 GGAAUCUUG).....:UGGUUGCUG Cleavage	pacid=371609	
25	833	854 UGGAUCUUI).....:UUGCUGCAG(Cleavage	pacid=371610	
26	836	857 UGGAUCUUI).....:UUGCUGCAG(Cleavage	pacid=371610	
27	938	959 UGGAUCUUI).....:UUGCUGCAG(Cleavage	pacid=371610	
28	941	962 UGGAUCUUI).....:UUGCUGCAG(Cleavage	pacid=371609	
29	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
30	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
31	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
32	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
33	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
34	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
35	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
36	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
37	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
38	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
39	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
40	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
41	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
42	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
43	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
44	504	525 GGAAUCUUG).....:UUGCAGAUAI Cleavage	pacid=371614	
45	501	525 GGAAUCUUG).....:GAGUUGCAG/ Cleavage	pacid=371614	
46	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
47	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
48	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
49	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
50	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
51	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
52	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
53	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
54	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
55	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
56	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
57	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
58	746	766 GGAAUCUUG).....: UUGUGGCAU Translation	pacid=371578	
59	20	40 GGAAUCUUG).....: CUGCAGCAAC Translation	pacid=371576	
60	20	40 GGAAUCUUG).....: CUGCAGCAAC Translation	pacid=371576	



1			
2	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
3	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
4	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
5	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
6	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
7	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
8	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
9	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
10	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
11	20	40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation	pacid=371576
12	17	40 GGAAUCUUG, : :::::::::: : ::::::::::UUUCUGCAG(Translation	pacid=371576
13			
14	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
15	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
16	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
17	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
18	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
19	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
20	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
21	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
22	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
23	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
24	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
25	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
26	567	587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage	pacid=371598
27	564	587 GGAAUCUUG, :: ::::::::::: ::::AGGCUGGAG(Cleavage	pacid=371598
28	567	588 UGGAUCUU, : ::::::::::: ::::: CUGGAGCAUI Cleavage	pacid=371598
29			
30	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
31	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
32	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
33	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
34	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
35	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
36	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
37	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
38	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
39	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
40	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
41	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
42	627	646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage	pacid=371604
43	1448	1470 UGGAUCUU, : ::::::::::: ::::: UUGUAUGUA Cleavage	pacid=371614
44	1154	1175 UGGAUCUU, : ::::::::::: ::::: AUGCGAAAU(Cleavage	pacid=371505
45	1154	1175 UGGAUCUU, : ::::::::::: ::::: AUGCGAAAU(Cleavage	pacid=371505
46			
47	94	114 UGGAUCUU, : ::::::::::: ::::: CAGCAGCAUC Translation	pacid=371511
48	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
49	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
50	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
51	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
52	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
53	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
54	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
55	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
56	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
57	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
58	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
59	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
60	1001	1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage	pacid=371502
	65	86 UGGAUCUU, : ::::::::::: ::::: UGAUAGCAU(Cleavage	pacid=371423



1					
2	441	462	UGGAAUCUUU	UUGCAACAUL	Cleavage pacid=371565
3	1075	1096	UGGAAUCUUU	GGUUAGUAA	Translation pacid=371565
4	1075	1096	UGGAAUCUUU	GGUUAGUAA	Translation pacid=371565
5					
6	1397	1418	UGGAAUCUUU	UUGCACCGUL	Cleavage pacid=371485
7	119	141	UGGAAUCUUU	GUGCAGCAGL	Cleavage pacid=371694
8	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
9					
10	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
11	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
12	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
13					
14	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
15	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
16	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
17					
18	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
19	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
20	1408	1428	GGAAUCUUGU	UUGCACCAUL	Cleavage pacid=371688
21					
22	1981	2001	UGGAAUCUUU	UUGCAGCAU	Cleavage pacid=371683
23	1989	2009	UGGAAUCUUU	UUGCAGCAU	Cleavage pacid=371683
24	1996	2016	UGGAAUCUUU	UUGCAGCAU	Cleavage pacid=371683
25					
26	1546	1567	UGGAAUCUUU	CUGAAGCAU	Cleavage pacid=371686
27	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
28	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
29					
30	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
31	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
32	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
33					
34	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
35	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
36	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
37					
38	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
39	1061	1080	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371777
40	1061	1081	UGGAAUCUUU	CUGCGGCAUL	Cleavage pacid=371777
41					
42	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
43	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
44	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
45	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
46					
47	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
48	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
49	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
50					
51	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
52	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
53	1230	1249	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371779
54					
55	1230	1250	UGGAAUCUUU	CUGCGGCAUL	Cleavage pacid=371779
56	1216	1235	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371765
57	1216	1235	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371765
58					
59	1216	1235	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371765
60	1216	1235	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371765
	1216	1235	GGAAUCUUGU	CUGCGGCAUL	Cleavage pacid=371765







1				
2	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
3	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
4	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
5	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
6	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
7	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
8	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
9	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
10	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
11	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
12	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
13	764	784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage		pacid=371673
14	1518	1539 UGGAUCUU)..... : : : : UUGCAGUAC(Cleavage		pacid=371650
15	2961	2984 GGAAUCUUG)..... : : : : UUAUGCAG(Cleavage		pacid=371581
16	2964	2985 UGGAUCUU)..... : : : : AUGCAGCAU(Cleavage		pacid=371581
17	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
18	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
19	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
20	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
21	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
22	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
23	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
24	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
25	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
26	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
27	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
28	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
29	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
30	1687	1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage		pacid=371596
31	1687	1708 UGGAUCUU)..... : : : : CUGUGGAA(Cleavage		pacid=371596
32	230	251 UGGAUCUU)..... : : : : CUGCAGAAU(Translation		pacid=371577
33	20	41 UGGAUCUU)..... : : : : CUGCAGCAAC(Cleavage		pacid=371576
34	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
35	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
36	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
37	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
38	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
39	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
40	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
41	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
42	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
43	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
44	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
45	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
46	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
47	203	223 GGAAUCUUG)..... : : : : CUGCAACAUC(Cleavage		pacid=371610
48	471	493 GGAAUCUUG)..... : : : : UUGCUGCAG-(Cleavage		pacid=371584
49	474	494 UGGAUCUU)..... : : : : CUGCAG-AUU(Cleavage		pacid=371584
50	163	186 GGAAUCUUG)..... : : : : CUGCAGCAAL(Cleavage		pacid=371613
51	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
52	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
53	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
54	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
55	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
56	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
57	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
58	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
59	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
60	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498
	1986	2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage		pacid=371498



1				
2	1986	2007 GGAAU-CUUG	UUGCUGCAU	pacid=371498
3	1986	2007 GGAAU-CUUG	UUGCUGCAU	pacid=371498
4	1986	2008 UGGAU-CUU	UUGCUGCAU	pacid=371498
5	3055	3078 GGAAUCUUG	UUGAUGCAA	pacid=371424
6	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
7	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
8	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
9	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
10	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
11	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
12	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
13	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
14	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
15	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
16	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
17	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
18	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
19	1147	1167 GGAAUCUUG	CUGCUGCAU	pacid=371560
20	2140	2162 UGGAUCUU	CUAUAGCUA	pacid=371559
21	1941	1962 UGGAUCUU	AUGUACCUU	pacid=371568
22	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
23	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
24	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
25	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
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27	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
28	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
29	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
30	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
31	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
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34	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
35	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
36	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
37	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
38	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
39	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
40	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
41	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
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43	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
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45	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
46	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
47	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
48	1075	1095 GGAAUCUUG	GGUUAGUAA	pacid=371565
49	1072	1095 GGAAUCUUG	UAAGGUUAG	pacid=371565
50	1072	1095 GGAAUCUUG	UAAGGUUAG	pacid=371565
51				
52				
53				
54				
55				
56				
57				
58				
59				
60				







1					
2	1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0 0
3	1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0 0
4	1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0 0
5					
6	1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0 0
7	1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0 0
8	1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0 0
9					
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11	1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0 0
12	1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0 0
13					
14	1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0 0
15	1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0 0
16	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
17	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
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24	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
25					
26	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
27	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
28	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
29					
30	1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24 PF00847	PTHR32467,P
31	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
32	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
33					
34	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
35	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
36	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
37	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
38					
39	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
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42					
43	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
44	1	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
45	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
46	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
47	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
48	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
49	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
50					
51	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
52	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
53	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
54					
55	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
56	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
57	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
58					
59	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
60	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0

1					
2	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
3	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
4	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
5	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
6	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
7	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
8	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
9	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
10	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
11	1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0 0
12	1	Phvul.001G233200.1	Phvul.001G233200	Phvul.001G23	0 0
13	1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07 PF00847	PTHR32467,P
14	1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07 PF00847	PTHR32467,P
15	1	Phvul.L000308.2	Phvul.L000308	Phvul.L000308 PF00847	PTHR32467,P
16	1	Phvul.L000308.1	Phvul.L000308	Phvul.L000308 PF00847	PTHR32467,P
17	1	Phvul.003G111500.1	Phvul.003G111500	Phvul.003G11 PF06351	PTHR31843,P
18	1	Phvul.005G118700.1	Phvul.005G118700	Phvul.005G11 PF07646,PF13	PTHR11668,P
19	1	Phvul.008G058700.2	Phvul.008G058700	Phvul.008G05 PF01657,PF07	PTHR27002,P
20	1	Phvul.008G058700.1	Phvul.008G058700	Phvul.008G05 PF01657,PF07	PTHR27002,P
21	1	Phvul.011G150100.1	Phvul.011G150100	Phvul.011G15 PF00954,PF08	PTHR27002,P
22	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
23	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
24	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
25	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
26	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
27	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
28	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
29	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
30	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
31	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
32	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
33	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
34	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
35	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
36	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
37	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
38	1	Phvul.001G033700.1	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
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53	1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03 PF10258	PTHR13135
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1 Phvul.010G002600.1	Phvul.010G002600	Phvul.010G00 PF03140	PTHR31549,P
1 Phvul.010G002600.1	Phvul.010G002600	Phvul.010G00 PF03140	PTHR31549,P
1 Phvul.010G002600.1	Phvul.010G002600	Phvul.010G00 PF03140	PTHR31549,P
1 Phvul.011G067401.1	Phvul.011G067401	Phvul.011G06PF11721,PF00PTHR27006,P	
1 Phvul.011G079800.1	Phvul.011G079800	Phvul.011G07PF00046,PF08PTHR24326,P	











































































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2	1	Phvul.009G092600.1	Phvul.009G092600	Phvul.009G09 PF07651	PTHR22951,P
3	1	Phvul.009G092600.1	Phvul.009G092600	Phvul.009G09 PF07651	PTHR22951,P
4	1	Phvul.009G092600.1	Phvul.009G092600	Phvul.009G09 PF07651	PTHR22951,P
5	1	Phvul.009G092600.1	Phvul.009G092600	Phvul.009G09 PF07651	PTHR22951,P
6	1	Phvul.010G053600.1	Phvul.010G053600	Phvul.010G05 PF00780,PF10	PTHR12894,P
7	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
8	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
9	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
10	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
11	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
12	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
13	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
14	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
15	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
16	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
17	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
18	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
19	1	Phvul.011G035700.2	Phvul.011G035700	Phvul.011G03 PF07716	PTHR23334,P
20	2	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0 0
21					
22	1	Phvul.011G147000.1	Phvul.011G147000	Phvul.011G14 PF08276,PF00	PTHR27002,P
23	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
24	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
25	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
26	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
27	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
28	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
29	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
30	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
31	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
32	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
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35	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
36	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
37	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
38	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
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41	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
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44	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
45	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
46	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
47	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
48	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
49	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
50	2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
51	2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15 PF08276,PF00	PTHR27002,P
52					
53					
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56					
57					
58					
59					
60					



	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol
1					
2					
3		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
4		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
5		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
6		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
7		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
8		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
9		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
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11		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
12		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
13		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
14		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
15		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
16		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
17		0	0 K09284	GO:0006355,(AT2G28550.3 RAP2.7,TOE1	
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19		0	0 K09284	GO:0006355,(AT4G36920.2 AP2,FL1,FLO2	
20		0	0 K09284	GO:0006355,(AT4G36920.2 AP2,FL1,FLO2	
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23		0	0 K09284	GO:0006355,(AT4G36920.2 AP2,FL1,FLO2	
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27		0	0 K09284	GO:0006355,(AT4G36920.2 AP2,FL1,FLO2	
28		0	0 K09284	GO:0006355,(AT4G36920.2 AP2,FL1,FLO2	
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		0	0 K09284	GO:0006355,(AT2G28550.1 RAP2.7,TOE1	



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2	0	0 K09284	GO:0006355,(AT2G28550.1	RAP2.7,TOE1		
3	0	0 K09284	GO:0006355,(AT2G28550.1	RAP2.7,TOE1		
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6	0	0 K09284	GO:0006355,(AT2G28550.1	RAP2.7,TOE1		
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8	0	0 K09284	GO:0006355,(AT2G28550.1	RAP2.7,TOE1		
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9		0	0	0	0	0	0
10		0	0	0	0	0	0
11		0	0	0	0	0	0
12		0	0	0	0	0	0
13		0	0	0	0	0	0
14		0	0 K09284	GO:0006355,(AT2G28550.1 RAP2.7,TOE1			
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18		0	0 K09284	GO:0006355,(AT2G28550.1 RAP2.7,TOE1			
19		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3			
20	KOG0374	3.1.3.16		0 GO:0005515,(AT2G27210.1 BSL3			
21							
22	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29			
23	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29			
24	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1			0
25							
26		0	0 K14291	0 AT3G20430.1			0
27		0	0 K14291	0 AT3G20430.1			0
28		0	0 K14291	0 AT3G20430.1			0
29		0	0 K14291	0 AT3G20430.1			0
30		0	0 K14291	0 AT3G20430.1			0
31		0	0 K14291	0 AT3G20430.1			0
32		0	0 K14291	0 AT3G20430.1			0
33		0	0 K14291	0 AT3G20430.1			0
34		0	0 K14291	0 AT3G20430.1			0
35		0	0 K14291	0 AT3G20430.1			0
36		0	0 K14291	0 AT3G20430.1			0
37		0	0 K14291	0 AT3G20430.1			0
38		0	0 K14291	0 AT3G20430.1			0
39		0	0 K14291	0 AT3G20430.1			0
40		0	0 K14291	0 AT3G20430.1			0
41		0	0 K14291	0 AT3G20430.1			0
42		0	0 K14291	0 AT3G20430.1			0
43		0	0 K14291	0 AT3G20430.1			0
44		0	0 K14291	0 AT3G20430.1			0
45		0	0 K14291	0 AT3G20430.1			0
46		0	0 K14291	0 AT3G20430.1			0
47		0	0 K14291	0 AT3G20430.1			0
48		0	0 K14291	0 AT3G20430.1			0
49		0	0 K14291	0 AT3G20430.1			0
50		0	0 K14291	0 AT3G20430.1			0
51		0	0 K14291	0 AT3G20430.1			0
52		0	0 K14291	0 AT3G20430.1			0
53		0	0 K14291	0 AT3G20430.1			0
54		0	0	0			0
55		0	0	0	0 AT1G06590.1		0
56		0	0	0	0 AT1G06590.1		0
57		0	0	0	0 AT1G06590.1		0
58		0	0	0	0 AT1G06590.1		0
59		0	0	0	0 AT1G06590.1		0
60		0	0	0	0 AT1G06590.1		0
		0	0	0	0 AT1G06590.1		0

1					
2	0	0	0	0 AT1G06590.1	0
3	0	0	0	0 AT1G06590.1	0
4	0	0	0	0 AT1G06590.1	0
5	0	0	0	0 AT1G06590.1	0
6	0	0	0	0 AT1G06590.1	0
7	0	0	0	0 AT1G06590.1	0
8	0	0	0	0 AT1G06590.1	0
9	0	0	0	0 AT1G06590.1	0
10	0	0	0	0 AT1G02610.1	0
11	0	0	0	0 AT1G02610.1	0
12	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
13	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
14	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
15	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
16	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
17	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
18	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
19	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
20	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
21	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
22	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
23	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
24	0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1 ATCKA1,CKA1		
25	0 2.3.1.45		0 0 AT2G34410.2		0
26	0 4.4.1.19		0 GO:0019295 AT4G21320.1 HSA32		
27	0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b		
28	0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b		
29					
30					
31	KOG1558	0 K14709	GO:0055085,(AT1G31260.1 ZIP10		
32	KOG1558	0 K14709	GO:0055085,(AT1G31260.1 ZIP10		
33					
34	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
35	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
36	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
37	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
38	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
39	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
40	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
41	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
42	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
43	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
44	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
45	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
46	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
47	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
48	0 2.7.11.1		0 GO:0048544,(AT4G27290.1		0
49	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1		0
50	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1		0
51	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1		0
52	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1		0
53	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3		
54					
55	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		
56	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		
57	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		
58	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		
59	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		
60	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		
	KOG1282	3.4.16.5 K16298	GO:0006508,(AT3G45010.1 scpl48		

1							
2	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
3	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
4	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
5	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
6	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
7	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
8	KOG1282	3.4.16.5	K16298	GO:0006508,(AT3G45010.1	scpl48		
9							
10		0	0	0	0	0	0
11		0	0	0	0	0	0
12	KOG1441		0	0	GO:0055085	AT3G11320.1	0
13	KOG1441		0	0	GO:0055085	AT3G11320.1	0
14	KOG1441		0	0	GO:0055085	AT3G11320.1	0
15	KOG1441		0	0	GO:0055085	AT3G11320.1	0
16	KOG1441		0	0	GO:0055085	AT3G11320.1	0
17	KOG1441		0	0	GO:0055085	AT3G11320.1	0
18	KOG1441		0	0	GO:0055085	AT3G11320.1	0
19	KOG1441		0	0	GO:0055085	AT3G11320.1	0
20	KOG1441		0	0	GO:0055085	AT3G11320.1	0
21	KOG1441		0	0	GO:0055085	AT3G11320.1	0
22	KOG1441		0	0	GO:0055085	AT3G11320.1	0
23	KOG1441		0	0	GO:0055085	AT3G11320.1	0
24	KOG1441		0	0	GO:0055085	AT3G11320.1	0
25	KOG1441		0	0	GO:0055085	AT3G11320.1	0
26	KOG1441		0	0	GO:0055085	AT3G11320.1	0
27		0	0	K09284	GO:0006355,(AT2G28550.2	RAP2.7,TOE1	
28		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
29		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
30		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
31		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
32		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
33		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
34		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
35		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
36		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
37		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
38		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
39		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
40		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
41		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
42		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
43		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
44		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
45		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
46		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
47		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
48		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
49		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
50		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
51		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
52		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
53		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
54		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
55		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
56		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
57		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
58		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
59		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
60		0	0	0	0	AT3G19640.1	MGT4,MRS2-3
		0	0	0	0	AT3G19640.1	MGT4,MRS2-3

1					
2	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
3	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
4	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
5	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
6	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
7	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
8	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
9	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
10	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
11	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
12	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
13	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
14	0	0	0	0	AT3G19640.1 MGT4,MRS2-3
15	0	0	K10523	GO:0005515	AT4G08455.1 0
16	0	0	K10523	GO:0005515	AT4G08455.1 0
17	0	0	K10523	GO:0005515	AT4G08455.1 0
18	0	0	K10523	GO:0005515	AT4G08455.1 0
19	0	0	K10523	GO:0005515	AT4G08455.1 0
20	0	0	K10523	GO:0005515	AT4G08455.1 0
21	0	0	K10523	GO:0005515	AT4G08455.1 0
22	0	0	K10523	GO:0005515	AT4G08455.1 0
23	0	0	K10523	GO:0005515	AT4G08455.1 0
24	0	0	K10523	GO:0005515	AT4G08455.1 0
25	0	0	K10523	GO:0005515	AT4G08455.1 0
26	0	0	K10523	GO:0005515	AT4G08455.1 0
27	0	0	K10523	GO:0005515	AT4G08455.1 0
28	0	0	K10523	GO:0005515	AT4G08455.1 0
29	0	0	0	0	AT5G50990.1 0
30	0	0	0	0	0 0
31	0	0	0	0	0 0
32	KOG1187	2.7.11.1		0	GO:0004674,(AT4G27290.1 0
33		0 2.7.11.1		0	GO:0048544,(AT4G27290.1 0
34		0 2.7.11.1		0	GO:0048544,(AT4G27290.1 0
35		0 2.7.11.1		0	GO:0048544,(AT4G27290.1 0
36	KOG1187	2.7.11.1		0	GO:0048544,(AT4G27290.1 0
37	KOG1187	2.7.11.1		0	GO:0048544,(AT4G27290.1 0
38	KOG1187	2.7.11.1		0	GO:0048544,(AT4G27290.1 0
39	KOG1187	2.7.11.1		0	GO:0048544,(AT4G27290.1 0
40	KOG1187	2.7.11.1		0	GO:0004674,(AT4G27290.1 0
41	KOG1187	2.7.11.1		0	GO:0048544,(AT4G27290.1 0
42					
43	0	0	K14291		AT3G20430.1 0
44	0	0	K14291		AT3G20430.1 0
45	0	0	0	0	AT2G36430.1 0
46	0	0	0	0	AT2G36430.1 0
47	0	0	0	0	AT2G36430.1 0
48	0	0	0	0	AT2G36430.1 0
49	0	0	0	0	AT2G36430.1 0
50	0	0	0	0	AT2G36430.1 0
51	0	0	0	0	AT2G36430.1 0
52	0	0	0	0	AT2G36430.1 0
53	0	0	0	0	AT2G36430.1 0
54	0	0	0	0	AT2G36430.1 0
55	0	0	0	0	AT2G36430.1 0
56	0	0	0	0	AT2G36430.1 0
57	0	0	0	0	AT2G36430.1 0
58	0	0	0	0	AT2G36430.1 0
59	0	0	0	0	AT2G36430.1 0
60	0	0	0	0	AT2G36430.1 0
	0	0	0	0	0 0



1							
2		0	0	0	0	0	0
3		0 2.7.11.1	K03097	GO:0006468,(AT5G67380.1	ATCKA1,CKA1		
4		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
5		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
6		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
7		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
8		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
9		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
10		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
11		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
12		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
13		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
14		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
15		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
16		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
17		0	0 K15032	GO:0006355,(AT2G03050.1	EMB93,SOLDAT1(		
18	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
19	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
20	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
21	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
22	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
23	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
24	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
25	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
26	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
27	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
28	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
29	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
30	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
31	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
32	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
33	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
34	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
35	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
36	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
37	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
38	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
39	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
40	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
41	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
42	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
43	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
44	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
45	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
46	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
47	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
48	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
49	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
50	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
51	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
52	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
53	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
54	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
55	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
56	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
57	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
58	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
59	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
60	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2	ATDGK2,DGK2		
	KOG1399	1.14.13.168	K11816	0 AT4G13260.1	YUC2		

1					
2	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
3	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
4	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
5	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
6	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
7	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
8	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
9	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
10	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
11	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
12	KOG1399	1.14.13.168	K11816	0	AT4G13260.1 YUC2
13					
14		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
15		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
16		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
17		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
18		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
19		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
20		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
21		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
22		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
23		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
24		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
25		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
26		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
27		0 2.4.1.15,3.1.3 K16055		GO:0005992,(AT1G60140.1 ATTPS10,TPS10	
28	KOG1809	0	0	0	AT1G48090.1 0
29	KOG1809	0	0	0	AT1G48090.1 0
30	KOG1809	0	0	0	AT1G48090.1 0
31	KOG1809	0	0	0	AT1G48090.1 0
32	KOG1809	0	0	0	AT1G48090.1 0
33	KOG1809	0	0	0	AT1G48090.1 0
34	KOG1809	0	0	0	AT1G48090.1 0
35	KOG1809	0	0	0	AT1G48090.1 0
36	KOG1809	0	0	0	AT1G48090.1 0
37	KOG1809	0	0	0	AT1G48090.1 0
38	KOG1809	0	0	0	AT1G48090.1 0
39	KOG1809	0	0	0	AT1G48090.1 0
40	KOG1809	0	0	0	AT1G48090.1 0
41	KOG1809	0	0	0	AT1G48090.1 0
42					
43		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
44		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
45		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
46		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
47		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
48		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
49		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
50		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
51		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
52		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
53		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
54		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
55		0 2.7.11.1 K03097		GO:0006468,(AT3G50000.1 ATCKA2,CKA2	
56	KOG1558	0 K14709		GO:0055085,(AT1G31260.1 ZIP10	
57	KOG1558	0 K14709		GO:0055085,(AT1G31260.1 ZIP10	
58	KOG1558	0 K14709		GO:0055085,(AT1G31260.1 ZIP10	
59	KOG1558	0 K14709		GO:0055085,(AT1G31260.1 ZIP10	
60	KOG1558	0 K14709		GO:0055085,(AT1G31260.1 ZIP10	
	KOG1558	0 K14709		GO:0055085,(AT1G31260.1 ZIP10	

1					
2	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
3	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
4	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
5	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
6	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
7	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
8	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
9	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
10	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
11	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
12	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
13	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
14	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
15	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
16	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
17	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
18	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
19	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
20	KOG1558		0 K14709	GO:0055085,(AT1G31260.1 ZIP10	
21	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
22	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
23	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
24	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
25	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
26	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
27	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
28	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
29	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
30	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
31	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
32	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
33	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
34	KOG0374	3.1.3.16	0	GO:0005515,(AT2G27210.1 BSL3	
35	KOG1471		0	0 AT5G47730.1	0
36	KOG1471		0	0 AT5G47730.1	0
37	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
38	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
39	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
40	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
41	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
42	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
43	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
44	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
45	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
46	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
47	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
48	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
49	KOG1919	5.4.99.24	0	GO:0009982,(AT4G21770.1	0
50					
51	0	0	0	0 AT5G03170.1 ATFLA11,FLA11	
52	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
53	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
54	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
55	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
56	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
57	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
58	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
59	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
60	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
	0	0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	

1					
2		0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
3		0	0 K14486	GO:0003677,(AT2G33860.1 ARF3,ETT	
4		0	0	0 GO:0016020,(AT3G52060.2	0
5		0	0	0 GO:0016020,(AT3G52060.2	0
6		0	0	0 GO:0016020,(AT3G52060.2	0
7		0	0	0 GO:0016020,(AT3G52060.2	0
8		0	0	0 GO:0016020,(AT3G52060.2	0
9		0	0	0 GO:0016020,(AT3G52060.2	0
10		0	0	0 GO:0016020,(AT3G52060.2	0
11		0	0	0 GO:0016020,(AT3G52060.2	0
12		0	0	0 GO:0016020,(AT3G52060.2	0
13		0	0	0 GO:0016020,(AT3G52060.2	0
14		0	0	0 GO:0016020,(AT3G52060.2	0
15		0	0	0 GO:0016020,(AT3G52060.2	0
16		0	0	0 GO:0016020,(AT3G52060.2	0
17		0	0	0 GO:0016020,(AT3G52060.2	0
18	KOG0522		0	0 AT1G04780.1	0
19	KOG0522		0	0 AT1G04780.1	0
20	KOG0522		0	0 AT1G04780.1	0
21	KOG0522		0	0 AT1G04780.1	0
22	KOG0522		0	0 AT1G04780.1	0
23	KOG0522		0	0 AT1G04780.1	0
24	KOG0522		0	0 AT1G04780.1	0
25	KOG0522		0	0 AT1G04780.1	0
26	KOG0522		0	0 AT1G04780.1	0
27	KOG0522		0	0 AT1G04780.1	0
28	KOG0522		0	0 AT1G04780.1	0
29	KOG0522		0	0 AT1G04780.1	0
30	KOG0522		0	0 AT1G04780.1	0
31	KOG0522		0	0 AT1G04780.1	0
32	KOG0522		0	0 AT1G04780.1	0
33	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
34	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
35	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
36	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
37	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
38	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
39	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
40	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
41	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
42	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
43	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
44	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
45	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
46	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
47	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
48	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
49	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
50	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
51	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
52	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
53	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
54	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
55	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
56	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
57	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
58	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
59	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
60	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	
	KOG1187	2.7.11.1		0 GO:0006468,(AT4G21410.1 CRK29	

1						
2	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
3	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
4	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
5	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
6	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
7	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
8	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
9	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
10	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
11	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
12	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
13	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
14	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
15	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
16	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
17	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
18	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
19	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
20	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
21	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
22	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
23	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
24	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
25	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
26	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
27	KOG4409	2.3.1.51	0	0	AT4G24160.1	0
28		0	0	0	AT5G17690.1 LHP1,TFL2	
29		0	0	0	AT5G17690.1 LHP1,TFL2	
30		0	0	0	AT5G17690.1 LHP1,TFL2	
31		0	0	0	AT5G17690.1 LHP1,TFL2	
32		0	0	0	AT5G17690.1 LHP1,TFL2	
33		0	0	0	AT5G17690.1 LHP1,TFL2	
34		0	0	0	AT5G17690.1 LHP1,TFL2	
35		0	0	0	AT5G17690.1 LHP1,TFL2	
36		0	0	0	AT5G17690.1 LHP1,TFL2	
37		0	0	0	AT5G17690.1 LHP1,TFL2	
38		0	0	0	AT5G17690.1 LHP1,TFL2	
39		0	0	0	AT5G17690.1 LHP1,TFL2	
40		0	0	0	AT5G17690.1 LHP1,TFL2	
41		0	0	0	AT5G17690.1 LHP1,TFL2	
42		0	0	0	AT5G17690.1 LHP1,TFL2	
43		0	0 K10523	GO:0005515	AT4G08455.1	0
44		0	0	0	AT3G50140.1	0
45		0	0	0	AT3G50140.1	0
46		0	0	0	AT3G50140.1	0
47		0	0	0	AT3G50140.1	0
48		0	0	0	AT3G50140.1	0
49		0	0	0	AT3G50140.1	0
50		0	0	0	AT3G50140.1	0
51		0	0	0	AT3G50140.1	0
52		0	0	0	AT3G50140.1	0
53		0	0	0	AT3G50140.1	0
54		0	0	0	AT3G50140.1	0
55		0	0	0	AT3G50140.1	0
56		0	0	0	AT3G50140.1	0
57		0	0	0	AT3G50140.1	0
58		0	0	0	AT3G50140.1	0
59		0	0	0	AT3G50140.1	0
60	KOG1187	2.7.11.1		0	GO:0006468,(AT3G14840.2	0
		0	0 K09338	GO:0003677,(AT5G60690.1	IFL1,IFL1,REV	

1					
2		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
3		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
4		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
5		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
6		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
7		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
8		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
9		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
10		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
11		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
12		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
13		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
14		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
15		0	0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
16	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
17	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
18	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
19	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
20	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
21	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
22	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
23	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
24	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
25	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
26	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
27	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
28	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
29	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
30	KOG1543	3.4.22.33	0	GO:0008234,(AT5G45890.1 SAG12	
31	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
32	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
33	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
34	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
35	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
36	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
37	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
38	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
39	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
40	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
41	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
42	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
43	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
44	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
45	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
46	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
47	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
48	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
49	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
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52	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
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54	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
55	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
56	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
57	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
58	KOG1187	2.7.11.1	0	GO:0048544,(AT4G27290.1	0
59	KOG1187	2.7.11.1	0	GO:0004674,(AT4G27290.1	0
60	KOG1187	2.7.11.1	0	GO:0004674,(AT4G27290.1	0
		0 3.1.1.3	0	GO:0016788 AT5G33370.1	0



1						
2		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
3		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
4		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
5		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
6		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
7		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
8		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
9		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
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11		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
12		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
13		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
14		0 3.1.1.3		0 GO:0016788	AT5G33370.1	0
15	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
16	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
17	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
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21	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
22	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
23	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
24	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
25	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
26	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
27	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
28	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
29	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
30	KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
31		0	0	0	AT2G48070.1 RPH1	
32	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
33	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
34	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
35	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
36	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
37	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
38	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
39	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
40	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
41	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
42	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
43	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
44	KOG3467		0 K11254	0	AT2G28740.1 HIS4	
45		0	0	0	AT3G53320.1	0
46		0	0	0	AT3G53320.1	0
47		0	0	0	AT3G53320.1	0
48		0	0	0	AT3G53320.1	0
49		0	0	0	AT3G53320.1	0
50		0	0	0	AT3G53320.1	0
51		0	0	0	AT3G53320.1	0
52		0	0	0	AT3G53320.1	0
53		0	0	0	AT3G53320.1	0
54		0	0	0	AT3G53320.1	0
55		0	0	0	AT3G53320.1	0
56		0	0	0	AT3G53320.1	0
57		0	0	0	AT3G53320.1	0
58		0	0	0	AT1G02610.1	0
59		0	0	0	AT1G02610.1	0
60		0	0	0	AT1G02610.1	0

1					
2		0	0	0	0 AT1G02610.1
3		0	0	0	0 AT1G02610.1
4		0	0	0	0 AT1G02610.1
5		0	0	0	0 AT1G02610.1
6		0	0	0	0 AT1G02610.1
7		0	0	0	0 AT1G02610.1
8		0	0	0	0 AT1G02610.1
9		0	0	0	0 AT1G02610.1
10		0	0	0	0 AT1G02610.1
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13		0	0	0	0 AT1G02610.1
14		0	0	0	0 AT1G02610.1
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19		0	0	0	0 AT1G02610.1
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21		0	0	0	0 AT1G02610.1
22		0	0	0	0 AT1G02610.1
23		0	0	0	0 AT1G02610.1
24	KOG2231		0	0	0 AT3G62240.1
25	KOG2231		0	0	0 AT3G62240.1
26	KOG2231		0	0	0 AT3G62240.1
27	KOG2231		0	0	0 AT3G62240.1
28	KOG2231		0	0	0 AT3G62240.1
29	KOG2231		0	0	0 AT3G62240.1
30	KOG2231		0	0	0 AT3G62240.1
31	KOG2231		0	0	0 AT3G62240.1
32	KOG2231		0	0	0 AT3G62240.1
33	KOG2231		0	0	0 AT3G62240.1
34	KOG2231		0	0	0 AT3G62240.1
35	KOG2231		0	0	0 AT3G62240.1
36	KOG2231		0	0	0 AT3G62240.1
37	KOG2231		0	0	0 AT3G62240.1
38	KOG2231		0	0	0 AT3G62240.1
39	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
40	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
41	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
42	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
43	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
44	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
45	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
46	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
47	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
48	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
49	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
50	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
51	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
52	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
53	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
54	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
55	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
56	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
57	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
58	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
59	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
60	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B
	KOG1187	2.7.11.1,2.7.11		0	GO:0006468,(AT2G28930.1 APK1B,PK1B

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2	KOG1187	2.7.11.1,2.7.11	0 GO:0006468,(AT2G28930.1 APK1B,PK1B	
3	KOG1187	2.7.11.1,2.7.11	0 GO:0006468,(AT2G28930.1 APK1B,PK1B	
4	KOG1187	2.7.11.1,2.7.11	0 GO:0006468,(AT2G28930.1 APK1B,PK1B	
5				
6	KOG1187	2.7.11.1,2.7.11	0 GO:0006468,(AT2G28930.1 APK1B,PK1B	
7		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
8		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
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10		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
11		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
12		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
13				
14		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
15		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
16		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
17				
18		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
19		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
20		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
21				
22		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
23		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
24		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
25				
26		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
27		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
28		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
29				
30		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
31		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
32		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
33		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
34		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
35		0 1.10.3.3	0 GO:0055114,(AT1G55570.1 sks12	
36		0 2.3.1.45	0 AT2G34410.2	0
37		0 2.3.1.45	0 AT2G34410.2	0
38				
39		0 2.3.1.45	0 AT2G34410.2	0
40		0 2.3.1.45	0 AT2G34410.2	0
41		0 2.3.1.45	0 AT2G34410.2	0
42				
43		0 2.3.1.45	0 AT2G34410.2	0
44		0 2.3.1.45	0 AT2G34410.2	0
45		0 2.3.1.45	0 AT2G34410.2	0
46				
47		0 2.3.1.45	0 AT2G34410.2	0
48		0 2.3.1.45	0 AT2G34410.2	0
49		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
50				
51		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
52		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
53		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
54				
55		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
56		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
57		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
58				
59		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
60		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	
		0 4.4.1.19	0 GO:0019295 AT4G21320.1 HSA32	

1					
2		0 4.4.1.19		0 GO:0019295 AT4G21320.1 HSA32	
3	KOG1235	3.6.3.46		0 AT5G64940.1 ATATH13,ATH13,,	
4		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
5		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
6		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
7		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
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9		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
10		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
11		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
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14		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
15		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
16		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
17		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
18		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
19		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
20		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
21		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
22		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
23		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
24		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
25		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
26		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
27		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
28		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
29		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
30		0	0	0 GO:0043047,(AT5G06310.1 AtPOT1b	
31		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
32		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
33		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
34		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
35		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
36		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
37		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
38		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
39		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
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41		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
42		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
43		0 5.3.99.6	K10525	GO:0016853,(AT3G25780.1 AOC3	
44	KOG1809		0	0 AT1G48090.1	0
45	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
46	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
47	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
48	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
49	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
50	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
51	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
52	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
53	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
54	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
55	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
56	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
57	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
58	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
59	KOG1187	2.7.11.1		0 GO:0005515,(AT5G56040.2	0
60		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096	
		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096	

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2		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
3		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
4		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
5		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
6		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
7		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
8		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
9		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
10		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
11		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
12		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
13		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
14		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
15		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
16		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
17		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
18		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
19		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
20		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
21		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
22		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
23		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
24		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
25		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
26		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
27		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096
28		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1 0
29	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
30	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
31	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
32	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
33	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
34	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
35	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
36	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
37	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
38	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
39	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
40	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
41	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
42	KOG2182	3.4.14.2		0 GO:0008236,(AT4G36195.1 0
43	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
44	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
45	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
46	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
47	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
48	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
49	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
50	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
51	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
52	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
53	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
54	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
55	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
56	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
57	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
58	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
59	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
60	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0
	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1 0

1					
2	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
3	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
4	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
5	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
6	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
7	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
8	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
9	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
10	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
11	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
12	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
13	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
14	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
15	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
16	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
17	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
18	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
19	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
20	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
21	KOG2182	3.4.21.26		0 GO:0008236,(AT4G36195.1	0
22	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
23	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
24	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
25	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
26	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
27	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
28	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
29	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
30	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
31	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
32	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
33	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
34	KOG4742	3.2.1.14	K01183	GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI	
35		0	0	0 AT4G13750.1 NOV	
36		0	0	0 AT4G13750.1 NOV	
37		0	0	0 AT4G13750.1 NOV	
38		0	0	0 AT4G13750.1 NOV	
39		0	0	0 AT4G13750.1 NOV	
40		0	0	0 AT4G13750.1 NOV	
41		0	0	0 AT4G13750.1 NOV	
42		0	0	0 AT4G13750.1 NOV	
43		0	0	0 AT4G13750.1 NOV	
44		0	0	0 AT4G13750.1 NOV	
45		0	0	0 AT4G13750.1 NOV	
46		0	0	0 AT4G13750.1 NOV	
47		0	0	0 AT4G13750.1 NOV	
48		0	0	0 AT4G13750.1 NOV	
49		0	0	0 AT4G13750.1 NOV	
50		0	0	0 AT4G13750.1 NOV	
51		0	0	0 AT4G13750.1 NOV	
52		0	0	0 AT4G13750.1 NOV	
53		0	0	0 AT4G13750.1 NOV	
54		0	0	0 AT4G13750.1 NOV	
55		0	0	0 AT4G13750.1 NOV	
56		0	0	0 AT4G13750.1 NOV	
57		0	0	0 AT4G13750.1 NOV	
58		0	0	0 AT4G13750.1 NOV	
59		0	0	0 AT4G13750.1 NOV	
60		0	0	0 AT4G13750.1 NOV	
		0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	



1				
2	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
3	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
4	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
5	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
6	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
7	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
8	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
9	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
10	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
11	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
12	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
13	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
14	0	0	0 GO:0016020 AT3G01100.1 ATHYP1,HYP1	
15	0	0	0 GO:0005515 AT5G22720.1	0
16	0	0	0 GO:0005515 AT5G22720.1	0
17				
18	0	0 K19041	GO:0008270,(AT1G53190.1	0
19	0	0 K19041	GO:0008270,(AT1G53190.1	0
20	0	0 K19041	GO:0008270,(AT1G53190.1	0
21	0	0 K19041	GO:0008270,(AT1G53190.1	0
22	0	0 K19041	GO:0008270,(AT1G53190.1	0
23	0	0 K19041	GO:0008270,(AT1G53190.1	0
24	0	0 K19041	GO:0008270,(AT1G53190.1	0
25	0	0 K19041	GO:0008270,(AT1G53190.1	0
26	0	0 K19041	GO:0008270,(AT1G53190.1	0
27	0	0 K19041	GO:0008270,(AT1G53190.1	0
28	0	0 K19041	GO:0008270,(AT1G53190.1	0
29	0	0 K19041	GO:0008270,(AT1G53190.1	0
30	0	0 K19041	GO:0008270,(AT1G53190.1	0
31	0	0 K19041	GO:0008270,(AT1G53190.1	0
32	0	0 K19041	GO:0008270,(AT1G53190.1	0
33	0	0 K19041	GO:0008270,(AT1G53190.1	0
34	0	0 K19041	GO:0008270,(AT1G53190.1	0
35	0	0 K19041	GO:0008270,(AT1G53190.1	0
36	0	0 K19041	GO:0008270,(AT1G53190.1	0
37	0	0 K19041	GO:0008270,(AT1G53190.1	0
38	0	0 K19041	GO:0008270,(AT1G53190.1	0
39	0	0 K19041	GO:0008270,(AT1G53190.1	0
40	0	0 K19041	GO:0008270,(AT1G53190.1	0
41	0	0 K19041	GO:0008270,(AT1G53190.1	0
42	0	0 K19041	GO:0008270,(AT1G53190.1	0
43	0	0 K19041	GO:0008270,(AT1G53190.1	0
44	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
45	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
46	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
47	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
48	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
49	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
50	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
51	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
52	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
53	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
54	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
55	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
56	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
57	KOG1187	2.7.11.1	0 GO:0004674,(AT4G21380.1 ARK3,RK3	
58	KOG0645		0 GO:0005515 AT1G52360.1	0
59	KOG0645		0 GO:0005515 AT1G52360.1	0
60	KOG0645		0 GO:0005515 AT1G52360.1	0

1					
2	KOG0645	0	0 GO:0005515	AT1G52360.1	0
3	KOG0645	0	0 GO:0005515	AT1G52360.1	0
4	KOG0645	0	0 GO:0005515	AT1G52360.1	0
5	KOG0645	0	0 GO:0005515	AT1G52360.1	0
6	KOG0645	0	0 GO:0005515	AT1G52360.1	0
7	KOG0645	0	0 GO:0005515	AT1G52360.1	0
8	KOG0645	0	0 GO:0005515	AT1G52360.1	0
9	KOG0645	0	0 GO:0005515	AT1G52360.1	0
10	KOG0645	0	0 GO:0005515	AT1G52360.1	0
11	KOG0645	0	0 GO:0005515	AT1G52360.1	0
12	KOG0645	0	0 GO:0005515	AT1G52360.1	0
13	KOG0645	0	0 GO:0005515	AT1G52360.1	0
14	KOG0645	0	0 GO:0005515	AT1G52360.1	0
15	KOG0645	0	0 GO:0005515	AT1G52360.1	0
16	KOG0645	0	0 GO:0005515	AT1G52360.1	0
17	KOG0645	0	0 GO:0005515	AT1G52360.1	0
18	KOG0645	0	0 GO:0005515	AT1G52360.1	0
19	KOG0645	0	0 GO:0005515	AT1G52360.1	0
20	KOG0645	0	0 GO:0005515	AT1G52360.1	0
21	KOG0645	0	0 GO:0005515	AT1G52360.1	0
22	KOG0645	0	0 GO:0005515	AT1G52360.1	0
23	KOG0645	0	0 GO:0005515	AT1G52360.1	0
24	KOG0645	0	0 GO:0005515	AT1G52360.1	0
25	KOG0645	0	0 GO:0005515	AT1G52360.1	0
26	KOG0645	0	0 GO:0005515	AT1G52360.1	0
27	KOG0645	0	0 GO:0005515	AT1G52360.1	0
28	KOG0645	0	0 GO:0005515	AT1G52360.1	0
29		0	0 GO:0006886,(	AT2G38020.1 EMB258,MAN,VC	
30		0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
31	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
32	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
33	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
34	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
35	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
36	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
37	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
38	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
39	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
40	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
41	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
42	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
43	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
44	KOG1902	0	0 K14404	0 AT1G30460.1 ATCPSF30,CPSF30	
45	KOG1441	0	0 GO:0055085	AT3G11320.1	0
46		0	0 K14486	GO:0003677,(	AT2G33860.1 ARF3,ETT
47		0	0 K14486	GO:0003677,(	AT2G33860.1 ARF3,ETT
48	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
49	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
50	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
51	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
52	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
53	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
54	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
55	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
56	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
57	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
58	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
59	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
60	KOG1187	2.7.11.1	0 GO:0005515,(	AT1G68400.1	0
		0 2.1.1.193	0 GO:0008168,(	AT1G50000.1	0

1					
2		0	0	0 GO:0006355,(AT4G09620.1	0
3		0	0	0 GO:0006355,(AT4G09620.1	0
4		0	0	0 GO:0006355,(AT4G09620.1	0
5		0	0	0 GO:0006355,(AT4G09620.1	0
6		0	0	0 GO:0006355,(AT4G09620.1	0
7		0	0	0 GO:0006355,(AT4G09620.1	0
8		0	0	0 GO:0006355,(AT4G09620.1	0
9		0	0	0 GO:0006355,(AT4G09620.1	0
10		0	0	0 GO:0006355,(AT4G09620.1	0
11		0	0	0 GO:0006355,(AT4G09620.1	0
12		0	0	0 GO:0006355,(AT4G09620.1	0
13		0	0	0 GO:0006355,(AT4G09620.1	0
14		0	0	0 GO:0006355,(AT4G09620.1	0
15		0	0	0 GO:0006355,(AT4G09620.1	0
16		0	0	0 GO:0006355,(AT4G09620.1	0
17		0	0	0 GO:0006355,(AT4G09620.1	0
18	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
19	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
20	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
21	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
22	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
23	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
24	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
25	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
26	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
27	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
28	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
29	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
30	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
31	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
32	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
33	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
34	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
35	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
36	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
37	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
38	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
39	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
40	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
41	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
42	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
43	KOG4793	2.7.7.7	0	0 AT5G26940.3	0
44		0	0	0 AT2G38570.1	0
45		0	0	0 AT2G38570.1	0
46		0	0	0 AT2G38570.1	0
47		0	0	0 AT2G38570.1	0
48		0	0	0 AT2G38570.1	0
49		0	0	0 AT2G38570.1	0
50		0	0	0 AT2G38570.1	0
51		0	0	0 AT2G38570.1	0
52		0	0	0 AT2G38570.1	0
53		0	0	0 AT2G38570.1	0
54		0	0	0 AT2G38570.1	0
55		0	0	0 AT2G38570.1	0
56		0	0	0 AT2G38570.1	0
57		0	0	0 AT2G38570.1	0
58		0	0	0 AT2G38570.1	0
59	KOG1586		0	0 GO:0006886 AT3G56190.1 ALPHA-SNAP2,AS	
60	KOG1586		0	0 GO:0006886 AT3G56190.1 ALPHA-SNAP2,AS	
	KOG1586		0	0 GO:0006886 AT3G56190.1 ALPHA-SNAP2,AS	

1					
2	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
3	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
4	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
5	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
6	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
7	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
8	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
9	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
10	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
11	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
12	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
13	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
14	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
15	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
16	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
17	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
18	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
19	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
20	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
21	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
22	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
23	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
24	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
25	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
26	KOG1586		0	0 GO:0006886	AT3G56190.1 ALPHA-SNAP2,AS
27	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
28	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
29	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
30	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
31	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
32	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
33	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
34	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
35	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
36	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
37	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
38	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
39	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
40	KOG0192	2.7.11.1		0 GO:0005515,(AT3G24715.1	0
41		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
42		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
43		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
44		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
45		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
46		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
47		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
48		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
49		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
50		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
51		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
52		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
53		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
54		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
55		0 1.3.3.3	K00228	GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L	
56		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
57		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
58		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
59		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
60		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	

1					
2		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
3		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
4		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
5		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
6		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
7		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
8		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
9		0		0 AT5G17690.1 LHP1,TFL2	
10		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
11		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
12		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
13		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
14		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
15		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
16		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
17		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
18		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
19		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
20		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
21		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
22		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
23		0	0	0 GO:0016788 AT1G53920.1 GLIP5	
24		0	0	0 AT3G02645.1	0
25					
26	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
27	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
28	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
29	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
30	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
31	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
32	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
33	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
34	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
35	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
36	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
37	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
38	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
39	KOG1187	2.7.11.1		0 GO:0006468,(AT3G51990.1	0
40		0	0 K07399	0 AT1G49380.1	0
41		0	0 K07399	0 AT1G49380.1	0
42					
43	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
44	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
45	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
46	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
47	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
48	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
49	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
50	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
51	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
52	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
53	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
54	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
55	KOG1187	2.7.11.1		0 GO:0006468,(AT3G14840.2	0
56	KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
57	KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
58	KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
59	KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
60	KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
	KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	

1				
2	KOG1543	3.4.22.33	0 GO:0008234,(AT5G45890.1 SAG12	
3	KOG1543	3.4.22.33	0 GO:0008234,(AT5G45890.1 SAG12	
4	KOG1543	3.4.22.33	0 GO:0008234,(AT5G45890.1 SAG12	
5	KOG1543	3.4.22.33	0 GO:0008234,(AT5G45890.1 SAG12	
6	KOG1543	3.4.22.33	0 GO:0008234,(AT5G45890.1 SAG12	
7	KOG1543	3.4.22.33	0 GO:0008234,(AT5G45890.1 SAG12	
8	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
9	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
10	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
11	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
12	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
13	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
14	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
15	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
16	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
17	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
18	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
19	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
20	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
21	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
22	KOG1187	2.7.11.1	0 GO:0004674,(AT4G27290.1	0
23		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
24		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
25		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
26		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
27		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
28		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
29		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
30		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
31		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
32		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
33		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
34		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
35		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
36		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
37		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
38		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
39		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
40		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
41		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
42		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
43		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
44		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
45		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
46		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
47		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
48		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
49		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
50		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
51		0 2.7.11.1	0 GO:0048544,(AT4G27290.1	0
52	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
53	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
54	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
55	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
56	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
57	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
58	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
59	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
60	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0
	KOG1187	2.7.11.1	0 GO:0048544,(AT4G27290.1	0





1					
2	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
3	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
4	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
5	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
6	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
7	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
8	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
9	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
10	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
11	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
12	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
13	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
14	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
15	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
16	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
17	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
18	KOG1187	2.7.11.1		0 GO:0048544,(AT4G27290.1	0
19		0	0 K10268	GO:0005515 AT4G02760.2	0
20		0	0 K10268	GO:0005515 AT4G02760.2	0
21		0	0 K10268	GO:0005515 AT4G02760.2	0
22		0	0 K10268	GO:0005515 AT4G02760.2	0
23		0	0 K10268	GO:0005515 AT4G02760.2	0
24		0	0 K10268	GO:0005515 AT4G02760.2	0
25		0	0 K10268	GO:0005515 AT4G02760.2	0
26		0	0 K10268	GO:0005515 AT4G02760.2	0
27		0	0 K10268	GO:0005515 AT4G02760.2	0
28		0	0 K10268	GO:0005515 AT4G02760.2	0
29		0	0 K10268	GO:0005515 AT4G02760.2	0
30		0	0 K10268	GO:0005515 AT4G02760.2	0
31		0	0 K10268	GO:0005515 AT4G02760.2	0
32		0	0 K10268	GO:0005515 AT4G02760.2	0
33		0	0	0 AT5G03150.1 JKD	
34		0	0	0 AT5G03150.1 JKD	
35		0	0	0 AT5G03150.1 JKD	
36		0	0	0 AT5G03150.1 JKD	
37		0	0	0 AT5G03150.1 JKD	
38		0	0	0 AT5G03150.1 JKD	
39		0	0	0 AT5G03150.1 JKD	
40		0	0	0 AT5G03150.1 JKD	
41		0	0	0 AT5G03150.1 JKD	
42		0	0	0 AT5G03150.1 JKD	
43		0	0	0 AT5G03150.1 JKD	
44		0	0	0 AT5G03150.1 JKD	
45		0	0	0 AT5G03150.1 JKD	
46		0	0	0 AT5G03150.1 JKD	
47		0	0	0 AT5G03150.1 JKD	
48		0 1.10.3.3		0 GO:0055114,(AT1G55570.1 sks12	
49		0 1.10.3.3		0 GO:0055114,(AT1G55570.1 sks12	
50		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
51		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
52		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
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55		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
56		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
57		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
58		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
59		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
60		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	
		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49	

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2		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49
3		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49
4		0 5.2.1.8	K10598	GO:0006457,(AT5G67530.1 ATPUB49,PUB49
5				
6		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
7		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
8		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
9				
10		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
11		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
12		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
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14		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
15		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
16		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
17		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
18		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
19		0 1.3.3.8		0 GO:0055114,(AT2G34790.1 EDA28,MEE23
20	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
21				
22	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
23	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
24	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
25				
26	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
27	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
28	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
29				
30	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
31	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
32	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
33				
34	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
35	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
36	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
37				
38	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
39	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
40	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
41				
42	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
43	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
44	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
45	KOG1187	2.7.11.1		0 GO:0006468,(AT5G10530.1 0
46				
47	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
48	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
49	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
50				
51	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
52	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
53	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
54				
55	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
56	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
57	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
58				
59	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
60	KOG1235	3.6.3.46	0	0 AT5G64940.1 ATATH13,ATH13,,
	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2 ATDGK2,DGK2

1				
2	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2 ATDGK2,DGK2
3	KOG1169	2.7.1.107		0 GO:0035556,(AT5G63770.2 ATDGK2,DGK2
4				
5		0	0	0 GO:0004519 AT2G15820.1 OTP51
6	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
7	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
8	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
9				
10	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
11	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
12	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
13				
14	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
15	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
16	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
17				
18	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
19	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
20	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
21				
22	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
23	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
24	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
25				
26	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
27	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
28	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
29				
30	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
31	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
32	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
33				
34	KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE
35	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
36	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
37	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
38				
39	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
40	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
41	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
42				
43	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
44	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
45	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
46				
47	KOG0748		0 K07297	GO:0016021 AT5G20270.1 HHP1
48		0	0	0 GO:0006355,(AT3G47500.1 CDF3
49		0	0	0 GO:0006355,(AT3G47500.1 CDF3
50				
51		0	0	0 GO:0006355,(AT3G47500.1 CDF3
52		0	0	0 GO:0006355,(AT3G47500.1 CDF3
53		0	0	0 GO:0006355,(AT3G47500.1 CDF3
54				
55		0	0	0 GO:0006355,(AT3G47500.1 CDF3
56		0	0	0 GO:0006355,(AT3G47500.1 CDF3
57		0	0	0 GO:0006355,(AT3G47500.1 CDF3
58				
59		0	0	0 GO:0006355,(AT3G47500.1 CDF3
60		0	0	0 GO:0006355,(AT3G47500.1 CDF3
		0	0	0 GO:0006355,(AT3G47500.1 CDF3

1					
2		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
3		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
4		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
5		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
6		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
7		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
8		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
9		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
10		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
11		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
12		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
13		0	0	0 GO:0006355,(AT3G47500.1 CDF3	
14	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
15	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
16	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
17	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
18	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
19	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
20	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
21	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
22	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
23	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
24	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
25	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
26	KOG0472	2.7.11.1		0 GO:0005515 AT4G20140.1 GSO1	
27		0	0	0 AT5G14410.1	0
28		0	0	0 AT5G14410.1	0
29		0	0	0 AT5G14410.1	0
30		0	0	0 AT5G14410.1	0
31		0	0	0 AT5G14410.1	0
32		0	0	0 AT5G14410.1	0
33		0	0	0 AT5G14410.1	0
34		0	0	0 AT5G14410.1	0
35		0	0	0 AT5G14410.1	0
36		0	0	0 AT5G14410.1	0
37		0	0	0 AT5G14410.1	0
38		0	0	0 AT5G14410.1	0
39		0	0	0 AT5G14410.1	0
40		0	0	0 AT5G14410.1	0
41		0	0	0 AT5G14410.1	0
42		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096	
43		0	0	0 GO:0006355,(AT5G46590.1 anac096,NAC096	
44		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
45		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
46		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
47		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
48		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
49		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
50		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
51		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
52		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
53		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
54		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
55		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
56		0 2.7.11.1	K03097	GO:0006468,(AT2G23070.1	0
57		0	0	0 GO:0007165,(AT5G17680.1	0
58		0	0	0 GO:0007165,(AT5G17680.1	0
59		0	0	0 GO:0007165,(AT5G17680.1	0
60		0	0	0 GO:0007165,(AT5G17680.1	0
		0	0	0 GO:0007165,(AT5G17680.1	0

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2		0	0	0 GO:0007165,(AT5G17680.1	0
3		0	0	0 GO:0007165,(AT5G17680.1	0
4		0	0	0 GO:0007165,(AT5G17680.1	0
5		0	0	0 GO:0007165,(AT5G17680.1	0
6		0	0	0 GO:0007165,(AT5G17680.1	0
7		0	0	0 GO:0007165,(AT5G17680.1	0
8		0	0	0 GO:0007165,(AT5G17680.1	0
9		0	0	0 GO:0007165,(AT5G17680.1	0
10		0	0	0 GO:0007165,(AT5G17680.1	0
11		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
12		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
13		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
14		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
15		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
16		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
17		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
18		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
19		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
20		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
21		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
22		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
23		0 2.4.1.142	K03842	GO:0016757 AT1G16570.1	0
24		0	0	0 GO:0005089 AT1G79860.1 ATROPGEF12,ME	
25					
26	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
27	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
28	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
29	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
30	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
31	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
32	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
33	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
34	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
35	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
36	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
37	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
38	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
39	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
40	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
41	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
42	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
43	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
44	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
45	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
46	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
47	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
48	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
49	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
50	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
51	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
52	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
53	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
54	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
55	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
56	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
57	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
58	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
59	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
60	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	



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2	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
3	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
4					
5		0	0	0 AT5G59320.1 LTP3	
6	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
7	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
8	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
9					
10	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
11	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
12	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
13					
14	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
15	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
16	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
17					
18	KOG0039	1.16.1.7		0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7	
19	KOG1471		0	0 AT5G47730.1	0
20	KOG1471		0	0 AT5G47730.1	0
21					
22	KOG1471		0	0 AT5G47730.1	0
23	KOG1471		0	0 AT5G47730.1	0
24	KOG1471		0	0 AT5G47730.1	0
25					
26	KOG1471		0	0 AT5G47730.1	0
27	KOG1471		0	0 AT5G47730.1	0
28	KOG1471		0	0 AT5G47730.1	0
29					
30	KOG1471		0	0 AT5G47730.1	0
31	KOG1471		0	0 AT5G47730.1	0
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26	KOG4793	2.7.7.7		0	0 AT5G26940.3		0
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28		0	0	0	0 AT3G01680.1		0
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38	0 2.5.1.55	K01627	GO:0009058,(AT1G79500.4	AtkdsA1		
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	KOG1187 2.7.11.1		0 GO:0005515,(AT3G47570.1			0

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13					
14	KOG2913		0 K12386	0 AT5G40670.1	0
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34	KOG0143	1.14.11.32		0 GO:0055114,(AT5G58660.1	0
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41	KOG0143	1.14.11.32		0 GO:0055114,(AT5G58660.1	0
42					
43		0 2.7.7.15		0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1	
44	KOG4409	2.3.1.51	0	0 AT4G24160.1	0
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46					
47		0	0	0 GO:0046983 AT4G00120.1 EDA33,GT140,IN[	
48	KOG1305		0 K14207	GO:0003333 AT3G30390.2	0
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		0	0	0 GO:0016788 AT1G53920.1 GLIP5	

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2	KOG1430	1.1.1.170	K07748	GO:0050662,(AT2G43420.1	0
3		0 2.7.11.1		0 GO:0048544,(AT4G27290.1	0
4		0 2.7.11.1		0 GO:0048544,(AT4G27290.1	0
5		0 3.1.1.3		0 GO:0016788 AT5G33370.1	0
6		0	0	0 AT4G36550.1	0
7		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
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9		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
10		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
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15		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
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17		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
18		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
19		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
20		0 3.1.1.3	K14674	GO:0006629,(AT5G04040.1 SDP1	
21		0	0	0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2	
22		0	0	0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2	
23		0	0	0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2	
24		0	0	0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2	
25	KOG2231			0 AT3G62240.1	0
26		0	0	0 GO:0006629 AT4G16070.1	0
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2		0	0	0 GO:0006629 AT4G16070.1	0
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10		0	0	0 GO:0006629 AT4G16070.1	0
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12	KOG1471		0	0 AT4G36490.1 ATSFH12,SFH12	
13	KOG1471		0	0 AT4G36490.1 ATSFH12,SFH12	
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28	KOG1138		0 K13146	GO:0032039,(AT3G07530.1	0
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31	KOG1028		0	0 GO:0005515 AT1G74720.1 QKY	
32	KOG1028		0	0 GO:0005515 AT1G74720.1 QKY	
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43	KOG1028		0	0 GO:0005515 AT1G74720.1 QKY	
44	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
45	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
46	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
47	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
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49	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
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51	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
52	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
53	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
54	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
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56	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
57	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
58	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
59	KOG1973	2.3.1.48		0 GO:0005515 AT4G14920.1	0
60	KOG2826		0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2	
	KOG2826		0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2	



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2	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
3	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
4	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
5	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
6	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
7	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
8	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
9	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
10	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
11	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
12	KOG2826	0 K05758	GO:0034314,(AT1G30825.1 ARPC2A,DIS2		
13					
14	0	0	0 GO:0005515 AT5G22720.1		0
15	0	0	0 GO:0005515 AT5G22720.1		0
16	0	0	0 GO:0005515 AT5G22720.1		0
17	0	0	0 GO:0005515 AT5G22720.1		0
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33	0	0	0 GO:0005515 AT5G22720.1		0
34	0	0	0 GO:0005515 AT5G22720.1		0
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42					
43	KOG2547	0	0 GO:0016757 AT2G19880.2		0
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54	KOG2547	0	0 GO:0016757 AT2G19880.2		0
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57	KOG2547	0	0 GO:0016757 AT2G19880.2		0
58					
59	0 2.4.1.142	K03842	GO:0016757 AT1G16570.1		0
60	0	0 K19041	GO:0008270,(AT1G53190.1		0
	0	0 K19041	GO:0008270,(AT1G53190.1		0

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14	KOG1698		0 K02884	GO:0006412,(AT4G11630.1	0
15	KOG0519	2.7.11.1	K14509	GO:0005515,(AT3G04580.2 EIN4	
16	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
17	KOG0519	2.7.11.1		0 GO:0007165,(AT3G04580.1 EIN4	
18					
19		0	0	0 AT5G59320.1 LTP3	
20		0	0	0 AT5G59320.1 LTP3	
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42		0	0	0 AT1G32583.1	0
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44		0	0	0 AT1G32583.1	0
45		0	0	0 AT1G32583.1	0
46		0	0	0 AT1G32583.1	0
47		0	0	0 AT2G45180.1	0
48	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
49	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
50	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
51	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
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54	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
55	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
56	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
57	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
58	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
59	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
60	KOG0809		0	0 GO:0005515 AT3G05710.2 ATSYP43,SYP43	
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2		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
3		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
4		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
5		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
6		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
7		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
8		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
9		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
10		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
11		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
12		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
13		0 2.5.1.36	K09833	GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1	
14		0 6.6.1.1	K03403	GO:0016851,(AT5G13630.1 ABAR,CCH,CCH1,(	
15		0	0	0 AT5G13390.1 NEF1	
16		0	0	0 AT5G13390.1 NEF1	
17		0	0	0 GO:0006412,(AT5G39785.1	0
18		0	0	0 GO:0006412,(AT5G39785.1	0
19		0	0	0 GO:0006412,(AT5G39785.1	0
20		0	0	0 GO:0006412,(AT5G39785.1	0
21		0	0	0 GO:0006412,(AT5G39785.1	0
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32		0	0	0 AT2G38570.1	0
33					
34	KOG1187	2.7.11.1		0 GO:0005515,(AT3G47570.1	0
35		0 2.5.1.54	K01626	GO:0009073,(AT1G22410.1	0
36		0 2.5.1.54	K01626	GO:0009073,(AT1G22410.1	0
37		0 2.5.1.54	K01626	GO:0009073,(AT1G22410.1	0
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41		0 2.5.1.54	K01626	GO:0009073,(AT1G22410.1	0
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48		0	0	0 AT3G59300.1	0
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51					
52	KOG0251		0	0 GO:0005543 AT2G25430.1	0
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60	KOG0251		0	0 GO:0005543 AT2G25430.1	0
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2	KOG0251	0	0	GO:0005543	AT2G25430.1		0
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4	KOG0251	0	0	GO:0005543	AT2G25430.1		0
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6	KOG2063	0	0	GO:0016192,(	AT1G22860.1		0
7		0	0	GO:0043565,(	AT2G16770.1	bZIP23	
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17		0	0	GO:0043565,(	AT2G16770.1	bZIP23	
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19		0	0	GO:0043565,(	AT2G16770.1	bZIP23	
20		0	0	0	0	0	0
21							
22	KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
23		0 2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
24		0 2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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26		0 2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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60							

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2	arabi-defline		
3	related to AP2.7	Phvul.001G17K09284 - AP2-	
4	related to AP2.7	Phvul.001G17K09284 - AP2-	
5	related to AP2.7	Phvul.001G17K09284 - AP2-	
6	related to AP2.7	Phvul.001G17K09284 - AP2-	
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12	related to AP2.7	Phvul.001G17K09284 - AP2-	
13	related to AP2.7	Phvul.001G17K09284 - AP2-	
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15	related to AP2.7	Phvul.001G17K09284 - AP2-	
16	related to AP2.7	Phvul.001G17K09284 - AP2-	
17			
18	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
19	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
20	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
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22	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
23	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
24	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
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31	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
32	Integrase-type DNA-binding superfamily protein	Phvul.003G24PTHR32467:SF	
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46	Integrase-type DNA-binding superfamily protein	Phvul.003G24PTHR32467:SF	
47	related to AP2.7	Phvul.011G07PTHR32467:SF	
48	related to AP2.7	Phvul.011G07PTHR32467:SF	
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55	related to AP2.7	Phvul.011G07PTHR32467:SF	
56	related to AP2.7	Phvul.011G07PTHR32467:SF	
57	related to AP2.7	Phvul.011G07PTHR32467:SF	
58	related to AP2.7	Phvul.011G07PTHR32467:SF	
59	related to AP2.7	Phvul.011G07PTHR32467:SF	
60	related to AP2.7	Phvul.011G07PTHR32467:SF	
	related to AP2.7	Phvul.011G07PTHR32467:SF	

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2	related to AP2.7	Phvul.011G07PTHR32467:SF	
3	related to AP2.7	Phvul.011G07PTHR32467:SF	
4	related to AP2.7	Phvul.011G07PTHR32467:SF	
5	related to AP2.7	Phvul.011G07PTHR32467:SF	
6	related to AP2.7	Phvul.011G07PTHR32467:SF	
7	related to AP2.7	Phvul.011G07PTHR32467:SF	
8	related to AP2.7	Phvul.011G07PTHR32467:SF	
9	related to AP2.7	Phvul.011G07PTHR32467:SF	
10	related to AP2.7	Phvul.011G07PTHR32467:SF	
11	related to AP2.7	Phvul.011G07PTHR32467:SF	
12	related to AP2.7	Phvul.011G07PTHR32467:SF	
13	related to AP2.7	Phvul.011G07PTHR32467:SF	
14	related to AP2.7	Phvul.011G07PTHR32467:SF	
15	related to AP2.7	Phvul.L00030PTHR32467:SF	
16	related to AP2.7	Phvul.L00030PTHR32467:SF	
17	related to AP2.7	Phvul.L00030PTHR32467:SF	
18	related to AP2.7	Phvul.L00030PTHR32467:SF	
19	related to AP2.7	Phvul.L00030PTHR32467:SF	
20	related to AP2.7	Phvul.L00030PTHR32467:SF	
21	related to AP2.7	Phvul.L00030PTHR32467:SF	
22	related to AP2.7	Phvul.L00030PTHR32467:SF	
23	related to AP2.7	Phvul.L00030PTHR32467:SF	
24	related to AP2.7	Phvul.L00030PTHR32467:SF	
25	related to AP2.7	Phvul.L00030PTHR32467:SF	
26	related to AP2.7	Phvul.L00030PTHR32467:SF	
27	related to AP2.7	Phvul.L00030PTHR32467:SF	
28	related to AP2.7	Phvul.L00030PTHR32467:SF	
29	related to AP2.7	Phvul.L00030PTHR32467:SF	
30	related to AP2.7	Phvul.L00030PTHR32467:SF	
31	related to AP2.7	Phvul.L00030PTHR32467:SF	
32	related to AP2.7	Phvul.L00030PTHR32467:SF	
33	related to AP2.7	Phvul.L00030PTHR32467:SF	
34	related to AP2.7	Phvul.L00030PTHR32467:SF	
35	related to AP2.7	Phvul.L00030PTHR32467:SF	
36	related to AP2.7	Phvul.L00030PTHR32467:SF	
37	related to AP2.7	Phvul.L00030PTHR32467:SF	
38	related to AP2.7	Phvul.L00030PTHR32467:SF	
39	related to AP2.7	Phvul.L00030PTHR32467:SF	
40	related to AP2.7	Phvul.L00030PTHR32467:SF	
41	related to AP2.7	Phvul.L00030PTHR32467:SF	
42	related to AP2.7	Phvul.L00030PTHR32467:SF	
43	related to AP2.7	Phvul.L00030PTHR32467:SF	
44	related to AP2.7	Phvul.001G17K09284 - AP2-	
45	Integrase-type DNA-binding superfamily protein	Phvul.002G01PTHR32467:SF	
46	Integrase-type DNA-binding superfamily protein	Phvul.003G24PTHR32467:SF	
47			
48		0	0
49		0	0
50		0	0
51		0	0
52		0	0
53		0	0
54		0	0
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56		0	0
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59		0	0
60		0	0



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13		0	0	0
14		0	0	0
15		0	0	0
16	related to AP2.7		Phvul.007G24PTHR32467:SF	
17	related to AP2.7		Phvul.007G24PTHR32467:SF	
18	related to AP2.7		Phvul.007G24PTHR32467:SF	
19	related to AP2.7		Phvul.007G24PTHR32467:SF	
20	related to AP2.7		Phvul.007G24PTHR32467:SF	
21	related to AP2.7		Phvul.007G24PTHR32467:SF	
22	related to AP2.7		Phvul.007G24PTHR32467:SF	
23	related to AP2.7		Phvul.007G24PTHR32467:SF	
24	related to AP2.7		Phvul.007G24PTHR32467:SF	
25	related to AP2.7		Phvul.007G24PTHR32467:SF	
26	related to AP2.7		Phvul.007G24PTHR32467:SF	
27	related to AP2.7		Phvul.007G24PTHR32467:SF	
28	related to AP2.7		Phvul.007G24PTHR32467:SF	
29	related to AP2.7		Phvul.007G24PTHR32467:SF	
30	related to AP2.7		Phvul.007G24PTHR32467:SF	
31		0	0	0
32		0	0	0
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34		0	0	0
35		0	0	0
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57		0	0	0
58		0	0	0
59		0	0	0
60		0	0	0

1				
2		0	0	0
3		0	0	0
4		0	0	0
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6		0	0	0
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9		0	0	0
10		0	0	0
11		0	0	0
12		0	0	0
13				
14	related to AP2.7		Phvul.011G07PTHR32467:SF	
15	related to AP2.7		Phvul.011G07PTHR32467:SF	
16	related to AP2.7		Phvul.L00030{PTHR32467:SF	
17	related to AP2.7		Phvul.L00030{PTHR32467:SF	
18	allene oxide cyclase 3		Phvul.003G11K10525 - allen	
19	BRI1 suppressor 1 (BSU1)-like 3		Phvul.005G11PTHR11668//I	
20	cysteine-rich RLK (RECEPTOR-like protein kinase) 29		Phvul.008G05PTHR27002:SF	
21	cysteine-rich RLK (RECEPTOR-like protein kinase) 29		Phvul.008G05PTHR27002:SF	
22	S-locus lectin protein kinase family protein		Phvul.011G15PTHR27002:SF	
23		0	Phvul.001G03PTHR13135 - C	
24		0	Phvul.001G03PTHR13135 - C	
25		0	Phvul.001G03PTHR13135 - C	
26		0	Phvul.001G03PTHR13135 - C	
27		0	Phvul.001G03PTHR13135 - C	
28		0	Phvul.001G03PTHR13135 - C	
29		0	Phvul.001G03PTHR13135 - C	
30		0	Phvul.001G03PTHR13135 - C	
31		0	Phvul.001G03PTHR13135 - C	
32		0	Phvul.001G03PTHR13135 - C	
33		0	Phvul.001G03PTHR13135 - C	
34		0	Phvul.001G03PTHR13135 - C	
35		0	Phvul.001G03PTHR13135 - C	
36		0	Phvul.001G03PTHR13135 - C	
37		0	Phvul.001G03PTHR13135 - C	
38		0	Phvul.001G03PTHR13135 - C	
39		0	Phvul.001G03PTHR13135 - C	
40		0	Phvul.001G03PTHR13135 - C	
41		0	Phvul.001G03PTHR13135 - C	
42		0	Phvul.001G03PTHR13135 - C	
43		0	Phvul.001G03PTHR13135 - C	
44		0	Phvul.001G03PTHR13135 - C	
45		0	Phvul.001G03PTHR13135 - C	
46		0	Phvul.001G03PTHR13135 - C	
47		0	Phvul.001G03PTHR13135 - C	
48		0	Phvul.001G03PTHR13135 - C	
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50		0	Phvul.001G03PTHR13135 - C	
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52		0	Phvul.001G03PTHR13135 - C	
53		0	Phvul.001G03PTHR13135 - C	
54		0	Phvul.001G03PTHR13135 - C	
55		0	0	0
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57		0	0	0
58		0	0	0
59		0	0	0
60		0	0	0

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6		0	0
7		0	0
8		0	0
9		0	0
10	RING/FYVE/PHD zinc finger superfamily protein		Phvul.001G21PTHR23012:SF
11	RING/FYVE/PHD zinc finger superfamily protein		Phvul.001G21PTHR23012:SF
12	casein kinase alpha 1		Phvul.002G01K03097 - case
13	casein kinase alpha 1		Phvul.002G01K03097 - case
14	casein kinase alpha 1		Phvul.002G01K03097 - case
15	casein kinase alpha 1		Phvul.002G01K03097 - case
16	casein kinase alpha 1		Phvul.002G01K03097 - case
17	casein kinase alpha 1		Phvul.002G01K03097 - case
18	casein kinase alpha 1		Phvul.002G01K03097 - case
19	casein kinase alpha 1		Phvul.002G01K03097 - case
20	casein kinase alpha 1		Phvul.002G01K03097 - case
21	casein kinase alpha 1		Phvul.002G01K03097 - case
22	casein kinase alpha 1		Phvul.002G01K03097 - case
23	casein kinase alpha 1		Phvul.002G01K03097 - case
24	casein kinase alpha 1		Phvul.002G01K03097 - case
25	O-acetyltransferase family protein		Phvul.002G19PTHR13533:SF
26	Aldolase-type TIM barrel family protein		Phvul.002G214.4.1.19 - Pho
27	Nucleic acid-binding, OB-fold-like protein		Phvul.002G33PTHR14513 - I
28	Nucleic acid-binding, OB-fold-like protein		Phvul.002G33PTHR14513 - I
29	zinc transporter 10 precursor		Phvul.003G26PTHR11040:SF
30	zinc transporter 10 precursor		Phvul.003G26PTHR11040:SF
31	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
32	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
33	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
34	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
35	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
36	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
37	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
38	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
39	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
40	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
41	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
42	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
43	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
44	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
45	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
46	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
47	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
48	S-locus lectin protein kinase family protein		Phvul.005G03PF00954//PFC
49	S-locus lectin protein kinase family protein		Phvul.005G08PF00954//PFC
50	S-locus lectin protein kinase family protein		Phvul.005G08PF00954//PFC
51	S-locus lectin protein kinase family protein		Phvul.005G08PF00954//PFC
52	S-locus lectin protein kinase family protein		Phvul.005G08PF00954//PFC
53	receptor kinase 3		Phvul.005G08PF00954//PFC
54	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin
55	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin
56	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin
57	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin
58	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin
59	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin
60	serine carboxypeptidase-like 48		Phvul.005G13K16298 - serin

1			
2	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
3	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
4	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
5	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
6	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
7	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
8	serine carboxypeptidase-like 48	Phvul.005G13K16298 - serin	
9			
10		0	0
11		0	0
12	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
13	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
14	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
15	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
16	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
17	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
18	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
19	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
20	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
21	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
22	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
23	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
24	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
25	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
26	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I	
27	related to AP2.7	Phvul.007G24PTHR32467:SF	
28	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
29	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
30	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
31	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
32	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
33	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
34	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
35	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
36	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
37	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
38	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
39	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
40	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
41	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
42	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
43	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
44	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
45	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
46	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
47	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
48	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
49	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
50	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
51	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
52	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
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54	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
55	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
56	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
57	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
58	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
59	magnesium transporter 4	Phvul.008G03PTHR13890:SF	
60	magnesium transporter 4	Phvul.008G03PTHR13890:SF	

1			
2	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
3	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
4	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
5	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
6	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
7	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
8	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
9	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
10	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
11	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
12	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
13	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
14	magnesium transporter 4	Phvul.008G03 PTHR13890:SF	
15	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
16	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
17	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
18	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
19	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
20	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
21	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
22	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
23	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
24	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
25	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
26	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
27	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
28	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec	
29	Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.009G24 PF01535//PF1	
30			
31		0	0
32	S-locus lectin protein kinase family protein	Phvul.011G15 PF00954//PFC	
33	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
34	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
35	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
36	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
37	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
38	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
39	S-locus lectin protein kinase family protein	Phvul.011G15 PTHR27002:SF	
40	S-locus lectin protein kinase family protein	Phvul.011G15 PF00954//PFC	
41	S-locus lectin protein kinase family protein	Phvul.011G16 PTHR27002:SF	
42			
43		0	0
44		0	0
45	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
46	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
47	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
48	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
49	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
50	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
51	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
52	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
53	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
54	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
55	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
56	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
57	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
58	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
59	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
60	Plant protein of unknown function (DUF247)	Phvul.001G18 PF03140 - Plai	
		0	0

1				
2		0	0	0
3	casein kinase alpha 1			Phvul.002G01K03097 - case
4	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
5	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
6	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
7	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
8	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
9	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
10	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
11	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
12	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
13	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
14	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
15	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
16	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
17	Mitochondrial transcription termination factor family protei			Phvul.002G08PTHR13068//I
18	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
19	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
20	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
21	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
22	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
23	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
24	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
25	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
26	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
27	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
28	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
29	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
30	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
31	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
32	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
33	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
34	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
35	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
36	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
37	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
38	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
39	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
40	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
41	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
42	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
43	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
44	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
45	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
46	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
47	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
48	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
49	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
50	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
51	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
52	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
53	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
54	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
55	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
56	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
57	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
58	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
59	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
60	diacylglycerol kinase 2			Phvul.002G27PTHR11255:SF
	Flavin-binding monooxygenase family protein			Phvul.002G31PTHR23023//I



1		
2	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
3	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
4	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
5	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
6	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
7	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
8	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
9	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
10	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
11	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
12	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
13	Flavin-binding monooxygenase family protein	Phvul.002G31PTHR23023//I
14	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
15	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
16	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
17	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
18	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
19	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
20	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
21	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
22	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
23	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
24	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
25	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
26	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
27	trehalose phosphate synthase	Phvul.003G052.4.1.15//3.1.
28	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
29	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
30	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
31	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
32	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
33	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
34	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
35	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
36	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
37	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
38	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
39	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
40	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
41	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
42	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
43	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
44	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
45	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
46	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
47	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
48	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
49	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
50	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
51	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
52	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
53	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
54	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
55	casein kinase II, alpha chain 2	Phvul.003G23K03097 - case
56	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
57	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
58	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
59	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
60	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF

1		
2	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
3	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
4	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
5	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
6	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
7	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
8	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
9	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
10	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
11	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
12	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
13	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
14	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
15	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
16	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
17	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
18	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
19	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
20	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
21	zinc transporter 10 precursor	Phvul.003G26PTHR11040:SF
22	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
23	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
24	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
25	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
26	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
27	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
28	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
29	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
30	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
31	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
32	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
33	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
34	BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11PTHR11668//I
35	Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13PTHR23324//I
36	Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13PTHR23324//I
37	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
38	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
39	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
40	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
41	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
42	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
43	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
44	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
45	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
46	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
47	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
48	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
49	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
50	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF
51	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF
52	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
53	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
54	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
55	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
56	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
57	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
58	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
59	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
60	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF



1		
2	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
3	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
4	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
5	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
6	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
7	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
8	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
9	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
10	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
11	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
12	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
13	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
14	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
15	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
16	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
17	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
18	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
19	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
20	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
21	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
22	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
23	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
24	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
25	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
26	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
27	alpha/beta-Hydrolases superfamily protein	Phvul.009G01 PTHR10992//I
28	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
29	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
30	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
31	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
32	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
33	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
34	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
35	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
36	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
37	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
38	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
39	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
40	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
41	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
42	like heterochromatin protein (LHP1)	Phvul.009G11 PTHR22812 - (
43	BTB/POZ domain-containing protein	Phvul.009G13 K10523 - spec
44	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
45	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
46	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
47	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
48	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
49	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
50	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
51	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
52	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
53	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
54	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
55	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
56	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
57	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
58	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
59	Plant protein of unknown function (DUF247)	Phvul.010G00 PF03140 - Plai
60	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06 PF00069//PF1
	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07 PF08670 - ME

1		
2	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
3	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
4	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
5	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
6	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
7	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
8	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
9	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
10	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
11	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
12	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
13	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
14	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
15	Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07PF08670 - ME
16	senescence-associated gene 12	Phvul.011G12PTHR12411//I
17	senescence-associated gene 12	Phvul.011G12PTHR12411//I
18	senescence-associated gene 12	Phvul.011G12PTHR12411//I
19	senescence-associated gene 12	Phvul.011G12PTHR12411//I
20	senescence-associated gene 12	Phvul.011G12PTHR12411//I
21	senescence-associated gene 12	Phvul.011G12PTHR12411//I
22	senescence-associated gene 12	Phvul.011G12PTHR12411//I
23	senescence-associated gene 12	Phvul.011G12PTHR12411//I
24	senescence-associated gene 12	Phvul.011G12PTHR12411//I
25	senescence-associated gene 12	Phvul.011G12PTHR12411//I
26	senescence-associated gene 12	Phvul.011G12PTHR12411//I
27	senescence-associated gene 12	Phvul.011G12PTHR12411//I
28	senescence-associated gene 12	Phvul.011G12PTHR12411//I
29	senescence-associated gene 12	Phvul.011G12PTHR12411//I
30	senescence-associated gene 12	Phvul.011G12PTHR12411//I
31	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
32	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
33	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
34	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
35	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
36	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
37	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
38	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
39	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
40	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
41	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
42	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
43	S-locus lectin protein kinase family protein	Phvul.011G14PF00954//PFC
44	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
45	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
46	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
47	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
48	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
49	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
50	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
51	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
52	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
53	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
54	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
55	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
56	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
57	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
58	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
59	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
60	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I



1			
2	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
3	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
4	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
5	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
6	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
7	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
8	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
9	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
10	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
11	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
12	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
13	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
14	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I	
15	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
16	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
17	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
18	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
19	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
20	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
21	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
22	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
23	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
24	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
25	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
26	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
27	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
28	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
29	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
30	Peptidase M20/M25/M40 family protein	Phvul.003G003.5.1.14 - N-ac	
31	resistance to phytophthora 1	Phvul.001G14PTHR36359:SF	
32	histone H4	Phvul.001G16K11254 - histc	
33	histone H4	Phvul.001G16K11254 - histc	
34	histone H4	Phvul.001G16K11254 - histc	
35	histone H4	Phvul.001G16K11254 - histc	
36	histone H4	Phvul.001G16K11254 - histc	
37	histone H4	Phvul.001G16K11254 - histc	
38	histone H4	Phvul.001G16K11254 - histc	
39	histone H4	Phvul.001G16K11254 - histc	
40	histone H4	Phvul.001G16K11254 - histc	
41	histone H4	Phvul.001G16K11254 - histc	
42	histone H4	Phvul.001G16K11254 - histc	
43	histone H4	Phvul.001G16K11254 - histc	
44	histone H4	Phvul.001G16K11254 - histc	
45		0	0
46		0	0
47		0	0
48		0	0
49		0	0
50		0	0
51		0	0
52		0	0
53		0	0
54		0	0
55		0	0
56		0	0
57		0	0
58			
59	RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21PTHR23012:SF	
60	RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21PTHR23012:SF	
	RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21PTHR23012:SF	





1		
2	protein kinase 1B	Phvul.001G232.7.10.2//2.7.
3	protein kinase 1B	Phvul.001G232.7.10.2//2.7.
4	protein kinase 1B	Phvul.001G232.7.10.2//2.7.
5	protein kinase 1B	Phvul.001G232.7.10.2//2.7.
6	protein kinase 1B	Phvul.001G232.7.10.2//2.7.
7	SKU5 similar 12	Phvul.001G26PTHR11709:SF
8	SKU5 similar 12	Phvul.001G26PTHR11709:SF
9	SKU5 similar 12	Phvul.001G26PTHR11709:SF
10	SKU5 similar 12	Phvul.001G26PTHR11709:SF
11	SKU5 similar 12	Phvul.001G26PTHR11709:SF
12	SKU5 similar 12	Phvul.001G26PTHR11709:SF
13	SKU5 similar 12	Phvul.001G26PTHR11709:SF
14	SKU5 similar 12	Phvul.001G26PTHR11709:SF
15	SKU5 similar 12	Phvul.001G26PTHR11709:SF
16	SKU5 similar 12	Phvul.001G26PTHR11709:SF
17	SKU5 similar 12	Phvul.001G26PTHR11709:SF
18	SKU5 similar 12	Phvul.001G26PTHR11709:SF
19	SKU5 similar 12	Phvul.001G26PTHR11709:SF
20	SKU5 similar 12	Phvul.001G26PTHR11709:SF
21	SKU5 similar 12	Phvul.001G26PTHR11709:SF
22	SKU5 similar 12	Phvul.001G26PTHR11709:SF
23	SKU5 similar 12	Phvul.001G26PTHR11709:SF
24	SKU5 similar 12	Phvul.001G26PTHR11709:SF
25	SKU5 similar 12	Phvul.001G26PTHR11709:SF
26	SKU5 similar 12	Phvul.001G26PTHR11709:SF
27	SKU5 similar 12	Phvul.001G26PTHR11709:SF
28	SKU5 similar 12	Phvul.001G26PTHR11709:SF
29	SKU5 similar 12	Phvul.001G26PTHR11709:SF
30	SKU5 similar 12	Phvul.001G26PTHR11709:SF
31	SKU5 similar 12	Phvul.001G26PTHR11709:SF
32	SKU5 similar 12	Phvul.001G26PTHR11709:SF
33	SKU5 similar 12	Phvul.001G26PTHR11709:SF
34	SKU5 similar 12	Phvul.001G26PTHR11709:SF
35	SKU5 similar 12	Phvul.001G26PTHR11709:SF
36	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
37	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
38	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
39	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
40	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
41	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
42	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
43	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
44	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
45	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
46	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
47	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
48	O-acetyltransferase family protein	Phvul.002G19PTHR13533:SF
49	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
50	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
51	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
52	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
53	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
54	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
55	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
56	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
57	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
58	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
59	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
60	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho

1		
2	Aldolase-type TIM barrel family protein	Phvul.002G214.4.1.19 - Pho
3	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
4	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
5	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
6	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
7	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
8	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
9	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
10	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
11	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
12	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
13	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
14	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
15	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
16	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
17	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
18	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
19	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
20	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
21	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
22	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
23	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
24	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
25	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
26	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
27	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
28	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
29	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
30	Nucleic acid-binding, OB-fold-like protein	Phvul.002G33PTHR14513 - I
31	allene oxide cyclase 3	Phvul.003G11K10525 - allen
32	allene oxide cyclase 3	Phvul.003G11K10525 - allen
33	allene oxide cyclase 3	Phvul.003G11K10525 - allen
34	allene oxide cyclase 3	Phvul.003G11K10525 - allen
35	allene oxide cyclase 3	Phvul.003G11K10525 - allen
36	allene oxide cyclase 3	Phvul.003G11K10525 - allen
37	allene oxide cyclase 3	Phvul.003G11K10525 - allen
38	allene oxide cyclase 3	Phvul.003G11K10525 - allen
39	allene oxide cyclase 3	Phvul.003G11K10525 - allen
40	allene oxide cyclase 3	Phvul.003G11K10525 - allen
41	allene oxide cyclase 3	Phvul.003G11K10525 - allen
42	allene oxide cyclase 3	Phvul.003G11K10525 - allen
43	allene oxide cyclase 3	Phvul.003G11K10525 - allen
44	calcium-dependent lipid-binding family protein	Phvul.003G11PTHR16166:SF
45	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
46	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
47	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
48	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
49	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
50	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
51	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
52	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
53	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
54	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
55	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
56	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
57	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
58	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
59	Leucine-rich receptor-like protein kinase family protein	Phvul.003G20PF00069//PFC
60	NAC domain containing protein 96	Phvul.003G22PTHR31989:SF
	NAC domain containing protein 96	Phvul.003G22PTHR31989:SF







1		
2	hypothetical protein 1	Phvul.004G03 PTHR13018//I
3	hypothetical protein 1	Phvul.004G03 PTHR13018//I
4	hypothetical protein 1	Phvul.004G03 PTHR13018//I
5	hypothetical protein 1	Phvul.004G03 PTHR13018//I
6	hypothetical protein 1	Phvul.004G03 PTHR13018//I
7	hypothetical protein 1	Phvul.004G03 PTHR13018//I
8	hypothetical protein 1	Phvul.004G03 PTHR13018//I
9	hypothetical protein 1	Phvul.004G03 PTHR13018//I
10	hypothetical protein 1	Phvul.004G03 PTHR13018//I
11	hypothetical protein 1	Phvul.004G03 PTHR13018//I
12	hypothetical protein 1	Phvul.004G03 PTHR13018//I
13	hypothetical protein 1	Phvul.004G03 PTHR13018//I
14	hypothetical protein 1	Phvul.004G03 PTHR13018//I
15	F-box/RNI-like superfamily protein	Phvul.004G11 PF00646 - F-b
16	F-box/RNI-like superfamily protein	Phvul.004G11 PF00646 - F-b
17		
18	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
19	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
20	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
21	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
22	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
23	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
24	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
25	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
26	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
27	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
28	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
29	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
30	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
31	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
32	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
33	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
34	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
35	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
36	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
37	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
38	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
39	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
40	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
41	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
42	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
43	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
44	receptor kinase 3	Phvul.005G08 PF00954//PFC
45	receptor kinase 3	Phvul.005G08 PF00954//PFC
46	receptor kinase 3	Phvul.005G08 PF00954//PFC
47	receptor kinase 3	Phvul.005G08 PF00954//PFC
48	receptor kinase 3	Phvul.005G08 PF00954//PFC
49	receptor kinase 3	Phvul.005G08 PF00954//PFC
50	receptor kinase 3	Phvul.005G08 PF00954//PFC
51	receptor kinase 3	Phvul.005G08 PF00954//PFC
52	receptor kinase 3	Phvul.005G08 PF00954//PFC
53	receptor kinase 3	Phvul.005G08 PF00954//PFC
54	receptor kinase 3	Phvul.005G08 PF00954//PFC
55	receptor kinase 3	Phvul.005G08 PF00954//PFC
56	receptor kinase 3	Phvul.005G08 PF00954//PFC
57	receptor kinase 3	Phvul.005G08 PF00954//PFC
58	Coatomer, beta\' subunit	Phvul.005G17 KOG0265//KC
59	Coatomer, beta\' subunit	Phvul.005G17 KOG0265//KC
60	Coatomer, beta\' subunit	Phvul.005G17 KOG0265//KC



1		
2	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
3	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
4	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
5	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
6	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
7	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
8	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
9	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
10	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
11	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
12	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
13	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
14	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
15	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
16	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
17	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
18	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
19	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
20	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
21	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
22	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
23	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
24	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
25	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
26	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
27	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
28	Coatomer, beta\' subunit	Phvul.005G17KOG0265//KC
29	vacuoleless1 (VCL1)	Phvul.006G02PTHR12811 - \
30		
31	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
32	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
33	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
34	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
35	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
36	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
37	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
38	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
39	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
40	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
41	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
42	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
43	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
44	cleavage and polyadenylation specificity factor 30	Phvul.006G13PTHR12357:SF
45	Nucleotide-sugar transporter family protein	Phvul.006G13PTHR11132//I
46		
47	Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18PTHR31384:SF
48	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
49	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
50	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
51	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
52	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
53	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
54	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
55	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
56	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
57	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
58	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
59	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
60	leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02PF00560//PFC
	methyltransferases	Phvul.007G042.1.1.193 - 16:

1			
2	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
3	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
4	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
5	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
6	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
7	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
8	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
9	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
10	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
11	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
12	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
13	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
14	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
15	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
16	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
17	Mitochondrial transcription termination factor family protei	Phvul.007G08PTR13068:SF	
18	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
19	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
20	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
21	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
22	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
23	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
24	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
25	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
26	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
27	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
28	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
29	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
30	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
31	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
32	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
33	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
34	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
35	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
36	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
37	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
38	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
39	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
40	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
41	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
42	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
43	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th	
44		0	0
45		0	0
46		0	0
47		0	0
48		0	0
49		0	0
50		0	0
51		0	0
52		0	0
53		0	0
54		0	0
55		0	0
56		0	0
57		0	0
58			
59	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alph	
60	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alph	
	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alph	

1		
2	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
3	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
4	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
5	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
6	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
7	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
8	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
9	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
10	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
11	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
12	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
13	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
14	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
15	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
16	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
17	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
18	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
19	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
20	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
21	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
22	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
23	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
24	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
25	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
26	alpha-soluble NSF attachment protein 2	Phvul.008G08K15296 - alpha
27	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
28	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
29	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
30	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
31	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
32	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
33	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
34	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
35	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
36	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
37	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
38	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
39	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
40	Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12 PTHR23257//I
41	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
42	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
43	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
44	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
45	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
46	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
47	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
48	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
49	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
50	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
51	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
52	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
53	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
54	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
55	Coproporphyrinogen III oxidase	Phvul.008G281.3.3.3 - Copro
56	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
57	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
58	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
59	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
60	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho

1		
2	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
3	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
4	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
5	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
6	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
7	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
8	phosphorylcholine cytidylyltransferase	Phvul.008G292.7.7.15 - Cho
9	like heterochromatin protein (LHP1)	Phvul.009G11PTHR22812 - (
10		
11	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
12	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
13	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
14	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
15	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
16	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
17	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
18	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
19	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
20	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
21	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
22	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
23	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF
24	Plant protein of unknown function (DUF247)	Phvul.010G15PF03140 - Plai
25		
26	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
27	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
28	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
29	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
30	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
31	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
32	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
33	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
34	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
35	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
36	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
37	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
38	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
39	Protein kinase superfamily protein	Phvul.011G012.7.11.1 - Non
40	cytochrome c biogenesis protein family	Phvul.011G04K07399 - cyto
41	cytochrome c biogenesis protein family	Phvul.011G04K07399 - cyto
42		
43	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
44	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
45	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
46	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
47	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
48	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
49	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
50	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
51	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
52	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
53	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
54	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
55	Leucine-rich repeat transmembrane protein kinase	Phvul.011G06PF00069//PF1
56	senescence-associated gene 12	Phvul.011G12PTHR12411//I
57	senescence-associated gene 12	Phvul.011G12PTHR12411//I
58	senescence-associated gene 12	Phvul.011G12PTHR12411//I
59	senescence-associated gene 12	Phvul.011G12PTHR12411//I
60	senescence-associated gene 12	Phvul.011G12PTHR12411//I









1		
2	S-locus lectin protein kinase family protein	Phvul.011G16PTHR27002:SF
3	S-locus lectin protein kinase family protein	Phvul.011G16PTHR27002:SF
4	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
5	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
6	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
7	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
8	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
9	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
10	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
11	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
12	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
13	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
14	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
15	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
16	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
17	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
18	S-locus lectin protein kinase family protein	Phvul.011G20PF00954//PFC
19	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
20	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
21	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
22	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
23	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
24	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
25	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
26	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
27	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
28	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
29	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
30	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
31	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
32	RNI-like superfamily protein	Phvul.001G15K10268 - F-bo
33	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
34	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
35	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
36	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
37	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
38	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
39	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
40	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
41	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
42	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
43	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
44	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
45	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
46	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
47	C2H2-like zinc finger protein	Phvul.001G17PTHR10593:SF
48	SKU5 similar 12	Phvul.001G26PTHR11709:SF
49	SKU5 similar 12	Phvul.001G26PTHR11709:SF
50	plant U-box 49	Phvul.002G01K10598 - pept
51	plant U-box 49	Phvul.002G01K10598 - pept
52	plant U-box 49	Phvul.002G01K10598 - pept
53	plant U-box 49	Phvul.002G01K10598 - pept
54	plant U-box 49	Phvul.002G01K10598 - pept
55	plant U-box 49	Phvul.002G01K10598 - pept
56	plant U-box 49	Phvul.002G01K10598 - pept
57	plant U-box 49	Phvul.002G01K10598 - pept
58	plant U-box 49	Phvul.002G01K10598 - pept
59	plant U-box 49	Phvul.002G01K10598 - pept
60	plant U-box 49	Phvul.002G01K10598 - pept

1		
2	plant U-box 49	Phvul.002G01K10598 - pept
3	plant U-box 49	Phvul.002G01K10598 - pept
4	plant U-box 49	Phvul.002G01K10598 - pept
5		
6	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
7	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
8	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
9		
10	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
11	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
12	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
13	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
14	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
15	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
16	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
17	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
18	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
19	FAD-binding Berberine family protein	Phvul.002G191.3.3.8 - Tetra
20	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
21	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
22	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
23	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
24	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
25	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
26	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
27	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
28	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
29	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
30	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
31	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
32	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PTHR27007:SF
33	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
34	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
35	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
36	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
37	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
38	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
39	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
40	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
41	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
42	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
43	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
44	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
45	Concanavalin A-like lectin protein kinase family protein	Phvul.002G21PF00139//PFC
46		
47	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
48	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
49	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
50		
51	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
52	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
53	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
54	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
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56	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
57	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
58	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
59	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
60	ABC2 homolog 13	Phvul.002G26PTHR10566:SF
	diacylglycerol kinase 2	Phvul.002G27PTHR11255:SF

1		
2	diacylglycerol kinase 2	Phvul.002G27PTHR11255:SI
3	diacylglycerol kinase 2	Phvul.002G27PTHR11255:SI
4	endonucleases	Phvul.002G30PF03161 - LAC
5		
6	ethylene-forming enzyme	Phvul.002G32K05933 - amir
7	ethylene-forming enzyme	Phvul.002G32K05933 - amir
8	ethylene-forming enzyme	Phvul.002G32K05933 - amir
9		
10	ethylene-forming enzyme	Phvul.002G32K05933 - amir
11	ethylene-forming enzyme	Phvul.002G32K05933 - amir
12	ethylene-forming enzyme	Phvul.002G32K05933 - amir
13		
14	ethylene-forming enzyme	Phvul.002G32K05933 - amir
15	ethylene-forming enzyme	Phvul.002G32K05933 - amir
16	ethylene-forming enzyme	Phvul.002G32K05933 - amir
17	ethylene-forming enzyme	Phvul.002G32K05933 - amir
18	ethylene-forming enzyme	Phvul.002G32K05933 - amir
19	ethylene-forming enzyme	Phvul.002G32K05933 - amir
20	ethylene-forming enzyme	Phvul.002G32K05933 - amir
21		
22	ethylene-forming enzyme	Phvul.002G32K05933 - amir
23	ethylene-forming enzyme	Phvul.002G32K05933 - amir
24	ethylene-forming enzyme	Phvul.002G32K05933 - amir
25	ethylene-forming enzyme	Phvul.002G32K05933 - amir
26	ethylene-forming enzyme	Phvul.002G32K05933 - amir
27	ethylene-forming enzyme	Phvul.002G32K05933 - amir
28	ethylene-forming enzyme	Phvul.002G32K05933 - amir
29	ethylene-forming enzyme	Phvul.002G32K05933 - amir
30	ethylene-forming enzyme	Phvul.002G32K05933 - amir
31	ethylene-forming enzyme	Phvul.002G32K05933 - amir
32	ethylene-forming enzyme	Phvul.002G32K05933 - amir
33	ethylene-forming enzyme	Phvul.002G32K05933 - amir
34	ethylene-forming enzyme	Phvul.002G32K05933 - amir
35	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
36	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
37	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
38	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
39	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
40	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
41	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
42	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
43	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
44	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
45	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
46	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
47	heptahelical transmembrane protein1	Phvul.003G17PTHR20855//I
48	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
49	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
50		
51	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
52	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
53	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
54	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
55	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
56	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
57	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
58	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
59	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
60	cycling DOF factor 3	Phvul.003G18PTHR31089:SI
	cycling DOF factor 3	Phvul.003G18PTHR31089:SI

1			
2	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
3	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
4	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
5	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
6	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
7	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
8	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
9	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
10	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
11	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
12	cycling DOF factor 3	Phvul.003G18PTHR31089:SF	
13			
14	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
15	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
16	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
17	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
18	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
19	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
20	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
21	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
22	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
23	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
24	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
25	Leucine-rich repeat transmembrane protein kinase	Phvul.003G20PF00560//PFC	
26			
27		0	0
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41	NAC domain containing protein 96	Phvul.003G22PTHR31989:SF	
42	NAC domain containing protein 96	Phvul.003G22PTHR31989:SF	
43	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
44	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
45	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
46	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
47	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
48	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
49	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
50	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
51	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
52	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
53	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
54	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
55	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
56	Protein kinase superfamily protein	Phvul.003G23PTHR24054:SF	
57	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04PTHR11017//I	
58	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04PTHR11017//I	
59	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04PTHR11017//I	
60	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04PTHR11017//I	





1 Signal transduction histidine kinase, hybrid-type, ethylene sePhvul.006G10K14509 - ethy  
2 Signal transduction histidine kinase, hybrid-type, ethylene sePhvul.006G10K14509 - ethy  
3 lipid transfer protein 3 Phvul.006G11PF00234 - Pro  
4 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
5 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
6 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
7 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
8 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
9 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
10 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
11 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
12 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
13 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
14 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
15 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
16 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
17 ferric reduction oxidase 7 Phvul.006G131.16.1.7 - Ferr  
18 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
19 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
20 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
21 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
22 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
23 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
24 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
25 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
26 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
27 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
28 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
29 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
30 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
31 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
32 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
33 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
34 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
35 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
36 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
37 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
38 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
39 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
40 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
41 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
42 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
43 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
44 Sec14p-like phosphatidylinositol transfer family protein Phvul.006G13PTHR23324//I  
45 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
46 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
47 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
48 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
49 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
50 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
51 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
52 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
53 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
54 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
55 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
56 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
57 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
58 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S ;Phvul.006G13PTHR31731:SF  
59 Pseudouridine synthase family protein Phvul.006G15PTHR11079:SF  
60 Pseudouridine synthase family protein Phvul.006G15PTHR11079:SF



1				
2	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF		
3	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF		
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11	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SF		
12	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
13	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
14	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
15	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
16	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
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19	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
20	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
21	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
22	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
23	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
24	FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17PTHR32077:SF		
25				
26	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th		
27	Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19KOG4793 - Th		
28		0 Phvul.007G28PF14577 - Sie		
29		0	0	0
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31		0	0	0
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29		0	0
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31		0	0
32	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
33	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
34	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
35	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
36	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
37	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
38	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
39	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
40	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
41	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
42	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
43	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
44	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
45	Aldolase-type TIM barrel family protein	Phvul.008G042.5.1.55 - 3-de	
46			
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60	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC	
	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC	

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2	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
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4	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
5	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
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8	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
9	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
10	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
11	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
12	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
13	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
14	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
15	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
16	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
17	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
18	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
19	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
20	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
21	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
22	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
23	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
24	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
25	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
26	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
27	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
28	PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14K12386 - cysti
29	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
30	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
31	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
32	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
33	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
34	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
35	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
36	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
37	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
38	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
39	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
40	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
41	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
42	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26PTHR10209:SF
43	phosphorylcholine cytidyltransferase	Phvul.008G292.7.7.15 - Cho
44	<b>alpha/beta-Hydrolases superfamily protein</b>	<b>Phvul.009G01PTHR10992//I</b>
45	<b>alpha/beta-Hydrolases superfamily protein</b>	<b>Phvul.009G01PTHR10992//I</b>
46	<b>alpha/beta-Hydrolases superfamily protein</b>	<b>Phvul.009G01PTHR10992//I</b>
47	basic helix-loop-helix (bHLH) DNA-binding superfamily protei	Phvul.009G14PTHR12565:SF
48	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
49	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
50	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
51	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
52	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
53	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
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58	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
59	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
60	Transmembrane amino acid transporter family protein	Phvul.009G19PTHR22950:SF
	GDSL-motif lipase 5	Phvul.010G12PTHR22835:SF

1		
2	3-beta hydroxysteroid dehydrogenase/isomerase family prot	Phvul.011G05PTHR10366:SF
3	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
4	S-locus lectin protein kinase family protein	Phvul.011G15PTHR27002:SF
5	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233;PTHR22835//I
6	ARM repeat superfamily protein	Phvul.001G01PTHR22849:SF
7	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
8	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
9	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
10	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
11	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
12	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
13	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
14	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
15	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
16	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
17	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
18	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
19	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
20	Patatin-like phospholipase family protein	Phvul.001G12K14674 - TAG
21	villin 2	Phvul.001G13PTHR11977:SF
22	villin 2	Phvul.001G13PTHR11977:SF
23	villin 2	Phvul.001G13PTHR11977:SF
24	RING/U-box superfamily protein	Phvul.001G21PTHR22938 - ;
25	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
26	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
27	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
28	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
29	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
30	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
31	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
32	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
33	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
34	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
35	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
36	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
37	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
38	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
39	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
40	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
41	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
42	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
43	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
44	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
45	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
46	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
47	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
48	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
49	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
50	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
51	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
52	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
53	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
54	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
55	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
56	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
57	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
58	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
59	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
60	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I

1		
2	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
3	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
4	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
5	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
6	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
7	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
8	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
9	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
10	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13PTHR21493//I
11	SEC14-like 12	Phvul.002G16PTHR23324:SF
12	SEC14-like 12	Phvul.002G16PTHR23324:SF
13	SEC14-like 12	Phvul.002G16PTHR23324:SF
14		Phvul.002G16PTHR23324:SF
15		0 Phvul.002G28K13146 - integ
16		0 Phvul.002G28K13146 - integ
17		0 Phvul.002G28K13146 - integ
18		0 Phvul.002G28K13146 - integ
19		0 Phvul.002G28K13146 - integ
20		0 Phvul.002G28K13146 - integ
21		0 Phvul.002G28K13146 - integ
22		0 Phvul.002G28K13146 - integ
23		0 Phvul.002G28K13146 - integ
24		0 Phvul.002G28K13146 - integ
25		0 Phvul.002G28K13146 - integ
26		0 Phvul.002G28K13146 - integ
27		0 Phvul.002G28K13146 - integ
28		0 Phvul.002G28K13146 - integ
29		0 Phvul.002G28K13146 - integ
30	<b>trehalose phosphate synthase</b>	<b>Phvul.003G052.4.1.15//3.1.</b>
31	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
32	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
33	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
34	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
35	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
36	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
37	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
38	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
39	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
40	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
41	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
42	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
43	C2 calcium/lipid-binding plant phosphoribosyltransferase far	Phvul.003G19PTHR10024:SF
44	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
45	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
46	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
47	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
48	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
49	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
50	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
51	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
52	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
53	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
54	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
55	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
56	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
57	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
58	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi	Phvul.003G22PTHR24098:SF
59	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
60	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin



1		
2	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
3	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
4	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
5	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
6	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
7	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
8	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
9	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
10	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
11	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
12	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
13	Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27K05758 - actin
14	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
15	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
16	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
17	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
18	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
19	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
20	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
21	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
22	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
23	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
24	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
25	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
26	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
27	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
28	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
29	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
30	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
31	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
32	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
33	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
34	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
35	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
36	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
37	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
38	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
39	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
40	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
41	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
42	F-box/RNI-like superfamily protein	Phvul.004G11PF00646 - F-box
43	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
44	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
45	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
46	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
47	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
48	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
49	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
50	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
51	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
52	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
53	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
54	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
55	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
56	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
57	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
58	Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17PTHR12726 - C
59	UDP-Glycosyltransferase superfamily protein	Phvul.005G052.4.1.142 - Ch
60	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul
	RING/U-box superfamily protein	Phvul.005G06K19041 - E3 ul



1			
2	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
3	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
4	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
5	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
6	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
7	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
8	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
9	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
10	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
11	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
12	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
13	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
14	Ribosomal protein L19 family protein	Phvul.006G05 PTHR15680:SF	
15	Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10K14509 - ethy	
16	Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10K14509 - ethy	
17	Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10K14509 - ethy	
18	Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10K14509 - ethy	
19	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
20	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
21	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
22	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
23	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
24	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
25	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
26	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
27	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
28	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
29	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
30	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
31	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
32	lipid transfer protein 3	Phvul.006G11 PF00234 - Pro	
33		0	0
34		0	0
35		0	0
36		0	0
37		0	0
38		0	0
39		0	0
40		0	0
41		0	0
42		0	0
43		0	0
44		0	0
45		0	0
46		0	0
47	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13 PTHR31731:SF	
48	syntaxin of plants 43	Phvul.007G19K08489 - synt	
49	syntaxin of plants 43	Phvul.007G19K08489 - synt	
50	syntaxin of plants 43	Phvul.007G19K08489 - synt	
51	syntaxin of plants 43	Phvul.007G19K08489 - synt	
52	syntaxin of plants 43	Phvul.007G19K08489 - synt	
53	syntaxin of plants 43	Phvul.007G19K08489 - synt	
54	syntaxin of plants 43	Phvul.007G19K08489 - synt	
55	syntaxin of plants 43	Phvul.007G19K08489 - synt	
56	syntaxin of plants 43	Phvul.007G19K08489 - synt	
57	syntaxin of plants 43	Phvul.007G19K08489 - synt	
58	syntaxin of plants 43	Phvul.007G19K08489 - synt	
59	syntaxin of plants 43	Phvul.007G19K08489 - synt	
60	syntaxin of plants 43	Phvul.007G19K08489 - synt	
	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih	

1		
2	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
3	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
4	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
5	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
6	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
7	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
8	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
9	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
10	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
11	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
12	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
13	homogentisate phytyltransferase 1	Phvul.007G222.5.1.36 - Trih
14	magnesium-chelatase subunit chlH, chloroplast, putative / M	Phvul.007G25K03403 - mag
15	no exine formation 1	Phvul.008G00PTHR35313:SF
16	no exine formation 1	Phvul.008G00PTHR35313:SF
17	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
18	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
19	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
20	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
21	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
22	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
23	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
24	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
25	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
26	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
27	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
28	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
29	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
30	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
31	Protein of unknown function (DUF1666)	Phvul.008G04PTHR10759//I
32		0 0 0
33	Leucine-rich repeat protein kinase family protein	Phvul.008G09PF00069//PFC
34	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
35	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
36	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
37	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
38	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
39	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
40	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
41	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
42	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
43	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
44	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
45	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
46	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
47	Class-II DAHP synthetase family protein	Phvul.008G172.5.1.54 - 3-de
48	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.008G19PTHR13343:SF
49	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.008G19PTHR13343:SF
50	Lateral organ boundaries (LOB) domain family protein	Phvul.008G25PTHR31301:SF
51	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
52	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
53	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
54	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
55	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
56	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
57	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
58	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
59	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I
60	epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09PTHR22951//I

1  
2 epsin N-terminal homology (ENTH) domain-containing prote Phvul.009G09PTHR22951//I  
3 epsin N-terminal homology (ENTH) domain-containing prote Phvul.009G09PTHR22951//I  
4 epsin N-terminal homology (ENTH) domain-containing prote Phvul.009G09PTHR22951//I  
5  
6 Vacuolar sorting protein 39 Phvul.010G05PTHR12894:SF  
7 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
8 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
9  
10 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
11 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
12 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
13 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
14 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
15 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
16 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
17 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
18 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
19 Basic-leucine zipper (bZIP) transcription factor family proteinPhvul.011G03PTHR23334 - (C  
20  
21  
22 S-locus lectin protein kinase family protein Phvul.011G14PF00954//PFC  
23 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
24 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
25 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
26 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
27 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
28 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
29 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
30 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
31 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
32 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
33 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
34 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
35 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
36 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
37 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
38 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
39 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
40 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
41 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
42 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
43 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
44 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
45 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
46 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
47 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
48 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
49 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
50 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
51 S-locus lectin protein kinase family protein Phvul.011G15PTHR27002:SF  
52  
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60













1 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
2 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
3 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
4 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
5 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
6 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
7 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
8 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
9 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1  
10 **Phvul.001G21 Protein home RING-v-class E3 ligase (original description: pacid=37167834 transcript**  
11 **Phvul.001G21 Protein home RING-v-class E3 ligase (original description: pacid=37167834 transcript**  
12 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
13 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
14 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
15 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
16 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
17 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
18 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
19 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
20 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
21 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
22 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
23 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
24 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac  
25 Phvul.002G19 Cell wall organ O-acetyltransferase (RWA) (original description: pacid=37175788 trans  
26 Phvul.002G21 not assigned.ε (original description: pacid=37176061 transcript=Phvul.002G218300.1  
27 Phvul.002G33 Cell cycle organ associated component POT of telomerase ribonucleoprotein complex (  
28 Phvul.002G33 Cell cycle organ associated component POT of telomerase ribonucleoprotein complex (  
29 Phvul.003G26 Solute transport metal cation transporter (ZIP) (original description: pacid=37145610 tr  
30 Phvul.003G26 Solute transport metal cation transporter (ZIP) (original description: pacid=37146252 tr  
31 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
32 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
33 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
34 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
35 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
36 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
37 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
38 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
39 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
40 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
41 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
42 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
43 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
44 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
45 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
46 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
47 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
48 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=  
49 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=  
50 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=  
51 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=  
52 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=  
53 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153816 transcript=  
54 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr  
55 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr  
56 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr  
57 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr  
58 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr  
59 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr  
60 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr

















































1 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
2 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
3 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
4 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
5 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
6 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
7 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
8 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:  
9 Phvul.009G11Chromatin organization modification reader component Pc of PRC1 histone mono-ubiquitinatio  
10 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
11 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
12 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
13 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
14 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
15 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
16 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
17 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
18 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
19 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
20 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
21 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
22 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
23 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1  
24 Phvul.010G15not assigned.α (original description: pacid=37143692 transcript=Phvul.010G158100.1  
25 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
26 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
27 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
28 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
29 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
30 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
31 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
32 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
33 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
34 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
35 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
36 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
37 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
38 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
39 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi  
40 Phvul.011G04Photosynthesis assembly factor CcsB of CCS cytochrome f/c6 maturation system (syste  
41 Phvul.011G04Photosynthesis assembly factor CcsB of CCS cytochrome f/c6 maturation system (syste  
42 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
43 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
44 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
45 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
46 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
47 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
48 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
49 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
50 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
51 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
52 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
53 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
54 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans  
55 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph  
56 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph  
57 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph  
58 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph  
59 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph  
60 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph











































1 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
2 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
3 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
4 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
5 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
6 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
7 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
8 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
9 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
10 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
11 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
12 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac  
13 Phvul.007G25Phytohormon ABAR chloroplast envelope-localized abscisic acid receptor (original de  
14 Phvul.008G00Cell wall orgarexine patterning factor (NEF1) (original description: pacid=37158156 tr  
15 Phvul.008G00Cell wall orgarexine patterning factor (NEF1) (original description: pacid=37158156 tr  
16 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
17 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
18 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
19 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
20 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
21 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
22 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
23 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
24 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
25 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
26 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
27 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
28 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
29 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
30 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
31 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G  
32 Phvul.008G08not assigned.r no hits & (original description: pacid=37157729 transcript=Phvul.008G  
33 Phvul.008G09Protein modif protein kinase (LRR-XII) (original description: pacid=37157650 transcrip  
34 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
35 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
36 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
37 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
38 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
39 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
40 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
41 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
42 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
43 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
44 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
45 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
46 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
47 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi  
48 Phvul.008G19not assigned.ã (original description: pacid=37158415 transcript=Phvul.008G199500.1  
49 Phvul.008G19not assigned.ã (original description: pacid=37158415 transcript=Phvul.008G199500.1  
50 Phvul.008G25RNA biosynthetranscription factor (AS2/LOB) (original description: pacid=37161314 tr  
51 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
52 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
53 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
54 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
55 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
56 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
57 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
58 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
59 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d  
60 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d

















































































































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3 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5\_arath : 98.6)  
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25 v2.1) &  
26 SS-ASSOCIATED 32 OS=Arabidopsis thaliana (sp|q8gwl1|hsa32\_arath : 383.0)  
27 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &  
28 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &  
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16 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845\_arath : 243.0)  
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29 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845\_arath : 243.0)  
30 epeat-containing protein At5g50990 OS=Arabidopsis thaliana (sp|q9fi49|pp428\_arath : 614.0)  
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46 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720\_arath : 274.0)  
47 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720\_arath : 274.0)  
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35 ol/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
36 ol/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
37 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
38 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
39 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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42 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
43 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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46 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
47 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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15 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)

16 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)

17 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)

18 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)

19 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)

20 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)

21 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)

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36 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)

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58 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22\_arath : 307.0)

59 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22\_arath : 307.0)

60 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22\_arath : 307.0)

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2 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22\_arath : 307.0)  
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28 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22\_arath : 307.0)  
29 00 ID=Phvul.006G022400.1.v2.1 annot-version=v2.1) &  
30 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &  
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44 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &  
45 phosphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311\_arath : 446.1  
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17 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1\_arath : 218.0)  
18 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1\_arath : 218.0)  
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58 attachment protein OS=Vitis vinifera (sp|p93798|snaa\_vitvi : 260.0)  
59 attachment protein OS=Vitis vinifera (sp|p93798|snaa\_vitvi : 260.0)  
60 attachment protein OS=Vitis vinifera (sp|p93798|snaa\_vitvi : 260.0)

1 attachment protein OS=Vitis vinifera (sp|p93798|snaa\_vitvi : 260.0)  
2 attachment protein OS=Vitis vinifera (sp|p93798|snaa\_vitvi : 260.0)  
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48 101 or related substance as donor(50.1.10 : 138.7) (original description: pacid=37170741 transcript=  
49 101 or related substance as donor(50.1.10 : 138.7) (original description: pacid=37168554 transcript=  
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6 va (sp|a6p6w0|casl1\_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!  
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8 va (sp|a6p6w0|casl1\_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!  
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36 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
37 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
38 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
39 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
40 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
41 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
42 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
43 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
44 )l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2\_arath : 95.1)  
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46 protein DC2.15 OS=Daucus carota (sp|p14009|14kd\_dauca : 82.8)  
47 protein DC2.15 OS=Daucus carota (sp|p14009|14kd\_dauca : 82.8)  
48 protein DC2.15 OS=Daucus carota (sp|p14009|14kd\_dauca : 82.8)  
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synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)

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2 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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6 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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11 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
12 ot-version=v2.1) &  
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14 ot-version=v2.1) &  
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24 ot-version=v2.1) &  
25 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1\_arath : 218.0)  
26 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1\_arath : 218.0)  
27 IENT OCCLUSION B OS=Arabidopsis thaliana (sp|q9ss87|seob\_arath : 168.0)  
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15 ; OS=Arabidopsis thaliana (sp|p57758|ctns\_arath : 363.0)  
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25 ; OS=Arabidopsis thaliana (sp|p57758|ctns\_arath : 363.0)  
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28 ; OS=Arabidopsis thaliana (sp|p57758|ctns\_arath : 363.0)  
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30 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript  
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se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5\_arath : 192.0)



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7 aining protein 5 OS=Arabidopsis thaliana (sp|o23225|pub5\_arath : 122.0)  
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11 [/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana \(sp|q9si13|sfh10\\_arath : 53](#)  
12 [/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana \(sp|q9si13|sfh10\\_arath : 53](#)  
13 [/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana \(sp|q9si13|sfh10\\_arath : 53](#)  
14 [/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana \(sp|q9si13|sfh10\\_arath : 53](#)  
15 [00.1.v2.1 annot-version=v2.1\) &](#)  
16 [00.1.v2.1 annot-version=v2.1\) &](#)  
17 [00.1.v2.1 annot-version=v2.1\) &](#)  
18 [00.1.v2.1 annot-version=v2.1\) &](#)  
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23 [00.1.v2.1 annot-version=v2.1\) &](#)  
24 [00.1.v2.1 annot-version=v2.1\) &](#)  
25 [00.1.v2.1 annot-version=v2.1\) &](#)  
26 [00.1.v2.1 annot-version=v2.1\) &](#)  
27 [00.1.v2.1 annot-version=v2.1\) &](#)  
28 [00.1.v2.1 annot-version=v2.1\) &](#)  
29 [ases.EC\\_2.4 glycosyltransferase\(50.2.4 : 568.2\) \(original description: pacid=37146124 transcript=Phv](#)  
30 [=Arabidopsis thaliana \(sp|b8xch5|qky\\_arath : 1272.0\)](#)  
31 [=Arabidopsis thaliana \(sp|b8xch5|qky\\_arath : 1272.0\)](#)  
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40 [=Arabidopsis thaliana \(sp|b8xch5|qky\\_arath : 1272.0\)](#)  
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44 [on=v2.1\) &](#)  
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59 [Phvul.003G274500.1.v2.1 annot-version=v2.1\) &](#)  
60 [Phvul.003G274500.1.v2.1 annot-version=v2.1\) &](#)

1 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
2 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
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7 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
8 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
9 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
10 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
11 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
12 Phvul.003G274500.1.v2.1 annot-version=v2.1) &  
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14 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
15 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
16 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
17 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
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22 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
23 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
24 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14\_arath : 87.4)  
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58 ot-version=v2.1) &  
59 **tin-protein ligase ZFP1 OS=*Oryza sativa* subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)**  
60 **tin-protein ligase ZFP1 OS=*Oryza sativa* subsp. japonica (sp|q5qlr5|zfp1\_orysj : 161.0)**

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47 protein DC2.15 OS=Daucus carota (sp|p14009|14kd\_dauca : 82.8)  
48 not-version=v2.1) &  
49 not-version=v2.1) &  
50 not-version=v2.1) &  
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13 G252700.1.v2.1 annot-version=v2.1) &  
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35 ul.008G176200.1.v2.1 annot-version=v2.1) &  
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37 ul.008G176200.1.v2.1 annot-version=v2.1) &  
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39 ul.008G176200.1.v2.1 annot-version=v2.1) &  
40 ul.008G176200.1.v2.1 annot-version=v2.1) &  
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1	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
2	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
3	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
4	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
5	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
6	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
7	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
8	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
9	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
10	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
11	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
12	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
13	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
14	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
15	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
16	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
17	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
18	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
19	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
20	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
21	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
22	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
23	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
24	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
25	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
26	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
27	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
28	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
29	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
30	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	21
31	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	21
32	uuccacagcuuu	Phvul.003G168301.2	1.5	-1	1	22
33	uuccacagcuuu	Phvul.003G168301.1	1.5	-1	1	22
34	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
35	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
36	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
37	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
38	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
39	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
40	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
41	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
42	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
43	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
44	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
45	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
46	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
47	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
48	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	21
49	uuccacagcuuu	Phvul.008G204300.1	1.5	-1	1	22
50	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21
51	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21
52	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21
53	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21
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58	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21
59	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21
60	uuccacagcuuu	Phvul.003G168400.1	2	-1	1	21

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2	uuccacagcuuu Phvul.003G168400.1	2	-1	1	21
3	uuccacagcuuu Phvul.003G168400.1	2	-1	1	21
4	uuccacagcuuu Phvul.003G168400.1	2	-1	1	22
5					
6	uuccacagcuuu Phvul.007G253900.1	2	-1	1	21
7	uuccacagcuuu Phvul.007G253900.1	2	-1	1	21
8	uuccacagcuuu Phvul.007G253900.1	2	-1	1	21
9					
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19	uuccacagcuuu Phvul.007G253900.1	2	-1	1	21
20	uuccacagcuuu Phvul.007G253900.1	2	-1	1	22
21					
22	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	21
23	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	21
24	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	21
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27	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	21
28	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	21
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35	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	21
36	uuccacagcuuu Phvul.001G155150.1	2.5	-1	1	22
37	uuccacagcuuu Phvul.002G254800.1	2.5	-1	1	21
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39	uuccacagcuuu Phvul.002G254800.1	2.5	-1	1	21
40	uuccacagcuuu Phvul.002G254800.1	2.5	-1	1	21
41	uuccacagcuuu Phvul.002G254800.1	2.5	-1	1	21
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43	uuccacagcuuu Phvul.002G254800.1	2.5	-1	1	21
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52	uuccacagcuuu Phvul.002G254800.1	2.5	-1	1	22
53	uuccacagcuuu Phvul.004G046200.1	2.5	-1	1	21
54					
55	uuccacagcuuu Phvul.004G046200.1	2.5	-1	1	21
56	uuccacagcuuu Phvul.004G046200.1	2.5	-1	1	21
57	uuccacagcuuu Phvul.004G046200.1	2.5	-1	1	21
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2	uuccacagcuuu	Phvul.004G046200.1	2.5	-1	1 21
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Do not distribute





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19	2613	2633	UUCCACAGCL ::::: : CAGUUAAG/Cleavage	pacid=371610	
20	2613	2633	UUCCACAGCL ::::: : CAGUUAAG/Cleavage	pacid=371610	
21	2613	2633	UUCCACAGCL ::::: : CAGUUAAG/Cleavage	pacid=371610	
22	2613	2633	UUCCACAGCL ::::: : CAGUUAAG/Cleavage	pacid=371610	
23	2612	2633	UUCCACAGCL ::::: : UCAGUUAAG(Cleavage	pacid=371610	
24	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
25	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
26	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
27	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
28	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
29	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
30	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
31	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
32	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
33	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
34	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
35	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
36	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
37	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
38	212	232	UUCCACAGCL ::::: : AUGUUAAG/Cleavage	pacid=371562	
39	211	232	UUCCACAGCL ::::: : AAUGUUAAG(Cleavage	pacid=371562	
40	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
41	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
42	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
43	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
44	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
45	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
46	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
47	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
48	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
49	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
50	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
51	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
52	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
53	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
54	1046	1067	UUCCACA-GC( ::::: : UCGUUAAG/Cleavage	pacid=371692	
55	1045	1067	UUCCACA-GC( : ::::: : AUCGUUAAG(Cleavage	pacid=371692	
56	814	834	UUCCACAGCL ::::: : AGGUUAAG.Cleavage	pacid=371706	
57	814	834	UUCCACAGCL ::::: : AGGUUAAG.Cleavage	pacid=371706	
58	814	834	UUCCACAGCL ::::: : AGGUUAAG.Cleavage	pacid=371706	
59	814	834	UUCCACAGCL ::::: : AGGUUAAG.Cleavage	pacid=371706	
60	814	834	UUCCACAGCL ::::: : AGGUUAAG.Cleavage	pacid=371706	





1				
2	235	256 UCCACA-GC	UCGUUCAAG/Cleavage	pacid=371782
3	670	691 UCCACA-GC	UCGUUCAAG/Cleavage	pacid=371782
4	235	256 UCCACA-GC	UCGUUCAAG/Cleavage	pacid=371782
5	670	691 UCCACA-GC	UCGUUCAAG/Cleavage	pacid=371782
6	235	256 UCCACA-GC	UCGUUCAAG/Cleavage	pacid=371782
7	670	691 UCCACA-GC	UCGUUCAAG/Cleavage	pacid=371782
8	234	256 UCCACA-GC	AUCGUUCAAC/Cleavage	pacid=371782
9	669	691 UCCACA-GC	AUCGUUCAAC/Cleavage	pacid=371782
10	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
11	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
12	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
13	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
14	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
15	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
16	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
17	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
18	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
19	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
20	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
21	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
22	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
23	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
24	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
25	794	814 UCCACAGCL	CGGUUCAAG/Cleavage	pacid=371752
26	793	814 UCCACAGCL	CCGGUUCAAC/Cleavage	pacid=371752
27	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
28	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
29	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
30	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
31	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
32	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
33	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
34	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
35	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
36	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
37	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
38	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
39	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
40	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
41	496	517 UCCACA-GC	CCGUUCAAG/Cleavage	pacid=371780
42	495	517 UCCACA-GC	ACCGUUCAAC/Cleavage	pacid=371780
43	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
44	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
45	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
46	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
47	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
48	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
49	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
50	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
51	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
52	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
53	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
54	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
55	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
56	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
57	483	503 UCCACAGCL	CUCUUCAAG/Cleavage	pacid=371758
58	482	503 UCCACAGCL	GCUCUUCAAC/Cleavage	pacid=371758
59	906	926 UCCACAGCL	GUGUACGAG/Cleavage	pacid=371778
60	906	926 UCCACAGCL	GUGUACGAG/Cleavage	pacid=371778









1			
2	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
3	860	881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
4	862	883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
5			
6	1029	1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
7	1032	1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
8	1028	1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
9			
10	1031	1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
11	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
12	349	370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
13			
14	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
15	860	881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
16	862	883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
17			
18	1029	1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
19	1032	1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
20	1028	1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
21			
22	1031	1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
23	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
24	349	370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
25			
26	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
27	860	881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
28	862	883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
29			
30	1029	1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
31	1032	1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
32	1028	1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
33			
34	1031	1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
35	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
36	349	370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
37			
38	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
39	860	881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
40	862	883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
41			
42	1029	1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
43	1032	1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
44	1028	1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
45			
46	1031	1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
47	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
48	349	370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
49			
50	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
51	860	881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
52	862	883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
53			
54	1029	1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
55	1032	1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
56	1028	1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
57			
58	1031	1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
59	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
60	349	370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
	394	415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509

1				
2	860	881 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
3	862	883 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
4	1029	1050 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
5	1032	1053 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
6	1028	1049 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
7	1031	1052 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
8				
9	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
10	349	370 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
11	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
12				
13	860	881 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
14	862	883 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
15	1029	1050 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
16	1032	1053 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
17	1028	1049 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
18	1031	1052 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
19				
20	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
21	349	370 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
22	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
23				
24	860	881 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
25	862	883 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
26	1029	1050 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
27	1032	1053 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
28	1028	1049 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
29	1031	1052 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
30				
31	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
32	349	370 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
33	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
34				
35	860	881 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
36	862	883 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
37	1029	1050 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
38	1032	1053 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
39	1028	1049 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
40	1031	1052 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
41				
42	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
43	349	370 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
44	394	415 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
45				
46	860	881 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
47	862	883 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
48	1029	1050 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
49	1032	1053 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
50	1028	1049 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
51	1031	1052 UCCACA-GCl: ::::::::::: :::::	CCGUUCAAG <sup>A</sup> Cleavage	pacid=371509
52				
53	393	415 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
54	348	370 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
55	393	415 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
56				
57	859	881 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
58	861	883 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
59	1028	1050 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
60	1031	1053 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
	1027	1049 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
	1030	1052 UCCACA-GCl: ::::::::::: :::::	CCCGUUCAAC Cleavage	pacid=371509
	1177	1197 UCCACAGCL : ::::::::::: :::::	CCCUAAAG <sup>A</sup> Cleavage	pacid=371498
	1177	1197 UCCACAGCL : ::::::::::: :::::	CCCUAAAG <sup>A</sup> Cleavage	pacid=371498
	1177	1197 UCCACAGCL : ::::::::::: :::::	CCCUAAAG <sup>A</sup> Cleavage	pacid=371498
	1177	1197 UCCACAGCL : ::::::::::: :::::	CCCUAAAG <sup>A</sup> Cleavage	pacid=371498







1				
2	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
3	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
4	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
5	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
6	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
7	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
8	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
9	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
10	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
11	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
12	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
13	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
14	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
15	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
16	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
17	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
18	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
19	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
20	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
21	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
22	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
23	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
24	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
25	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
26	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
27	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
28	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
29	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
30	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
31	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
32	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
33	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
34	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
35	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
36	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371426
37	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
38	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
39	760	781 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
40	766	787 UCCACA-GCl	UCGUUCAAG/Cleavage	pacid=371425
41	759	781 UCCACA-GCl:	AUCGUUCAAC/Cleavage	pacid=371426
42	765	787 UCCACA-GCl:	AUCGUUCAAC/Cleavage	pacid=371425
43	765	787 UCCACA-GCl:	AUCGUUCAAC/Cleavage	pacid=371425
44	759	781 UCCACA-GCl:	AUCGUUCAAC/Cleavage	pacid=371425
45	765	787 UCCACA-GCl:	AUCGUUCAAC/Cleavage	pacid=371425
46	765	787 UCCACA-GCl:	AUCGUUCAAC/Cleavage	pacid=371425
47	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
48	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
49	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
50	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
51	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
52	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
53	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
54	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
55	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
56	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
57	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
58	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
59	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
60	1938	1959 UCCACA-GCl:	CCGUUCAAG <sup>A</sup> /Cleavage	pacid=371432
	1937	1959 UCCACA-GCl:	ACCGUUCAAC/Cleavage	pacid=371432







1				
2	942	962 UUCCACAGCL	::: :: CGGUUCAAG	Cleavage pacid=371452
3	540	560 UUCCACAGCL	::: :: CGGUUCAAG	Cleavage pacid=371452
4	942	962 UUCCACAGCL	::: :: CGGUUCAAG	Cleavage pacid=371452
5				
6	539	560 UUCCACAGCL	::: :: UCGGUUCAA	Cleavage pacid=371452
7	941	962 UUCCACAGCL	::: :: UCGGUUCAA	Cleavage pacid=371452
8	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
9				
10	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
11	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
12	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
13				
14	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
15	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
16	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
17				
18	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
19	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
20	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
21				
22	984	1004 UUCCACAGCL	::: :: GAGCUCAUG	Cleavage pacid=371455
23	983	1004 UUCCACAGCL	::: :: CGAGCUCAU	Cleavage pacid=371455
24	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
25	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
26	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
27	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
28	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
29	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
30	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
31	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
32	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
33	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
34	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
35	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
36	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
37	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
38	1055	1075 UUCCACAGCL	::: :: AUGGCCAAG	Cleavage pacid=371618
39	1054	1075 UUCCACAGCL	::: :: AAUGGCCAA	Cleavage pacid=371618
40	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
41	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
42	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
43	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
44	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
45	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
46	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
47	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
48	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
49	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
50	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
51	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
52	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
53	149	169 UUCCACAGCL	::: :: AAGUUCAAG	Cleavage pacid=371545
54	148	169 UUCCACAGCL	::: :: UAAGUUCAA	Cleavage pacid=371545
55	574	594 UUCCACAGCL	::: :: CAGAUUGAG	Cleavage pacid=371713
56	574	594 UUCCACAGCL	::: :: CAGAUUGAG	Cleavage pacid=371713
57	574	594 UUCCACAGCL	::: :: CAGAUUGAG	Cleavage pacid=371713
58	574	594 UUCCACAGCL	::: :: CAGAUUGAG	Cleavage pacid=371713
59	574	594 UUCCACAGCL	::: :: CAGAUUGAG	Cleavage pacid=371713
60	574	594 UUCCACAGCL	::: :: CAGAUUGAG	Cleavage pacid=371713































1			
2	491	511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
3	750	770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
4	790	810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
5			
6	491	511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
7	750	770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
8	790	810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
9			
10	491	511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
11	750	770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
12	790	810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
13			
14	491	511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
15	750	770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
16	790	810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
17			
18	491	511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
19	750	770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
20	790	810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
21			
22	491	511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
23	750	770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
24	790	810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage	pacid=371463
25			
26	490	511 UUCCACAGCL :..... :.....:UCGGUUCAA(Cleavage	pacid=371463
27	749	770 UUCCACAGCL :..... :.....:UCGGUUCAA(Cleavage	pacid=371463
28	789	810 UUCCACAGCL :..... :.....:UCGGUUCAA(Cleavage	pacid=371463
29			
30	2392	2413 UUCCACAGCL:..... :.....:AUAGUGAGAI Cleavage	pacid=371483
31	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
32	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
33	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
34	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
35	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
36	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
37	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
38	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
39	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
40	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
41	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
42	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
43	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
44	556	576 UUCCACAGCL ::.....: .....: AAGAUCAAG(Cleavage	pacid=371476
45	555	576 UUCCACAGCL: ::.....: .....:AAAGAUCAAG(Cleavage	pacid=371476
46			
47	3519	3540 UUCCACAGCL:..... :.....: :ACUGUUCAA(Cleavage	pacid=371474
48	3671	3692 UUCCACAGCL:..... :.....: :ACUGUUCAA(Cleavage	pacid=371451
49	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
50			
51	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
52	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
53	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
54	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
55	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
56	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
57	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
58	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
59	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455
60	812	832 UUCCACAGCL :.....:.....: :: GAGUUCGAG/Cleavage	pacid=371455

























1					
2	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
3	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
4	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
5					
6	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
7	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
8	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
9					
10	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
11	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
12	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
13					
14	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
15	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
16	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
17					
18	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
19	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
20	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
21					
22	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
23	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
24	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
25					
26	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
27	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
28	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
29					
30	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
31	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
32	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
33					
34	892	912 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
35	994	1014 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
36	1474	1494 UCCACAGCL	:::.....::: AUUAUCGAG/ Cleavage		pacid=371423
37					
38	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
39	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
40	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
41	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
42	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
43	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
44	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
45	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
46	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
47	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
48	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
49	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
50	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
51	430	450 UCCACAGCL	:::.....::: ACCAUCAACA Cleavage		pacid=371556
52	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
53	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
54	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
55	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
56	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
57	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
58	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
59	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564
60	291	311 UCCACAGCL	:::.....::: CCUAUUGAG( Cleavage		pacid=371564

1				
2	291	311 UCCACAGCL	..... CCUAUUGAG	Cleavage pacid=371564
3	291	311 UCCACAGCL	..... CCUAUUGAG	Cleavage pacid=371564
4	291	311 UCCACAGCL	..... CCUAUUGAG	Cleavage pacid=371564
5	291	311 UCCACAGCL	..... CCUAUUGAG	Cleavage pacid=371564
6	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
7	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
8	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
9	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
10	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
11	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
12	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
13	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
14	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
15	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
16	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
17	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
18	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
19	292	312 UCCACAGCL	..... CAGCUGGAG	Cleavage pacid=371562
20	291	312 UCCACAGCL	..... GCAGCUGGA	Cleavage pacid=371562
21				
22	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
23	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
24	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
25	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
26	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
27	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
28	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
29	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
30	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
31	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
32	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
33	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
34	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
35	1161	1180 UCCACAGCL	..... CAGAU CAGG	Cleavage pacid=371690
36	1160	1180 UCCACAGCL	..... GCAGAU CAG	Cleavage pacid=371690
37				
38	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
39	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
40	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
41	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
42	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
43	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
44	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
45	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
46	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
47	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
48	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
49	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
50	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
51	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
52	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
53	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
54	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
55	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
56	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
57	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
58	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
59	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710
60	977	997 UCCACAGCL	..... AAGUUUGAG	Cleavage pacid=371710







1			
2	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
3	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
4	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
5			
6	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
7	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
8			
9	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
10	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
11	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
12			
13	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
14	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
15	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
16	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
17			
18	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
19	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
20	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
21			
22	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
23	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
24	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
25			
26	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
27	627	647 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
28	715	735 UUCCACAGCL :::: ::::: : :::	CAGAUCAAG <sup>A</sup> Cleavage pacid=371624
29			
30	626	647 UUCCACAGCL :::: ::::: : :::	GCAGAUCAAG <sup>A</sup> Cleavage pacid=371624
31	714	735 UUCCACAGCL :::: ::::: : :::	GCAGAUCAAG <sup>A</sup> Cleavage pacid=371624
32	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
33	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
34			
35	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
36	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
37			
38	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
39	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
40	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
41	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
42			
43	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
44	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
45	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
46			
47	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
48	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
49	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
50			
51	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
52	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
53	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
54			
55	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
56	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
57	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
58			
59	352	372 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
60	413	433 UUCCACAGCL ::::: : : ::::	UAGUUCAGG <sup>G</sup> Cleavage pacid=371540
	351	372 UUCCACAGCL ::::: : : ::::	AUAGUUCAGG <sup>G</sup> Cleavage pacid=371540



1			
2	412	433 UUCCACAGCL:::.....: : ::::AUAGUUCAG(Cleavage	pacid=371540
3	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
4	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
5	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
6	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
7	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
8	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
9	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
10	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
11	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
12	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
13	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
14	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
15	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
16	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
17	1224	1244 UUCCACAGCL :: :.....: :. CAGCUUAGG/Cleavage	pacid=371714
18	1223	1244 UUCCACAGCL :: :.....: :. UCAGCUUAG(Cleavage	pacid=371714
19	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
20	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
21	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
22	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
23	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
24	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
25	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
26	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
27	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
28	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
29	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
30	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
31	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
32	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
33	283	303 UUCCACAGCL .....: :. AGGUUCGGG(Cleavage	pacid=371729
34	282	303 UUCCACAGCL .....: :. CAGGUUCGG(Cleavage	pacid=371729
35	1264	1285 UUCCACAGCL:::.....: :.AUUUUCAA(Cleavage	pacid=371673
36	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
37	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
38	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
39	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
40	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
41	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
42	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
43	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
44	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
45	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
46	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
47	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
48	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
49	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
50	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
51	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
52	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
53	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
54	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
55	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
56	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
57	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
58	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
59	280	300 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611
60	451	471 UUCCACAGCL .....: :. :. CAGUUCAGG(Cleavage	pacid=371611











1				
2	631	651 UCCACAGCL :: ::::::::::::::	CAUCUCAAGA	Cleavage pacid=371526
3	631	651 UCCACAGCL :: ::::::::::::::	CAUCUCAAGA	Cleavage pacid=371526
4	631	651 UCCACAGCL :: ::::::::::::::	CAUCUCAAGA	Cleavage pacid=371526
5	631	651 UCCACAGCL :: ::::::::::::::	CAUCUCAAGA	Cleavage pacid=371526
6	631	651 UCCACAGCL :: ::::::::::::::	CAUCUCAAGA	Cleavage pacid=371526
7	631	651 UCCACAGCL :: ::::::::::::::	CAUCUCAAGA	Cleavage pacid=371526
8	630	651 UCCACAGCL :: ::::::::::::::	UCAUCUCAAC	Cleavage pacid=371526
9				
10	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
11	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
12	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
13	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
14	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
15	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
16	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
17	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
18	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
19	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
20	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
21	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
22	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
23	1758	1778 UCCACAGCL :::::::::::::: ::	CAGUUCGAG	Cleavage pacid=371726
24	1757	1778 UCCACAGCL :::::::::::::: ::	UCAGUUCGA	Cleavage pacid=371726
25				
26	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
27	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
28	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
29	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
30	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
31	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
32	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
33	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
34	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
35	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
36	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
37	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
38	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
39	863	884 UCCACAGCL :: :: ::::::::::::::	CAUUUCAAU	Cleavage pacid=371722
40	862	884 UCCACAGCL :: :: ::::::::::::::	ACAUUUCAAL	Cleavage pacid=371722
41	939	960 UCCACAGCL :: :: :: :: :: :: ::	GCAGUUCG	Cleavage pacid=371713
42				
43	603	623 UCCACAGCL :::::::::::::: ::	AUAGUUUAA	Cleavage pacid=371643
44	644	664 UCCACAGCL :::::::::::::: ::	AUAGUUUAA	Cleavage pacid=371643
45				
46	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
47	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
48	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
49	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
50	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
51	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
52	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
53	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
54	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
55	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
56	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
57	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
58	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
59	4525	4545 UCCACAGCL :: :::::::::::::: ..	CGGAACAAGA	Cleavage pacid=371668
60	1780	1801 UCCACAGCL :: :: :: :: :: :: ::	ACAGUACAAC	Cleavage pacid=371656
	1898	1919 UCCACAGCL :: :: :: :: :: :: ::	ACAGUACAAC	Cleavage pacid=371656





1			
2	685	703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage	pacid=371569
3	685	703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage	pacid=371569
4	685	703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage	pacid=371569
5	685	703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage	pacid=371569
6	685	703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage	pacid=371569
7	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
8	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
9	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
10	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
11	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
12	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
13	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
14	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
15	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
16	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
17	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
18	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
19	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
20	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
21	1397	1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage	pacid=371790
22	1396	1417 UUCCACAGCL ::::::::::: UCGGUUCGG(Cleavage	pacid=371790
23			
24			
25			
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1				
2	1	Phvul.002G248200.1	Phvul.002G248200	Phvul.002G248200 PF13894
3	1	Phvul.002G248200.1	Phvul.002G248200	Phvul.002G248200 PF13894
4	1	Phvul.002G248200.1	Phvul.002G248200	Phvul.002G248200 PF13894
5				
6	1	Phvul.002G330600.1	Phvul.002G330600	Phvul.002G330600 PF08238
7	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
8	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
9				
10	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
11	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
12	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
13				
14	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
15	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
16	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
17				
18	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
19	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
20	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
21				
22	1	Phvul.003G105600.1	Phvul.003G105600	Phvul.003G105600 PF06827,PF08
23	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
24	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
25				
26	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
27	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
28	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
29				
30	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
31	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
32	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
33				
34	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
35	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
36	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
37	1	Phvul.003G127400.1	Phvul.003G127400	Phvul.003G127400 PF11995,PF00
38	1	Phvul.003G140200.2	Phvul.003G140200	Phvul.003G140200 PF00690,PF12
39	1	Phvul.003G140200.1	Phvul.003G140200	Phvul.003G140200 PF00690,PF12
40	1	Phvul.003G140200.2	Phvul.003G140200	Phvul.003G140200 PF00690,PF12
41	1	Phvul.003G140200.1	Phvul.003G140200	Phvul.003G140200 PF00690,PF12
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43	1	Phvul.003G140200.2	Phvul.003G140200	Phvul.003G140200 PF00690,PF12
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1 Phvul.003G205600.1	Phvul.003G205600	Phvul.003G205600	PF03144,PF03
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1 Phvul.003G205600.1	Phvul.003G205600	Phvul.003G205600	PF03144,PF03
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1 Phvul.004G012700.2	Phvul.004G012700	Phvul.004G012700	PF00122,PF12
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23	1	Phvul.007G188900.1	Phvul.007G188900	Phvul.007G188900 PF14432,PF01
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26	1	Phvul.007G189100.1	Phvul.007G189100	Phvul.007G189100 PF13041,PF01
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8	1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041
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12	1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041
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18	1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041
19	1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041
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23	1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041
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33	1	Phvul.008G118100.2	Phvul.008G118100	Phvul.008G118100	0
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35	1	Phvul.008G118100.3	Phvul.008G118100	Phvul.008G118100	0
36	1	Phvul.008G118100.1	Phvul.008G118100	Phvul.008G118100	0
37	1	Phvul.008G118100.2	Phvul.008G118100	Phvul.008G118100	0
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28	1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
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32	1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
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34	1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
35	1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
36	1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
37	1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
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49	1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
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51	1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
52	1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
53	1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
54					
55	1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00
56	1	Phvul.009G037300.1	Phvul.009G037300	Phvul.009G037300	PF01486,PF00
57	1	Phvul.009G037300.1	Phvul.009G037300	Phvul.009G037300	PF01486,PF00
58					
59	1	Phvul.009G037300.1	Phvul.009G037300	Phvul.009G037300	PF01486,PF00
60	1	Phvul.009G037300.1	Phvul.009G037300	Phvul.009G037300	PF01486,PF00
	1	Phvul.009G037300.1	Phvul.009G037300	Phvul.009G037300	PF01486,PF00

























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2	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
3	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
4	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
5					
6	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
7	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
8	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
9					
10	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
11	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
12	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
13					
14	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
15	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
16	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
17					
18	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
19	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
20	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
21					
22	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
23	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
24	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
25					
26	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
27	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
28	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
29	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
30					
31	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
32	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
33					
34	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
35	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
36	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
37	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
38					
39	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
40	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
41	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
42					
43	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
44	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
45	1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
46					
47	1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
48	1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
49	1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
50					
51	1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
52	1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
53	1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
54					
55	1	Phvul.007G184400.3	Phvul.007G184400	Phvul.007G184400	PF00400
56	1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
57	1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
58					
59	1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
60	1	Phvul.007G184400.3	Phvul.007G184400	Phvul.007G184400	PF00400
	1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400



























1					
2	1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
3	1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
4	1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
5					
6	1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
7	1	Phvul.008G055200.1	Phvul.008G055200	Phvul.008G055200	PF03547
8	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
9					
10	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
11	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
12	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
13					
14	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
15	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
16	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
17					
18	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
19	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
20	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
21					
22	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
23	1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
24	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
25					
26	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
27	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
28	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
29					
30	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
31	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
32	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
33					
34	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
35	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
36	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
37	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
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39	1	Phvul.008G192200.1	Phvul.008G192200	Phvul.008G192200	0
40	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
41	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
42					
43	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
44	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
45	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
46					
47	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
48	1	Phvul.008G277900.1	Phvul.008G277900	Phvul.008G277900	PF01095
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56	1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
57	1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
58					
59	1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
60	1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
	1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04

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1 Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1 Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1 Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1 Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1 Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1 Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1 Phvul.009G086300.2	Phvul.009G086300	Phvul.009G086300	PF12776
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1 Phvul.009G086300.1	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G086300.2	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G086300.1	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G086300.2	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G086300.1	Phvul.009G086300	Phvul.009G086300	PF12776
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1 Phvul.009G086300.1	Phvul.009G086300	Phvul.009G086300	PF12776
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1 Phvul.009G086300.1	Phvul.009G086300	Phvul.009G086300	PF12776
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1 Phvul.009G086300.2	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G086300.1	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G086300.2	Phvul.009G086300	Phvul.009G086300	PF12776
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
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1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1 Phvul.010G131100.2	Phvul.010G131100	Phvul.010G131100	PF00067
1 Phvul.010G140600.2	Phvul.010G140600	Phvul.010G140600	PF00664,PF00
1 Phvul.010G140600.2	Phvul.010G140600	Phvul.010G140600	PF00664,PF00
1 Phvul.010G140600.2	Phvul.010G140600	Phvul.010G140600	PF00664,PF00
1 Phvul.010G140600.2	Phvul.010G140600	Phvul.010G140600	PF00664,PF00







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2	1	Phvul.005G105400.1	Phvul.005G105400	Phvul.005G105400 PF03168
3	1	Phvul.005G105400.1	Phvul.005G105400	Phvul.005G105400 PF03168
4	1	Phvul.005G105400.1	Phvul.005G105400	Phvul.005G105400 PF03168
5				
6	1	Phvul.005G105400.1	Phvul.005G105400	Phvul.005G105400 PF03168
7	1	Phvul.005G105400.1	Phvul.005G105400	Phvul.005G105400 PF03168
8	1	Phvul.005G105400.1	Phvul.005G105400	Phvul.005G105400 PF03168
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10	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
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12	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
13				
14	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
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16	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
17				
18	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
19	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
20	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
21				
22	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
23	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
24	1	Phvul.006G142000.1	Phvul.006G142000	Phvul.006G142000 PF00083
25				
26	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
27	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
28	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
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31	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
32	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
33				
34	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
35	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
36	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
37	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
38				
39	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
40	1	Phvul.006G157700.1	Phvul.006G157700	Phvul.006G157700 PF12937,PF13
41	1	Phvul.006G200900.1	Phvul.006G200900	Phvul.006G200900 PF04576
42				
43	1	Phvul.007G083600.1	Phvul.007G083600	Phvul.007G083600 PF10994
44	1	Phvul.007G083600.2	Phvul.007G083600	Phvul.007G083600 PF10994
45	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
46	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
47	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
48	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
49	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
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53	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
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55	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
56	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
57	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
58	2	Phvul.007G136300.1	Phvul.007G136300	Phvul.007G136300 PF00400,PF04
59	1	Phvul.007G175300.2	Phvul.007G175300	Phvul.007G175300 PF13385,PF00
60	1	Phvul.007G175300.3	Phvul.007G175300	Phvul.007G175300 PF13385,PF00



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2	1 Phvul.011G090600.1	Phvul.011G090600	Phvul.011G090600	PF00300
3	1 Phvul.011G090600.1	Phvul.011G090600	Phvul.011G090600	PF00300
4	1 Phvul.011G090600.1	Phvul.011G090600	Phvul.011G090600	PF00300
5				
6	1 Phvul.011G090600.1	Phvul.011G090600	Phvul.011G090600	PF00300
7	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
8	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
9				
10	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
11	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
12	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
13	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
14	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
15	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
16	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
17	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
18	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
19	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
20	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
21	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
22	1 Phvul.L001616.1	Phvul.L001616	Phvul.L001616	PF04564,PF00
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2		0	0	0	0	0	0
3		0	0	0	0	0	0
4		0	0	0	0	0	0
5		0	0	0	0	0	0
6	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
7	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
8	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
9	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
10	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
11	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
12	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
13	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
14	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
15	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
16	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
17	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
18	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
19	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
20	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
21	PTHR33142,P <sup>-</sup>	0	0	0	0	AT3G20898.1	0
22	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
23	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
24	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
25	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
26	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
27	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
28	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
29	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
30	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
31	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
32	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
33	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
34	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
35	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
36	PTHR24093,P <sup>-</sup>	0 3.6.3.8		0	0	AT3G63380.1	0
37	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
38	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
39	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
40	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
41	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
42	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
43	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
44	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
45	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
46	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
47	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
48	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
49	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
50	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
51	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
52	PTHR22904,P <sup>-</sup> KOG0548,KOC		0 K09527		0	AT5G65160.1	0
53	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
54	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
55	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
56	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
57	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
58	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
59	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
60	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0
	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C	AT3G22910.1		0

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2	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C AT3G22910.1	0
3	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C AT3G22910.1	0
4	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C AT3G22910.1	0
5	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C AT3G22910.1	0
6	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C AT3G22910.1	0
7	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0046872,C AT3G22910.1	0
8	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
9	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
10	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
11	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
12	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
13	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
14	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
15	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
16	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
17	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
18	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
19	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
20	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
21	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
22	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
23	PTHR11361,P <sup>-</sup>	0	0	0 GO:0030983,C AT5G54090.1	0
24	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
25	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
26	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
27	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
28	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
29	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
30	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
31	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
32	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
33	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
34	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
35	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
36	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
37	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
38	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
39	PTHR12217,P <sup>-</sup>	0	0 K15027	GO:0006413,C AT1G71350.1	0
40	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
41	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
42	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
43	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
44	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
45	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
46	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
47	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
48	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
49	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
50	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
51	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
52	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
53	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
54	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
55	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1	0
56	PTHR16019,P <sup>-</sup>	0	0	0 0 AT1G03350.1	0
57	PTHR16019,P <sup>-</sup>	0	0	0 0 AT1G03350.1	0
58	PTHR16019,P <sup>-</sup>	0	0	0 0 AT1G03350.1	0
59	PTHR16019,P <sup>-</sup>	0	0	0 0 AT1G03350.1	0
60	PTHR16019,P <sup>-</sup>	0	0	0 0 AT1G03350.1	0
	PTHR16019,P <sup>-</sup>	0	0	0 0 AT1G03350.1	0







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2	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
3	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
4	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
5	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
6	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
7	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
8	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
9	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
10	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
11	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
12	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
13	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
14	PTHR11246,P <sup>-</sup>	0	0 K12869	GO:0005515,(AT5G41770.1		0
15	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
16	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
17	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
18	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
19	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
20	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
21	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
22	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
23	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
24	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
25	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
26	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
27	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
28	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
29	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
30	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(AT1G10900.1		0
31	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
32	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
33	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
34	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
35	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
36	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
37	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
38	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
39	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
40	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
41	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
42	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
43	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
44	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
45	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
46	PTHR24015,P <sup>-</sup>	0	0	0 AT1G31430.1		0
47	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
48	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
49	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
50	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
51	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
52	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
53	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
54	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
55	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
56	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
57	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
58	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
59	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
60	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0
	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5		0

1						
2	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
3	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
4	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
5	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
6	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
7	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
8	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
9	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
10	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
11	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
12	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
13	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
14	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
15	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
16	PTHR19375,P <sup>-</sup>	0	0 K03283	0 AT1G16030.1 Hsp70b		
17						
18	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
19	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
20	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
21	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
22	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
23	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
24	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
25	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
26	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
27	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
28	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
29	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
30	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
31	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
32	PTHR22904,P <sup>-</sup> KOG4412		0	0 GO:0005515 AT3G04710.3		0
33						
34	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
35	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
36	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
37	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
38	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
39	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
40	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
41	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
42	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
43	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
44	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
45	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
46	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
47	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
48	PTHR19957,P <sup>-</sup> KOG0810		0 K08486	GO:0005515,( AT1G61290.1 ATSYP124,SYP		
49						
50	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
51	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
52	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
53	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
54	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
55	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
56	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
57	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
58	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
59	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
60	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		
	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,( AT2G36400.1 AtGRF3,GRF3		

1						
2	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT2G36400.1 AtGRF3,GRF3	
3	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT2G36400.1 AtGRF3,GRF3	
4	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
5						
6	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
7	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
8	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
9						
10	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
11	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
12	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
13						
14	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
15	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
16	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
17	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
18	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
19	PTHR24177 KOG4214		0	0	GO:0008270 AT3G54070.1	0
20	PTHR24177	0	0	0	AT3G54070.1	0
21	PTHR24177	0	0	0	AT3G54070.1	0
22	PTHR24177	0	0	0	AT3G54070.1	0
23	PTHR24177	0	0	0	AT3G54070.1	0
24	PTHR24177	0	0	0	AT3G54070.1	0
25	PTHR24177	0	0	0	AT3G54070.1	0
26	PTHR24177	0	0	0	AT3G54070.1	0
27	PTHR24177	0	0	0	AT3G54070.1	0
28	PTHR24177	0	0	0	AT3G54070.1	0
29	PTHR24177	0	0	0	AT3G54070.1	0
30	PTHR24177	0	0	0	AT3G54070.1	0
31	PTHR24177	0	0	0	AT3G54070.1	0
32	PTHR24177	0	0	0	AT3G54070.1	0
33	PTHR24177	0	0	0	AT3G54070.1	0
34	PTHR24177	0	0	0	AT3G54070.1	0
35	PTHR24177	0	0	0	AT3G54070.1	0
36	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
37	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
38	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
39	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
40	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
41	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
42	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
43	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
44	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
45	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
46	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
47	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
48	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
49	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
50	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
51	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
52	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
53	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
54	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
55	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
56	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
57	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
58	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
59	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
60	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	
	PTHR31602,P <sup>-</sup>	0	0	0	GO:0006355,C AT4G37740.1 AtGRF2,GRF2	













1				
2	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
3	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
4	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
5	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
6	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
7	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
8	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
9	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
10	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
11	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
12	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
13	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
14	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
15	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
16	PTHR11771,P <sup>-</sup>	0	1.13.11.58	0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1
17	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
18	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
19	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
20	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
21	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
22	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
23	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
24	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
25	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
26	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
27	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
28	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
29	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
30	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
31	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
32	PTHR31602,P <sup>-</sup>	0	0	0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5
33	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
34	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
35	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
36	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
37	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
38	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
39	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
40	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
41	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
42	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
43	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
44	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
45	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
46	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
47	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
48	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13		0 GO:0016787,(AT5G26742.2 emb1138
49	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
50	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
51	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
52	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
53	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
54	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
55	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
56	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
57	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
58	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
59	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3
60	PTHR32409,P <sup>-</sup>	0	0	0 GO:0045040,(AT3G27080.1 TOM20-3

1							
2	PTHR32409,P <sup>-</sup>	0	0	0	GO:0045040,C	AT3G27080.1	TOM20-3
3	PTHR32409,P <sup>-</sup>	0	0	0	GO:0045040,C	AT3G27080.1	TOM20-3
4	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
5	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
6	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
7	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
8	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
9	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
10	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
11	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
12	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
13	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
14	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
15	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
16	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
17	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
18	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
19	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
20	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
21	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
22	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
23	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
24	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
25	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
26	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
27	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
28	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
29	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
30	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
31	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
32	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
33	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
34	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
35	PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,C	AT4G17510.1	UCH3
36	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
37	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
38	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
39	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
40	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
41	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
42	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
43	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
44	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
45	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
46	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
47	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
48	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
49	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
50	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
51	PTHR11727,P <sup>-</sup>	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
52	PTHR14003	0	0	0	0	AT4G06634.1	0
53	PTHR14003	0	0	0	0	AT4G06634.1	0
54	PTHR14003	0	0	0	0	AT4G06634.1	0
55	PTHR14003	0	0	0	0	AT4G06634.1	0
56	PTHR14003	0	0	0	0	AT4G06634.1	0
57	PTHR14003	0	0	0	0	AT4G06634.1	0
58	PTHR14003	0	0	0	0	AT4G06634.1	0
59	PTHR14003	0	0	0	0	AT4G06634.1	0
60	PTHR14003	0	0	0	0	AT4G06634.1	0
	PTHR14003	0	0	0	0	AT4G06634.1	0



1						
2	PTHR14003	0	0	0	0 AT4G06634.1	0
3	PTHR14003	0	0	0	0 AT4G06634.1	0
4	PTHR14003	0	0	0	0 AT4G06634.1	0
5						
6	PTHR11102,P <sup>-</sup> KOG1550		0 K14026		0 AT1G18260.1	0
7	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
8	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
9						
10	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
11	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
12	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
13						
14	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
15	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
16	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
17						
18	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
19	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
20	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
21						
22	PTHR11946,P <sup>-</sup>	0 6.1.1.5	K01870		GO:0006418,(AT5G49030.3 OVA2	
23	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
24	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
25						
26	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
27	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
28	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
29						
30	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
31	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
32	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
33						
34	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
35	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
36	PTHR24115,P <sup>-</sup> KOG0242	3.6.4.4	K11498		GO:0008017,(AT3G43210.1 ATNACK2,NAC	
37						
38	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
39	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
40	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
41						
42	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
43	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
44	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
45	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
46						
47	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
48	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
49	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
50						
51	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
52	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
53						
54	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
55	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
56	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
57						
58	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
59	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
60	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	
	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537		GO:0005516,(AT5G57110.2 ACA8,AT-ACA	



1						
2	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0005516,( AT5G57110.2 ACA8,AT-ACA8		
3	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0005516,( AT5G57110.2 ACA8,AT-ACA8		
4	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0005516,( AT5G57110.2 ACA8,AT-ACA8		
5	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0005516,( AT5G57110.2 ACA8,AT-ACA8		
6	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0005516,( AT5G57110.2 ACA8,AT-ACA8		
7	PTHR24093,P <sup>-</sup>	0 3.6.3.8	K01537	GO:0005516,( AT5G57110.2 ACA8,AT-ACA8		
8	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
9	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
10	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
11	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
12	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
13	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
14	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
15	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
16	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
17	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
18	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
19	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
20	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
21	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
22	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
23	PTHR23115,P <sup>-</sup>	0 3.6.5.3	K02358	GO:0005525 AT4G20360.1 ATRAB8D,ATR		
24	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
25	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
26	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
27	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
28	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
29	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
30	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
31	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
32	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
33	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
34	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
35	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
36	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
37	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
38	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
39	PTHR24092,P <sup>-</sup>	0 3.6.3.1	K01530	GO:0046872,( AT3G27870.1		0
40	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
41	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
42	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
43	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
44	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
45	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
46	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
47	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
48	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
49	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
50	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
51	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
52	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
53	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
54	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
55	PTHR33178,P <sup>-</sup>	0	0	0 AT5G22580.1		0
56	PTHR18359	0	0 K14553	GO:0005515 AT5G14050.1		0
57	PTHR18359	0	0 K14553	GO:0005515 AT5G14050.1		0
58	PTHR18359	0	0 K14553	GO:0005515 AT5G14050.1		0
59	PTHR18359	0	0 K14553	GO:0005515 AT5G14050.1		0
60	PTHR18359	0	0 K14553	GO:0005515 AT5G14050.1		0
	PTHR18359	0	0 K14553	GO:0005515 AT5G14050.1		0

1						
2	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
3	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
4	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
5	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
6	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
7	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
8	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
9	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
10	PTHR18359	0	0 K14553	GO:0005515	AT5G14050.1	0
11	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
13	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
14	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
15	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
16	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
17	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
18	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
19	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
20	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
21	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
22	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
23	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
24	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
25	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
26	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
27	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
28	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
29	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
30	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
31	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
32	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
33	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
34	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
35	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
36	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
37	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
38	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
39	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
40	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G11460.1	0
41	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
42	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
43	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
44	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
45	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
46	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
47	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
48	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
49	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
50	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
51	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
52	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
53	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
54	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
55	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
56	PTHR24096,P <sup>-</sup>	0 6.2.1.3	K01897	GO:0008152,(	AT2G47240.1 CER8,LACS1	
57	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1	0
58	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1	0
59	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1	0
60	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1	0

1					
2	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
3	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
4	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
5	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
6	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
7	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
8	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
9	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
10	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
11	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
12	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
13	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
14	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
15	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
16	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
17	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
18	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
19	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
20	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
21	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
22	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
23	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
24	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
25	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
26	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
27	PTHR23241,P <sup>-</sup> KOG4744		0	0	0 AT3G53040.1
28	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
29	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
30	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
31	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
32	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
33	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
34	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
35	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
36	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
37	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
38	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
39	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
40	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
41	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
42	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
43	PTHR31642,P <sup>-</sup>	0 2.3.1.196		0 GO:0016747	AT5G17540.1
44	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
45	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
46	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
47	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
48	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
49	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
50	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
51	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
52	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
53	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
54	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
55	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
56	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
57	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
58	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,C	AT4G10780.1
59	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1
60	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1
	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1

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2	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
3	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
4	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
5	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
6	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
7	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
8	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
9	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
10	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
11	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
13	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
14	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
15	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
16	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
17	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
18	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
19	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
20	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
21	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
22	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
23	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
24	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
25	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
26	PTHR24015,P <sup>-</sup>	0	0	0	0 AT4G19890.1	0
27	0	0	0	0	0 AT5G02130.1 NDP1	
28	0	0	0	0	0 AT5G02130.1 NDP1	
29	0	0	0	0	0 AT5G02130.1 NDP1	
30	0	0	0	0	0 AT5G02130.1 NDP1	
31	0	0	0	0	0 AT5G02130.1 NDP1	
32	0	0	0	0	0 AT5G02130.1 NDP1	
33	0	0	0	0	0 AT5G02130.1 NDP1	
34	0	0	0	0	0 AT5G02130.1 NDP1	
35	0	0	0	0	0 AT5G02130.1 NDP1	
36	0	0	0	0	0 AT5G02130.1 NDP1	
37	0	0	0	0	0 AT5G02130.1 NDP1	
38	0	0	0	0	0 AT5G02130.1 NDP1	
39	0	0	0	0	0 AT5G02130.1 NDP1	
40	0	0	0	0	0 AT5G02130.1 NDP1	
41	0	0	0	0	0 AT5G02130.1 NDP1	
42	0	0	0	0	0 AT5G02130.1 NDP1	
43	0	0	0	0	0 AT5G02130.1 NDP1	
44	0	0	0	0	0 AT5G02130.1 NDP1	
45	0	0	0	0	0 AT5G02130.1 NDP1	
46	0	0	0	0	0 AT5G02130.1 NDP1	
47	0	0	0	0	0 AT5G02130.1 NDP1	
48	0	0	0	0	0 AT5G02130.1 NDP1	
49	0	0	0	0	0 AT5G02130.1 NDP1	
50	0	0	0	0	0 AT5G02130.1 NDP1	
51	0	0	0	0	0 AT5G02130.1 NDP1	
52	0	0	0	0	0 AT5G02130.1 NDP1	
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56	0	0	0	0	0 AT5G02130.1 NDP1	
57	0	0	0	0	0 AT5G02130.1 NDP1	
58	0	0	0	0	0 AT5G02130.1 NDP1	
59	0	0	0	0	0 AT5G02130.1 NDP1	
60	0	0	0	0	0 AT5G02130.1 NDP1	
	0	0	0	0	0 AT5G02130.1 NDP1	

1						
2		0	0	0	0	0 AT5G02130.1 NDP1
3		0	0	0	0	0 AT5G02130.1 NDP1
4		0	0	0	0	0 AT5G02130.1 NDP1
5		0	0	0	0	0 AT5G02130.1 NDP1
6		0	0	0	0	0 AT5G02130.1 NDP1
7		0	0	0	0	0 AT5G02130.1 NDP1
8		0	0	0	0	0 AT5G02130.1 NDP1
9		0	0	0	0	0 AT5G02130.1 NDP1
10	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
11	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
12	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
13	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
14	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
15	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
16	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
17	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
18	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
19	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
20	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
21	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
22	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
23	PTHR13522	KOG3102		0	0 GO:0034477,(AT5G51170.1	0
24	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
25	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
26	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
27	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
28	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
29	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
30	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
31	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
32	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
33	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
34	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
35	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
36	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
37	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
38	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
39	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
40	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
41	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
42	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
43	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
44	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
45	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
46	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
47	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
48	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
49	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
50	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
51	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
52	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
53	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
54	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
55	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.23		0 GO:0003723,(AT1G76050.2	0
56	PTHR11945,P <sup>-</sup>	KOG0014		0	0 GO:0006355,(AT2G22540.1 AGL22,SVP	
57	PTHR11945,P <sup>-</sup>	KOG0014		0	0 GO:0006355,(AT2G22540.1 AGL22,SVP	
58	PTHR11945,P <sup>-</sup>	KOG0014		0	0 GO:0006355,(AT2G22540.1 AGL22,SVP	
59	PTHR11945,P <sup>-</sup>	KOG0014		0	0 GO:0006355,(AT2G22540.1 AGL22,SVP	
60	PTHR11945,P <sup>-</sup>	KOG0014		0	0 GO:0006355,(AT2G22540.1 AGL22,SVP	

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2	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
3	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
4	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
5	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
6	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
7	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
8	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
9	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
10	PTHR11945,P <sup>-</sup> KOG0014		0	0	GO:0006355,C AT2G22540.1 AGL22,SVP	
11	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
12	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
13	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
14	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
15	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
16	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
17	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
18	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
19	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
20	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
21	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
22	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
23	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
24	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
25	PTHR24015,P <sup>-</sup>	0	0	0	AT2G04860.1	0
26	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
27	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
28	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
29	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
30	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
31	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
32	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
33	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
34	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
35	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
36	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
37	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
38	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
39	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
40	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
41	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
42	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
43	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
44	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
45	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
46	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
47	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
48	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
49	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
50	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
51	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
52	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
53	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
54	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
55	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
56	PTHR31115,P <sup>-</sup>	0	0	0	AT4G29790.1	0
57	PTHR13780,P <sup>-</sup>	0	0	0	AT1G09020.1 ATSNF4,SNF4	
58	PTHR13780,P <sup>-</sup>	0	0	0	AT1G09020.1 ATSNF4,SNF4	
59	PTHR13780,P <sup>-</sup>	0	0	0	AT1G09020.1 ATSNF4,SNF4	
60	PTHR13780,P <sup>-</sup>	0	0	0	AT1G09020.1 ATSNF4,SNF4	



1					
2	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
3	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
4	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
5	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
6	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
7	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
8	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
9	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
10	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
11	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
12	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
13	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
14	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
15	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
16	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
17	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
18	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
19	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
20	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
21	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
22	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
23	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
24	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
25	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
26	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
27	PTHR13780,P <sup>-</sup>	0	0	0	0 AT1G09020.1 ATSNF4,SNF4
28	PTHR11771,P <sup>-</sup>	0 1.13.11.58	K15718	GO:0005515,(	AT1G55020.1 ATLOX1,LOX1
29	PTHR11771,P <sup>-</sup>	0 1.13.11.58	K15718	GO:0005515,(	AT1G55020.1 ATLOX1,LOX1
30	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
31	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
32	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
33	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
34	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
35	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
36	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
37	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
38	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
39	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
40	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
41	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
42	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
43	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
44	PTHR13878,P <sup>-</sup>	0 1.5.99.12	K00279	GO:0055114,(	AT3G63440.1 ATCKX6,ATCK
45	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
46	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
47	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
48	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
49	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
50	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
51	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
52	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
53	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
54	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
55	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
56	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
57	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
58	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
59	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
60	PTHR23428 KOG1744		0 K11252	GO:0003677,(	AT1G08170.1 0
	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17		0 GO:0016757,(	AT4G33330.2 GUX2,PGSIP3

1			
2	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
3	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
4	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
5			
6	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
7	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
8	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
9			
10	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
11	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
12	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
13	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
14	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
15	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
16	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
17	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
18	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
19	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
20	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
21	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
22	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
23	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
24	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
25	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
26	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
27	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
28	PTHR11183,P <sup>-</sup> KOG1950	2.4.1.17	0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3
29			
30	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
31	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
32	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
33	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
34	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
35	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
36	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
37	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
38	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
39	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
40	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
41	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
42	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
43	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
44	PTHR10209,P <sup>-</sup> KOG0143	0 K04124	GO:0055114,(AT1G15550.1 ATGA3OX1,G/
45	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
46	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
47	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
48	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
49	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
50	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
51	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
52	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
53	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
54	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
55	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
56	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
57	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
58	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
59	PTHR10277,P <sup>-</sup>	0 2.3.3.13	0 GO:0009098,(AT1G18500.1 IPMS1,MAML
60	PTHR10277,P <sup>-</sup>	0 2.3.3.14	0 GO:0009098,(AT1G74040.1 IMS1,IPMS2,N
	PTHR10277,P <sup>-</sup>	0 2.3.3.14	0 GO:0009098,(AT1G74040.1 IMS1,IPMS2,N

1					
2	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
3	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
4	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
5	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
6	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
7	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
8	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
9	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
10	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
11	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
12	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
13	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
14	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
15	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
16	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
17	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
18	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
19	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
20	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
21	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
22	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
23	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
24	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
25	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
26	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
27	PTHR10277,P <sup>-</sup>	0	2.3.3.14	0	GO:0009098,C AT1G74040.1 IMS1,IPMS2,N
28	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
29	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
30	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
31	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
32	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
33	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
34	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
35	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
36	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
37	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
38	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
39	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
40	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
41	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
42	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
43	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0	GO:0006508,C AT1G66180.1 0
44	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
45	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
46	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
47	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
48	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
49	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
50	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
51	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
52	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
53	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
54	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
55	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
56	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
57	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
58	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
59	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0
60	PTHR33732,P <sup>-</sup>	0	0	0	AT1G67360.2 0

1						
2	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
3	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
4	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
5	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
6	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
7	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
8	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
9	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
10	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
11	PTHR33732,P <sup>-</sup>	0	0	0	0 AT1G67360.2	0
12	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
13	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
14	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
15	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
16	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
17	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
18	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
19	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
20	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
21	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
22	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
23	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
24	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
25	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
26	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
27	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
28	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
29	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
30	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
31	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
32	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
33	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
34	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
35	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
36	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
37	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
38	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
39	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
40	PTHR31113,P <sup>-</sup>	0	0	0	0 AT2G18630.1	0
41	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
42	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
43	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
44	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
45	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
46	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
47	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
48	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
49	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
50	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
51	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
52	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
53	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
54	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
55	PTHR11679,P <sup>-</sup>	0	0	0	0 GO:0016192,(AT2G17980.1 ATSLY1	
56	PTHR10209,P <sup>-</sup> KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EF		
57	PTHR10209,P <sup>-</sup> KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EF		
58	PTHR10209,P <sup>-</sup> KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EF		
59	PTHR10209,P <sup>-</sup> KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EF		
60	PTHR10209,P <sup>-</sup> KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EF		
	PTHR10209,P <sup>-</sup> KOG0143	1.14.17.4	K05933	GO:0055114,(AT1G05010.1 ACO4,EAT1,EF		





1						
2	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
3	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
4	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
5	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
6	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
7	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
8	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
9	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
10	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
11	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
12	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
13	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
14	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
15	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
16	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
17	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
18	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
19	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
20	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
21	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
22	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
23	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
24	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
25	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
26	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
27	PTHR34778,P <sup>-</sup>	0	0	0	0 AT1G19010.1	0
28	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
29	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
30	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
31	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
32	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
33	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
34	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
35	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
36	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
37	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
38	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
39	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
40	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
41	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
42	PTHR12626,P <sup>-</sup>	0	0	0	0 AT5G63190.1	0
43	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
44	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
45	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
46	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
47	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
48	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
49	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
50	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
51	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
52	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
53	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
54	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
55	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
56	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
57	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
58	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
59	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
60	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	
	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26			0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C	



1					
2	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
3	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
4	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
5	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
6	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
7	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
8	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
9	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
10	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
11	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
12	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
13	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
14	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
15	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
16	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
17	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
18	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
19	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
20	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
21	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
22	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
23	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
24	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
25	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
26	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
27	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
28	PTHR11654,P <sup>-</sup> KOG1237	3.6.3.26	0	GO:0016020,C AT1G12110.1 ATNRT1,B-1,C	
29	PTHR12029,P <sup>-</sup>	0 2.1.1.34	0	GO:0008173,C AT4G17610.1	0
30	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
31	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
32	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
33	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
34	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
35	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
36	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
37	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
38	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
39	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
40	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
41	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
42	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
43	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
44	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
45	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
46	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14	0	GO:0008234,C AT3G19390.1	0
47	PTHR14237,P <sup>-</sup>	0 2.8.1.9	0	AT2G23520.1	0
48	PTHR14237,P <sup>-</sup>	0 2.8.1.9	0	AT2G23520.1	0
49	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
50	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
51	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
52	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
53	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
54	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
55	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
56	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
57	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
58	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
59	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
60	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0
	PTHR23324,P <sup>-</sup> KOG1471	0	0	AT1G55690.3	0











1						
2	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13	K16911	GO:0008270,C	AT5G26742.2 emb1138	
3	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13	K16911	GO:0008270,C	AT5G26742.2 emb1138	
4	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13	K16911	GO:0008270,C	AT5G26742.2 emb1138	
5	PTHR24031,P <sup>-</sup> KOG0331	3.6.4.13	K16911	GO:0008270,C	AT5G26742.2 emb1138	
6	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
7	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
8	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
9	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
10	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
11	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
12	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
13	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
14	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
15	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
16	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
17	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
18	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
19	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
20	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
21	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
22	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
23	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
24	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
25	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
26	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
27	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
28	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
29	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
30	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
31	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
32	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
33	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
34	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
35	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
36	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
37	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
38	PTHR10221,P <sup>-</sup> KOG2549		0 K03131	GO:0006352,C	AT1G04950.1 ATTA6,TAF6,	
39	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
40	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
41	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
42	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
43	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
44	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
45	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
46	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
47	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
48	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
49	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
50	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
51	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
52	PTHR36795,P <sup>-</sup>	0	0	0	AT5G14410.1	0
53	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
54	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
55	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
56	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
57	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
58	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
59	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
60	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0
	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2	0



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2	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2		0
3	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2		0
4	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2		0
5	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2		0
6	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2		0
7	PTHR24012,P <sup>-</sup> KOG0131		0 K12741	GO:0003676	AT2G41060.2		0
8	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
9	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
10	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
11	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
13	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
14	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
15	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
16	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
17	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
18	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
19	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
20	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
21	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
22	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G02650.1		0
23	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
24	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
25	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
26	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
27	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
28	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
29	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
30	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
31	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
32	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
33	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
34	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
35	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
36	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
37	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
38	PTHR13683,P <sup>-</sup> KOG1339	3.4.23.12		0 GO:0006508,C	AT1G66180.1		0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0
56	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0
57	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0
58	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0
59	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0
60	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0
	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1		0

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2	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1	0
3	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1	0
4	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1	0
5	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1	0
6	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1	0
7	PTHR10445,P <sup>-</sup> KOG2905	3.6.4.12	K03139	GO:0006367,C	AT1G75510.1	0
8	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
9	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
10	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
11	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
13	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
14	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
15	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
16	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
17	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
18	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
19	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
20	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
21	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
22	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
23	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G05670.2	0
24	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
25	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
26	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
27	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
28	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
29	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
30	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
31	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
32	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
33	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
34	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
35	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
36	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
37	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
38	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
39	PTHR10410,P <sup>-</sup>	0 3.4.25.1	K09613	GO:0005515	AT1G71230.1 AJH2,CSN5,CS	
40	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
41	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
42	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
43	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
44	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
45	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
46	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
47	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
48	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
49	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
50	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
51	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
52	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
53	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
54	PTHR26312,P <sup>-</sup>	0	0	0	0 AT4G39470.1	0
55	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
56	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
57	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
58	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
59	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
60	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0

1						
2	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
3	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
4	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
5	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
6	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
7	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
8	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
9	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
10	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
11	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
13	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
14	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
15	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
16	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
17	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
18	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
19	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
20	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
21	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
22	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G79540.1	0
23	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
24	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
25	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
26	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
27	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
28	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
29	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
30	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
31	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
32	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
33	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
34	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
35	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
36	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
37	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
38	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
39	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
40	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
41	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
42	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
43	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
44	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
45	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
46	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
47	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
48	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
49	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
50	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
51	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
52	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
53	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
54	PTHR31388,P <sup>-</sup>	0 1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
55	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	
56	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	
57	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	
58	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	
59	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	
60	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	
	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,(	AT5G01310.1 APTX	

1				
2	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
3	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
4	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
5	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
6	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
7	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
8	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
9	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
10	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
11	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
12	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
13	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
14	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
15	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
16	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
17	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
18	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
19	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
20	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
21	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
22	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
23	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
24	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
25	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
26	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
27	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
28	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
29	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
30	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
31	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
32	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
33	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
34	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
35	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
36	PTHR12486,P <sup>-</sup> KOG0562		0	0 GO:0033699,C AT5G01310.1 APTX
37	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
38	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
39	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
40	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
41	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
42	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
43	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
44	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
45	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
46	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
47	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
48	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
49	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
50	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
51	PTHR10252,P <sup>-</sup>	0 2.7.7.7	0	0 AT1G07980.1 NF-YC10
52	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
53	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
54	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
55	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
56	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
57	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
58	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
59	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
60	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1
	PTHR31633	0	0 K14763	GO:0042254,C AT1G03530.1 ATNAF1,NAF1

1						
2	PTHR31633	0	0 K14763	GO:0042254,(	AT1G03530.1 ATNAF1,NAF1	
3	PTHR31633	0	0 K14763	GO:0042254,(	AT1G03530.1 ATNAF1,NAF1	
4	PTHR31633	0	0 K14763	GO:0042254,(	AT1G03530.1 ATNAF1,NAF1	
5						
6	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
7	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
8	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
9						
10	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
11	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
12	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
13						
14	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
15	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
16	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
17						
18	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
19	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
20	PTHR24326,P <sup>-</sup>	0	0	0 GO:0003677	AT5G53980.1 ATHB52,HB52	
21						
22	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
23	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
24	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
25						
26	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
27	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
28	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
29						
30	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
31	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
32	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
33						
34	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
35	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
36	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.14		0 GO:0008234,(	AT1G47128.1 RD21,RD21A	
37						
38	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
39	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
40	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
41						
42	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
43	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
44	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
45	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
46						
47	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
48	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
49						
50	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
51	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
52	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
53						
54	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
55	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
56	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
57	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
58						
59	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
60	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0
	PTHR24015,P <sup>-</sup>	0	0	0	AT3G04130.2	0

1						
2	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G04130.2	0
3	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G04130.2	0
4	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G04130.2	0
5	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G04130.2	0
6	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G04130.2	0
7	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
8	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
9	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
10	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
11	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
12	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
13	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
14	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
15	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
16	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
17	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
18	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
19	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
20	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
21	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
22	PTHR31422,P <sup>-</sup>	0	0	0	0 AT5G06560.1	0
23	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
24	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
25	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
26	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
27	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
28	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
29	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
30	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
31	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
32	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
33	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
34	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
35	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
36	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
37	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
38	PTHR31669,P <sup>-</sup>	0	0	0	GO:0008270,C AT4G38180.1 FRS5	
39	PTHR33101,P <sup>-</sup>	0	0	0	GO:0005089 AT1G31650.1 ATROPGEF14,	
40	PTHR33101,P <sup>-</sup>	0	0	0	GO:0005089 AT1G31650.1 ATROPGEF14,	
41	PTHR10168,P <sup>-</sup> KOG2824		0 K17479		GO:0045454,C AT4G10630.1	0
42	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
43	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
44	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
45	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
46	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
47	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
48	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
49	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
50	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
51	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
52	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
53	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
54	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
55	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
56	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
57	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
58	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
59	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
60	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0
	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723 AT4G29750.1	0



1							
2	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
3	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
4	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
5	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
6	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
7	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
8	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
9	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
10	PTHR31846,P <sup>-</sup> KOG1990		0	0	GO:0003723	AT4G29750.1	0
11	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
12	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
13	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
14	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
15	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
16	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
17	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
18	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
19	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
20	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
21	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
22	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
23	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
24	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
25	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
26	PTHR24015,P <sup>-</sup>	0	0	0	0	AT4G30700.1	0
27	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
28	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
29	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
30	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
31	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
32	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
33	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
34	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
35	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
36	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
37	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
38	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
39	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
40	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
41	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
42	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
43	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
44	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
45	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
46	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
47	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
48	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
49	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
50	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
51	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
52	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
53	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
54	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
55	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
56	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
57	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
58	PTHR34778,P <sup>-</sup>	0	0	0	0	AT1G19010.1	0
59	PTHR31009,P <sup>-</sup>	0	2.1.1.274	K08241	GO:0008168	AT5G04380.1	0
60	PTHR24015,P <sup>-</sup>	0	0	0	0	AT2G15690.1	0
	PTHR10264,P <sup>-</sup> KOG2620		0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1



1								
2	PTHR12526,P <sup>-</sup> KOG0853		0	0	0	AT3G15940.2		0
3	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
4	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
5	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
6	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
7	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
8	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
9	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
10	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
11	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
12	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
13	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
14	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
15	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
16	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
17	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
18	PTHR24223,P <sup>-</sup>	0 3.6.3.44			0	GO:0055085,C AT3G13080.1	ATMRP3,MRP	
19	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0
35	PTHR11817,P <sup>-</sup>	0 2.7.1.40	K00873		GO:0030955,C AT3G52990.1			0
36	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
37	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
38	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
39	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
40	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
41	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
42	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
43	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
44	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
45	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
46	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
47	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
48	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
49	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
50	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
51	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
52	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
53	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
54	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
55	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
56	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
57	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
58	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
59	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
60	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0
	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2			0	GO:0005975 AT5G13420.1		0

1						
2	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2		0 GO:0005975	AT5G13420.1	0
3	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2		0 GO:0005975	AT5G13420.1	0
4	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2		0 GO:0005975	AT5G13420.1	0
5						
6	PTHR10683,P <sup>-</sup> KOG2772	2.2.1.2		0 GO:0005975	AT5G13420.1	0
7	PTHR31752,P <sup>-</sup>	0	0 K13947	GO:0055085,C	AT5G16530.1 PIN5	
8	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
9						
10	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
11	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
12	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
13						
14	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
15	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
16	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
17						
18	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
19	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
20	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
21						
22	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
23	PTHR10887,P <sup>-</sup> KOG1801		0 K10706		0 AT4G15570.1 MAA3	
24	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
25	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
26	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
27	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
28	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
29	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
30	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
31	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
32	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
33	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
34	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
35	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
36	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
37	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
38	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
39	PTHR24078,P <sup>-</sup>	0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
40	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
41	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
42	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
43	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
44	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
45	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
46	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
47	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
48	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
49	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
50	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
51	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
52	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
53	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
54	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
55	PTHR31321,P <sup>-</sup>	0 3.1.1.11	K01051	GO:0042545,C	AT5G55590.1 QRT1	
56	PTHR12670,P <sup>-</sup>	0 3.5.1.23	K12349		0 AT1G07380.1	0
57	PTHR12670,P <sup>-</sup>	0 3.5.1.23	K12349		0 AT1G07380.1	0
58	PTHR12670,P <sup>-</sup>	0 3.5.1.23	K12349		0 AT1G07380.1	0
59	PTHR12670,P <sup>-</sup>	0 3.5.1.23	K12349		0 AT1G07380.1	0
60	PTHR12670,P <sup>-</sup>	0 3.5.1.23	K12349		0 AT1G07380.1	0

1						
2	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
3	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
4	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
5	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
6	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
7	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
8	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
9	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
10	PTHR12670,P <sup>-</sup>	0	3.5.1.23	K12349	0	AT1G07380.1
11	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
12	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
13	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
14	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
15	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
16	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
17	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
18	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
19	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
20	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
21	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
22	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
23	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
24	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
25	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
26	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
27	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
28	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
29	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
30	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
31	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
32	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
33	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
34	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
35	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
36	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
37	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
38	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
39	PTHR31704,P <sup>-</sup>	0	0	0	0	AT2G24960.2
40	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
41	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
42	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
43	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
44	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
45	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
46	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
47	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
48	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
49	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
50	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
51	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
52	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
53	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
54	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
55	PTHR11119,P <sup>-</sup>	0	0	K06901	GO:0055085,C	AT3G10960.1 ATAZG1,AZG1
56	PTHR24286,P <sup>-</sup>	0	0	0	GO:0055114,C	AT1G05160.1 ATKAO1,CYP8
57	PTHR24223,P <sup>-</sup>	0	3.6.3.44	0	GO:0055085,C	AT3G60160.1 ATMRP9,MRP
58	PTHR24223,P <sup>-</sup>	0	3.6.3.44	0	GO:0055085,C	AT3G60160.1 ATMRP9,MRP
59	PTHR24223,P <sup>-</sup>	0	3.6.3.44	0	GO:0055085,C	AT3G60160.1 ATMRP9,MRP
60	PTHR24223,P <sup>-</sup>	0	3.6.3.44	0	GO:0055085,C	AT3G60160.1 ATMRP9,MRP

1				
2	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
3	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
4	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
5	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
6	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
7	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
8	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
9	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
10	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
11	PTHR24223,P <sup>-</sup>	0 3.6.3.44		0 GO:0055085,C AT3G60160.1 ATM RP9,MRP
12	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
13	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
14	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
15	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
16	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
17	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
18	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
19	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
20	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
21	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
22	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
23	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
24	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
25	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
26	PTHR22953,P <sup>-</sup> KOG1378	3.1.4.1		0 GO:0016787 AT4G24890.1 ATPAP24,PAP.
27	PTHR10774,P <sup>-</sup>	0	0	0 GO:0005515 AT3G19830.1 NTMC2T5.2,N
28	PTHR10774,P <sup>-</sup>	0	0	0 GO:0005515 AT3G19830.1 NTMC2T5.2,N
29	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
30	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
31	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
32	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
33	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
34	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
35	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
36	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
37	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
38	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
39	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
40	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
41	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
42	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
43	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
44	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
45	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
46	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
47	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
48	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
49	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
50	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
51	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
52	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
53	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
54	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
55	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
56	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
57	PTHR10795,P <sup>-</sup>	0 3.4.14.10		0 GO:0006508,C AT2G04160.1 AIR3
58	PTHR22870,P <sup>-</sup> KOG1427		0	0 GO:0046872 AT1G69710.1
59	PTHR22870,P <sup>-</sup> KOG1427		0	0 GO:0046872 AT1G69710.1
60	PTHR23070,P <sup>-</sup>	0	0 K08900	GO:0005524,C AT5G57480.1



1					
2	PTHR11746,P <sup>-</sup> KOG1509		0	0 GO:0005737 AT5G66550.1	0
3	PTHR11746,P <sup>-</sup> KOG1509		0	0 GO:0005737 AT5G66550.1	0
4	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
5					
6	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
7	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
8	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
9	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
10	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
11	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
12	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
13	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
14	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
15	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
16	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
17	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
18	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
19	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
20	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
21	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
22	PTHR21330,P <sup>-</sup>	0	0	0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
23	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
24	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
25	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
26	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
27	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
28	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
29	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
30	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
31	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
32	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
33	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
34	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
35	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
36	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
37	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
38	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
39	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
40	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
41	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
42	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
43	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
44	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
45	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
46	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
47	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
48	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
49	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
50	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
51	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
52	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
53	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
54	PTHR21330,P <sup>-</sup>	0 3.4.22.16		0 GO:0030915,(AT3G15150.1 ATMMS21,HP	
55	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0
56	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0
57	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0
58	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0
59	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0
60	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0
	PTHR31852,P <sup>-</sup>	0	0	0 AT2G35460.1	0

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2	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
3	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
4	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
5	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
6	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
7	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
8	PTHR31852,P <sup>-</sup>	0	0	0	0 AT2G35460.1	0
9						
10	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
11	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
12	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
13	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
14	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
15	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
16	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
17	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
18	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
19	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
20	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
21	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
22	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
23	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
24	PTHR23500,P <sup>-</sup> KOG0254		0 K08150		GO:0055085,C AT4G16480.1 ATINT4,INT4	
25	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
26	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
27	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
28	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
29	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
30	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
31	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
32	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
33	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
34	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
35	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
36	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
37	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
38	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
39	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
40	PTHR24006,P <sup>-</sup> KOG1947		0 K10268		GO:0005515 AT4G15475.1	0
41	PTHR31422,P <sup>-</sup>	0	0	0	0 AT1G18265.1	0
42						
43	PTHR11532,P <sup>-</sup> KOG2649	3.4.17.22		0	0 AT1G71696.1 SOL1	
44	PTHR11532,P <sup>-</sup> KOG2649	3.4.17.22		0	0 AT1G71696.1 SOL1	
45	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
46	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
47	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
48	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
49	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
50	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
51	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
52	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
53	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
54	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
55	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
56	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
57	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
58	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
59	PTHR22849,P <sup>-</sup> KOG0279	2.7.11.7		0	GO:0005515,C AT3G06880.2	0
60	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT1G03060.1 SPI	
	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT1G03060.1 SPI	

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2	PTHR13743,P <sup>-</sup>	0	0	0	GO:0005515 AT1G03060.1 SPI	
3	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
4	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
5	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
6	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
7	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
8	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
9	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
10	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
11	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
12	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
13	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
14	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
15	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
16	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
17	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
18	PTHR31282,P <sup>-</sup>	0	0	0	GO:0043565,CAT2G30590.1 WRKY21	
19	PTHR31549,P <sup>-</sup>	0	0	0	0 AT4G31980.1	0
20	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
21	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
22	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
23	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
24	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
25	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
26	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
27	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
28	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
29	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
30	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
31	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
32	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
33	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
34	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
35	PTHR24031,P <sup>-</sup>	0	3.6.4.13	K17679	GO:0016787,CAT5G08610.1	0
36	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
37	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
38	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
39	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
40	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
41	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
42	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
43	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
44	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
45	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
46	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
47	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
48	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
49	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
50	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
51	PTHR22970,P <sup>-</sup>	0		0	0 GO:0003677 AT3G43240.1	0
52	PTHR11851,P <sup>-</sup>	0	1.10.2.2,3.4.2	K01412	0 AT1G51980.1	0
53	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
54	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
55	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
56	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
57	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
58	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
59	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
60	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0
	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63		K15634	0 AT5G22620.1	0

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2	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63	K15634	0 AT5G22620.1	0
3	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63	K15634	0 AT5G22620.1	0
4	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63	K15634	0 AT5G22620.1	0
5					
6	PTHR23029,P <sup>-</sup> KOG0235	3.1.3.63	K15634	0 AT5G22620.1	0
7	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
8	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
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10	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
11	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
12	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
13					
14	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
15	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
16	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
17	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
18	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
19	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
20	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
21					
22	PTHR23315,P <sup>-</sup>	0 6.3.2.19		0 GO:0016567,C AT5G40140.1	0
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not distribute

	arabi-defline	ID	Annot_defline	IDENTIFIER	NAME
1					
2					
3		0	0	0 Phvul.003G16	not assigned.r
4		0	0	0 Phvul.003G16	not assigned.r
5		0	0	0 Phvul.003G16	not assigned.r
6		0	0	0 Phvul.003G16	not assigned.r
7		0	0	0 Phvul.003G16	not assigned.r
8		0	0	0 Phvul.003G16	not assigned.r
9		0	0	0 Phvul.003G16	not assigned.r
10		0	0	0 Phvul.003G16	not assigned.r
11		0	0	0 Phvul.003G16	not assigned.r
12		0	0	0 Phvul.003G16	not assigned.r
13		0	0	0 Phvul.003G16	not assigned.r
14		0	0	0 Phvul.003G16	not assigned.r
15		0	0	0 Phvul.003G16	not assigned.r
16		0	0	0 Phvul.003G16	not assigned.r
17		0	0	0 Phvul.003G16	not assigned.r
18		0	0	0 Phvul.003G16	not assigned.r
19		0	0	0 Phvul.003G16	not assigned.r
20		0	0	0 Phvul.003G16	not assigned.r
21		0	0	0 Phvul.003G16	not assigned.r
22		0	0	0 Phvul.003G16	not assigned.r
23		0	0	0 Phvul.003G16	not assigned.r
24		0	0	0 Phvul.003G16	not assigned.r
25		0	0	0 Phvul.003G16	not assigned.r
26		0	0	0 Phvul.003G16	not assigned.r
27		0	0	0 Phvul.003G16	not assigned.r
28		0	0	0 Phvul.003G16	not assigned.r
29		0	0	0 Phvul.003G16	not assigned.r
30		0	0	0 Phvul.003G16	not assigned.r
31		0	0	0 Phvul.003G16	not assigned.r
32		0	0	0 Phvul.003G16	not assigned.r
33		0	0	0 Phvul.003G16	not assigned.r
34		0	0	0 Phvul.003G16	not assigned.r
35	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
36	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
37	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
38	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
39	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
40	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
41	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
42	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
43	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
44	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
45	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
46	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
47	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
48	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
49	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
50	Ankyrin-repeat containing protein		Phvul.008G20PF13962 - Dor	Phvul.008G20	not assigned.r
51		0	0	0 Phvul.003G16	not assigned.r
52		0	0	0 Phvul.003G16	not assigned.r
53		0	0	0 Phvul.003G16	not assigned.r
54		0	0	0 Phvul.003G16	not assigned.r
55		0	0	0 Phvul.003G16	not assigned.r
56		0	0	0 Phvul.003G16	not assigned.r
57		0	0	0 Phvul.003G16	not assigned.r
58		0	0	0 Phvul.003G16	not assigned.r
59		0	0	0 Phvul.003G16	not assigned.r
60		0	0	0 Phvul.003G16	not assigned.r





































































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25		0	0
26		0	0
27		0	0
28	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
29	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
30	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
31	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
32	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
33	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
34	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
35	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
36	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
37	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
38	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
39	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
40	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
41	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
42	MA3 domain-containing protein	Phvul.003G20PTHR12626:SI	Phvul.003G20Multi-process
43	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
44	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
45	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
46	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
47	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
48	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
49	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
50	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
51	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
52	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
53	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
54	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
55	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
56	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
57	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
58	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
59	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc
60	nitrate transporter 1.1	Phvul.003G21PTHR11654:SI	Phvul.003G21Solute transpc

















1 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
2 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
3 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
4 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
5 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
6 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
7 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a  
8 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
9 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
10 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
11 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
12 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
13 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
14 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
15 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
16 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
17 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
18 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
19 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
20 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
21 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
22 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a  
23 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
24 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
25 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
26 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
27 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
28 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
29 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
30 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
31 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
32 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
33 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
34 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
35 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
36 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
37 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
38 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home  
39 0 0 0 Phvul.009G01not assigned.r  
40 0 0 0 Phvul.009G01not assigned.r  
41 0 0 0 Phvul.009G01not assigned.r  
42 0 0 0 Phvul.009G01not assigned.r  
43 0 0 0 Phvul.009G01not assigned.r  
44 0 0 0 Phvul.009G01not assigned.r  
45 0 0 0 Phvul.009G01not assigned.r  
46 0 0 0 Phvul.009G01not assigned.r  
47 0 0 0 Phvul.009G01not assigned.r  
48 0 0 0 Phvul.009G01not assigned.r  
49 0 0 0 Phvul.009G01not assigned.r  
50 0 0 0 Phvul.009G01not assigned.r  
51 0 0 0 Phvul.009G01not assigned.r  
52 0 0 0 Phvul.009G01not assigned.r  
53 0 0 0 Phvul.009G01not assigned.r  
54  
55 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe  
56 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe  
57 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe  
58 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe  
59 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe  
60 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe













1 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a  
2 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a  
3 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a  
4 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a  
5 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a  
6 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
7 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
8 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
9 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
10 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
11 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
12 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
13 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
14 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
15 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
16 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
17 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
18 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
19 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
20 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
21 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
22 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SlPhvul.001G19not assigned.a  
23 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
24 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
25 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
26 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
27 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
28 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
29 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
30 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
31 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
32 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
33 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
34 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
35 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
36 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
37 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
38 FAR1-related sequence 5 Phvul.002G11PTHR31669:SlPhvul.002G11RNA biosynthe  
39 RHO guanyl-nucleotide exchange factor Phvul.002G12PTHR33101:SlPhvul.002G12Multi-process  
40 RHO guanyl-nucleotide exchange factor Phvul.002G12PTHR33101:SlPhvul.002G12Multi-process  
41 Glutaredoxin family protein Phvul.002G32PTHR10168:SlPhvul.002G32not assigned.a  
42 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
43 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
44 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
45 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
46 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
47 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
48 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
49 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
50 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
51 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
52 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
53 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
54 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
55 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
56 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
57 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
58 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
59 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
60 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a

1 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
2 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
3 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
4 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
5 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
6 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
7 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
8 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
9 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a  
10 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
11 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
12 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
13 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
14 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
15 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
16 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
17 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
18 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
19 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
20 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
21 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
22 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
23 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
24 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
25 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
26 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a  
27 0 0 0 Phvul.003G19not assigned.r  
28 0 0 0 Phvul.003G19not assigned.r  
29 0 0 0 Phvul.003G19not assigned.r  
30 0 0 0 Phvul.003G19not assigned.r  
31 0 0 0 Phvul.003G19not assigned.r  
32 0 0 0 Phvul.003G19not assigned.r  
33 0 0 0 Phvul.003G19not assigned.r  
34 0 0 0 Phvul.003G19not assigned.r  
35 0 0 0 Phvul.003G19not assigned.r  
36 0 0 0 Phvul.003G19not assigned.r  
37 0 0 0 Phvul.003G19not assigned.r  
38 0 0 0 Phvul.003G19not assigned.r  
39 0 0 0 Phvul.003G19not assigned.r  
40 0 0 0 Phvul.003G19not assigned.r  
41 0 0 0 Phvul.003G19not assigned.r  
42 0 0 0 Phvul.003G19not assigned.r  
43 0 0 0 Phvul.003G19not assigned.r  
44 0 0 0 Phvul.003G19not assigned.r  
45 0 0 0 Phvul.003G19not assigned.r  
46 0 0 0 Phvul.003G19not assigned.r  
47 0 0 0 Phvul.003G19not assigned.r  
48 0 0 0 Phvul.003G19not assigned.r  
49 0 0 0 Phvul.003G19not assigned.r  
50 0 0 0 Phvul.003G19not assigned.r  
51 0 0 0 Phvul.003G19not assigned.r  
52 0 0 0 Phvul.003G19not assigned.r  
53 0 0 0 Phvul.003G19not assigned.r  
54 0 0 0 Phvul.003G19not assigned.r  
55 0 0 0 Phvul.003G19not assigned.r  
56 0 0 0 Phvul.003G19not assigned.r  
57 0 0 0 Phvul.003G19not assigned.r  
58 S-adenosyl-L-methionine-dependent mePhvul.003G252.1.1.274 - SalPhvul.003G25Enzyme classifi  
59 Tetratricopeptide repeat (TPR)-like supePhvul.003G29PF01535//PF1Phvul.003G29RNA processir  
60 SPFH/Band 7/PHB domain-containing mPhvul.004G02PTHR10264//IPhvul.004G02not assigned.a







1	
2	Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate
3	Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate
4	Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate
5	Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate
6	Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate
7	Auxin efflux carrier family protein Phvul.008G05PTHR31752:SiPhvul.008G05Solute transp
8	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
9	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
10	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
11	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
12	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
13	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
14	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
15	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
16	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
17	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
18	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
19	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
20	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
21	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
22	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
23	P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SiPhvul.008G16not assigned.a
24	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
25	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
26	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
27	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
28	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
29	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
30	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
31	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
32	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
33	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
34	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
35	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
36	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
37	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
38	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
39	RAD-like 6 Phvul.008G19PTHR24078:SiPhvul.008G19RNA biosynthe
40	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
41	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
42	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
43	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
44	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
45	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
46	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
47	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
48	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
49	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
50	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
51	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
52	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
53	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
54	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
55	Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SiPhvul.008G27Cell wall orgar
56	Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
57	Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
58	Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
59	Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
60	Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli

1 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
2 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
3 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
4 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
5 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
6 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
7 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
8 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
9 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli  
10  
11 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
12 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
13 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
14 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
15 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
16 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
17 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
18 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
19 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
20 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
21 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
22 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
23 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
24 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
25 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
26 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
27 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
28 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
29 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
30 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
31 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
32 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
33 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
34 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
35 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
36 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
37 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
38 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
39 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a  
40 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
41 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
42 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
43 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
44 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
45 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
46 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
47 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
48 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
49 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
50 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
51 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
52 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
53 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
54 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
55 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc  
56 cytochrome P450, family 88, subfamily 1Phvul.010G13PTHR24286:SfPhvul.010G13Enzyme classif  
57 multidrug resistance-associated protein Phvul.010G14PTHR24223:SfPhvul.010G14Solute transpc  
58 multidrug resistance-associated protein Phvul.010G14PTHR24223:SfPhvul.010G14Solute transpc  
59 multidrug resistance-associated protein Phvul.010G14PTHR24223:SfPhvul.010G14Solute transpc  
60 multidrug resistance-associated protein Phvul.010G14PTHR24223:SfPhvul.010G14Solute transpc







1		
2	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
3	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
4	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
5	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
6	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
7	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
8	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
9	Late embryogenesis abundant (LEA) hyd	Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r
10	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
11	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
12	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
13	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
14	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
15	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
16	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
17	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
18	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
19	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
20	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
21	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
22	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
23	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
24	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
25	inositol transporter 4	Phvul.006G14K08150 - MFS Phvul.006G14Solute transp
26	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
27	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
28	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
29	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
30	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
31	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
32	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
33	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
34	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
35	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
36	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
37	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
38	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
39	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
40	F-box/RNI-like superfamily protein	Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a
41	Protein of unknown function, DUF593	Phvul.006G20PTHR31422:SlPhvul.006G20not assigned.r
42	carboxypeptidase D, putative	Phvul.007G083.4.17.22 - MεPhvul.007G08Protein home
43	carboxypeptidase D, putative	Phvul.007G083.4.17.22 - MεPhvul.007G08Protein home
44	carboxypeptidase D, putative	Phvul.007G083.4.17.22 - MεPhvul.007G08Protein home
45	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
46	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
47	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
48	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
49	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
50	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
51	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
52	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
53	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
54	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
55	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
56	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
57	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
58	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
59	Transducin/WD40 repeat-like superfami	Phvul.007G13PTHR22849//IPhvul.007G13External stimu
60	Beige/BEACH domain ;WD domain, G-βε	Phvul.007G17PTHR13743:SlPhvul.007G17not assigned.a
	Beige/BEACH domain ;WD domain, G-βε	Phvul.007G17PTHR13743:SlPhvul.007G17not assigned.a

1 Beige/BEACH domain ;WD domain, G-bcPhvul.007G17PTHR13743:SfPhvul.007G17 not assigned.a  
2 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
3 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
4 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
5 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
6 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
7 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
8 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
9 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
10 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
11 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
12 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
13 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
14 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
15 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
16 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
17 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
18 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe  
19 0 Phvul.008G10PF03140 - PlaPhvul.008G10 not assigned.a  
20 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
21 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
22 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
23 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
24 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
25 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
26 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
27 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
28 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
29 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
30 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
31 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
32 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
33 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
34 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
35 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a  
36 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
37 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
38 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
39 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
40 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
41 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
42 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
43 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
44 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
45 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
46 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
47 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
48 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
49 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
50 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
51 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe  
52 Insulinase (Peptidase family M16) prote Phvul.010G143.4.24.64 - Mi Phvul.010G14 Protein modif  
53 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
54 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
55 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
56 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
57 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
58 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
59 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi  
60 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi



1 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi  
2 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi  
3 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi  
4 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi  
5 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi  
6 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home  
7 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home  
8 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home  
9 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home  
10 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home  
11 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home  
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4 carboxy-D-arabinitol-1-phosphatase (CA1PP) (original description: pacid=37156982 transcript=Phv  
5 carboxy-D-arabinitol-1-phosphatase (CA1PP) (original description: pacid=37156982 transcript=Phv  
6 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F  
7 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F  
8 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F  
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58 original description: pacid=37147951 transcript=Phvul.003G255900.1 locus=Phvul.003G255900 ID=  
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Do not distribute

(50.2.7 : 376.0) (original description: pacid=37167361 transcript=Phvul.007G244900.1 locus=Phvul.l

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9 is thaliana (sp|b6sfa4|maa3\_arath : 916.0)  
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miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	
1					
2					
3	ucuucccaauuccgcccauucc	Phvul.004G048000.1	0.5	-1	1
4	ucuucccuacaccucccauacc	Phvul.001G224800.1	2	-1	1
5	ucuucccuacaccucccauacc	Phvul.001G224800.2	2	-1	1
6	ucuucccuacaccucccauacc	Phvul.001G224800.1	2	-1	1
7	ucuucccuacaccucccauacc	Phvul.001G224800.2	2	-1	1
8	ucuucccuacaccucccauacc	Phvul.007G201700.1	2	-1	1
9	ucuucccuacaccucccauacc	Phvul.007G201700.1	2	-1	1
10	ucuucccuacaccucccauacc	Phvul.008G061300.2	2	-1	1
11	ucuucccuacaccucccauacc	Phvul.008G061300.1	2	-1	1
12	ucuucccuacaccucccauacc	Phvul.008G061300.2	2	-1	1
13	ucuucccuacaccucccauacc	Phvul.008G061300.1	2	-1	1
14	ucuucccaauuccgcccauucc	Phvul.002G079200.1	2.5	-1	1
15	ucuucccaauuccgcccauucc	Phvul.001G217600.1	3	-1	1
16	ucuucccuacaccucccauacc	Phvul.002G001500.1	3	-1	1
17	ucuucccuacaccucccauacc	Phvul.002G001500.1	3	-1	1
18	ucuucccaauuccgcccauucc	Phvul.003G072500.1	3	-1	1
19	ucuucccaauuccgcccauucc	Phvul.003G244225.3	3	-1	1
20	ucuucccaauuccgcccauucc	Phvul.003G244225.2	3	-1	1
21	ucuucccaauuccgcccauucc	Phvul.003G244225.1	3	-1	1
22	ucuucccaauuccgcccauucc	Phvul.004G137300.1	3	-1	1
23	ucuucccaauuccgcccauucc	Phvul.005G029400.1	3	-1	1
24	ucuucccaauuccgcccauucc	Phvul.005G029400.3	3	-1	1
25	ucuucccaauuccgcccauucc	Phvul.005G029400.2	3	-1	1
26	ucuucccuacaccucccauacc	Phvul.007G210600.1	3	-1	1
27	ucuucccuacaccucccauacc	Phvul.007G210600.1	3	-1	1
28	ucuucccaauuccgcccauucc	Phvul.008G055500.1	3	-1	1
29	ucuucccuacaccucccauacc	Phvul.008G280900.1	3	-1	1
30	ucuucccuacaccucccauacc	Phvul.008G280900.1	3	-1	1
31	ucuucccaauuccgcccauucc	Phvul.010G064700.1	3	-1	1
32	ucuucccaauuccgcccauucc	Phvul.010G136700.1	3	-1	1
33	ucuucccaauuccgcccauucc	Phvul.011G149100.7	3	-1	1
34	ucuucccaauuccgcccauucc	Phvul.011G149100.6	3	-1	1
35	ucuucccaauuccgcccauucc	Phvul.011G149100.5	3	-1	1
36	ucuucccaauuccgcccauucc	Phvul.011G149100.2	3	-1	1
37	ucuucccaauuccgcccauucc	Phvul.011G149100.1	3	-1	1
38	ucuucccaauuccgcccauucc	Phvul.011G149100.4	3	-1	1
39	ucuucccaauuccgcccauucc	Phvul.011G149100.3	3	-1	1
40	ucuucccaauuccgcccauucc	Phvul.011G166100.1	3	-1	1
41	ucuucccaauuccgcccauucc	Phvul.001G128200.2	3.5	-1	1
42	ucuucccuacaccucccauacc	Phvul.001G134000.1	3.5	-1	1
43	ucuucccuacaccucccauacc	Phvul.001G134000.1	3.5	-1	1
44	ucuucccuacaccucccauacc	Phvul.001G243900.1	3.5	-1	1
45	ucuucccuacaccucccauacc	Phvul.001G243900.1	3.5	-1	1
46	ucuucccaauuccgcccauucc	Phvul.002G057300.2	3.5	-1	1
47	ucuucccaauuccgcccauucc	Phvul.002G057300.1	3.5	-1	1
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2	ucuucccaauuccgcccauucc	Phvul.002G122200.1	3.5	-1	1
3	ucuucccaauuccgcccauucc	Phvul.002G187600.1	3.5	-1	1
4	ucuucccuacaccucccauacc	Phvul.002G261500.1	3.5	-1	1
5	ucuucccuacaccucccauacc	Phvul.002G261500.1	3.5	-1	1
6	ucuucccuacaccucccauacc	Phvul.003G101200.1	3.5	-1	1
7	ucuucccuacaccucccauacc	Phvul.003G101200.1	3.5	-1	1
8	ucuucccuacaccucccauacc	Phvul.003G202900.1	3.5	-1	1
9	ucuucccuacaccucccauacc	Phvul.003G202900.1	3.5	-1	1
10	ucuucccuacaccucccauacc	Phvul.004G026200.1	3.5	-1	1
11	ucuucccuacaccucccauacc	Phvul.004G140400.1	3.5	-1	1
12	ucuucccuacaccucccauacc	Phvul.004G140400.1	3.5	-1	1
13	ucuucccuacaccucccauacc	Phvul.005G038200.1	3.5	-1	1
14	ucuucccuacaccucccauacc	Phvul.005G038200.1	3.5	-1	1
15	ucuucccuacaccucccauacc	Phvul.005G087100.1	3.5	-1	1
16	ucuucccuacaccucccauacc	Phvul.005G087100.1	3.5	-1	1
17	ucuucccaauuccgcccauucc	Phvul.006G102700.1	3.5	-1	1
18	ucuucccuacaccucccauacc	Phvul.008G072300.2	3.5	-1	1
19	ucuucccuacaccucccauacc	Phvul.008G072300.1	3.5	-1	1
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21	ucuucccuacaccucccauacc	Phvul.008G072300.1	3.5	-1	1
22	ucuucccaauuccgcccauucc	Phvul.008G202300.1	3.5	-1	1
23	ucuucccuacaccucccauacc	Phvul.008G259600.2	3.5	-1	1
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25	ucuucccuacaccucccauacc	Phvul.008G259600.2	3.5	-1	1
26	ucuucccaauuccgcccauucc	Phvul.010G131650.1	3.5	-1	1
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32	ucuucccuacaccucccauacc	Phvul.010G151400.4	3.5	-1	1
33	ucuucccaauuccgcccauucc	Phvul.011G140300.1	3.5	-1	1
34	ucuucccaauuccgcccauucc	Phvul.011G140400.1	3.5	-1	1
35	ucuucccaauuccgcccauucc	Phvul.011G151300.1	3.5	-1	1
36	ucuucccuacaccucccauacc	Phvul.011G181700.1	3.5	-1	1
37	ucuucccuacaccucccauacc	Phvul.011G181700.1	3.5	-1	1
38	ucuucccaauuccgcccauucc	Phvul.011G192400.1	3.5	-1	1
39	ucuucccaauuccgcccauucc	Phvul.011G192600.1	3.5	-1	1
40	ucuucccaauuccgcccauucc	Phvul.011G193100.1	3.5	-1	1
41	ucuucccaauuccgcccauucc	Phvul.011G193500.1	3.5	-1	1
42	ucuucccaauuccgcccauucc	Phvul.011G193600.1	3.5	-1	1
43	ucuucccaauuccgcccauucc	Phvul.011G194800.1	3.5	-1	1
44	ucuucccaauuccgcccauucc	Phvul.011G194900.1	3.5	-1	1
45	ucuucccaauuccgcccauucc	Phvul.011G195000.1	3.5	-1	1
46	ucuucccaauuccgcccauucc	Phvul.011G195200.1	3.5	-1	1
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2	ucuuccaauuccgcccauucc	Phvul.011G195400.1	3.5	-1	1
3	ucuuccaauuccgcccauucc	Phvul.011G195500.1	3.5	-1	1
4	ucuuccaauuccgcccauucc	Phvul.011G196000.1	3.5	-1	1
5	ucuuccaauuccgcccauucc	Phvul.011G196066.1	3.5	-1	1
6	ucuuccaauuccgcccauucc	Phvul.011G196066.1	3.5	-1	1
7	ucuuccuacaccucccauacc	Phvul.011G200820.1	3.5	-1	1
8	ucuuccuacaccucccauacc	Phvul.011G200820.1	3.5	-1	1
9	ucuuccuacaccucccauacc	Phvul.011G200820.1	3.5	-1	1
10	ucuuccuacaccucccauacc	Phvul.011G202100.1	3.5	-1	1
11	ucuuccuacaccucccauacc	Phvul.011G202100.1	3.5	-1	1
12	ucuuccuacaccucccauacc	Phvul.011G202300.1	3.5	-1	1
13	ucuuccuacaccucccauacc	Phvul.011G202300.1	3.5	-1	1
14	ucuuccuacaccucccauacc	Phvul.011G202300.1	3.5	-1	1
15	ucuuccuacaccucccauacc	Phvul.011G203100.1	3.5	-1	1
16	ucuuccuacaccucccauacc	Phvul.011G203100.1	3.5	-1	1
17	ucuuccuacaccucccauacc	Phvul.011G203100.1	3.5	-1	1
18	ucuuccuacaccucccauacc	Phvul.L002337.2	3.5	-1	1
19	ucuuccuacaccucccauacc	Phvul.L002337.1	3.5	-1	1
20	ucuuccuacaccucccauacc	Phvul.L002337.2	3.5	-1	1
21	ucuuccuacaccucccauacc	Phvul.L002337.2	3.5	-1	1
22	ucuuccuacaccucccauacc	Phvul.L002337.1	3.5	-1	1
23	ucuuccuacaccucccauacc	Phvul.001G015600.1	4	-1	1
24	ucuuccuacaccucccauacc	Phvul.001G015600.2	4	-1	1
25	ucuuccuacaccucccauacc	Phvul.001G015600.1	4	-1	1
26	ucuuccuacaccucccauacc	Phvul.001G015600.1	4	-1	1
27	ucuuccuacaccucccauacc	Phvul.001G015600.2	4	-1	1
28	ucuuccaauuccgcccauucc	Phvul.001G085500.2	4	-1	1
29	ucuuccaauuccgcccauucc	Phvul.001G085500.1	4	-1	1
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34	ucuuccaauuccgcccauucc	Phvul.002G041400.4	4	-1	1
35	ucuuccaauuccgcccauucc	Phvul.002G041400.1	4	-1	1
36	ucuuccaauuccgcccauucc	Phvul.002G041400.2	4	-1	1
37	ucuuccaauuccgcccauucc	Phvul.002G041400.3	4	-1	1
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40	ucuuccuacaccucccauacc	Phvul.003G010900.1	4	-1	1
41	ucuuccuacaccucccauacc	Phvul.003G010900.1	4	-1	1
42	ucuuccuacaccucccauacc	Phvul.003G010900.1	4	-1	1
43	ucuuccaauuccgcccauucc	Phvul.003G195800.2	4	-1	1
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51	ucuuccaauuccgcccauucc	Phvul.003G295800.2	4	-1	1
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53	ucuucccaauuccgcccauucc	Phvul.003G244225.2	5	-1	1
54	ucuucccaauuccgcccauucc	Phvul.003G244225.1	5	-1	1
55	ucuucccaauuccgcccauucc	Phvul.003G282200.3	5	-1	1
56	ucuucccaauuccgcccauucc	Phvul.003G282200.3	5	-1	1
57	ucuucccaauuccgcccauucc	Phvul.003G282200.2	5	-1	1
58	ucuucccaauuccgcccauucc	Phvul.003G282200.2	5	-1	1
59	ucuucccaauuccgcccauucc	Phvul.003G282250.1	5	-1	1
60	ucuucccaauuccgcccauucc	Phvul.004G011100.1	5	-1	1
	ucuucccaauuccgcccauucc	Phvul.004G086300.2	5	-1	1



1					
2	ucuucccaauuccgcccauucc	Phvul.004G086300.1	5	-1	1
3	ucuucccuacaccucccauacc	Phvul.005G041300.1	5	-1	1
4	ucuucccuacaccucccauacc	Phvul.005G041300.1	5	-1	1
5	ucuucccuacaccucccauacc	Phvul.005G069700.1	5	-1	1
6	ucuucccuacaccucccauacc	Phvul.005G069700.1	5	-1	1
7	ucuucccuacaccucccauacc	Phvul.005G072000.1	5	-1	1
8	ucuucccaauuccgcccauucc	Phvul.005G072000.1	5	-1	1
9	ucuucccuacaccucccauacc	Phvul.006G027500.1	5	-1	1
10	ucuucccuacaccucccauacc	Phvul.006G027500.1	5	-1	1
11	ucuucccuacaccucccauacc	Phvul.006G100600.1	5	-1	1
12	ucuucccaauuccgcccauucc	Phvul.006G100600.1	5	-1	1
13	ucuucccuacaccucccauacc	Phvul.006G126400.1	5	-1	1
14	ucuucccuacaccucccauacc	Phvul.006G126400.1	5	-1	1
15	ucuucccuacaccucccauacc	Phvul.006G126400.1	5	-1	1
16	ucuucccaauuccgcccauucc	Phvul.006G170700.1	5	-1	1
17	ucuucccuacaccucccauacc	Phvul.008G107400.1	5	-1	1
18	ucuucccuacaccucccauacc	Phvul.008G107400.1	5	-1	1
19	ucuucccuacaccucccauacc	Phvul.008G206300.1	5	-1	1
20	ucuucccaauuccgcccauucc	Phvul.008G206300.1	5	-1	1
21	ucuucccaauuccgcccauucc	Phvul.009G103100.1	5	-1	1
22	ucuucccaauuccgcccauucc	Phvul.010G008500.1	5	-1	1
23	ucuucccaauuccgcccauucc	Phvul.010G013500.1	5	-1	1
24	ucuucccaauuccgcccauucc	Phvul.010G013500.1	5	-1	1
25	ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
26	ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
27	ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
28	ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
29	ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
30	ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
31	ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
32	ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
33	ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
34	ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
35	ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
36	ucuucccaauuccgcccauucc	Phvul.010G145600.1	5	-1	1
37	ucuucccaauuccgcccauucc	Phvul.011G181700.1	5	-1	1
38	ucuucccaauuccgcccauucc	Phvul.011G181700.1	5	-1	1
39	ucuucccaauuccgcccauucc	Phvul.011G200820.1	5	-1	1
40	ucuucccaauuccgcccauucc	Phvul.011G202100.1	5	-1	1
41	ucuucccaauuccgcccauucc	Phvul.011G202300.1	5	-1	1
42	ucuucccaauuccgcccauucc	Phvul.011G202300.1	5	-1	1
43	ucuucccaauuccgcccauucc	Phvul.011G203100.1	5	-1	1
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miRNA_end	Target_start	Target_end	miRNA_align	alignment	Target_align	Inhibition
	22	667	688	UCUUCCCAAL	GGAAUGGGG	Cleavage
	22	1158	1179	UCUUCCCUAC	UAUAUGGCG	Cleavage
	22	993	1014	UCUUCCCUAC	UAUAUGGCG	Cleavage
	22	1158	1179	UCUUCCCUAC	UAUAUGGCG	Cleavage
	22	993	1014	UCUUCCCUAC	UAUAUGGCG	Cleavage
	22	1110	1131	UCUUCCCUAC	UAUAUGGCG	Cleavage
	22	1110	1131	UCUUCCCUAC	UAUAUGGCG	Cleavage
	22	1023	1044	UCUUCCCUAC	GGUAUGGGG	Cleavage
	22	1520	1541	UCUUCCCUAC	GGUAUGGGG	Cleavage
	22	1023	1044	UCUUCCCUAC	GGUAUGGGG	Cleavage
	22	1520	1541	UCUUCCCUAC	GGUAUGGGG	Cleavage
	22	863	884	UCUUCCCAAL	GGAAUGGGU	Cleavage
	22	104	125	UCUUCCCAAL	UGUGUGGUU	Cleavage
	22	2120	2141	UCUUCCCUAC	AUUGUGGGA	Cleavage
	22	2120	2141	UCUUCCCUAC	AUUGUGGGA	Cleavage
	22	782	803	UCUUCCCAAL	GGGAUGGGU	Cleavage
	22	2213	2234	UCUUCCCAAL	CAGAUGGGG	Cleavage
	22	2213	2234	UCUUCCCAAL	CAGAUGGGG	Cleavage
	22	2209	2230	UCUUCCCAAL	CAGAUGGGG	Cleavage
	22	763	784	UCUUCCCAAL	GGAAUAGGU	Cleavage
	22	986	1007	UCUUCCCAAL	GAGGUGGGU	Cleavage
	22	1081	1102	UCUUCCCAAL	GAGGUGGGU	Cleavage
	22	1155	1176	UCUUCCCAAL	GAGGUGGGU	Cleavage
	22	516	537	UCUUCCCUAC	GAUUUGAGG	Cleavage
	22	516	537	UCUUCCCUAC	GAUUUGAGG	Cleavage
	22	78	99	UCUUCCCAAL	UGCGUGUGU	Cleavage
	22	864	885	UCUUCCCUAC	AAGAUUGGA	Cleavage
	22	864	885	UCUUCCCUAC	AAGAUUGGA	Cleavage
	22	571	592	UCUUCCCAAL	GGCAUGGGU	Cleavage
	22	811	832	UCUUCCCAAL	GGUAUGGGU	Cleavage
	22	781	802	UCUUCCCAAL	GAGGAGGGU	Cleavage
	22	781	802	UCUUCCCAAL	GAGGAGGGU	Cleavage
	22	781	802	UCUUCCCAAL	GAGGAGGGU	Cleavage
	22	781	802	UCUUCCCAAL	GAGGAGGGU	Cleavage
	22	781	802	UCUUCCCAAL	GAGGAGGGU	Cleavage
	22	781	802	UCUUCCCAAL	GAGGAGGGU	Cleavage
	22	517	538	UCUUCCCAAL	GGUAUGGGC	Cleavage
	22	746	767	UCUUCCCAAL	GGCAUGGGU	Translation
	22	709	730	UCUUCCCUAC	GGGAUGGGA	Translation
	22	709	730	UCUUCCCUAC	GGGAUGGGA	Translation
	22	1008	1029	UCUUCCCUAC	GACGUGGAG	Cleavage
	22	1008	1029	UCUUCCCUAC	GACGUGGAG	Cleavage
	22	513	534	UCUUCCCAAL	AGGAUGGGU	Cleavage
	22	613	634	UCUUCCCAAL	AGGAUGGGU	Cleavage

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2	22	1221	1242 UCUUCCCAAL :: :: : ::::::::::: AUAAGGGUCI Cleavage	
3	22	493	514 UCUUCCCAAL ::::::::::: CCUACUGGGUC Cleavage	
4	22	138	159 UCUUCCCUAC ::::::::::: ::UGGCAGGGA Cleavage	
5	22	138	159 UCUUCCCUAC ::::::::::: ::UGGCAGGGA Cleavage	
6	22	126	147 UCUUCCCUAC :: :: :: :: :: GAGGUGGAA Cleavage	
7	22	126	147 UCUUCCCUAC :: :: :: :: :: GAGGUGGAA Cleavage	
8	22	2611	2632 UCUUCCCUAC: :: :: : ::::::::::: GCUAUGUCAI Cleavage	
9	22	2611	2632 UCUUCCCUAC: :: :: : ::::::::::: GCUAUGUCAI Cleavage	
10	22	487	508 UCUUCCCAAL . :: :: :: :: :: :: UUAGCGGGC Cleavage	
11	22	661	682 UCUUCCCUAC: :: :: :: :: :: :: GGAUUGGGC Cleavage	
12	22	661	682 UCUUCCCUAC: :: :: :: :: :: :: GGAUUGGGC Cleavage	
13	22	844	865 UCUUCCCUAC :: :: :: :: :: :: :: UGUUUGGGA Translation	
14	22	844	865 UCUUCCCUAC :: :: :: :: :: :: :: UGUUUGGGA Translation	
15	22	508	529 UCUUCCCUAC: :: :: :: :: :: :: : GGCAUGGGA Translation	
16	22	508	529 UCUUCCCUAC: :: :: :: :: :: :: : GGCAUGGGA Translation	
17	22	2091	2112 UCUUCCCAAL: :: :: :: :: :: :: :: GGGGUUGGC Translation	
18	22	550	571 UCUUCCCUAC: . :: :: :: :: :: :: :: GGGGUUGGA Cleavage	
19	22	550	571 UCUUCCCUAC: . :: :: :: :: :: :: :: GGGGUUGGA Cleavage	
20	22	550	571 UCUUCCCUAC: . :: :: :: :: :: :: :: GGGGUUGGA Cleavage	
21	22	550	571 UCUUCCCUAC: . :: :: :: :: :: :: :: GGGGUUGGA Cleavage	
22	22	1939	1960 UCUUCCCAAL :: :: :: :: :: :: :: AUAGUAGGC Cleavage	
23	22	113	134 UCUUCCCUAC : :: :: :: :: :: :: :: AUUUUGAGG Cleavage	
24	22	113	134 UCUUCCCUAC : :: :: :: :: :: :: :: AUUUUGAGG Cleavage	
25	22	113	134 UCUUCCCUAC : :: :: :: :: :: :: :: AUUUUGAGG Cleavage	
26	22	113	134 UCUUCCCUAC : :: :: :: :: :: :: :: AUUUUGAGG Cleavage	
27	22	750	771 UCUUCCCAAL: :: :: :: :: :: :: :: GGCAUGGGU Translation	
28	22	747	768 UCUUCCCAAL: :: :: :: :: :: :: :: GGCAUGGGU Translation	
29	22	802	823 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGG Cleavage	
30	22	59	80 UCUUCCCUAC :: :: :: :: :: :: :: UUAUUGGUA Cleavage	
31	22	59	80 UCUUCCCUAC :: :: :: :: :: :: :: UUAUUGGUA Cleavage	
32	22	59	80 UCUUCCCUAC :: :: :: :: :: :: :: UUAUUGGUA Cleavage	
33	22	59	80 UCUUCCCUAC :: :: :: :: :: :: :: UUAUUGGUA Cleavage	
34	22	680	701 UCUUCCCAAL: :: :: :: :: :: :: :: GGGAUUGGGU Cleavage	
35	22	720	741 UCUUCCCAAL: :: :: :: :: :: :: :: GGGAUUGGGU Cleavage	
36	22	586	607 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
37	22	658	679 UCUUCCCUAC: :: :: :: :: :: :: :: GGAAUGGGA Translation	
38	22	658	679 UCUUCCCUAC: :: :: :: :: :: :: :: GGAAUGGGA Translation	
39	22	793	814 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
40	22	589	610 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
41	22	703	724 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
42	22	798	819 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
43	22	723	744 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
44	22	532	553 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
45	22	589	610 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
46	22	656	677 UCUUCCCAAL: :: :: :: :: :: :: :: GGUAUGGGC Cleavage	
47	22	636	657 UCUUCCCAAL: :: :: :: :: :: :: :: GGCAUGGGC Cleavage	

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2	22	589	610 UCUUCCCAAL:: : : : :GGUAUGGGC Cleavage
3	22	589	610 UCUUCCCAAL : : : : :GCUAUGGGC Cleavage
4	22	842	863 UCUUCCCAAL:: : : : :GGUAUGGGC Cleavage
5	22	39	60 UCUUCCCAAL:: : : : :GGGAUGGGC Cleavage
6	22	716	737 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
7	22	716	737 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
8	22	601	622 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
9	22	601	622 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
10	22	604	625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
11	22	604	625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
12	22	604	625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
13	22	604	625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
14	22	752	773 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
15	22	752	773 UCUUCCCUAC:: : : : :GGAAUGGGA Translation
16	22	211	232 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage
17	22	516	537 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage
18	22	211	232 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage
19	22	516	537 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage
20	22	1599	1620 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage
21	22	1681	1702 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage
22	22	1599	1620 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage
23	22	1681	1702 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage
24	22	757	778 UCUUCCCAAL:: : : : :GGAAGGGGA Cleavage
25	22	757	778 UCUUCCCAAL:: : : : :GGAAGGGGA Cleavage
26	22	647	668 UCUUCCCUAC : : : : :AACGUGGGA Cleavage
27	22	647	668 UCUUCCCUAC : : : : :AACGUGGGA Cleavage
28	22	414	435 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage
29	22	724	745 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage
30	22	720	741 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage
31	22	801	822 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage
32	22	1183	1204 UCUUCCCAAL : : : : :UUGAUGGGU Translation
33	22	2066	2087 UCUUCCCUAC : : : : :CUUGUGGAA Cleavage
34	22	2066	2087 UCUUCCCUAC : : : : :CUUGUGGAA Cleavage
35	22	804	825 UCUUCCCAAL: : : : :GGGGUGGGU Cleavage
36	22	804	825 UCUUCCCAAL: : : : :GGGGUGGGU Cleavage
37	22	505	526 UCUUCCCUAC : : : : :AUUAUUGGA Cleavage
38	22	505	526 UCUUCCCUAC : : : : :AUUAUUGGA Cleavage
39	22	83	104 UCUUCCCAAL : : : : :AAAUGGGGA Cleavage
40	22	83	104 UCUUCCCAAL : : : : :AAAUGGGGA Cleavage
41	22	83	104 UCUUCCCAAL : : : : :AAAUGGGGA Cleavage
42	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
43	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
44	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
45	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
46	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
47	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
48	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
49	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
50	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
51	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
52	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
53	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
54	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
55	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
56	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
57	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
58	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
59	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation
60	22	1325	1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation

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2	22	667	688 UCUUCCCUAC:: : : : :GGAAUGGGC(Translation
3	22	667	688 UCUUCCCUAC:: : : : :GGAAUGGGC(Translation
4	22	326	347 UCUUCCCUAC:: : : : :GGCAAGGGC( Cleavage
5	22	326	347 UCUUCCCUAC:: : : : :GGCAAGGGC( Cleavage
6	22	326	347 UCUUCCCUAC:: : : : :GGCAAGGGC( Cleavage
7	22	791	812 UCUUCCCAAL : : : : :UGAGUGGGC( Cleavage
8	22	837	858 UCUUCCCUAC : : : : :UGUAUGGGU( Cleavage
9	22	837	858 UCUUCCCUAC : : : : :UGUAUGGGU( Cleavage
10	22	837	858 UCUUCCCUAC : : : : :UGUAUGGGU( Cleavage
11	22	634	655 UCUUCCCAAL : : : : :GGAAUGGGU( Cleavage
12	22	666	687 UCUUCCCAAL : : : : :AAUGUGGGU( Cleavage
13	22	1615	1636 UCUUCCCAAL : : : : :GGCAUGGGU( Cleavage
14	22	619	640 UCUUCCCUAC : : : : :GGCAAAGGA( Cleavage
15	22	619	640 UCUUCCCUAC : : : : :GGCAAAGGA( Cleavage
16	22	619	640 UCUUCCCUAC : : : : :GGCAAAGGA( Cleavage
17	22	265	287 UCUUCCCAAL : : : : :GUGAUGGGU( Cleavage
18	22	265	287 UCUUCCCAAL : : : : :GUGAUGGGU( Cleavage
19	22	312	333 UCUUCCCAAL : : : : :GGGAAAGGA( Cleavage
20	22	1781	1802 UCUUCCCAAL : : : : :GGAAUAGGU( Cleavage
21	22	1891	1912 UCUUCCCUAC : : : : :CGUGUGGGA( Cleavage
22	22	1891	1912 UCUUCCCUAC : : : : :CGUGUGGGA( Cleavage
23	22	1891	1912 UCUUCCCUAC : : : : :CGUGUGGGA( Cleavage
24	22	404	425 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation
25	22	479	500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation
26	22	479	500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation
27	22	404	425 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation
28	22	479	500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation
29	22	479	500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation
30	22	1415	1436 UCUUCCCAAL : : : : :AAGCAGGGU( Cleavage
31	22	715	736 UCUUCCCUAC : : : : :GAUGUGGAA( Cleavage
32	22	728	749 UCUUCCCUAC : : : : :GAUGUGGAA( Cleavage
33	22	715	736 UCUUCCCUAC : : : : :GAUGUGGAA( Cleavage
34	22	715	736 UCUUCCCUAC : : : : :GAUGUGGAA( Cleavage
35	22	728	749 UCUUCCCUAC : : : : :GAUGUGGAA( Cleavage
36	22	811	832 UCUUCCCAAL : : : : :GGGAUGGGG( Translation
37	22	811	832 UCUUCCCUAC : : : : :GGGAUGGGG( Translation
38	22	811	832 UCUUCCCUAC : : : : :GGGAUGGGG( Translation
39	22	811	832 UCUUCCCUAC : : : : :GGGAUGGGG( Translation
40	22	1673	1694 UCUUCCCAAL : : : : :GGGAUGGGGA( Cleavage
41	22	1698	1719 UCUUCCCAAL : : : : :GGGAUGGGGA( Cleavage
42	22	1698	1719 UCUUCCCAAL : : : : :GGGAUGGGGA( Cleavage
43	22	1135	1156 UCUUCCCUAC : : : : :UGAAUGGGGA( Cleavage
44	22	1135	1156 UCUUCCCUAC : : : : :UGAAUGGGGA( Cleavage
45	22	596	617 UCUUCCCAAL : : : : :GGCAUGGGC( Cleavage
46	22	596	617 UCUUCCCAAL : : : : :GGCAUGGGC( Cleavage
47	22	2364	2385 UCUUCCCAAL : : : : :AAAUGGGGA( Cleavage
48	22	409	430 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
49	22	719	740 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
50	22	719	740 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
51	22	722	743 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
52	22	722	743 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
53	22	719	740 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
54	22	719	740 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
55	22	770	791 UCUUCCCAAL : : : : :GCAAUGGCUI( Cleavage
56	22	568	589 UCUUCCCAAL : : : : :GGCAUGGGG( Translation
57	22	568	589 UCUUCCCUAC : : : : :GGCAUGGGG( Translation
58	22	568	589 UCUUCCCUAC : : : : :GGCAUGGGG( Translation
59	22	568	589 UCUUCCCUAC : : : : :GGCAUGGGG( Translation
60	22	180	201 UCUUCCCAAL : : : : :GCGAUGGGC( Cleavage
	22	159	180 UCUUCCCAAL : : : : :GCGAUGGGC( Cleavage





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2	22	816	837 UCUUCCCAAL::: : : : : : : : : :GGGAUCGCU( Cleavage
3	22	449	470 UCUUCCCAAL::: : : : : : : : : :GGGUUGGGU Cleavage
4	22	449	470 UCUUCCCAAL::: : : : : : : : : :GGGUUGGGU Cleavage
5	22	1711	1732 UCUUCCCUAC : : : : : : : : : :UUUAUGGGU Cleavage
6	22	1711	1732 UCUUCCCUAC : : : : : : : : : :UUUAUGGGU Cleavage
7	22	529	550 UCUUCCCAAL : : : : : : : : : :CUACAGGGC( Cleavage
8	22	525	546 UCUUCCCUAC : : : : : : : : : :AAUAUGGGC( Cleavage
9	22	525	546 UCUUCCCUAC : : : : : : : : : :AAUAUGGGC( Cleavage
10	22	843	864 UCUUCCCUAC: : : : : : : : : :GGUUUGGUG Cleavage
11	22	843	864 UCUUCCCUAC: : : : : : : : : :GGUUUGGUG Cleavage
12	22	822	843 UCUUCCCAAL: : : : : : : : : :GGAAUGGGA( Cleavage
13	22	248	269 UCUUCCCUAC: : : : : : : : : :GGAGUGGCA( Cleavage
14	22	248	269 UCUUCCCUAC: : : : : : : : : :GGAGUGGCA( Cleavage
15	22	1667	1688 UCUUCCCAAL : : : : : : : : : :UGGGUGGAU Cleavage
16	22	1756	1777 UCUUCCCAAL : : : : : : : : : :UGGGUGGAU Cleavage
17	22	1759	1780 UCUUCCCAAL : : : : : : : : : :UGGGUGGAU Cleavage
18	22	181	202 UCUUCCCAAL: : : : : : : : : :GAAUUGGAU( Cleavage
19	22	634	655 UCUUCCCUAC: : : : : : : : : :GGAAUGGGU Translation
20	22	634	655 UCUUCCCUAC: : : : : : : : : :GGAAUGGGU Translation
21	22	704	725 UCUUCCCAAL: : : : : : : : : :GGCAUGGGU( Cleavage
22	22	704	725 UCUUCCCAAL: : : : : : : : : :GGCAUGGGU( Cleavage
23	22	732	753 UCUUCCCUAC: : : : : : : : : :GGUAUGGGU Translation
24	22	732	753 UCUUCCCUAC: : : : : : : : : :GGUAUGGGU Translation
25	22	544	565 UCUUCCCUAC: : : : : : : : : :GGUGUUGGU Cleavage
26	22	544	565 UCUUCCCUAC: : : : : : : : : :GGUGUUGGU Cleavage
27	22	494	516 UCUUC-CCAAI : : : : : : : : : :CUUGUGGGU Cleavage
28	22	750	772 UCUUC-CCAAI : : : : : : : : : :CUUGUGGGU Cleavage
29	22	620	641 UCUUCCCAAL: : : : : : : : : :GGAGAGGGU Cleavage
30	22	271	292 UCUUCCCUAC : : : : : : : : : :GGAUGGGGA Cleavage
31	22	271	292 UCUUCCCUAC : : : : : : : : : :GGAUGGGGA Cleavage
32	22	226	247 UCUUCCCUAC : : : : : : : : : :GGGGACGGA( Cleavage
33	22	226	247 UCUUCCCUAC : : : : : : : : : :GGGGACGGA( Cleavage
34	22	226	247 UCUUCCCUAC : : : : : : : : : :GGGGACGGA( Cleavage
35	22	226	247 UCUUCCCUAC : : : : : : : : : :GGGGACGGA( Cleavage
36	22	244	265 UCUUCCCAAL: : : : : : : : : :GGUAUGAGC( Cleavage
37	22	673	694 UCUUCCCAAL: : : : : : : : : :GGAAUGGGA( Cleavage
38	22	646	667 UCUUCCCAAL: : : : : : : : : :GGAAUGGGA( Cleavage
39	22	566	587 UCUUCCCAAL: : : : : : : : : :GGCAUGGGU( Cleavage
40	22	286	306 UCUUCCCAAL: : : : : : : : : :GAAUUGGGU( Cleavage
41	22	1001	1022 UCUUCCCAAL : : : : : : : : : :AAAUUGGGU(Translation
42	22	468	489 UCUUCCCUAC: : : : : : : : : :GUUAUGGGU Cleavage
43	22	468	489 UCUUCCCUAC: : : : : : : : : :GUUAUGGGU Cleavage
44	22	1083	1104 UCUUCCCAAL : : : : : : : : : :UGAAUUGGC( Cleavage
45	22	817	838 UCUUCCCUAC: : : : : : : : : :GGAAUGGGU Translation
46	22	817	838 UCUUCCCUAC: : : : : : : : : :GGAAUGGGU Translation
47	22	716	737 UCUUCCCUAC: : : : : : : : : :GGGAUGGGC( Translation

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2	22	716	737 UCUUCCCUAC:: : : : : :GGGAUGGGC Translation
3	22	1231	1252 UCUUCCCAAL:: : : : : :GGAAUGGGA Cleavage
4	22	1231	1252 UCUUCCCAAL:: : : : : :GGAAUGGGA Cleavage
5	22	634	655 UCUUCCCUAC:: : : : : :GGAAUGGGU Translation
6	22	634	655 UCUUCCCUAC:: : : : : :GGAAUGGGU Translation
7	22	634	655 UCUUCCCUAC:: : : : : :GGAAUGGGU Translation
8	22	640	661 UCUUCCCUAC:: : : : : :GGCAUGGGU Translation
9	22	640	661 UCUUCCCUAC:: : : : : :GGCAUGGGU Translation
10	22	640	661 UCUUCCCUAC:: : : : : :GGCAUGGGU Translation
11	22	238	259 UCUUCCCUAC:: : : : : :GGAAUGCGA Translation
12	22	238	259 UCUUCCCUAC:: : : : : :GGAAUGCGA Translation
13	22	238	259 UCUUCCCUAC:: : : : : :GGAAUGCGA Translation
14	22	1714	1735 UCUUCCCUAC:: : : : : :GGGAUGAGA Cleavage
15	22	1714	1735 UCUUCCCUAC:: : : : : :GGGAUGAGA Cleavage
16	22	318	339 UCUUCCCAAL : : : : : :AGGGUGGGU Cleavage
17	22	394	415 UCUUCCCAAL : : : : : :AGGGUGGGU Cleavage
18	22	394	415 UCUUCCCAAL : : : : : :AGGGUGGGU Cleavage
19	22	394	415 UCUUCCCAAL : : : : : :AGGGUGGGU Cleavage
20	22	394	415 UCUUCCCAAL : : : : : :AGGGUGGGU Cleavage
21	22	334	355 UCUUCCCUAC : : : : : :CGUUUGGGG Translation
22	22	334	355 UCUUCCCUAC : : : : : :CGUUUGGGG Translation
23	22	334	355 UCUUCCCUAC : : : : : :CGUUUGGGG Translation
24	22	838	859 UCUUCCCAAL:: : : : : :GGAAUCGGG Cleavage
25	22	321	342 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
26	22	321	342 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
27	22	321	342 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
28	22	383	404 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
29	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
30	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
31	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
32	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
33	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
34	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
35	22	383	404 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
36	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
37	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
38	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
39	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
40	22	434	455 UCUUCCCUAC : : : : : :ACUGUGGGA Cleavage
41	22	1054	1075 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
42	22	1054	1075 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
43	22	1360	1381 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
44	22	1452	1473 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
45	22	1054	1075 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
46	22	1054	1075 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
47	22	1360	1381 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
48	22	1452	1473 UCUUCCCUAC:: : : : : :GGUGAGAGU Cleavage
49	22	923	944 UCUUCCCAAL:: : : : : :GGAGUGGUC Cleavage
50	22	945	966 UCUUCCCAAL:: : : : : :GGAGUGGUC Cleavage
51	22	945	966 UCUUCCCAAL:: : : : : :GGAGUGGUC Cleavage
52	22	5224	5245 UCUUCCCAAL : : : : : :GAAGUGCGU Cleavage
53	22	5224	5245 UCUUCCCAAL : : : : : :GAAGUGCGU Cleavage
54	22	5224	5245 UCUUCCCAAL : : : : : :GAAGUGCGU Cleavage
55	22	5220	5241 UCUUCCCAAL : : : : : :GAAGUGCGU Cleavage
56	22	1887	1908 UCUUCCCAAL : : : : : :AAGAUGGGC Cleavage
57	22	1887	1908 UCUUCCCAAL : : : : : :AAGAUGGGC Cleavage
58	22	1887	1908 UCUUCCCAAL : : : : : :AAGAUGGGC Cleavage
59	22	3331	3352 UCUUCCCAAL : : : : : :AAGAUGGGC Cleavage
60	22	623	644 UCUUCCCAAL:: : : : : :GGAAUGGUU Cleavage
	22	733	754 UCUUCCCAAL:: : : : : :GGAAGGGGU Translation

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2	22	1265	1286 UCUUCCCAAL:::: ::::: ::::: :::::GGAAGGGGU Translation
3	22	1508	1528 UCUUCCCUAC ::::: ::::: :::::UGUAUGCGA\ Cleavage
4	22	1508	1528 UCUUCCCUAC ::::: ::::: :::::UGUAUGCGA\ Cleavage
5			
6	22	11	30 UCUUCCCUAC::::: ::::: :::::GGUAUGG-AC\ Cleavage
7	22	11	30 UCUUCCCUAC::::: ::::: :::::GGUAUGG-AC\ Cleavage
8			
9	22	519	540 UCUUCCCAAL::: : : ::::: GGGGUUGGG Cleavage
10	22	525	546 UCUUCCCUAC ::::: ::::: ::::: UUCAUGGGA\ Cleavage
11	22	525	546 UCUUCCCUAC ::::: ::::: ::::: UUCAUGGGA\ Cleavage
12			
13	22	81	102 UCUUCCCAAL ::::: : : ::::: UGAAUGGGG Cleavage
14	22	46	67 UCUUCCCUAC ::::: ::::: ::::: CUAGUGGGA\ Cleavage
15	22	46	67 UCUUCCCUAC ::::: ::::: ::::: CUAGUGGGA\ Cleavage
16			
17	22	81	102 UCUUCCCAAL ::::: ::::: :::::UGAGUGGGG Cleavage
18	22	845	866 UCUUCCCUAC ::::: ::::: :::::AGUGUGGGA Translation
19	22	845	866 UCUUCCCUAC ::::: ::::: :::::AGUGUGGGA Translation
20			
21	22	419	440 UCUUCCCAAL::: : : ::::: GGAGUUGGG Cleavage
22	22	1622	1643 UCUUCCCAAL::: : : ::::: GGAAGGGU Cleavage
23	22	1951	1974 UCUUCCCAAL::::: ::::: :::::GGAUUGGGA\ Cleavage
24	22	716	737 UCUUCCCAAL ::::: ::::: ::::: CCAGUGGGA\ Cleavage
25			
26	22	1608	1629 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage
27	22	643	664 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation
28	22	1537	1558 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage
29			
30	22	688	709 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation
31	22	1608	1629 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage
32	22	643	664 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation
33			
34	22	1537	1558 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage
35	22	688	709 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation
36	22	3093	3114 UCUUCCCAAL::: : : :::::GGAGUUAGU Cleavage
37	22	658	679 UCUUCCCAAL::::: ::::: :::::GGAUUGGGA\ Cleavage
38			
39	22	716	737 UCUUCCCAAL::::: ::::: :::::GGAUUGGGA\ Cleavage
40	22	601	622 UCUUCCCAAL::::: ::::: :::::GGAUUGGGA\ Cleavage
41			
42	22	604	625 UCUUCCCAAL::::: ::::: :::::GGAUUGGGA\ Cleavage
43	22	752	773 UCUUCCCAAL::::: ::::: :::::GGAUUGGGA\ Cleavage
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	Target_Desc.	Multiplicity	Target_Acc.	ID	locusName	Pfam
1						
2						
3	pacid=371636	1	Phvul.004G048000.1	Phvul.004G048000	Phvul.004G04	PF00931
4	pacid=371689	1	Phvul.001G224800.1	Phvul.001G224800	Phvul.001G22	PF01344,PF13
5						
6	pacid=371689	1	Phvul.001G224800.2	Phvul.001G224800	Phvul.001G22	PF01344,PF13
7	pacid=371689	1	Phvul.001G224800.1	Phvul.001G224800	Phvul.001G22	PF01344,PF13
8	pacid=371689	1	Phvul.001G224800.2	Phvul.001G224800	Phvul.001G22	PF01344,PF13
9						
10	pacid=371656	1	Phvul.007G201700.1	Phvul.007G201700	Phvul.007G20	PF01344,PF13
11	pacid=371656	1	Phvul.007G201700.1	Phvul.007G201700	Phvul.007G20	PF01344,PF13
12	pacid=371606	1	Phvul.008G061300.2	Phvul.008G061300	Phvul.008G06	PF13855,PF00
13						
14	pacid=371606	1	Phvul.008G061300.1	Phvul.008G061300	Phvul.008G06	PF13855,PF00
15	pacid=371606	1	Phvul.008G061300.2	Phvul.008G061300	Phvul.008G06	PF13855,PF00
16	pacid=371606	1	Phvul.008G061300.1	Phvul.008G061300	Phvul.008G06	PF13855,PF00
17						
18	pacid=371779	1	Phvul.002G079200.1	Phvul.002G079200	Phvul.002G07	PF05729,PF13
19	pacid=371683	1	Phvul.001G217600.1	Phvul.001G217600	Phvul.001G21	0
20	pacid=371775	1	Phvul.002G001500.1	Phvul.002G001500	Phvul.002G00	PF13919,PF00
21						
22	pacid=371775	1	Phvul.002G001500.1	Phvul.002G001500	Phvul.002G00	PF13919,PF00
23	pacid=371469	1	Phvul.003G072500.1	Phvul.003G072500	Phvul.003G07	PF13676,PF00
24	pacid=371456	2	Phvul.003G244225.3	Phvul.003G244225	Phvul.003G24	0
25						
26	pacid=371456	2	Phvul.003G244225.2	Phvul.003G244225	Phvul.003G24	0
27	pacid=371456	2	Phvul.003G244225.1	Phvul.003G244225	Phvul.003G24	0
28	pacid=371634	1	Phvul.004G137300.1	Phvul.004G137300	Phvul.004G13	PF13676,PF00
29	pacid=371543	1	Phvul.005G029400.1	Phvul.005G029400	Phvul.005G02	PF03145
30						
31	pacid=371543	1	Phvul.005G029400.3	Phvul.005G029400	Phvul.005G02	PF03145
32	pacid=371543	1	Phvul.005G029400.2	Phvul.005G029400	Phvul.005G02	PF03145
33	pacid=371662	1	Phvul.007G210600.1	Phvul.007G210600	Phvul.007G21	PF03110
34						
35	pacid=371662	1	Phvul.007G210600.1	Phvul.007G210600	Phvul.007G21	PF03110
36	pacid=371605	1	Phvul.008G055500.1	Phvul.008G055500	Phvul.008G05	PF00005
37	pacid=371577	1	Phvul.008G280900.1	Phvul.008G280900	Phvul.008G28	PF01594
38						
39	pacid=371577	1	Phvul.008G280900.1	Phvul.008G280900	Phvul.008G28	PF01594
40	pacid=371428	1	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G06	PF00931
41	pacid=371426	1	Phvul.010G136700.1	Phvul.010G136700	Phvul.010G13	PF07725,PF13
42						
43	pacid=371549	1	Phvul.011G149100.7	Phvul.011G149100	Phvul.011G14	0
44	pacid=371549	1	Phvul.011G149100.6	Phvul.011G149100	Phvul.011G14	0
45	pacid=371549	1	Phvul.011G149100.5	Phvul.011G149100	Phvul.011G14	0
46	pacid=371549	1	Phvul.011G149100.2	Phvul.011G149100	Phvul.011G14	0
47	pacid=371549	1	Phvul.011G149100.1	Phvul.011G149100	Phvul.011G14	0
48	pacid=371549	1	Phvul.011G149100.4	Phvul.011G149100	Phvul.011G14	0
49	pacid=371549	1	Phvul.011G149100.3	Phvul.011G149100	Phvul.011G14	0
50						
51	pacid=371569	1	Phvul.011G166100.1	Phvul.011G166100	Phvul.011G16	PF00931
52						
53	pacid=371711	1	Phvul.001G128200.2	Phvul.001G128200	Phvul.001G12	PF07725,PF13
54						
55	pacid=371696	1	Phvul.001G134000.1	Phvul.001G134000	Phvul.001G13	PF13855,PF00
56	pacid=371696	1	Phvul.001G134000.1	Phvul.001G134000	Phvul.001G13	PF13855,PF00
57	pacid=371708	1	Phvul.001G243900.1	Phvul.001G243900	Phvul.001G24	PF02861,PF07
58	pacid=371708	1	Phvul.001G243900.1	Phvul.001G243900	Phvul.001G24	PF02861,PF07
59	pacid=371772	1	Phvul.002G057300.2	Phvul.002G057300	Phvul.002G05	PF08458,PF05
60	pacid=371772	1	Phvul.002G057300.1	Phvul.002G057300	Phvul.002G05	PF08458,PF05

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2	pacid=371769	1 Phvul.002G122200.1	Phvul.002G122200	Phvul.002G12 PF00067	
3	pacid=371750	1 Phvul.002G187600.1	Phvul.002G187600	Phvul.002G18	0
4	pacid=371773	1 Phvul.002G261500.1	Phvul.002G261500	Phvul.002G26 PF00076	
5	pacid=371773	1 Phvul.002G261500.1	Phvul.002G261500	Phvul.002G26 PF00076	
6	pacid=371475	1 Phvul.003G101200.1	Phvul.003G101200	Phvul.003G10 PF04535	
7	pacid=371475	1 Phvul.003G101200.1	Phvul.003G101200	Phvul.003G10 PF04535	
8	pacid=371460	1 Phvul.003G202900.1	Phvul.003G202900	Phvul.003G20 PF02657,PF02	
9	pacid=371460	1 Phvul.003G202900.1	Phvul.003G202900	Phvul.003G20 PF02657,PF02	
10	pacid=371627	1 Phvul.004G026200.1	Phvul.004G026200	Phvul.004G02 PF00505,PF08	
11	pacid=371631	1 Phvul.004G140400.1	Phvul.004G140400	Phvul.004G14 PF05729,PF13	
12	pacid=371631	1 Phvul.004G140400.1	Phvul.004G140400	Phvul.004G14 PF05729,PF13	
13	pacid=371524	1 Phvul.005G038200.1	Phvul.005G038200	Phvul.005G03 PF00590	
14	pacid=371524	1 Phvul.005G038200.1	Phvul.005G038200	Phvul.005G03 PF00590	
15	pacid=371534	1 Phvul.005G087100.1	Phvul.005G087100	Phvul.005G08 PF13855,PF00	
16	pacid=371534	1 Phvul.005G087100.1	Phvul.005G087100	Phvul.005G08 PF13855,PF00	
17	pacid=371730	1 Phvul.006G102700.1	Phvul.006G102700	Phvul.006G10 PF11721,PF00	
18	pacid=371579	1 Phvul.008G072300.2	Phvul.008G072300	Phvul.008G07 PF00931	
19	pacid=371579	1 Phvul.008G072300.1	Phvul.008G072300	Phvul.008G07 PF00931	
20	pacid=371579	1 Phvul.008G072300.2	Phvul.008G072300	Phvul.008G07 PF00931	
21	pacid=371579	1 Phvul.008G072300.1	Phvul.008G072300	Phvul.008G07 PF00931	
22	pacid=371579	1 Phvul.008G202300.1	Phvul.008G202300	Phvul.008G20 PF04031	
23	pacid=371595	1 Phvul.008G259600.2	Phvul.008G259600	Phvul.008G25 PF02705	
24	pacid=371595	1 Phvul.008G259600.1	Phvul.008G259600	Phvul.008G25 PF02705	
25	pacid=371595	1 Phvul.008G259600.2	Phvul.008G259600	Phvul.008G25 PF02705	
26	pacid=371595	1 Phvul.008G259600.1	Phvul.008G259600	Phvul.008G25 PF02705	
27	pacid=371424	1 Phvul.010G131650.1	Phvul.010G131650	Phvul.010G13 PF07725,PF13	
28	pacid=371433	1 Phvul.010G132333.1	Phvul.010G132333	Phvul.010G13 PF07725	
29	pacid=371436	1 Phvul.010G136800.1	Phvul.010G136800	Phvul.010G13 PF07725,PF13	
30	pacid=371426	1 Phvul.010G151400.6	Phvul.010G151400	Phvul.010G15 PF16994	
31	pacid=371426	1 Phvul.010G151400.4	Phvul.010G151400	Phvul.010G15 PF16994	
32	pacid=371426	1 Phvul.010G151400.6	Phvul.010G151400	Phvul.010G15 PF16994	
33	pacid=371426	1 Phvul.010G151400.4	Phvul.010G151400	Phvul.010G15 PF16994	
34	pacid=371547	1 Phvul.011G140300.1	Phvul.011G140300	Phvul.011G14 PF07725,PF13	
35	pacid=371561	1 Phvul.011G140400.1	Phvul.011G140400	Phvul.011G14 PF13676,PF13	
36	pacid=371574	1 Phvul.011G151300.1	Phvul.011G151300	Phvul.011G15 PF00931	
37	pacid=371561	1 Phvul.011G181700.1	Phvul.011G181700	Phvul.011G18 PF00931	
38	pacid=371561	1 Phvul.011G181700.1	Phvul.011G181700	Phvul.011G18 PF00931	
39	pacid=371570	1 Phvul.011G192400.1	Phvul.011G192400	Phvul.011G19 PF00931	
40	pacid=371555	1 Phvul.011G192600.1	Phvul.011G192600	Phvul.011G19 PF13855,PF00	
41	pacid=371558	1 Phvul.011G193100.1	Phvul.011G193100	Phvul.011G19 PF00931	
42	pacid=371551	1 Phvul.011G193500.1	Phvul.011G193500	Phvul.011G19 PF13855,PF00	
43	pacid=371558	1 Phvul.011G193600.1	Phvul.011G193600	Phvul.011G19 PF13855,PF00	
44	pacid=371550	1 Phvul.011G194800.1	Phvul.011G194800	Phvul.011G19 PF00931	
45	pacid=371546	1 Phvul.011G194900.1	Phvul.011G194900	Phvul.011G19 PF00931	
46	pacid=371570	1 Phvul.011G195000.1	Phvul.011G195000	Phvul.011G19 PF00931	
47	pacid=371563	1 Phvul.011G195200.1	Phvul.011G195200	Phvul.011G19 PF00931	



1				
2	pacid=371572	1 Phvul.011G195400.1	Phvul.011G195400	Phvul.011G19 PF00931
3	pacid=371554	1 Phvul.011G195500.1	Phvul.011G195500	Phvul.011G19 PF00931
4	pacid=371565	1 Phvul.011G196000.1	Phvul.011G196000	Phvul.011G19PF13855,PF00
5				
6	pacid=371571	1 Phvul.011G196066.1	Phvul.011G196066	Phvul.011G19 PF00931
7	pacid=371573	1 Phvul.011G200820.1	Phvul.011G200820	Phvul.011G20 PF00931
8	pacid=371573	1 Phvul.011G200820.1	Phvul.011G200820	Phvul.011G20 PF00931
9				
10	pacid=371560	1 Phvul.011G202100.1	Phvul.011G202100	Phvul.011G20 PF00931
11	pacid=371560	1 Phvul.011G202100.1	Phvul.011G202100	Phvul.011G20 PF00931
12	pacid=371555	1 Phvul.011G202300.1	Phvul.011G202300	Phvul.011G20 PF00931
13				
14	pacid=371555	1 Phvul.011G202300.1	Phvul.011G202300	Phvul.011G20 PF00931
15	pacid=371563	1 Phvul.011G203100.1	Phvul.011G203100	Phvul.011G20 PF00931
16	pacid=371563	1 Phvul.011G203100.1	Phvul.011G203100	Phvul.011G20 PF00931
17				
18	pacid=371575	1 Phvul.L002337.2	Phvul.L002337	Phvul.L002337:PF00107,PF08
19	pacid=371575	1 Phvul.L002337.1	Phvul.L002337	Phvul.L002337:PF00107,PF08
20	pacid=371575	1 Phvul.L002337.2	Phvul.L002337	Phvul.L002337:PF00107,PF08
21				
22	pacid=371575	1 Phvul.L002337.1	Phvul.L002337	Phvul.L002337:PF00107,PF08
23	pacid=371699	1 Phvul.001G015600.1	Phvul.001G015600	Phvul.001G01 PF01553
24	pacid=371699	1 Phvul.001G015600.2	Phvul.001G015600	Phvul.001G01 PF01553
25				
26	pacid=371699	1 Phvul.001G015600.1	Phvul.001G015600	Phvul.001G01 PF01553
27	pacid=371699	1 Phvul.001G015600.2	Phvul.001G015600	Phvul.001G01 PF01553
28	pacid=371677	1 Phvul.001G085500.2	Phvul.001G085500	Phvul.001G08 PF00010
29	pacid=371677	1 Phvul.001G085500.1	Phvul.001G085500	Phvul.001G08 PF00010
30				
31	pacid=371685	1 Phvul.001G232600.1	Phvul.001G232600	Phvul.001G23 PF03330,PF01
32	pacid=371685	1 Phvul.001G232600.1	Phvul.001G232600	Phvul.001G23 PF03330,PF01
33	pacid=371756	1 Phvul.002G041400.4	Phvul.002G041400	Phvul.002G04 PF04640
34				
35	pacid=371756	1 Phvul.002G041400.1	Phvul.002G041400	Phvul.002G04 PF04640
36	pacid=371756	1 Phvul.002G041400.2	Phvul.002G041400	Phvul.002G04 PF04640
37	pacid=371756	1 Phvul.002G041400.3	Phvul.002G041400	Phvul.002G04 PF04640
38				
39	pacid=371778	1 Phvul.002G298800.1	Phvul.002G298800	Phvul.002G29 PF01764
40	pacid=371450	1 Phvul.003G010900.1	Phvul.003G010900	Phvul.003G01 PF00503
41	pacid=371450	1 Phvul.003G010900.1	Phvul.003G010900	Phvul.003G01 PF00503
42				
43	pacid=371453	1 Phvul.003G195800.2	Phvul.003G195800	Phvul.003G19PF01535,PF13
44	pacid=371453	1 Phvul.003G195800.1	Phvul.003G195800	Phvul.003G19PF01535,PF13
45	pacid=371455	1 Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25 PF12171
46				
47	pacid=371455	1 Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25 PF12171
48	pacid=371465	1 Phvul.003G295800.4	Phvul.003G295800	Phvul.003G29PF12624,PF09
49	pacid=371465	1 Phvul.003G295800.3	Phvul.003G295800	Phvul.003G29PF12624,PF09
50				
51	pacid=371465	1 Phvul.003G295800.2	Phvul.003G295800	Phvul.003G29PF12624,PF09
52	pacid=371636	1 Phvul.004G032300.4	Phvul.004G032300	Phvul.004G03 PF14008,PF16
53	pacid=371636	1 Phvul.004G032300.2	Phvul.004G032300	Phvul.004G03 PF14008,PF16
54				
55	pacid=371636	1 Phvul.004G032300.3	Phvul.004G032300	Phvul.004G03 PF14008,PF16
56	pacid=371636	1 Phvul.004G032300.1	Phvul.004G032300	Phvul.004G03 PF14008,PF16
57	pacid=371636	1 Phvul.004G032300.4	Phvul.004G032300	Phvul.004G03 PF14008,PF16
58	pacid=371636	1 Phvul.004G032300.2	Phvul.004G032300	Phvul.004G03 PF14008,PF16
59	pacid=371636	1 Phvul.004G032300.3	Phvul.004G032300	Phvul.004G03 PF14008,PF16
60	pacid=371636	1 Phvul.004G032300.1	Phvul.004G032300	Phvul.004G03 PF14008,PF16



1					
2	pacid=371636	1 Phvul.004G048000.1	Phvul.004G048000	Phvul.004G04 PF00931	
3	pacid=371636	1 Phvul.004G048000.1	Phvul.004G048000	Phvul.004G04 PF00931	
4	pacid=371625	1 Phvul.004G106800.2	Phvul.004G106800	Phvul.004G10 PF01656	
5	pacid=371625	1 Phvul.004G106800.2	Phvul.004G106800	Phvul.004G10 PF01656	
6	pacid=371628	1 Phvul.004G133100.1	Phvul.004G133100	Phvul.004G13 PF12695	
7	pacid=371545	1 Phvul.005G165800.1	Phvul.005G165800	Phvul.005G16 PF01535,PF12	
8	pacid=371545	1 Phvul.005G165800.1	Phvul.005G165800	Phvul.005G16 PF01535,PF12	
9	pacid=371714	1 Phvul.006G066800.1	Phvul.006G066800	Phvul.006G06 PF00931	
10	pacid=371738	1 Phvul.006G086800.1	Phvul.006G086800	Phvul.006G08 PF03330,PF01	
11	pacid=371723	1 Phvul.006G148800.1	Phvul.006G148800	Phvul.006G14	0
12	pacid=371734	1 Phvul.006G180900.1	Phvul.006G180900	Phvul.006G18 PF08100,PF00	
13	pacid=371734	1 Phvul.006G180900.1	Phvul.006G180900	Phvul.006G18 PF08100,PF00	
14	pacid=371673	1 Phvul.007G027400.1	Phvul.007G027400	Phvul.007G02	0
15	pacid=371669	1 Phvul.007G096800.1	Phvul.007G096800	Phvul.007G09 PF01656	
16	pacid=371591	1 Phvul.008G158100.1	Phvul.008G158100	Phvul.008G15 PF08263,PF13	
17	pacid=371493	1 Phvul.009G020000.1	Phvul.009G020000	Phvul.009G02 PF08241,PF08	
18	pacid=371493	1 Phvul.009G020000.1	Phvul.009G020000	Phvul.009G02 PF08241,PF08	
19	pacid=371498	1 Phvul.009G065500.1	Phvul.009G065500	Phvul.009G06 PF00170	
20	pacid=371498	1 Phvul.009G065500.2	Phvul.009G065500	Phvul.009G06 PF00170	
21	pacid=371498	1 Phvul.009G065500.1	Phvul.009G065500	Phvul.009G06 PF00170	
22	pacid=371498	1 Phvul.009G065500.2	Phvul.009G065500	Phvul.009G06 PF00170	
23	pacid=371487	1 Phvul.009G213300.1	Phvul.009G213300	Phvul.009G21 PF13812,PF01	
24	pacid=371497	1 Phvul.009G226300.2	Phvul.009G226300	Phvul.009G22 PF14416,PF13	
25	pacid=371497	1 Phvul.009G226300.1	Phvul.009G226300	Phvul.009G22 PF14416,PF13	
26	pacid=371497	1 Phvul.009G226300.2	Phvul.009G226300	Phvul.009G22 PF14416,PF13	
27	pacid=371497	1 Phvul.009G226300.1	Phvul.009G226300	Phvul.009G22 PF14416,PF13	
28	pacid=371517	1 Phvul.009G233700.1	Phvul.009G233700	Phvul.009G23 PF00931	
29	pacid=371517	1 Phvul.009G233700.1	Phvul.009G233700	Phvul.009G23 PF00931	
30	pacid=371517	1 Phvul.009G233700.1	Phvul.009G233700	Phvul.009G23 PF00931	
31	pacid=371439	1 Phvul.010G008700.2	Phvul.010G008700	Phvul.010G00 PF00931	
32	pacid=371439	1 Phvul.010G008700.1	Phvul.010G008700	Phvul.010G00 PF00931	
33	pacid=371428	1 Phvul.010G056500.1	Phvul.010G056500	Phvul.010G05 PF13041	
34	pacid=371428	1 Phvul.010G056500.1	Phvul.010G056500	Phvul.010G05 PF13041	
35	pacid=371423	1 Phvul.010G063100.1	Phvul.010G063100	Phvul.010G06 PF00931	
36	pacid=371428	1 Phvul.010G070584.1	Phvul.010G070584	Phvul.010G07 PF00890,PF05	
37	pacid=371439	1 Phvul.010G146900.6	Phvul.010G146900	Phvul.010G14 PF07766	
38	pacid=371439	1 Phvul.010G146900.2	Phvul.010G146900	Phvul.010G14 PF07766	
39	pacid=371439	1 Phvul.010G146900.3	Phvul.010G146900	Phvul.010G14 PF07766	
40	pacid=371438	1 Phvul.010G146900.1	Phvul.010G146900	Phvul.010G14 PF07766	
41	pacid=371438	1 Phvul.010G146900.4	Phvul.010G146900	Phvul.010G14 PF07766	
42	pacid=371439	1 Phvul.010G146900.5	Phvul.010G146900	Phvul.010G14 PF07766	
43	pacid=371563	1 Phvul.011G014500.2	Phvul.011G014500	Phvul.011G01 PF00931	
44	pacid=371563	1 Phvul.011G014500.2	Phvul.011G014500	Phvul.011G01 PF00931	
45	pacid=371563	1 Phvul.011G014500.2	Phvul.011G014500	Phvul.011G01 PF00931	
46	pacid=371573	1 Phvul.011G082700.3	Phvul.011G082700	Phvul.011G08	0
47	pacid=371573	1 Phvul.011G082700.2	Phvul.011G082700	Phvul.011G08	0

1					
2	pacid=371573	1 Phvul.011G082700.1	Phvul.011G082700	Phvul.011G08	0
3	pacid=371549	1 Phvul.011G149400.1	Phvul.011G149400	Phvul.011G14 PF00931	
4	pacid=371549	1 Phvul.011G149400.1	Phvul.011G149400	Phvul.011G14 PF00931	
5	pacid=371566	1 Phvul.011G181500.1	Phvul.011G181500	Phvul.011G18 PF00931	
6	pacid=371546	1 Phvul.011G182900.1	Phvul.011G182900	Phvul.011G18 PF00407	
7	pacid=371546	1 Phvul.011G182900.1	Phvul.011G182900	Phvul.011G18 PF00407	
8	pacid=371551	1 Phvul.011G191600.1	Phvul.011G191600	Phvul.011G19PF13191,PF13	
9	pacid=371571	1 Phvul.011G191800.1	Phvul.011G191800	Phvul.011G19 PF00931	
10	pacid=371553	1 Phvul.011G192200.1	Phvul.011G192200	Phvul.011G19 PF00931	
11	pacid=371553	1 Phvul.011G192900.1	Phvul.011G192900	Phvul.011G19 PF00931	
12	pacid=371553	1 Phvul.011G192900.1	Phvul.011G192900	Phvul.011G19 PF00931	
13	pacid=371552	1 Phvul.011G195751.1	Phvul.011G195751	Phvul.011G19 PF00931	
14	pacid=371555	1 Phvul.011G198400.1	Phvul.011G198400	Phvul.011G19PF13855,PF00	
15	pacid=371548	1 Phvul.011G201000.1	Phvul.011G201000	Phvul.011G20 PF00931	
16	pacid=371569	1 Phvul.011G201101.1	Phvul.011G201101	Phvul.011G20 PF00931	
17	pacid=371680	1 Phvul.001G027100.1	Phvul.001G027100	Phvul.001G02 PF00646	
18	pacid=371711	1 Phvul.001G123000.2	Phvul.001G123000	Phvul.001G12 PF01055	
19	pacid=371712	1 Phvul.001G132516.1	Phvul.001G132516	Phvul.001G13 PF00931	
20	pacid=371712	1 Phvul.001G132516.1	Phvul.001G132516	Phvul.001G13 PF00931	
21	pacid=371694	1 Phvul.001G132701.1	Phvul.001G132701	Phvul.001G13 PF13855,PF00	
22	pacid=371694	1 Phvul.001G132701.1	Phvul.001G132701	Phvul.001G13 PF13855,PF00	
23	pacid=371700	1 Phvul.001G132800.1	Phvul.001G132800	Phvul.001G13 PF13855,PF00	
24	pacid=371700	1 Phvul.001G132800.1	Phvul.001G132800	Phvul.001G13 PF13855,PF00	
25	pacid=371678	1 Phvul.001G132864.1	Phvul.001G132864	Phvul.001G13 PF13855,PF00	
26	pacid=371678	1 Phvul.001G132864.1	Phvul.001G132864	Phvul.001G13 PF13855,PF00	
27	pacid=371687	1 Phvul.001G133100.1	Phvul.001G133100	Phvul.001G13 PF13855,PF00	
28	pacid=371687	1 Phvul.001G133100.1	Phvul.001G133100	Phvul.001G13 PF13855,PF00	
29	pacid=371684	1 Phvul.001G133101.1	Phvul.001G133101	Phvul.001G13 PF13855,PF00	
30	pacid=371684	1 Phvul.001G133101.1	Phvul.001G133101	Phvul.001G13 PF13855,PF00	
31	pacid=371712	1 Phvul.001G185400.1	Phvul.001G185400	Phvul.001G18PF08263,PF00	
32	pacid=371712	1 Phvul.001G185400.1	Phvul.001G185400	Phvul.001G18PF08263,PF00	
33	pacid=371700	1 Phvul.001G217800.1	Phvul.001G217800	Phvul.001G21 PF07885	
34	pacid=371778	1 Phvul.002G063500.1	Phvul.002G063500	Phvul.002G06 PF00295	
35	pacid=371778	1 Phvul.002G063500.1	Phvul.002G063500	Phvul.002G06 PF00295	
36	pacid=371754	1 Phvul.002G104200.1	Phvul.002G104200	Phvul.002G10PF00614,PF00	
37	pacid=371754	1 Phvul.002G104200.1	Phvul.002G104200	Phvul.002G10PF00614,PF00	
38	pacid=371780	1 Phvul.002G279500.1	Phvul.002G279500	Phvul.002G27PF03470,PF03	
39	pacid=371464	2 Phvul.003G050200.2	Phvul.003G050200	Phvul.003G05	0
40	pacid=371464	2 Phvul.003G050200.1	Phvul.003G050200	Phvul.003G05	0
41	pacid=371478	1 Phvul.003G076900.1	Phvul.003G076900	Phvul.003G07 PF00067	
42	pacid=371478	1 Phvul.003G076900.1	Phvul.003G076900	Phvul.003G07 PF00067	
43	pacid=371447	1 Phvul.003G104900.1	Phvul.003G104900	Phvul.003G10 PF00403	
44	pacid=371447	1 Phvul.003G104900.1	Phvul.003G104900	Phvul.003G10 PF00403	
45	pacid=371471	1 Phvul.003G157600.1	Phvul.003G157600	Phvul.003G15 PF05182	
46	pacid=371466	1 Phvul.003G158700.1	Phvul.003G158700	Phvul.003G15PF07714,PF00	
47	pacid=371466	1 Phvul.003G158700.1	Phvul.003G158700	Phvul.003G15PF07714,PF00	

1				
2	pacid=371463	1 Phvul.003G162300.1	Phvul.003G162300	Phvul.003G16PF12854,PF14
3	pacid=371483	1 Phvul.003G209600.2	Phvul.003G209600	Phvul.003G20PF07521,PF00
4	pacid=371483	1 Phvul.003G209600.1	Phvul.003G209600	Phvul.003G20PF07521,PF00
5				
6	pacid=371483	1 Phvul.003G288300.1	Phvul.003G288300	Phvul.003G28 PF00069
7	pacid=371483	1 Phvul.003G288300.1	Phvul.003G288300	Phvul.003G28 PF00069
8	pacid=371628	1 Phvul.004G011400.1	Phvul.004G011400	Phvul.004G01 PF13921
9				
10	pacid=371621	1 Phvul.004G064300.1	Phvul.004G064300	Phvul.004G06 PF00415
11	pacid=371621	1 Phvul.004G064300.1	Phvul.004G064300	Phvul.004G06 PF00415
12	pacid=371634	1 Phvul.004G131300.1	Phvul.004G131300	Phvul.004G13 PF01535,PF12
13				
14	pacid=371634	1 Phvul.004G131300.1	Phvul.004G131300	Phvul.004G13 PF01535,PF12
15	pacid=371542	1 Phvul.005G031200.1	Phvul.005G031200	Phvul.005G03 PF00931
16	pacid=371542	1 Phvul.005G071300.1	Phvul.005G071300	Phvul.005G07 PF00304
17				
18	pacid=371542	1 Phvul.005G071300.1	Phvul.005G071300	Phvul.005G07 PF00304
19	pacid=371723	1 Phvul.006G057000.1	Phvul.006G057000	Phvul.006G05 PF00076
20	pacid=371721	1 Phvul.006G057100.5	Phvul.006G057100	Phvul.006G05 PF00076
21				
22	pacid=371721	1 Phvul.006G057100.4	Phvul.006G057100	Phvul.006G05 PF00076
23	pacid=371716	1 Phvul.006G057700.2	Phvul.006G057700	Phvul.006G05 PF02146
24	pacid=371714	1 Phvul.006G066800.1	Phvul.006G066800	Phvul.006G06 PF00931
25				
26	pacid=371714	1 Phvul.006G066800.1	Phvul.006G066800	Phvul.006G06 PF00931
27	pacid=371653	1 Phvul.007G086300.2	Phvul.007G086300	Phvul.007G08 PF00931
28	pacid=371653	1 Phvul.007G086300.1	Phvul.007G086300	Phvul.007G08 PF00931
29				
30	pacid=371596	1 Phvul.008G014700.1	Phvul.008G014700	Phvul.008G01 PF00931
31	pacid=371596	1 Phvul.008G014700.1	Phvul.008G014700	Phvul.008G01 PF00931
32	pacid=371582	1 Phvul.008G072032.1	Phvul.008G072032	Phvul.008G07 PF13855,PF00
33				
34	pacid=371582	1 Phvul.008G072032.1	Phvul.008G072032	Phvul.008G07 PF13855,PF00
35	pacid=371605	1 Phvul.008G168300.2	Phvul.008G168300	Phvul.008G16 0
36	pacid=371604	1 Phvul.008G168300.1	Phvul.008G168300	Phvul.008G16 0
37				
38	pacid=371505	1 Phvul.009G039200.1	Phvul.009G039200	Phvul.009G03 PF00892
39	pacid=371497	1 Phvul.009G079700.1	Phvul.009G079700	Phvul.009G07 PF00433,PF07
40	pacid=371497	1 Phvul.009G079700.1	Phvul.009G079700	Phvul.009G07 PF00433,PF07
41				
42	pacid=371486	1 Phvul.009G180800.1	Phvul.009G180800	Phvul.009G18 PF08477
43	pacid=371486	1 Phvul.009G180800.2	Phvul.009G180800	Phvul.009G18 PF08477
44	pacid=371486	1 Phvul.009G180800.1	Phvul.009G180800	Phvul.009G18 PF08477
45	pacid=371486	1 Phvul.009G180800.2	Phvul.009G180800	Phvul.009G18 PF08477
46				
47	pacid=371520	1 Phvul.009G249500.1	Phvul.009G249500	Phvul.009G24 PF03242
48	pacid=371428	1 Phvul.010G025000.1	Phvul.010G025000	Phvul.010G02 PF13676,PF00
49	pacid=371440	1 Phvul.010G025700.1	Phvul.010G025700	Phvul.010G02 PF13676,PF00
50				
51	pacid=371426	1 Phvul.010G063700.2	Phvul.010G063700	Phvul.010G06 PF00931
52	pacid=371437	1 Phvul.010G101700.1	Phvul.010G101700	Phvul.010G10 0
53	pacid=371429	1 Phvul.010G141400.1	Phvul.010G141400	Phvul.010G14 PF02701
54				
55	pacid=371432	1 Phvul.010G149500.1	Phvul.010G149500	Phvul.010G14 PF13307,PF06
56	pacid=371432	1 Phvul.010G149500.1	Phvul.010G149500	Phvul.010G14 PF13307,PF06
57				
58	pacid=371571	1 Phvul.011G015000.1	Phvul.011G015000	Phvul.011G01 PF03514
59	pacid=371566	1 Phvul.011G181500.1	Phvul.011G181500	Phvul.011G18 PF00931
60	pacid=371566	1 Phvul.011G181500.1	Phvul.011G181500	Phvul.011G18 PF00931
	pacid=371548	1 Phvul.011G198000.1	Phvul.011G198000	Phvul.011G19 PF00931

1					
2	pacid=371548	1 Phvul.011G198000.1	Phvul.011G198000	Phvul.011G19	PF00931
3	pacid=371547	1 Phvul.011G200880.2	Phvul.011G200880	Phvul.011G20	PF00931
4	pacid=371547	1 Phvul.011G200880.1	Phvul.011G200880	Phvul.011G20	PF00931
5					
6	pacid=371548	1 Phvul.011G201000.1	Phvul.011G201000	Phvul.011G20	PF00931
7	pacid=371548	1 Phvul.011G201000.1	Phvul.011G201000	Phvul.011G20	PF00931
8	pacid=371569	1 Phvul.011G201101.1	Phvul.011G201101	Phvul.011G20	PF00931
9					
10	pacid=371569	1 Phvul.011G201101.1	Phvul.011G201101	Phvul.011G20	PF00931
11	pacid=371566	1 Phvul.011G202366.1	Phvul.011G202366	Phvul.011G20	PF13191
12	pacid=371566	1 Phvul.011G202366.1	Phvul.011G202366	Phvul.011G20	PF13191
13					
14	pacid=371639	1 Phvul.L004500.1	Phvul.L004500	Phvul.L004500	(PF00332
15	pacid=371639	1 Phvul.L004500.1	Phvul.L004500	Phvul.L004500	(PF00332
16	pacid=371683	1 Phvul.001G183400.2	Phvul.001G183400	Phvul.001G18	PF04640
17	pacid=371683	1 Phvul.001G183400.3	Phvul.001G183400	Phvul.001G18	PF04640
18	pacid=371683	1 Phvul.001G183400.4	Phvul.001G183400	Phvul.001G18	PF04640
19	pacid=371683	1 Phvul.001G183400.1	Phvul.001G183400	Phvul.001G18	PF04640
20					
21	pacid=371768	1 Phvul.002G089800.1	Phvul.002G089800	Phvul.002G08	PF08536
22	pacid=371768	1 Phvul.002G089800.1	Phvul.002G089800	Phvul.002G08	PF08536
23	pacid=371777	1 Phvul.002G171400.1	Phvul.002G171400	Phvul.002G17	PF13676,PF13
24	pacid=371778	1 Phvul.002G244900.1	Phvul.002G244900	Phvul.002G24	PF01925
25	pacid=371778	1 Phvul.002G244900.1	Phvul.002G244900	Phvul.002G24	PF01925
26	pacid=371757	1 Phvul.002G245000.5	Phvul.002G245000	Phvul.002G24	PF01925
27	pacid=371757	1 Phvul.002G245000.4	Phvul.002G245000	Phvul.002G24	PF01925
28	pacid=371757	1 Phvul.002G245000.3	Phvul.002G245000	Phvul.002G24	PF01925
29	pacid=371757	1 Phvul.002G245000.1	Phvul.002G245000	Phvul.002G24	PF01925
30	pacid=371757	1 Phvul.002G245000.2	Phvul.002G245000	Phvul.002G24	PF01925
31	pacid=371757	1 Phvul.002G245000.5	Phvul.002G245000	Phvul.002G24	PF01925
32	pacid=371757	1 Phvul.002G245000.4	Phvul.002G245000	Phvul.002G24	PF01925
33	pacid=371757	1 Phvul.002G245000.3	Phvul.002G245000	Phvul.002G24	PF01925
34	pacid=371757	1 Phvul.002G245000.1	Phvul.002G245000	Phvul.002G24	PF01925
35	pacid=371757	1 Phvul.002G245000.2	Phvul.002G245000	Phvul.002G24	PF01925
36	pacid=371757	1 Phvul.002G245000.5	Phvul.002G245000	Phvul.002G24	PF01925
37	pacid=371757	1 Phvul.002G245000.4	Phvul.002G245000	Phvul.002G24	PF01925
38	pacid=371757	1 Phvul.002G245000.3	Phvul.002G245000	Phvul.002G24	PF01925
39	pacid=371757	1 Phvul.002G245000.1	Phvul.002G245000	Phvul.002G24	PF01925
40	pacid=371757	1 Phvul.002G245000.2	Phvul.002G245000	Phvul.002G24	PF01925
41	pacid=371449	1 Phvul.003G002200.5	Phvul.003G002200	Phvul.003G00	PF00612,PF00
42	pacid=371449	1 Phvul.003G002200.4	Phvul.003G002200	Phvul.003G00	PF00612,PF00
43	pacid=371449	1 Phvul.003G002200.3	Phvul.003G002200	Phvul.003G00	PF00612,PF00
44	pacid=371449	1 Phvul.003G002200.5	Phvul.003G002200	Phvul.003G00	PF00612,PF00
45	pacid=371449	1 Phvul.003G002200.4	Phvul.003G002200	Phvul.003G00	PF00612,PF00
46	pacid=371449	1 Phvul.003G002200.3	Phvul.003G002200	Phvul.003G00	PF00612,PF00
47	pacid=371464	2 Phvul.003G050200.2	Phvul.003G050200	Phvul.003G05	0
48	pacid=371464	2 Phvul.003G050200.1	Phvul.003G050200	Phvul.003G05	0
49	pacid=371456	2 Phvul.003G244225.3	Phvul.003G244225	Phvul.003G24	0
50	pacid=371456	2 Phvul.003G244225.2	Phvul.003G244225	Phvul.003G24	0
51	pacid=371456	2 Phvul.003G244225.1	Phvul.003G244225	Phvul.003G24	0
52	pacid=371459	1 Phvul.003G282200.3	Phvul.003G282200	Phvul.003G28	PF00856,PF05
53	pacid=371459	1 Phvul.003G282200.2	Phvul.003G282200	Phvul.003G28	PF00856,PF05
54	pacid=371464	1 Phvul.003G282250.1	Phvul.003G282250	Phvul.003G28	PF01535,PF13
55	pacid=371615	1 Phvul.004G011100.1	Phvul.004G011100	Phvul.004G01	PF03726,PF00
56	pacid=371618	1 Phvul.004G086300.2	Phvul.004G086300	Phvul.004G08	PF00069

1				
2	pacid=371618	1 Phvul.004G086300.1	Phvul.004G086300	Phvul.004G08 PF00069
3	pacid=371544	1 Phvul.005G041300.1	Phvul.005G041300	Phvul.005G04 PF13041,PF01
4	pacid=371544	1 Phvul.005G041300.1	Phvul.005G041300	Phvul.005G04 PF13041,PF01
5				
6	pacid=371528	1 Phvul.005G069700.1	Phvul.005G069700	Phvul.005G06 0
7	pacid=371528	1 Phvul.005G069700.1	Phvul.005G069700	Phvul.005G06 0
8	pacid=371525	1 Phvul.005G072000.1	Phvul.005G072000	Phvul.005G07 PF04765
9				
10	pacid=371724	1 Phvul.006G027500.1	Phvul.006G027500	Phvul.006G02 PF00400
11	pacid=371724	1 Phvul.006G027500.1	Phvul.006G027500	Phvul.006G02 PF00400
12	pacid=371735	1 Phvul.006G100600.1	Phvul.006G100600	Phvul.006G10 PF06026
13				
14	pacid=371715	1 Phvul.006G126400.1	Phvul.006G126400	Phvul.006G12 0
15	pacid=371715	1 Phvul.006G126400.1	Phvul.006G126400	Phvul.006G12 0
16	pacid=371718	1 Phvul.006G170700.1	Phvul.006G170700	Phvul.006G17 PF12796,PF13
17				
18	pacid=371615	1 Phvul.008G107400.1	Phvul.008G107400	Phvul.008G10 PF01535,PF12
19	pacid=371615	1 Phvul.008G107400.1	Phvul.008G107400	Phvul.008G10 PF01535,PF12
20	pacid=371598	1 Phvul.008G206300.1	Phvul.008G206300	Phvul.008G20 PF05383
21				
22	pacid=371492	1 Phvul.009G103100.1	Phvul.009G103100	Phvul.009G10 PF13855,PF08
23	pacid=371436	1 Phvul.010G008500.1	Phvul.010G008500	Phvul.010G00 PF05340
24	pacid=371429	1 Phvul.010G013500.1	Phvul.010G013500	Phvul.010G01 PF02701
25				
26	pacid=371430	2 Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04 PF02493
27	pacid=371430	2 Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04 PF02493
28	pacid=371430	2 Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04 PF02493
29	pacid=371430	2 Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04 PF02493
30	pacid=371430	2 Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04 PF02493
31	pacid=371430	2 Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04 PF02493
32	pacid=371430	2 Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04 PF02493
33	pacid=371430	2 Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04 PF02493
34	pacid=371430	2 Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04 PF02493
35	pacid=371430	2 Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04 PF02493
36	pacid=371432	1 Phvul.010G145600.1	Phvul.010G145600	Phvul.010G14 PF14510,PF08
37	pacid=371561	1 Phvul.011G181700.1	Phvul.011G181700	Phvul.011G18 PF00931
38				
39	pacid=371573	1 Phvul.011G200820.1	Phvul.011G200820	Phvul.011G20 PF00931
40	pacid=371560	1 Phvul.011G202100.1	Phvul.011G202100	Phvul.011G20 PF00931
41	pacid=371555	1 Phvul.011G202300.1	Phvul.011G202300	Phvul.011G20 PF00931
42				
43	pacid=371563	1 Phvul.011G203100.1	Phvul.011G203100	Phvul.011G20 PF00931
44				
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60				



1	Panther	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol	
2	PTHR23155,P <sup>-</sup>		0	0	0 GO:0043531	AT4G27220.1	0
3	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
4	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
5	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
6	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
7	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
8	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
9	PTHR23244,P <sup>-</sup>		0	0	0 GO:0005515	AT1G74150.1	0
10	PTHR23244,P <sup>-</sup> KOG4693			0	0 GO:0005515	AT1G74150.1	0
11	PTHR23244,P <sup>-</sup> KOG4693			0	0 GO:0005515	AT1G74150.1	0
12	PTHR23155,P <sup>-</sup>		0	0 K13459	GO:0005515,(	AT5G63020.1	0
13	PTHR23155,P <sup>-</sup>		0	0 K13459	GO:0005515,(	AT5G63020.1	0
14	PTHR23155,P <sup>-</sup>		0	0 K13459	GO:0005515,(	AT5G63020.1	0
15	PTHR23155,P <sup>-</sup>		0	0 K13459	GO:0005515,(	AT5G63020.1	0
16	PTHR23155,P <sup>-</sup>		0	0 K13459	GO:0005515,(	AT5G63020.1	0
17	PTHR11017,P <sup>-</sup> KOG4658			0	0 GO:0007165,(	AT1G27170.1	0
18	PTHR24078,P <sup>-</sup>		0	0	0	0 AT1G75250.1 ATRL6,RL6,RSI	
19	PTHR10071,P <sup>-</sup>		0	0	0 GO:0043565,(	AT4G17570.3 GATA26	
20	PTHR10071,P <sup>-</sup>		0	0	0 GO:0043565,(	AT4G17570.3 GATA26	
21	PTHR10071,P <sup>-</sup>		0	0	0 GO:0043565,(	AT4G17570.3 GATA26	
22	PTHR10071,P <sup>-</sup>		0	0	0 GO:0043565,(	AT4G17570.3 GATA26	
23	PTHR11017,P <sup>-</sup> KOG4658			0	0 GO:0007165,(	AT1G27170.1	0
24	PTHR32093,P <sup>-</sup>		0	0	0	0 AT3G50370.1	0
25	PTHR32093,P <sup>-</sup>		0	0	0	0 AT3G50370.1	0
26	PTHR32093,P <sup>-</sup>		0	0	0	0 AT3G50370.1	0
27	PTHR32093,P <sup>-</sup>		0	0	0	0 AT3G50370.1	0
28	PTHR11017,P <sup>-</sup> KOG4658			0	0 GO:0007165,(	AT5G36930.2	0
29	PTHR10315,P <sup>-</sup> KOG3002	6.3.2.19		K04506	GO:0007275,(	AT3G61790.1	0
30	PTHR10315,P <sup>-</sup> KOG3002	6.3.2.19		K04506	GO:0007275,(	AT3G61790.1	0
31	PTHR10315,P <sup>-</sup> KOG3002	6.3.2.19		K04506	GO:0007275,(	AT3G61790.1	0
32	PTHR10315,P <sup>-</sup> KOG3002	6.3.2.19		K04506	GO:0007275,(	AT3G61790.1	0
33	PTHR31251,P <sup>-</sup>		0	0	0 GO:0005634,(	AT2G47070.1 SPL1	
34	PTHR31251,P <sup>-</sup>		0	0	0 GO:0005634,(	AT2G47070.1 SPL1	
35	PTHR31251,P <sup>-</sup>		0	0	0 GO:0005634,(	AT2G47070.1 SPL1	
36	PTHR24220,P <sup>-</sup>		0 3.6.3.25		0 GO:0016887,(	AT1G65410.1 ATNAP11,NAF	
37	PTHR21716,P <sup>-</sup> KOG2365			0	0	0 AT5G55960.1	0
38	PTHR21716,P <sup>-</sup> KOG2365			0	0	0 AT5G55960.1	0
39	PTHR21716,P <sup>-</sup> KOG2365			0	0	0 AT5G55960.1	0
40	PTHR23155,P <sup>-</sup> KOG4658			0	0 GO:0043531	AT3G14470.1	0
41	PTHR11017,P <sup>-</sup>		0	0	0 GO:0007165,(	AT5G17680.1	0
42	PTHR11017,P <sup>-</sup>		0	0	0 GO:0007165,(	AT5G17680.1	0
43	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
44	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
45	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
46	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
47	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
48	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
49	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
50	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
51	PTHR14221,P <sup>-</sup>		0	0	0	0 AT5G54200.1	0
52	PTHR23155,P <sup>-</sup> KOG4658			0	0 GO:0043531	AT3G14470.1	0
53	PTHR11017,P <sup>-</sup> KOG0472			0	0	0 AT5G17680.1	0
54	PTHR11017,P <sup>-</sup> KOG0472			0	0	0 AT5G17680.1	0
55	PTHR23155,P <sup>-</sup> KOG4658			0	0 GO:0005515,(	AT3G14470.1	0
56	PTHR23155,P <sup>-</sup> KOG4658			0	0 GO:0005515,(	AT3G14470.1	0
57	PTHR11638,P <sup>-</sup> KOG1051			0	0 GO:0019538,(	AT2G40130.2	0
58	PTHR11638,P <sup>-</sup> KOG1051			0	0 GO:0019538,(	AT2G40130.2	0
59	PTHR11638,P <sup>-</sup> KOG1051			0	0 GO:0019538,(	AT2G40130.2	0
60	PTHR31351,P <sup>-</sup>		0	0	0	0 AT4G17350.1	0
	PTHR31351,P <sup>-</sup>		0	0	0	0 AT4G17350.1	0



1					
2	PTHR24286,P <sup>-</sup> KOG0157	1.14.13.93		0 GO:0055114,(AT4G19230.1 CYP707A1	
3	PTHR36320,P <sup>-</sup>	0	0	0 AT1G30880.1	0
4	PTHR24012,P <sup>-</sup> KOG4209		0 K14396	GO:0003676 AT5G10350.1	0
5	PTHR24012,P <sup>-</sup> KOG4209		0 K14396	GO:0003676 AT5G10350.1	0
6	PTHR11615,P <sup>-</sup>	0	0	0 AT4G15630.1	0
7	PTHR11615,P <sup>-</sup>	0	0	0 AT4G15630.1	0
8	PTHR30573,P <sup>-</sup>	0 2.5.1.72	K03517	GO:0051539,(AT5G50210.1 OLD5,QS,SUFF	
9	PTHR30573,P <sup>-</sup>	0 2.5.1.72	K03517	GO:0051539,(AT5G50210.1 OLD5,QS,SUFF	
10	PTHR13711,P <sup>-</sup>	0	0 K09272	0 AT3G28730.1 ATHMG,HMG,	
11	PTHR11017,P <sup>-</sup>	0	0	0 GO:0007165,(AT5G17680.1	0
12	PTHR11017,P <sup>-</sup>	0	0	0 GO:0007165,(AT5G17680.1	0
13	PTHR21091,P <sup>-</sup> KOG1527		0	0 GO:0008168,(AT5G40850.1 UPM1	
14	PTHR21091,P <sup>-</sup> KOG1527		0	0 GO:0008168,(AT5G40850.1 UPM1	
15	PTHR23155,P <sup>-</sup> KOG4658		0 K13459	GO:0005515,(AT4G27220.1	0
16	PTHR23155,P <sup>-</sup> KOG4658		0 K13459	GO:0005515,(AT4G27220.1	0
17	PTHR27003,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,(AT3G04690.1 ANX1	
18	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT1G63350.1	0
19	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT1G63350.1	0
20	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT1G63350.1	0
21	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT1G63350.1	0
22	PTHR15002 KOG2425		0 K16912	0 AT5G12220.1	0
23	PTHR30540,P <sup>-</sup>	0	0	0 GO:0071805,(AT2G30070.1 ATK1,ATK1F	
24	PTHR30540,P <sup>-</sup>	0	0	0 GO:0071805,(AT2G30070.1 ATK1,ATK1F	
25	PTHR30540,P <sup>-</sup>	0	0	0 GO:0071805,(AT2G30070.1 ATK1,ATK1F	
26	PTHR30540,P <sup>-</sup>	0	0	0 GO:0071805,(AT2G30070.1 ATK1,ATK1F	
27	PTHR11017,P <sup>-</sup> KOG4658		0	0 GO:0007165,(AT5G41750.1	0
28	PTHR11017,P <sup>-</sup> KOG0617		0	0 AT5G41750.2	0
29	PTHR11017,P <sup>-</sup> KOG4658		0	0 GO:0007165,(AT5G17680.1	0
30	PTHR12526,P <sup>-</sup> KOG0853		0	0 AT3G15940.2	0
31	PTHR12526,P <sup>-</sup> KOG0853		0	0 AT3G15940.2	0
32	PTHR12526,P <sup>-</sup> KOG0853		0	0 AT3G15940.2	0
33	PTHR12526,P <sup>-</sup> KOG0853		0	0 AT3G15940.2	0
34	PTHR11017,P <sup>-</sup> KOG4658		0	0 GO:0007165,(AT5G17680.1	0
35	PTHR11017,P <sup>-</sup> KOG4658		0	0 GO:0007165,(AT5G17680.1	0
36	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
37	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
38	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
39	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
40	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
41	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,(AT3G14470.1	0
42	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
43	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,(AT3G14470.1	0
44	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,(AT3G14470.1	0
45	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,(AT3G14470.1	0
46	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14460.1	0
47	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
48	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
49	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
50	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
51	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
52	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
53	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
54	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
55	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
56	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
57	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
58	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
59	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0
60	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531 AT3G14470.1	0

1						
2	PTHR23155,P <sup>-</sup>	0	0	0 GO:0043531	AT3G14460.1	0
3	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
4	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0005515,(	AT3G14470.1	0
5						
6	PTHR23155,P <sup>-</sup>	0	0	0 GO:0043531	AT3G14470.1	0
7	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
8	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
9						
10	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
11	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
12	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
13						
14	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
15	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
16	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
17						
18	PTHR11695,P <sup>-</sup> KOG0022	1.1.1.1		0 GO:0055114,(	AT5G42250.1	0
19	PTHR11695,P <sup>-</sup> KOG0022	1.1.1.1		0 GO:0055114,(	AT5G42250.1	0
20	PTHR11695,P <sup>-</sup> KOG0022	1.1.1.1		0 GO:0055114,(	AT5G42250.1	0
21						
22	PTHR11695,P <sup>-</sup> KOG0022	1.1.1.1		0 GO:0055114,(	AT5G42250.1	0
23	PTHR23063,P <sup>-</sup> KOG4666	2.3.1.25	K13510	GO:0016746,(	AT1G80950.1	0
24	PTHR23063,P <sup>-</sup> KOG4666	2.3.1.25	K13510	GO:0016746,(	AT1G80950.1	0
25	PTHR23063,P <sup>-</sup> KOG4666	2.3.1.25	K13510	GO:0016746,(	AT1G80950.1	0
26						
27	PTHR23063,P <sup>-</sup> KOG4666	2.3.1.25	K13510	GO:0016746,(	AT1G80950.1	0
28						
29	PTHR31945,P <sup>-</sup>	0	0	0 GO:0046983	AT3G26744.1 ATICE1,ICE1,S	
30	PTHR31945,P <sup>-</sup>	0	0	0 GO:0046983	AT3G26744.1 ATICE1,ICE1,S	
31	PTHR31867,P <sup>-</sup>	0	0	0	0 AT2G39700.1 ATEXP4,ATEXI	
32	PTHR31867,P <sup>-</sup>	0	0	0	0 AT2G39700.1 ATEXP4,ATEXI	
33						
34	PTHR31065,P <sup>-</sup>	0	0	0	0 AT1G32700.1	0
35	PTHR31065,P <sup>-</sup>	0	0	0	0 AT1G32700.1	0
36	PTHR31065,P <sup>-</sup>	0	0	0	0 AT1G32700.1	0
37	PTHR31065,P <sup>-</sup>	0	0	0	0 AT1G32700.1	0
38						
39	PTHR31479,P <sup>-</sup>	0	0	0 GO:0006629	AT4G10955.1	0
40	PTHR10218,P <sup>-</sup> KOG0082		0	0 GO:0031683,(	AT2G23460.1 ATXLG1,XLG1	
41	PTHR10218,P <sup>-</sup> KOG0082		0	0 GO:0031683,(	AT2G23460.1 ATXLG1,XLG1	
42						
43	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G74850.1 PTAC2	
44	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G74850.1 PTAC2	
45	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G66730.1	0
46	PTHR10593,P <sup>-</sup>	0	0	0	0 AT5G66730.1	0
47						
48	PTHR13190,P <sup>-</sup> KOG2993		0 K17906	GO:0006914	AT3G19190.1 ATATG2,ATG2	
49	PTHR13190,P <sup>-</sup> KOG2993		0 K17906	GO:0006914	AT3G19190.1 ATATG2,ATG2	
50						
51	PTHR13190,P <sup>-</sup> KOG2993		0 K17906	GO:0006914	AT3G19190.1 ATATG2,ATG2	
52	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
53	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
54	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
55	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
56	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
57	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
58	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
59	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
60	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	
	PTHR22953,P <sup>-</sup> KOG1378	3.6.1.7,3.1.3.2		0 GO:0016787	AT4G13700.1 ATPAP23,PAP.	

1								
2	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531	AT4G27220.1	0	
3	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531	AT4G27220.1	0	
4	PTHR13696,P <sup>-</sup> KOG3022		0	K03609	0	AT5G24020.1	ARC11,ATMIN	
5								
6	PTHR13696,P <sup>-</sup> KOG3022		0	K03609	0	AT5G24020.1	ARC11,ATMIN	
7	PTHR23024,P <sup>-</sup> KOG1515	3.1.1.1			0	0	AT5G23530.1	AtCXE18,CXE1
8	PTHR24015,P <sup>-</sup>	0	0	0	0	0	AT3G49730.1	0
9								
10	PTHR24015,P <sup>-</sup>	0	0	0	0	0	AT3G49730.1	0
11	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14470.1	0	
12	PTHR31867,P <sup>-</sup>	0	0	0	0	0	AT3G03220.1	ATEXP13,ATE)
13								
14	0	0	0	0	0	0	0	0
15	PTHR11746,P <sup>-</sup> KOG3178		0	0	GO:0046983,(	AT4G35160.1	0	
16	PTHR11746,P <sup>-</sup> KOG3178		0	0	GO:0046983,(	AT4G35160.1	0	
17								
18	0	0	0	0	0	0	AT1G68500.1	0
19	PTHR10803 KOG2825	3.6.3.16	K01551		GO:0016887,(	AT3G10350.1	0	
20	PTHR27008,P <sup>-</sup> KOG1187	2.7.11.1			0	GO:0005515,(	AT5G35390.1	0
21								
22	PTHR10108,P <sup>-</sup> KOG1269	2.1.1.143,2.1.	K08242		GO:0008168,(	AT1G20330.1	CVP1,FRL1,SV	
23	PTHR10108,P <sup>-</sup> KOG1269	2.1.1.143,2.1.	K08242		GO:0008168,(	AT1G20330.1	CVP1,FRL1,SV	
24	PTHR22952,P <sup>-</sup>	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A	
25	PTHR22952,P <sup>-</sup>	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A	
26	PTHR22952,P <sup>-</sup>	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A	
27	PTHR22952,P <sup>-</sup>	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A	
28	PTHR22952,P <sup>-</sup>	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A	
29								
30	PTHR24015,P <sup>-</sup>	0	0	K17964	0	0	AT1G19290.1	0
31	PTHR13533,P <sup>-</sup>	0	0	0	0	0	AT5G20680.1	TBL16
32	PTHR13533,P <sup>-</sup>	0	0	0	0	0	AT5G20680.1	TBL16
33	PTHR13533,P <sup>-</sup>	0	0	0	0	0	AT5G20680.1	TBL16
34	PTHR13533,P <sup>-</sup>	0	0	0	0	0	AT5G20680.1	TBL16
35	PTHR13533,P <sup>-</sup>	0	0	0	0	0	AT5G20680.1	TBL16
36	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT1G50180.1	0	
37	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT1G50180.1	0	
38								
39	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT1G50180.1	0	
40	PTHR11017,P <sup>-</sup>	0	0	0	GO:0043531	AT5G36930.2	0	
41	PTHR11017,P <sup>-</sup>	0	0	0	GO:0043531	AT5G36930.2	0	
42								
43	PTHR24015,P <sup>-</sup>	0	0	0	0	0	AT2G17670.1	0
44	PTHR24015,P <sup>-</sup>	0	0	0	0	0	AT2G17670.1	0
45	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14460.1	0	
46								
47	PTHR10668,P <sup>-</sup> KOG1238	1.1.3.20	K17756		GO:0055114,(	AT3G23410.1	ATFAO3,FAO3	
48	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
49	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
50								
51	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
52	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
53	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
54	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
55	PTHR14009,P <sup>-</sup>	0	0	0	0	0	AT3G11560.2	0
56	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G46530.1	RPP13	
57	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G46530.1	RPP13	
58	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G46530.1	RPP13	
59								
60	PTHR33477,P <sup>-</sup>	0	0	0	0	0	AT5G60760.1	0
	PTHR33477,P <sup>-</sup>	0	0	0	0	0	AT5G60760.1	0

1						
2	PTHR33477,P <sup>-</sup>	0	0	0	0 AT5G60760.1	0
3	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT4G26090.1 RPS2	
4	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT4G26090.1 RPS2	
5	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1	0
6	PTHR31907,P <sup>-</sup>	0	0	0	GO:0009607,C AT1G70890.1 MLP43	
7	PTHR31907,P <sup>-</sup>	0	0	0	GO:0009607,C AT1G70890.1 MLP43	
8	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515 AT3G14470.1	0
9	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1	0
10	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1	0
11	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1	0
12	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1	0
13	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1	0
14	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
15	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1	0
16	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1	0
17	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
18	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1	0
19	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531 AT3G14470.1	0
20	PTHR32133,P <sup>-</sup>	0	0	0	GO:0005515 AT5G43190.1	0
21	PTHR22762,P <sup>-</sup>	0	3.2.1.20	0	GO:0005975,C AT5G63840.1 PSL5,RSW3	
22	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531 AT3G14470.1	0
23	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531 AT3G14470.1	0
24	PTHR23155,P <sup>-</sup> KOG0617		0	0	GO:0005515,C AT3G14470.1	0
25	PTHR23155,P <sup>-</sup> KOG0617		0	0	GO:0005515,C AT3G14470.1	0
26	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
27	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
28	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
29	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
30	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
31	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
32	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
33	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
34	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
35	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
36	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
37	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
38	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0005515,C AT3G14470.1	0
39	PTHR27008,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,C AT2G36570.1	0
40	PTHR27008,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,C AT2G36570.1	0
41	PTHR11003,P <sup>-</sup>	0	0	K05389	0 AT4G01840.1 ATKCO5,ATTP	
42	PTHR31375,P <sup>-</sup>	0	3.2.1.15	K01213	GO:0005975,C AT3G26610.1	0
43	PTHR31375,P <sup>-</sup>	0	3.2.1.15	K01213	GO:0005975,C AT3G26610.1	0
44	PTHR18896,P <sup>-</sup>	0	3.1.4.4	K01115	GO:0003824,C AT4G35790.2 ATPLDELTA,I	
45	PTHR18896,P <sup>-</sup>	0	3.1.4.4	K01115	GO:0003824,C AT4G35790.2 ATPLDELTA,I	
46	PTHR21596,P <sup>-</sup>	0	0	0	GO:0031047 AT5G23570.1 ATSGS3,SGS3	
47	PTHR37076,P <sup>-</sup>	0	0	0	0	0
48	PTHR37076,P <sup>-</sup>	0	0	0	0	0
49	PTHR24298,P <sup>-</sup> KOG0156		0	0	GO:0055114,C AT1G11600.1 CYP77B1	
50	PTHR24298,P <sup>-</sup> KOG0156		0	0	GO:0055114,C AT1G11600.1 CYP77B1	
51	PTHR22814,P <sup>-</sup> KOG1603		0	0	GO:0046872,C AT5G27690.1	0
52	PTHR22814,P <sup>-</sup> KOG1603		0	0	GO:0046872,C AT5G27690.1	0
53	PTHR36884	0	0	0	0 AT5G58040.1 ATFIP1[V],ATF	
54	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,C AT4G23180.1 CRK10,RLK4	
55	PTHR27002,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,C AT4G23180.1 CRK10,RLK4	

1					
2	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G08070.1 OTP82
3	PTHR11203,P <sup>-</sup> KOG1137	3.5.2.6		0	GO:0046872,(AT5G63420.1 emb2746
4	PTHR11203,P <sup>-</sup> KOG1137	3.5.2.6		0	GO:0046872,(AT5G63420.1 emb2746
5					
6	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT5G10520.1 RBK1
7	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT5G10520.1 RBK1
8	PTHR10641,P <sup>-</sup>	0	0	0	0 AT3G27785.1 ATMYB118,M
9					
10	PTHR22870,P <sup>-</sup> KOG1427		0	0	0 AT5G16040.1
11	PTHR22870,P <sup>-</sup> KOG1427		0	0	0 AT5G16040.1
12	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G12775.1
13					
14	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G12775.1
15	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1
16	PTHR33147	0	0	0	0 AT2G02130.1 LCR68,PDF2.3
17					
18	PTHR33147	0	0	0	0 AT2G02130.1 LCR68,PDF2.3
19	PTHR24012,P <sup>-</sup>	0	0 K14398	GO:0003676	AT5G55670.1
20	PTHR24012,P <sup>-</sup>	0	0 K14398	GO:0003676	AT5G55670.1
21					
22	PTHR24012,P <sup>-</sup>	0	0 K14398	GO:0003676	AT5G55670.1
23	PTHR11085,P <sup>-</sup> KOG1905		0 K11416	GO:0070403	AT5G55760.1 SRT1
24	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1
25					
26	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1
27	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1
28	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1
29					
30	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G46530.1 RPP13
31	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G46530.1 RPP13
32	PTHR23155,P <sup>-</sup>	0	0	0	GO:0005515,(AT4G27190.1
33					
34	PTHR23155,P <sup>-</sup>	0	0	0	GO:0005515,(AT4G27190.1
35	PTHR34112,P <sup>-</sup>	0	0	0	0 AT1G36990.1
36	PTHR34112,P <sup>-</sup>	0	0	0	0 AT1G36990.1
37					
38	PTHR31218,P <sup>-</sup>	0	0	0	GO:0016021,(AT1G09380.1
39	PTHR24356,P <sup>-</sup>	0 2.7.11.1		0	GO:0006468,(AT4G33080.2
40	PTHR24356,P <sup>-</sup>	0 2.7.11.1		0	GO:0006468,(AT4G33080.2
41					
42	PTHR24072,P <sup>-</sup> KOG0393	3.6.5.2	K04392	GO:0007264,(AT3G48040.1	ARAC8,ATAC
43	PTHR24072,P <sup>-</sup> KOG0393	3.6.5.2	K04392	GO:0007264,(AT3G48040.1	ARAC8,ATAC
44	PTHR24072,P <sup>-</sup> KOG0393	3.6.5.2	K04392	GO:0007264,(AT3G48040.1	ARAC8,ATAC
45	PTHR24072,P <sup>-</sup> KOG0393	3.6.5.2	K04392	GO:0007264,(AT3G48040.1	ARAC8,ATAC
46					
47	PTHR33509,P <sup>-</sup>	0	0	0	GO:0006950 AT4G15910.1 ATDI21,DI21
48	PTHR11017,P <sup>-</sup>	0	0	0	GO:0007165,(AT5G36930.2
49	PTHR11017,P <sup>-</sup>	0	0	0	GO:0007165,(AT5G36930.2
50					
51	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14460.1
52	PTHR31016,P <sup>-</sup>	0	0	0	0 AT2G30530.1
53	<b>PTHR31992,P<sup>-</sup></b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>GO:0006355,(AT1G51700.1 ADOF1,DOF1</b>
54					
55	PTHR11472,P <sup>-</sup>	0 3.6.4.13	K11273	GO:0016818,(AT1G79890.1	
56	PTHR11472,P <sup>-</sup>	0 3.6.4.13	K11273	GO:0016818,(AT1G79890.1	
57	PTHR31636,P <sup>-</sup>	0	0	0	0 AT1G50420.1 SCL-3,SCL3
58					
59	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1
60	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1
	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531 AT3G14470.1

1								
2	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14470.1		0
3	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14460.1		0
4	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14460.1		0
5	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14460.1		0
6	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14460.1		0
7	PTHR23155,P <sup>-</sup> KOG4658		0	0	GO:0043531	AT3G14460.1		0
8	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531	AT3G14470.1		0
9	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531	AT3G14470.1		0
10	PTHR23155,P <sup>-</sup>	0	0	0	GO:0043531	AT3G14470.1		0
11	PTHR23155,P <sup>-</sup>	0	0	0	0	AT3G14470.1		0
12	PTHR23155,P <sup>-</sup>	0	0	0	0	AT3G14470.1		0
13	PTHR23155,P <sup>-</sup>	0	0	0	0	AT3G14470.1		0
14	PTHR32227,P <sup>-</sup>	0	3.2.1.39	0	GO:0005975,(	AT1G32860.1		0
15	PTHR32227,P <sup>-</sup>	0	3.2.1.39	0	GO:0005975,(	AT1G32860.1		0
16	PTHR31065,P <sup>-</sup>	0	0	0	0	AT2G27930.1		0
17	PTHR31065,P <sup>-</sup>	0	0	0	0	AT2G27930.1		0
18	PTHR31065,P <sup>-</sup>	0	0	0	0	AT2G27930.1		0
19	PTHR31065,P <sup>-</sup>	0	0	0	0	AT2G27930.1		0
20	PTHR31065,P <sup>-</sup>	0	0	0	0	AT2G27930.1		0
21	PTHR31065,P <sup>-</sup>	0	0	0	0	AT2G27930.1		0
22	PTHR31745,P <sup>-</sup>	0	0	0	0	AT1G14410.1	ATWHY1,PTA(	
23	PTHR31745,P <sup>-</sup>	0	0	0	0	AT1G14410.1	ATWHY1,PTA(	
24	PTHR11017,P <sup>-</sup> KOG0617		0	0	GO:0007165,(	AT5G17680.1		0
25	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
26	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
27	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
28	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
29	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
30	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
31	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
32	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
33	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
34	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
35	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
36	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
37	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
38	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
39	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
40	PTHR14255,P <sup>-</sup>	0	0	0	GO:0016021	AT2G25737.1		0
41	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
42	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
43	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
44	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
45	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
46	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
47	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
48	PTHR13140,P <sup>-</sup>	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1	
49	PTHR37076,P <sup>-</sup>	0	0	0	0	0	0	0
50	PTHR37076,P <sup>-</sup>	0	0	0	0	0	0	0
51	PTHR37076,P <sup>-</sup>	0	0	0	0	0	0	0
52	PTHR32093,P <sup>-</sup>	0	0	0	0	AT3G50370.1		0
53	PTHR32093,P <sup>-</sup>	0	0	0	0	AT3G50370.1		0
54	PTHR32093,P <sup>-</sup>	0	0	0	0	AT3G50370.1		0
55	PTHR32093,P <sup>-</sup>	0	0	0	0	AT3G50370.1		0
56	PTHR22884,P <sup>-</sup> KOG1082	2.1.1.43	K11420	0	GO:0005515,(	AT4G13460.1	SDG22,SET22,	
57	PTHR22884,P <sup>-</sup> KOG1082	2.1.1.43	K11420	0	GO:0005515,(	AT4G13460.1	SDG22,SET22,	
58	PTHR24015,P <sup>-</sup>	0	0	0	0	AT2G03380.1		0
59	PTHR24015,P <sup>-</sup>	0	0	0	0	AT2G03380.1		0
60	PTHR11252,P <sup>-</sup>	0	2.7.7.8	K00962	0	GO:0006396,(	AT5G14580.1	
	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1,2.7.10		0	0	GO:0006468,(	AT1G71830.1	ATSERK1,SERK



1						
2	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1,2.7.11		0 GO:0006468,C	AT1G71830.1 ATSERK1,SERK	
3	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G03510.1	0
4	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G03510.1	0
5						
6	PTHR23198,P <sup>-</sup>	0	0 K14297		0 AT1G10390.2	0
7	PTHR23198,P <sup>-</sup>	0	0 K14297		0 AT1G10390.2	0
8	PTHR12956,P <sup>-</sup>	0	0	0	0 AT1G53040.1	0
9						
10	PTHR22838,P <sup>-</sup>	0	0	0 GO:0005515	AT5G08560.1	0
11	PTHR22838,P <sup>-</sup>	0	0	0 GO:0005515	AT5G08560.1	0
12	PTHR11934,P <sup>-</sup> KOG3075	5.3.1.6	K01807	GO:0009052,C	AT3G04790.1	0
13						
14	PTHR31656,P <sup>-</sup>	0 2.4.1.10		0	0 AT3G19430.1	0
15	PTHR31656,P <sup>-</sup>	0 2.4.1.10		0	0 AT3G19430.1	0
16	PTHR24177,P <sup>-</sup> KOG4412	2.7.11.1		0	0 AT3G18670.1	0
17						
18	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G09060.1	0
19	PTHR24015,P <sup>-</sup>	0	0	0	0 AT3G09060.1	0
20	PTHR22792,P <sup>-</sup> KOG2590		0 K18757		0 AT5G21160.3	0
21						
22	PTHR27008,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0005515,C	AT5G35390.1	0
23	PTHR31659,P <sup>-</sup>	0	0	0	0 AT3G09070.1	0
24	PTHR31992,P <sup>-</sup>	0	0	0 GO:0006355,C	AT3G55370.2 OBP3	
25						
26	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
27	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
28	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
29	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
30	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
31	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
32	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
33	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
34	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
35	PTHR23084,P <sup>-</sup>	0 2.7.1.68		0	0 AT4G17080.1	0
36	PTHR19241,P <sup>-</sup>	0 3.6.3.25		0 GO:0016887,C	AT1G59870.1 ABCG36,ATAB	
37	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
38						
39	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
40	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
41	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14470.1	0
42	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
43	PTHR23155,P <sup>-</sup> KOG4658		0	0 GO:0043531	AT3G14460.1	0
44						
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arabi-defline	ID	Annot_defline	IDENTIFIER
NB-ARC domain-containing disease resistance pro	Phvul.004G04	PTHR23155//I	Phvul.004G04
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.007G20	PTHR23244//I	Phvul.007G20
Galactose oxidase/kelch repeat superfamily protei	Phvul.007G20	PTHR23244//I	Phvul.007G20
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:S	Phvul.008G06
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:S	Phvul.008G06
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:S	Phvul.008G06
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:S	Phvul.008G06
transmembrane receptors;ATP binding	Phvul.002G07	PTHR11017:S	Phvul.002G07
RAD-like 6	Phvul.001G21	PTHR24078:S	Phvul.001G21
GATA transcription factor 26	Phvul.002G00	PTHR10071:S	Phvul.002G00
GATA transcription factor 26	Phvul.002G00	PTHR10071:S	Phvul.002G00
transmembrane receptors;ATP binding	Phvul.003G07	PTHR11017:S	Phvul.003G07
	0	0	0 Phvul.003G24
	0	0	0 Phvul.003G24
	0	0	0 Phvul.003G24
Disease resistance protein (TIR-NBS-LRR class) fam	Phvul.004G13	PTHR11017//I	Phvul.004G13
Protein with RING/U-box and TRAF-like domains	Phvul.005G02	PTHR10315//I	Phvul.005G02
Protein with RING/U-box and TRAF-like domains	Phvul.005G02	PTHR10315//I	Phvul.005G02
Protein with RING/U-box and TRAF-like domains	Phvul.005G02	PTHR10315//I	Phvul.005G02
squamosa promoter binding protein-like 1	Phvul.007G21	PTHR31251:S	Phvul.007G21
squamosa promoter binding protein-like 1	Phvul.007G21	PTHR31251:S	Phvul.007G21
<b>non-intrinsic ABC protein 11</b>	<b>Phvul.008G05</b>	<b>PTHR24220:S</b>	<b>Phvul.008G05</b>
	0	Phvul.008G28	PTHR21716 - `Phvul.008G28
	0	Phvul.008G28	PTHR21716 - `Phvul.008G28
NB-ARC domain-containing disease resistance pro	Phvul.010G06	PTHR23155//I	Phvul.010G06
disease resistance protein (TIR-NBS-LRR class), put	Phvul.010G13	PTHR11017//I	Phvul.010G13
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
<b>Transducin/WD40 repeat-like superfamily protein</b>	<b>Phvul.011G14</b>	<b>PTHR14221:S</b>	<b>Phvul.011G14</b>
NB-ARC domain-containing disease resistance pro	Phvul.011G16	PTHR23155//I	Phvul.011G16
disease resistance protein (TIR-NBS-LRR class), put	Phvul.001G12	PF07725//PF1	Phvul.001G12
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
Double Clp-N motif-containing P-loop nucleoside t	Phvul.001G24	PTHR11638:S	Phvul.001G24
Double Clp-N motif-containing P-loop nucleoside t	Phvul.001G24	PTHR11638:S	Phvul.001G24
Plant protein of unknown function (DUF828) with	Phvul.002G05	PF05703 - Au	Phvul.002G05
Plant protein of unknown function (DUF828) with	Phvul.002G05	PF05703 - Au	Phvul.002G05

1			
2	cytochrome P450, family 707, subfamily A, polypeptide	Phvul.002G12PTHR24286:SI	Phvul.002G12
3		0	0
4			0 Phvul.002G18
5	<b>RNA-binding (RRM/RBD/RNP motifs) family protein</b>	<b>Phvul.002G26K14396 - poly:</b>	<b>Phvul.002G26</b>
6	<b>RNA-binding (RRM/RBD/RNP motifs) family protein</b>	<b>Phvul.002G26K14396 - poly:</b>	<b>Phvul.002G26</b>
7	Uncharacterised protein family (UPF0497)	Phvul.003G10PTHR11615://I	Phvul.003G10
8	Uncharacterised protein family (UPF0497)	Phvul.003G10PTHR11615://I	Phvul.003G10
9	quinolinate synthase	Phvul.003G20K03517 - quin	Phvul.003G20
10	quinolinate synthase	Phvul.003G20K03517 - quin	Phvul.003G20
11	high mobility group	Phvul.004G02K09272 - struc	Phvul.004G02
12	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G14PF05729//PF1	Phvul.004G14
13	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G14PF05729//PF1	Phvul.004G14
14	uroporphyrin methylase 1	Phvul.005G03PTHR21091:SI	Phvul.005G03
15	uroporphyrin methylase 1	Phvul.005G03PTHR21091:SI	Phvul.005G03
16	NB-ARC domain-containing disease resistance protein	Phvul.005G08PTHR23155:SI	Phvul.005G08
17	NB-ARC domain-containing disease resistance protein	Phvul.005G08PTHR23155:SI	Phvul.005G08
18	Malectin/receptor-like protein kinase family protein	Phvul.006G10PTHR27003:SI	Phvul.006G10
19	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
20	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
21	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
22	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
23	las1-like family protein	Phvul.008G20K16912 - ribosome	Phvul.008G20
24	potassium transporter 1	Phvul.008G25PTHR30540:SI	Phvul.008G25
25	potassium transporter 1	Phvul.008G25PTHR30540:SI	Phvul.008G25
26	potassium transporter 1	Phvul.008G25PTHR30540:SI	Phvul.008G25
27	potassium transporter 1	Phvul.008G25PTHR30540:SI	Phvul.008G25
28	Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G13PF00931//PFC	Phvul.010G13
29	Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G13PF07725 - Leu	Phvul.010G13
30	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.010G13PTHR11017://I	Phvul.010G13
31	UDP-Glycosyltransferase superfamily protein	Phvul.010G15PTHR12526://I	Phvul.010G15
32	UDP-Glycosyltransferase superfamily protein	Phvul.010G15PTHR12526://I	Phvul.010G15
33	UDP-Glycosyltransferase superfamily protein	Phvul.010G15PTHR12526://I	Phvul.010G15
34	UDP-Glycosyltransferase superfamily protein	Phvul.010G15PTHR12526://I	Phvul.010G15
35	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.011G14PF00931//PFC	Phvul.011G14
36	disease resistance protein (TIR-NBS-LRR class), putative	Phvul.011G14PF00931//PF1	Phvul.011G14
37	NB-ARC domain-containing disease resistance protein	Phvul.011G15PTHR23155://I	Phvul.011G15
38	NB-ARC domain-containing disease resistance protein	Phvul.011G18PTHR23155://I	Phvul.011G18
39	NB-ARC domain-containing disease resistance protein	Phvul.011G18PTHR23155://I	Phvul.011G18
40	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
41	NB-ARC domain-containing disease resistance protein	Phvul.011G19PF00931//PF1	Phvul.011G19
42	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
43	NB-ARC domain-containing disease resistance protein	Phvul.011G19PF00931//PF1	Phvul.011G19
44	NB-ARC domain-containing disease resistance protein	Phvul.011G19PF00931//PF1	Phvul.011G19
45	LRR and NB-ARC domains-containing disease resistance	Phvul.011G19PTHR23155://I	Phvul.011G19
46	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
47	LRR and NB-ARC domains-containing disease resistance	Phvul.011G19PTHR23155://I	Phvul.011G19
48	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
49	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
50	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
51	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
52	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
53	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
54	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
55	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
56	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
57	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
58	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
59	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19
60	NB-ARC domain-containing disease resistance protein	Phvul.011G19PTHR23155://I	Phvul.011G19

1 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvul.011G19  
 2 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19  
 3 NB-ARC domain-containing disease resistance pro Phvul.011G19PF00931//PF1Phvul.011G19  
 4 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19  
 5 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 6 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 7 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 8 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 9 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 10 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 11 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 12 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 13 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:  
 14 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:  
 15 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:  
 16 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:  
 17 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01  
 18 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01  
 19 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01  
 20 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01  
 21 basic helix-loop-helix (bHLH) DNA-binding superfa Phvul.001G08PTHR31945:SIPhvul.001G08  
 22 basic helix-loop-helix (bHLH) DNA-binding superfa Phvul.001G08PTHR31945:SIPhvul.001G08  
 23 expansin A4 Phvul.001G23PTHR31867:SIPhvul.001G23  
 24 expansin A4 Phvul.001G23PTHR31867:SIPhvul.001G23  
 25 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04  
 26 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04  
 27 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04  
 28 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04  
 29 alpha/beta-Hydrolases superfamily protein Phvul.002G29PTHR31479:SIPhvul.002G29  
 30 extra-large G-protein 1 Phvul.003G01PTHR10218:SIPhvul.003G01  
 31 extra-large G-protein 1 Phvul.003G01PTHR10218:SIPhvul.003G01  
 32 plastid transcriptionally active 2 Phvul.003G19PF01535//PF1Phvul.003G19  
 33 plastid transcriptionally active 2 Phvul.003G19PF01535//PF1Phvul.003G19  
 34 C2H2-like zinc finger protein Phvul.003G25PTHR10593:SIPhvul.003G25  
 35 C2H2-like zinc finger protein Phvul.003G25PTHR10593:SIPhvul.003G25  
 36 **autophagy 2 Phvul.003G29K17906 - autoPhvul.003G29**  
 37 **autophagy 2 Phvul.003G29K17906 - autoPhvul.003G29**  
 38 **autophagy 2 Phvul.003G29K17906 - autoPhvul.003G29**  
 39 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 40 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 41 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 42 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 43 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 44 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 45 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 46 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 47 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 48 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 49 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 50 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03  
 51 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03

1				
2	NB-ARC domain-containing disease resistance pro	Phvul.004G04PTHR23155//I	Phvul.004G04	
3	NB-ARC domain-containing disease resistance pro	Phvul.004G04PTHR23155//I	Phvul.004G04	
4	septum site-determining protein (MIND)	Phvul.004G10K03609 - sept	Phvul.004G10	
5	septum site-determining protein (MIND)	Phvul.004G10K03609 - sept	Phvul.004G10	
6	septum site-determining protein (MIND)	Phvul.004G10K03609 - sept	Phvul.004G10	
7	carboxyesterase 18	Phvul.004G13PTHR23024//I	Phvul.004G13	
8	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G16PF01535//PF1	Phvul.005G16	
9	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G16PF01535//PF1	Phvul.005G16	
10	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G16PF01535//PF1	Phvul.005G16	
11	NB-ARC domain-containing disease resistance pro	Phvul.006G06PTHR23155//I	Phvul.006G06	
12	expansin A13	Phvul.006G08PTHR31867:Sf	Phvul.006G08	
13				
14		0	0	0 Phvul.006G14
15	O-methyltransferase family protein	Phvul.006G18PTHR11746//I	Phvul.006G18	
16	O-methyltransferase family protein	Phvul.006G18PTHR11746//I	Phvul.006G18	
17				
18		0	0	0 Phvul.007G02
19	P-loop containing nucleoside triphosphate hydrolase	Phvul.007G093.6.3.16 - Arse	Phvul.007G09	
20	Leucine-rich repeat protein kinase family protein	Phvul.008G15PF07714//PFC	Phvul.008G15	
21	sterol methyltransferase 2	Phvul.009G022.1.1.142 - Cy	Phvul.009G02	
22	sterol methyltransferase 2	Phvul.009G022.1.1.142 - Cy	Phvul.009G02	
23	sterol methyltransferase 2	Phvul.009G022.1.1.142 - Cy	Phvul.009G02	
24	abscisic acid responsive elements-binding factor 2	Phvul.009G06PTHR22952//I	Phvul.009G06	
25	abscisic acid responsive elements-binding factor 2	Phvul.009G06PTHR22952//I	Phvul.009G06	
26	abscisic acid responsive elements-binding factor 2	Phvul.009G06PTHR22952//I	Phvul.009G06	
27	abscisic acid responsive elements-binding factor 2	Phvul.009G06PTHR22952//I	Phvul.009G06	
28	abscisic acid responsive elements-binding factor 2	Phvul.009G06PTHR22952//I	Phvul.009G06	
29	abscisic acid responsive elements-binding factor 2	Phvul.009G06PTHR22952//I	Phvul.009G06	
30	Pentatricopeptide repeat (PPR) superfamily protei	Phvul.009G21K17964 - leuci	Phvul.009G21	
31	TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22PF14416 - PM	Phvul.009G22	
32	TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22PF14416 - PM	Phvul.009G22	
33	TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22PF14416 - PM	Phvul.009G22	
34	TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22PF14416 - PM	Phvul.009G22	
35	TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22PF14416 - PM	Phvul.009G22	
36	NB-ARC domain-containing disease resistance pro	Phvul.009G23PTHR23155:Sf	Phvul.009G23	
37	NB-ARC domain-containing disease resistance pro	Phvul.009G23PTHR23155:Sf	Phvul.009G23	
38	NB-ARC domain-containing disease resistance pro	Phvul.009G23PTHR23155:Sf	Phvul.009G23	
39	NB-ARC domain-containing disease resistance pro	Phvul.009G23PTHR23155:Sf	Phvul.009G23	
40	Disease resistance protein (TIR-NBS-LRR class) far	Phvul.010G00PF00931//PF1	Phvul.010G00	
41	Disease resistance protein (TIR-NBS-LRR class) far	Phvul.010G00PF00931//PF1	Phvul.010G00	
42	Disease resistance protein (TIR-NBS-LRR class) far	Phvul.010G00PF00931//PF1	Phvul.010G00	
43	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.010G05PF13041 - PPF	Phvul.010G05	
44	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.010G05PF13041 - PPF	Phvul.010G05	
45	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.010G05PF13041 - PPF	Phvul.010G05	
46	LRR and NB-ARC domains-containing disease resis	Phvul.010G06PTHR23155//I	Phvul.010G06	
47	fatty alcohol oxidase 3	Phvul.010G07K17756 - long	Phvul.010G07	
48	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
49	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
50	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
51	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
52	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
53	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
54	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
55	LETM1-like protein	Phvul.010G14PTHR14009//I	Phvul.010G14	
56	NB-ARC domain-containing disease resistance pro	Phvul.011G01PTHR23155:Sf	Phvul.011G01	
57	NB-ARC domain-containing disease resistance pro	Phvul.011G01PTHR23155:Sf	Phvul.011G01	
58	NB-ARC domain-containing disease resistance pro	Phvul.011G01PTHR23155:Sf	Phvul.011G01	
59	NB-ARC domain-containing disease resistance pro	Phvul.011G01PTHR23155:Sf	Phvul.011G01	
60	P-loop containing nucleoside triphosphate hydrolase	Phvul.011G08PTHR33477:Sf	Phvul.011G08	
	P-loop containing nucleoside triphosphate hydrolase	Phvul.011G08PTHR33477:Sf	Phvul.011G08	



**P-loop containing nucleoside triphosphate hydrolase** Phvul.011G08PTHR33477:SI Phvul.011G08  
 NB-ARC domain-containing disease resistance pro Phvul.011G14PTHR23155//IPhvul.011G14  
 NB-ARC domain-containing disease resistance pro Phvul.011G14PTHR23155//IPhvul.011G14  
 NB-ARC domain-containing disease resistance pro Phvul.011G18PTHR23155//IPhvul.011G18  
 MLP-like protein 43 Phvul.011G18PF00407 - Pat Phvul.011G18  
 MLP-like protein 43 Phvul.011G18PF00407 - Pat Phvul.011G18  
 NB-ARC domain-containing disease resistance pro Phvul.011G19PF13191//PF1Phvul.011G19  
 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19  
 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvul.011G19  
 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvul.011G19  
 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvul.011G19  
 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19  
 NB-ARC domain-containing disease resistance pro Phvul.011G19PF00931//PF1Phvul.011G19  
 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 Galactose oxidase/kelch repeat superfamily protein Phvul.001G02PF00646 - F-b Phvul.001G02  
 Glycosyl hydrolases family 31 protein Phvul.001G12PTHR22762//IPhvul.001G12  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvul.001G13  
 Leucine-rich repeat protein kinase family protein Phvul.001G18PF00069//PFCPhvul.001G18  
 Leucine-rich repeat protein kinase family protein Phvul.001G18PF00069//PFCPhvul.001G18  
 Ca<sup>2+</sup> activated outward rectifying K<sup>+</sup> channel 5 Phvul.001G21PTHR11003:SI Phvul.001G21  
 Pectin lyase-like superfamily protein Phvul.002G06PTHR31375:SI Phvul.002G06  
 Pectin lyase-like superfamily protein Phvul.002G06PTHR31375:SI Phvul.002G06  
 phospholipase D delta Phvul.002G10PTHR18896:SI Phvul.002G10  
 phospholipase D delta Phvul.002G10PTHR18896:SI Phvul.002G10  
 XS domain-containing protein / XS zinc finger dom Phvul.002G27PTHR21596:SI Phvul.002G27  
 0 0 0 Phvul.003G05  
 0 0 0 Phvul.003G05  
 cytochrome P450, family 77, subfamily B, polypep Phvul.003G07PTHR24298:SI Phvul.003G07  
 cytochrome P450, family 77, subfamily B, polypep Phvul.003G07PTHR24298:SI Phvul.003G07  
 Heavy metal transport/detoxification superfamily Phvul.003G10PTHR22814//IPhvul.003G10  
 Heavy metal transport/detoxification superfamily Phvul.003G10PTHR22814//IPhvul.003G10  
 homolog of yeast FIP1 [V] Phvul.003G15PF05182 - Fip:Phvul.003G15  
 cysteine-rich RLK (RECEPTOR-like protein kinase) 1Phvul.003G15PF00704//PFCPhvul.003G15  
 cysteine-rich RLK (RECEPTOR-like protein kinase) 1Phvul.003G15PF00704//PFCPhvul.003G15



1				
2	Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.003G16PF01535//PF1	Phvul.003G16	
3	RNA-metabolising metallo-beta-lactamase family	Phvul.003G203.5.2.6 - Beta-	Phvul.003G20	
4	RNA-metabolising metallo-beta-lactamase family	Phvul.003G203.5.2.6 - Beta-	Phvul.003G20	
5				
6	ROP binding protein kinases 1	Phvul.003G28PTHR27001:SI	Phvul.003G28	
7	ROP binding protein kinases 1	Phvul.003G28PTHR27001:SI	Phvul.003G28	
8	myb domain protein 118	Phvul.004G01PTHR10641:SI	Phvul.004G01	
9				
10	Regulator of chromosome condensation (RCC1) fa	Phvul.004G06PTHR22870//I	Phvul.004G06	
11	Regulator of chromosome condensation (RCC1) fa	Phvul.004G06PTHR22870//I	Phvul.004G06	
12	Pentatricopeptide repeat (PPR) superfamily protei	Phvul.004G13PTHR24015:SI	Phvul.004G13	
13	Pentatricopeptide repeat (PPR) superfamily protei	Phvul.004G13PTHR24015:SI	Phvul.004G13	
14				
15	LRR and NB-ARC domains-containing disease resis	Phvul.005G03PTHR23155//I	Phvul.005G03	
16	low-molecular-weight cysteine-rich 68	Phvul.005G07PF00304 - Gar	Phvul.005G07	
17	low-molecular-weight cysteine-rich 68	Phvul.005G07PF00304 - Gar	Phvul.005G07	
18				
19	RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.006G05K14398 - clea	Phvul.006G05	
20	RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.006G05K14398 - clea	Phvul.006G05	
21				
22	RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.006G05K14398 - clea	Phvul.006G05	
23	sirtuin 1	Phvul.006G05K11416 - mon	Phvul.006G05	
24	NB-ARC domain-containing disease resistance pro	Phvul.006G06PTHR23155//I	Phvul.006G06	
25	NB-ARC domain-containing disease resistance pro	Phvul.006G06PTHR23155//I	Phvul.006G06	
26				
27	LRR and NB-ARC domains-containing disease resis	Phvul.007G08PTHR23155//I	Phvul.007G08	
28	LRR and NB-ARC domains-containing disease resis	Phvul.007G08PTHR23155//I	Phvul.007G08	
29				
30	NB-ARC domain-containing disease resistance pro	Phvul.008G01PTHR23155:SI	Phvul.008G01	
31	NB-ARC domain-containing disease resistance pro	Phvul.008G01PTHR23155:SI	Phvul.008G01	
32	NB-ARC domain-containing disease resistance pro	Phvul.008G07PTHR23155//I	Phvul.008G07	
33	NB-ARC domain-containing disease resistance pro	Phvul.008G07PTHR23155//I	Phvul.008G07	
34				
35		0	0	0 Phvul.008G16
36		0	0	0 Phvul.008G16
37				
38	nodulin MtN21 /EamA-like transporter family prot	Phvul.009G03PF00892 - Ean	Phvul.009G03	
39	AGC (cAMP-dependent, cGMP-dependent and prc	Phvul.009G07PTHR24356:SI	Phvul.009G07	
40	AGC (cAMP-dependent, cGMP-dependent and prc	Phvul.009G07PTHR24356:SI	Phvul.009G07	
41				
42	RHO-related protein from plants 10	Phvul.009G18PTHR24072:SI	Phvul.009G18	
43	RHO-related protein from plants 10	Phvul.009G18PTHR24072:SI	Phvul.009G18	
44	RHO-related protein from plants 10	Phvul.009G18PTHR24072:SI	Phvul.009G18	
45	RHO-related protein from plants 10	Phvul.009G18PTHR24072:SI	Phvul.009G18	
46				
47	drought-induced 21	Phvul.009G24PTHR33509:SI	Phvul.009G24	
48	Disease resistance protein (TIR-NBS-LRR class) far	Phvul.010G02PF00931//PF1	Phvul.010G02	
49	Disease resistance protein (TIR-NBS-LRR class) far	Phvul.010G02PF00931//PF1	Phvul.010G02	
50				
51	LRR and NB-ARC domains-containing disease resis	Phvul.010G06PTHR23155//I	Phvul.010G06	
52		0	0	0 Phvul.010G10
53	<b>DOF zinc finger protein 1</b>	<b>Phvul.010G14PF02701 - Dof</b>	<b>Phvul.010G14</b>	
54				
55	RAD3-like DNA-binding helicase protein	Phvul.010G14K11273 - chro	Phvul.010G14	
56	RAD3-like DNA-binding helicase protein	Phvul.010G14K11273 - chro	Phvul.010G14	
57	scarecrow-like 3	Phvul.011G01PF03514 - GR	Phvul.011G01	
58				
59	NB-ARC domain-containing disease resistance pro	Phvul.011G18PTHR23155//I	Phvul.011G18	
60	NB-ARC domain-containing disease resistance pro	Phvul.011G18PTHR23155//I	Phvul.011G18	
	NB-ARC domain-containing disease resistance pro	Phvul.011G19PTHR23155//I	Phvul.011G19	

1 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19  
 2 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 3 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 4 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 5 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 6 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20  
 7 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 8 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 9 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20  
 10 NB-ARC domain-containing disease resistance pro Phvul.011G20PF13191 - AA/Phvul.011G20  
 11 NB-ARC domain-containing disease resistance pro Phvul.011G20PF13191 - AA/Phvul.011G20  
 12 Glycosyl hydrolase superfamily protein Phvul.L00450(PTHR32227:SfPhvul.L00450(
 13 Glycosyl hydrolase superfamily protein Phvul.L00450(PTHR32227:SfPhvul.L00450(
 14 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 15 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 16 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 17 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 18 ssDNA-binding transcriptional regulator Phvul.002G08PTHR31745:SfPhvul.002G08
 19 ssDNA-binding transcriptional regulator Phvul.002G08PTHR31745:SfPhvul.002G08
 20 disease resistance protein (TIR-NBS-LRR class), put Phvul.002G17PF00931//PF1Phvul.002G17
 21 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 22 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 23 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 24 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 25 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 26 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 27 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 28 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 29 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
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 31 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 32 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 33 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 34 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
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 36 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 37 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 38 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 39 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 40 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 41 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 42 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 43 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
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 48 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 49 0 0 0 Phvul.003G05
 50 0 0 0 Phvul.003G05
 51 0 0 0 Phvul.003G24
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 54 0 0 0 Phvul.003G24
 55 SU(VAR)3-9 homolog 9 Phvul.003G28PTHR22884:SfPhvul.003G28
 56 SU(VAR)3-9 homolog 9 Phvul.003G28PTHR22884:SfPhvul.003G28
 57 Pentatricopeptide repeat (PPR) superfamily proteiPhvul.003G28PF01535//PF1Phvul.003G28
 58 polyribonucleotide nucleotidyltransferase, putativPhvul.004G012.7.7.8 - Polyr Phvul.004G01
 59 somatic embryogenesis receptor-like kinase 1 Phvul.004G08K13418 - som:Phvul.004G08

1 somatic embryogenesis receptor-like kinase 1 Phvul.004G08K13418 - som:Phvul.004G08  
2 Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G04PF01535//PF1Phvul.005G04  
3 Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G04PF01535//PF1Phvul.005G04  
4 Nucleoporin autopeptidase Phvul.005G06K14297 - nucl:Phvul.005G06  
5 Nucleoporin autopeptidase Phvul.005G06K14297 - nucl:Phvul.005G06  
6 Protein of unknown function (DUF616) Phvul.005G07PTHR12956//I Phvul.005G07  
7 transducin family protein / WD-40 repeat family p Phvul.006G02PTHR22838:SI Phvul.006G02  
8 transducin family protein / WD-40 repeat family p Phvul.006G02PTHR22838:SI Phvul.006G02  
9 Ribose 5-phosphate isomerase, type A protein Phvul.006G10PTHR11934:SI Phvul.006G10  
10 late embryogenesis abundant protein-related / LE:Phvul.006G122.4.1.10 - Lev:Phvul.006G12  
11 late embryogenesis abundant protein-related / LE:Phvul.006G122.4.1.10 - Lev:Phvul.006G12  
12 Ankyrin repeat family protein Phvul.006G17PF12796//PF1 Phvul.006G17  
13 Pentatricopeptide repeat (PPR) superfamily protei Phvul.008G10PF01535//PF1 Phvul.008G10  
14 Pentatricopeptide repeat (PPR) superfamily protei Phvul.008G10PF01535//PF1 Phvul.008G10  
15 LA RNA-binding protein Phvul.008G20PTHR22792:SI Phvul.008G20  
16 Leucine-rich repeat protein kinase family protein Phvul.009G10PF07714//PFC Phvul.009G10  
17 Protein of unknown function (DUF740) Phvul.010G00PF05340 - Pro Phvul.010G00  
18 OBF-binding protein 3 Phvul.010G01PF02701 - Dof Phvul.010G01  
19 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
20 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
21 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
22 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
23 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
24 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
25 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
26 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
27 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
28 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04  
29 ABC-2 and Plant PDR ABC-type transporter family Phvul.010G14PTHR19241:SI Phvul.010G14  
30 NB-ARC domain-containing disease resistance pro Phvul.011G18PTHR23155//I Phvul.011G18  
31 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//I Phvul.011G20  
32 LRR and NB-ARC domains-containing disease resis: Phvul.011G20PTHR23155//I Phvul.011G20  
33 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//I Phvul.011G20  
34 LRR and NB-ARC domains-containing disease resis: Phvul.011G20PTHR23155//I Phvul.011G20  
35  
36  
37  
38  
39  
40  
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42  
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44  
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3	not assigned.ε	(original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.C
4	not assigned.ε	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C
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8	not assigned.ε	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C
9	not assigned.ε	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C
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13	not assigned.ε	(original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C
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17	not assigned.ε	(original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C
18	External stimu	effector receptor (NLR) (original description: pacid=37177951 transcript=Phvul.002G
19	RNA biosynth	transcription factor (MYB-related) (original description: pacid=37168368 transcript=F
20	RNA biosynth	transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0
21	RNA biosynth	transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0
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23	External stimu	effector receptor (NLR) (original description: pacid=37146968 transcript=Phvul.003G
24	not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
25	not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
26	not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
27	not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
28	External stimu	effector receptor (NLR) (original description: pacid=37163438 transcript=Phvul.004G
29	Protein home	SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029
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32	Protein home	SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029
33	RNA biosynth	transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007
34	RNA biosynth	transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007
35	RNA biosynth	transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007
36	Lipid metaboli	ATPase component TGD3 of TGD lipid importer complex (original description: pacid=
37	not assigned.r	no hits & (original description: pacid=37157769 transcript=Phvul.008G280900.1 locu
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40	not assigned.ε	(original description: pacid=37142899 transcript=Phvul.010G064700.1 locus=Phvul.C
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47	not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
48	not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
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52	not assigned.ε	(original description: pacid=37156909 transcript=Phvul.011G166100.1 locus=Phvul.C
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55	not assigned.ε	(original description: pacid=37169603 transcript=Phvul.001G134000.1 locus=Phvul.C
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57	Phytohormon	SMXL strigolactone signal transducer (original description: pacid=37170890 transcrip
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60	not assigned.r	no hits & (original description: pacid=37177208 transcript=Phvul.002G057300.2 locu
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1 Phytohormon abscisic acid hydroxylase (original description: pacid=37176949 transcript=Phvul.002  
2 not assigned.r no hits & (original description: pacid=37175068 transcript=Phvul.002G187600.1 locu  
3 **RNA processir poly(A) RNA polymerase regulatory protein (original description: pacid=37177379 tra**  
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5 not assigned.ε (original description: pacid=37147525 transcript=Phvul.003G101200.1 locus=Phvul.C  
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7 Coenzyme me component SUF-E2/-E3 of plastidial SUF system assembly phase (original description  
8 Coenzyme me component SUF-E2/-E3 of plastidial SUF system assembly phase (original description  
9 Chromatin org component SSRP of FACT histone chaperone complex (original description: pacid=37  
10 External stimu effector receptor (NLR) (original description: pacid=37163195 transcript=Phvul.004G  
11 External stimu effector receptor (NLR) (original description: pacid=37163195 transcript=Phvul.004G  
12 Coenzyme me uroporphyrinogen III methyltransferase (original description: pacid=37152438 transc  
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16 Protein modif protein kinase (CrIRLK1) (original description: pacid=37173044 transcript=Phvul.006C  
17 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C  
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20 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C  
21 Protein biosyr LAS1 pre-rRNA cleavage factor involved in ITS2 rRNA removal (original description: p  
22 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr  
23 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr  
24 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr  
25 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr  
26 External stimu effector receptor (NLR) (original description: pacid=37142428 transcript=Phvul.010G  
27 not assigned.ε (original description: pacid=37143313 transcript=Phvul.010G132333.3 locus=Phvul.C  
28 External stimu effector receptor (NLR) (original description: pacid=37143628 transcript=Phvul.010G  
29 not assigned.r no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu  
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32 not assigned.r no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu  
33 External stimu effector receptor (NLR) (original description: pacid=37154763 transcript=Phvul.011G  
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35 not assigned.ε (original description: pacid=37157447 transcript=Phvul.011G151300.1 locus=Phvul.C  
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26 not assigned.ε (original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.C  
27 External stimu transcription factor (ICE1|2) (original description: pacid=37167713 transcript=Phvul.(  
28 External stimu transcription factor (ICE1|2) (original description: pacid=37167713 transcript=Phvul.(  
29 Cell wall orgar alpha-class expansin (original description: pacid=37168526 transcript=Phvul.001G23:  
30 Cell wall orgar alpha-class expansin (original description: pacid=37168526 transcript=Phvul.001G23:  
31 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0  
32 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0  
33 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0  
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35 not assigned.ε (original description: pacid=37177875 transcript=Phvul.002G298800.1 locus=Phvul.C  
36 External stimu G-alpha component XLG of non-canonical heterotrimeric G-protein complex (original  
37 External stimu G-alpha component XLG of non-canonical heterotrimeric G-protein complex (original  
38 RNA biosynth PAP2/TAC2 cofactor of plastid-encoded RNA polymerase (original description: pacid=  
39 RNA biosynth PAP2/TAC2 cofactor of plastid-encoded RNA polymerase (original description: pacid=  
40 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript  
41 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript  
42 **Protein home component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origir**  
43 **Protein home component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origir**  
44 **Protein home component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origir**  
45 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
46 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
47 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
48 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
49 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
50 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
51 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
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54 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
55 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
56 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
57 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
58 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
59 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C  
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1 not assigned.ε (original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.C  
2 not assigned.ε (original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.C  
3 Cell cycle orgaMinD plastid division FtsZ assembly factor (original description: pacid=37162532 trar  
4 Cell cycle orgaMinD plastid division FtsZ assembly factor (original description: pacid=37162532 trar  
5 not assigned.ε (original description: pacid=37162837 transcript=Phvul.004G133100.1 locus=Phvul.C  
6 not assigned.ε (original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.C  
7 not assigned.ε (original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.C  
8 not assigned.ε (original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.C  
9 Cell wall orgar alpha-class expansin (original description: pacid=37173891 transcript=Phvul.006G08  
10 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu  
11 Enzyme classiiTrans-resveratrol di-O-methyltransferase OS=Vitis vinifera (sp|b6vjs4|romt\_vitvi : 34  
12 Enzyme classiiTrans-resveratrol di-O-methyltransferase OS=Vitis vinifera (sp|b6vjs4|romt\_vitvi : 34  
13 not assigned.r no hits & (original description: pacid=37167355 transcript=Phvul.007G027400.1 locu  
14 Enzyme classiiATPase ARSA1 OS=Chlamydomonas reinhardtii (sp|a8jgb0|asna1\_chlre : 369.0) & En  
15 Protein modif protein kinase (LRR-III) (original description: pacid=37159143 transcript=Phvul.008G1  
16 Lipid metabolisterol C-24 methyltransferase (original description: pacid=37149363 transcript=Phvu  
17 Lipid metabolisterol C-24 methyltransferase (original description: pacid=37149363 transcript=Phvu  
18 RNA biosynthtranscription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00  
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22 not assigned.ε (original description: pacid=37148715 transcript=Phvul.009G213300.1 locus=Phvul.C  
23 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C  
24 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C  
25 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C  
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27 not assigned.ε (original description: pacid=37151719 transcript=Phvul.009G233700.1 locus=Phvul.C  
28 not assigned.ε (original description: pacid=37151719 transcript=Phvul.009G233700.1 locus=Phvul.C  
29 not assigned.ε (original description: pacid=37151719 transcript=Phvul.009G233700.1 locus=Phvul.C  
30 not assigned.ε (original description: pacid=37143979 transcript=Phvul.010G008700.2 locus=Phvul.C  
31 not assigned.ε (original description: pacid=37143979 transcript=Phvul.010G008700.2 locus=Phvul.C  
32 not assigned.ε (original description: pacid=37142864 transcript=Phvul.010G056500.1 locus=Phvul.C  
33 not assigned.ε (original description: pacid=37142864 transcript=Phvul.010G056500.1 locus=Phvul.C  
34 not assigned.ε (original description: pacid=37142368 transcript=Phvul.010G063100.1 locus=Phvul.C  
35 not assigned.ε (original description: pacid=37142879 transcript=Phvul.010G070584.1 locus=Phvul.C  
36 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu  
37 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu  
38 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu  
39 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu  
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41 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu  
42 not assigned.ε (original description: pacid=37156367 transcript=Phvul.011G014500.2 locus=Phvul.C  
43 not assigned.ε (original description: pacid=37156367 transcript=Phvul.011G014500.2 locus=Phvul.C  
44 not assigned.ε (original description: pacid=37156367 transcript=Phvul.011G014500.2 locus=Phvul.C  
45 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C  
46 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C

1 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C  
2 not assigned.ε (original description: pacid=37154977 transcript=Phvul.011G149400.1 locus=Phvul.C  
3 not assigned.ε (original description: pacid=37154977 transcript=Phvul.011G149400.1 locus=Phvul.C  
4 not assigned.ε (original description: pacid=37156674 transcript=Phvul.011G181500.1 locus=Phvul.C  
5 not assigned.r no hits & (original description: pacid=37154681 transcript=Phvul.011G182900.1 locu  
6 not assigned.r no hits & (original description: pacid=37154681 transcript=Phvul.011G182900.1 locu  
7 not assigned.ε (original description: pacid=37155164 transcript=Phvul.011G191600.1 locus=Phvul.C  
8 not assigned.ε (original description: pacid=37157159 transcript=Phvul.011G191800.1 locus=Phvul.C  
9 not assigned.ε (original description: pacid=37155368 transcript=Phvul.011G192200.1 locus=Phvul.C  
10 not assigned.ε (original description: pacid=37155339 transcript=Phvul.011G192900.1 locus=Phvul.C  
11 not assigned.ε (original description: pacid=37155339 transcript=Phvul.011G192900.1 locus=Phvul.C  
12 not assigned.ε (original description: pacid=37155272 transcript=Phvul.011G195751.1 locus=Phvul.C  
13 not assigned.ε (original description: pacid=37155563 transcript=Phvul.011G198400.1 locus=Phvul.C  
14 not assigned.ε (original description: pacid=37154846 transcript=Phvul.011G201000.1 locus=Phvul.C  
15 not assigned.ε (original description: pacid=37156971 transcript=Phvul.011G201101.1 locus=Phvul.C  
16 not assigned.ε (original description: pacid=37168061 transcript=Phvul.001G027100.1 locus=Phvul.C  
17 not assigned.ε (original description: pacid=37171176 transcript=Phvul.001G123000.2 locus=Phvul.C  
18 not assigned.ε (original description: pacid=37171258 transcript=Phvul.001G132516.1 locus=Phvul.C  
19 not assigned.ε (original description: pacid=37171258 transcript=Phvul.001G132516.1 locus=Phvul.C  
20 not assigned.ε (original description: pacid=37169452 transcript=Phvul.001G132701.1 locus=Phvul.C  
21 not assigned.ε (original description: pacid=37169452 transcript=Phvul.001G132701.1 locus=Phvul.C  
22 not assigned.ε (original description: pacid=37170073 transcript=Phvul.001G132800.1 locus=Phvul.C  
23 not assigned.ε (original description: pacid=37170073 transcript=Phvul.001G132800.1 locus=Phvul.C  
24 not assigned.ε (original description: pacid=37167899 transcript=Phvul.001G132864.1 locus=Phvul.C  
25 not assigned.ε (original description: pacid=37167899 transcript=Phvul.001G132864.1 locus=Phvul.C  
26 not assigned.ε (original description: pacid=37168771 transcript=Phvul.001G133100.1 locus=Phvul.C  
27 not assigned.ε (original description: pacid=37168771 transcript=Phvul.001G133100.1 locus=Phvul.C  
28 not assigned.ε (original description: pacid=37168444 transcript=Phvul.001G133101.1 locus=Phvul.C  
29 not assigned.ε (original description: pacid=37168444 transcript=Phvul.001G133101.1 locus=Phvul.C  
30 Protein modif protein kinase (LRR-III) (original description: pacid=37171243 transcript=Phvul.001G1  
31 Protein modif protein kinase (LRR-III) (original description: pacid=37171243 transcript=Phvul.001G1  
32 Solute transpcvoltage-gated potassium cation channel (TPK/KCO) (original description: pacid=37171  
33 Cell wall orgar polygalacturonase (PGX1) (original description: pacid=37177802 transcript=Phvul.00  
34 Cell wall orgar polygalacturonase (PGX1) (original description: pacid=37177802 transcript=Phvul.00  
35 Lipid metaboliphospholipase D (PLD-delta) (original description: pacid=37175497 transcript=Phvul.  
36 Lipid metaboliphospholipase D (PLD-delta) (original description: pacid=37175497 transcript=Phvul.  
37 Chromatin orgSGS3 stabilization factor of DNA methylation pathway (original description: pacid=37  
38 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu  
39 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu  
40 Enzyme classiiCytochrome P450 77A1 (Fragment) OS=Solanum melongena (sp|p37123|c77a1\_soln  
41 Enzyme classiiCytochrome P450 77A1 (Fragment) OS=Solanum melongena (sp|p37123|c77a1\_soln  
42 not assigned.ε (original description: pacid=37144721 transcript=Phvul.003G104900.1 locus=Phvul.C  
43 not assigned.ε (original description: pacid=37144721 transcript=Phvul.003G104900.1 locus=Phvul.C  
44 RNA processir component Fip1 of Cleavage and Polyadenylation Specificity Factor (CPSF) complex (r  
45 Protein modif protein kinase (SD-1) (original description: pacid=37146603 transcript=Phvul.003G15  
46 Protein modif protein kinase (SD-1) (original description: pacid=37146603 transcript=Phvul.003G15

1 RNA processir RNA editing factor (OTP82) (original description: pacid=37146356 transcript=Phvul.01  
2 RNA processir exo-/endoribonuclease (RNase J) (original description: pacid=37148378 transcript=Phvul.01  
3 RNA processir exo-/endoribonuclease (RNase J) (original description: pacid=37148378 transcript=Phvul.01  
4 Multi-process GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37148383 tr  
5 Multi-process GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37148383 tr  
6 RNA biosynthtranscription factor (MYB) (original description: pacid=37162815 transcript=Phvul.00  
7 not assigned.ε (original description: pacid=37162157 transcript=Phvul.004G064300.1 locus=Phvul.C  
8 not assigned.ε (original description: pacid=37162157 transcript=Phvul.004G064300.1 locus=Phvul.C  
9 not assigned.ε (original description: pacid=37163473 transcript=Phvul.004G131300.1 locus=Phvul.C  
10 not assigned.ε (original description: pacid=37163473 transcript=Phvul.004G131300.1 locus=Phvul.C  
11 not assigned.ε (original description: pacid=37154207 transcript=Phvul.005G031200.1 locus=Phvul.C  
12 External stimu defensin (PDF1) (original description: pacid=37154287 transcript=Phvul.005G071300  
13 External stimu defensin (PDF1) (original description: pacid=37154287 transcript=Phvul.005G071300  
14 RNA processir component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description:  
15 RNA processir component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description:  
16 RNA processir component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description:  
17 Chromatin org histone deacetylase (SRT) (original description: pacid=37171603 transcript=Phvul.006  
18 not assigned.ε (original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.C  
19 not assigned.ε (original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.C  
20 not assigned.ε (original description: pacid=37165347 transcript=Phvul.007G086300.2 locus=Phvul.C  
21 not assigned.ε (original description: pacid=37165347 transcript=Phvul.007G086300.2 locus=Phvul.C  
22 not assigned.ε (original description: pacid=37159623 transcript=Phvul.008G014700.1 locus=Phvul.C  
23 not assigned.ε (original description: pacid=37159623 transcript=Phvul.008G014700.1 locus=Phvul.C  
24 not assigned.ε (original description: pacid=37158229 transcript=Phvul.008G072032.1 locus=Phvul.C  
25 not assigned.ε (original description: pacid=37158229 transcript=Phvul.008G072032.1 locus=Phvul.C  
26 not assigned.r no hits & (original description: pacid=37160500 transcript=Phvul.008G168300.2 locu  
27 not assigned.r no hits & (original description: pacid=37160500 transcript=Phvul.008G168300.2 locu  
28 Solute transpc solute transporter (UmamiT) (original description: pacid=37150535 transcript=Phvul.  
29 Protein modif protein kinase (AGC-VII/NDR) (original description: pacid=37149778 transcript=Phvul  
30 Protein modif protein kinase (AGC-VII/NDR) (original description: pacid=37149778 transcript=Phvul  
31 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180  
32 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180  
33 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180  
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35 not assigned.r no hits & (original description: pacid=37152061 transcript=Phvul.009G249500.1 locu  
36 External stimu effector receptor (NLR) (original description: pacid=37142827 transcript=Phvul.010G  
37 External stimu effector receptor (NLR) (original description: pacid=37144038 transcript=Phvul.010G  
38 not assigned.ε (original description: pacid=37142695 transcript=Phvul.010G063700.2 locus=Phvul.C  
39 not assigned.r no hits & (original description: pacid=37143741 transcript=Phvul.010G101700.1 locu  
40 **RNA biosynthtranscription factor (DOF) (original description: pacid=37142901 transcript=Phvul.011**  
41 not assigned.ε (original description: pacid=37143246 transcript=Phvul.010G149500.1 locus=Phvul.C  
42 not assigned.ε (original description: pacid=37143246 transcript=Phvul.010G149500.1 locus=Phvul.C  
43 RNA biosynthtranscription factor (GRAS) (original description: pacid=37157104 transcript=Phvul.0:  
44 not assigned.ε (original description: pacid=37156674 transcript=Phvul.011G181500.1 locus=Phvul.C  
45 not assigned.ε (original description: pacid=37156674 transcript=Phvul.011G181500.1 locus=Phvul.C  
46 not assigned.ε (original description: pacid=37154890 transcript=Phvul.011G198000.1 locus=Phvul.C



1 not assigned.ε (original description: pacid=37154890 transcript=Phvul.011G198000.1 locus=Phvul.C  
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9 not assigned.ε (original description: pacid=37156646 transcript=Phvul.011G202366.1 locus=Phvul.C  
10 not assigned.ε (original description: pacid=37156646 transcript=Phvul.011G202366.1 locus=Phvul.C  
11 Enzyme classiiGlucan endo-1,3-beta-glucosidase 11 OS=Arabidopsis thaliana (sp|q8l868|e1311\_ar  
12 Enzyme classiiGlucan endo-1,3-beta-glucosidase 11 OS=Arabidopsis thaliana (sp|q8l868|e1311\_ar  
13 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0  
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15 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0  
16 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0  
17 RNA processirWhirly-type plastidial RNA splicing factor (original description: pacid=37176882 trans  
18 RNA processirWhirly-type plastidial RNA splicing factor (original description: pacid=37176882 trans  
19 External stimuleffector receptor (NLR) (original description: pacid=37177710 transcript=Phvul.002G  
20 Solute transpctransport protein (TSUP) (original description: pacid=37177847 transcript=Phvul.002  
21 Solute transpctransport protein (TSUP) (original description: pacid=37177847 transcript=Phvul.002  
22 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002  
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27 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002  
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29 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002  
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40 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002  
41 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
42 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
43 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
44 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
45 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
46 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
47 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
48 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371  
49 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu  
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51 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu  
52 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu  
53 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu  
54 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu  
55 Chromatin orgSUVH2/9 methyl-DNA-binding factor of DNA methylation pathway (original descripti  
56 Chromatin orgSUVH2/9 methyl-DNA-binding factor of DNA methylation pathway (original descripti  
57 not assigned.ε (original description: pacid=37146499 transcript=Phvul.003G282250.1 locus=Phvul.C  
58 RNA processir polynucleotide phosphorylase (PNP) (original description: pacid=37161570 transcript  
59 Protein modif protein kinase (LRR-II) (original description: pacid=37161848 transcript=Phvul.004G0

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60 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A

1 J04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote  
2 J04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote  
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4 rscript=Phvul.004G106800.2 locus=Phvul.004G106800 ID=Phvul.004G106800.2.v2.1 annot-version=  
5 J04G133100 ID=Phvul.004G133100.1.v2.1 annot-version=v2.1) & Probable carboxylesterase 18 OS=  
6 J05G165800 ID=Phvul.005G165800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
7 J05G165800 ID=Phvul.005G165800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
8 J06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
9 6800.1 locus=Phvul.006G086800 ID=Phvul.006G086800.1.v2.1 annot-version=v2.1) &  
10 rs=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)  
11 46.0) & Enzyme classification.EC\_2 transferases.EC\_2.1 transferase transferring one-carbon group(5  
12 46.0) & Enzyme classification.EC\_2 transferases.EC\_2.1 transferase transferring one-carbon group(5  
13 rs=Phvul.007G027400 ID=Phvul.007G027400.1.v2.1 annot-version=v2.1)  
14 rzyme classification.EC\_3 hydrolases.EC\_3.6 hydrolase acting on acid anhydride(50.3.6 : 133.9) (orig  
15 158100.1 locus=Phvul.008G158100 ID=Phvul.008G158100.1.v2.1 annot-version=v2.1) &  
16 il.009G020000.1 locus=Phvul.009G020000 ID=Phvul.009G020000.1.v2.1 annot-version=v2.1) &  
17 il.009G020000.1 locus=Phvul.009G020000 ID=Phvul.009G020000.1.v2.1 annot-version=v2.1) &  
18 9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &  
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21 9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &  
22 J09G213300 ID=Phvul.009G213300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat  
23 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik  
24 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik  
25 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik  
26 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik  
27 J09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-  
28 J09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-  
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30 J10G008700 ID=Phvul.010G008700.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nicc  
31 J10G008700 ID=Phvul.010G008700.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nicc  
32 J10G056500 ID=Phvul.010G056500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
33 J10G056500 ID=Phvul.010G056500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
34 J10G063100 ID=Phvul.010G063100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
35 J10G070584 ID=Phvul.010G070584.1.v2.1 annot-version=v2.1) & Long-chain-alcohol oxidase FAO1  
36 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)  
37 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)  
38 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)  
39 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)  
40 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)  
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42 J11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13  
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44 J11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13  
45 J11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing  
46 J11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing

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2 **011G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing**  
3  
4 011G149400 ID=Phvul.011G149400.1.v2.1 annot-version=v2.1) & Disease resistance protein At4g27  
5 011G149400 ID=Phvul.011G149400.1.v2.1 annot-version=v2.1) & Disease resistance protein At4g27  
6 011G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
7  
8  
9  
10 011G191600 ID=Phvul.011G191600.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
11 011G191800 ID=Phvul.011G191800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
12 011G192200 ID=Phvul.011G192200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
13 011G192900 ID=Phvul.011G192900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
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16 011G195751 ID=Phvul.011G195751.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
17 011G198400 ID=Phvul.011G198400.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
18 011G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
19 011G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
20 011G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
21 001G027100 ID=Phvul.001G027100.1.v2.1 annot-version=v2.1) & F-box/kelch-repeat protein At5g4  
22 001G123000 ID=Phvul.001G123000.2.v2.1 annot-version=v2.1) & Alpha-glucosidase OS=Spinacia oler  
23 001G132516 ID=Phvul.001G132516.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
24 001G132516 ID=Phvul.001G132516.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
25 001G132701 ID=Phvul.001G132701.1.v2.1 annot-version=v2.1) & Disease resistance protein RGA2 (C  
26 001G132701 ID=Phvul.001G132701.1.v2.1 annot-version=v2.1) & Disease resistance protein RGA2 (C  
27 001G132800 ID=Phvul.001G132800.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
28 001G132800 ID=Phvul.001G132800.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
29 001G132864 ID=Phvul.001G132864.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
30 001G132864 ID=Phvul.001G132864.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
31 001G133100 ID=Phvul.001G133100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
32 001G133100 ID=Phvul.001G133100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
33 001G133101 ID=Phvul.001G133101.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
34 001G133101 ID=Phvul.001G133101.1.v2.1 annot-version=v2.1) & Putative disease resistance protei  
35 185400.1 locus=Phvul.001G185400 ID=Phvul.001G185400.1.v2.1 annot-version=v2.1) &  
36 185400.1 locus=Phvul.001G185400 ID=Phvul.001G185400.1.v2.1 annot-version=v2.1) &  
37 0086 transcript=Phvul.001G217800.1 locus=Phvul.001G217800 ID=Phvul.001G217800.1.v2.1 annot  
38 2G063500.1 locus=Phvul.002G063500 ID=Phvul.002G063500.1.v2.1 annot-version=v2.1) &  
39 2G063500.1 locus=Phvul.002G063500 ID=Phvul.002G063500.1.v2.1 annot-version=v2.1) &  
40 002G104200.1 locus=Phvul.002G104200 ID=Phvul.002G104200.1.v2.1 annot-version=v2.1) &  
41 002G104200.1 locus=Phvul.002G104200 ID=Phvul.002G104200.1.v2.1 annot-version=v2.1) &  
42 178074 transcript=Phvul.002G279500.1 locus=Phvul.002G279500 ID=Phvul.002G279500.1.v2.1 an  
43  
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1 03G162300.1 locus=Phvul.003G162300 ID=Phvul.003G162300.1.v2.1 annot-version=v2.1) &  
2 hvul.003G209600.2 locus=Phvul.003G209600 ID=Phvul.003G209600.2.v2.1 annot-version=v2.1) &  
3 hvul.003G209600.2 locus=Phvul.003G209600 ID=Phvul.003G209600.2.v2.1 annot-version=v2.1) &  
4 ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versic  
5 ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versic  
6 04G011400.1 locus=Phvul.004G011400 ID=Phvul.004G011400.1.v2.1 annot-version=v2.1) &  
7 04G064300 ID=Phvul.004G064300.1.v2.1 annot-version=v2.1) & Ultraviolet-B receptor UVR8 OS=A  
8 04G064300 ID=Phvul.004G064300.1.v2.1 annot-version=v2.1) & Ultraviolet-B receptor UVR8 OS=A  
9 04G131300 ID=Phvul.004G131300.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
10 04G131300 ID=Phvul.004G131300.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
11 05G031200 ID=Phvul.005G031200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
12 ).1 locus=Phvul.005G071300 ID=Phvul.005G071300.1.v2.1 annot-version=v2.1) &  
13 ).1 locus=Phvul.005G071300 ID=Phvul.005G071300.1.v2.1 annot-version=v2.1) &  
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15 : pacid=37172194 transcript=Phvul.006G057100.5 locus=Phvul.006G057100 ID=Phvul.006G057100  
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17 06G057700.2 locus=Phvul.006G057700 ID=Phvul.006G057700.2.v2.1 annot-version=v2.1) &  
18 06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
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21 07G086300 ID=Phvul.007G086300.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
22 08G014700 ID=Phvul.008G014700.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP13  
23 08G014700 ID=Phvul.008G014700.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP13  
24 08G072032 ID=Phvul.008G072032.1.v2.1 annot-version=v2.1) & Probable disease resistance prote  
25 08G072032 ID=Phvul.008G072032.1.v2.1 annot-version=v2.1) & Probable disease resistance prote  
26 rs=Phvul.008G168300 ID=Phvul.008G168300.2.v2.1 annot-version=v2.1)  
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28 .009G039200.1 locus=Phvul.009G039200 ID=Phvul.009G039200.1.v2.1 annot-version=v2.1) &  
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31 0800.2 locus=Phvul.009G180800 ID=Phvul.009G180800.2.v2.1 annot-version=v2.1) &  
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35 rs=Phvul.009G249500 ID=Phvul.009G249500.1.v2.1 annot-version=v2.1)  
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37 i025700.1 locus=Phvul.010G025700 ID=Phvul.010G025700.1.v2.1 annot-version=v2.1) &  
38 010G063700 ID=Phvul.010G063700.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
39 rs=Phvul.010G101700 ID=Phvul.010G101700.1.v2.1 annot-version=v2.1)  
40 **010G141400.1 locus=Phvul.010G141400 ID=Phvul.010G141400.1.v2.1 annot-version=v2.1) &**  
41 010G149500 ID=Phvul.010G149500.1.v2.1 annot-version=v2.1) & Regulator of telomere elongation  
42 010G149500 ID=Phvul.010G149500.1.v2.1 annot-version=v2.1) & Regulator of telomere elongation  
43 11G015000.1 locus=Phvul.011G015000 ID=Phvul.011G015000.1.v2.1 annot-version=v2.1) &  
44 11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
45 11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
46 11G198000 ID=Phvul.011G198000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

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3 J11G200880 ID=Phvul.011G200880.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
4 J11G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
5 J11G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
6 J11G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
7 J11G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
8 J11G202366 ID=Phvul.011G202366.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
9 J11G202366 ID=Phvul.011G202366.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
10 ath : 469.0) & Enzyme classification.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 354.6) (original des  
11 ath : 469.0) & Enzyme classification.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 354.6) (original des  
12 J01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &  
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15 J01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &  
16 script=Phvul.002G089800.1 locus=Phvul.002G089800 ID=Phvul.002G089800.1.v2.1 annot-version=v  
17 script=Phvul.002G089800.1 locus=Phvul.002G089800 ID=Phvul.002G089800.1.v2.1 annot-version=v  
18 i171400.1 locus=Phvul.002G171400 ID=Phvul.002G171400.1.v2.1 annot-version=v2.1) &  
19 G244900.1 locus=Phvul.002G244900 ID=Phvul.002G244900.1.v2.1 annot-version=v2.1) &  
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35 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &  
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37 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &  
38 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &  
39 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &  
40 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &  
41 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
42 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
43 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
44 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
45 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
46 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
47 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
48 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno  
49 us=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)  
50 us=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)  
51 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)  
52 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)  
53 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)  
54 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)  
55 on: pacid=37145910 transcript=Phvul.003G282200.3 locus=Phvul.003G282200 ID=Phvul.003G28220  
56 on: pacid=37145910 transcript=Phvul.003G282200.3 locus=Phvul.003G282200 ID=Phvul.003G28220  
57 J03G282250 ID=Phvul.003G282250.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
58 t=Phvul.004G011100.1 locus=Phvul.004G011100 ID=Phvul.004G011100.1.v2.1 annot-version=v2.1)  
59 J086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-version=v2.1) &



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2 )86300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-version=v2.1) &  
3 )05G041300 ID=Phvul.005G041300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat  
4 )05G041300 ID=Phvul.005G041300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat  
5 )05G069700 ID=Phvul.005G069700.1.v2.1 annot-version=v2.1) & Nuclear pore complex protein NU  
6 )05G069700 ID=Phvul.005G069700.1.v2.1 annot-version=v2.1) & Nuclear pore complex protein NU  
7  
8 )s=Phvul.005G072000 ID=Phvul.005G072000.1.v2.1 annot-version=v2.1)  
9  
10 )06G027500 ID=Phvul.006G027500.1.v2.1 annot-version=v2.1) & WD repeat-containing protein 26  
11 )06G027500 ID=Phvul.006G027500.1.v2.1 annot-version=v2.1) & WD repeat-containing protein 26  
12 )l.006G100600.1 locus=Phvul.006G100600 ID=Phvul.006G100600.1.v2.1 annot-version=v2.1) &  
13 )s=Phvul.006G126400 ID=Phvul.006G126400.1.v2.1 annot-version=v2.1)  
14 )s=Phvul.006G126400 ID=Phvul.006G126400.1.v2.1 annot-version=v2.1)  
15 )s=Phvul.006G170700 ID=Phvul.006G170700.1.v2.1 annot-version=v2.1)  
16  
17 )08G107400 ID=Phvul.008G107400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
18 )08G107400 ID=Phvul.008G107400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
19 cript=Phvul.008G206300.1 locus=Phvul.008G206300 ID=Phvul.008G206300.1.v2.1 annot-version=v2.1) &  
20 )10G008500 ID=Phvul.010G008500.1.v2.1 annot-version=v2.1) & no description available(sp|q9ss8  
21 )0G013500.1 locus=Phvul.010G013500 ID=Phvul.010G013500.1.v2.1 annot-version=v2.1) &  
22 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
23 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
24 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
25 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
26 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
27 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
28 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
29 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
30 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
31 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
32 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
33 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
34 )s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)  
35 )10G145600.1 locus=Phvul.010G145600 ID=Phvul.010G145600.1.v2.1 annot-version=v2.1) &  
36 )11G181700 ID=Phvul.011G181700.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
37 )11G200820 ID=Phvul.011G200820.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
38 )11G202100 ID=Phvul.011G202100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
39 )11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
40 )11G203100 ID=Phvul.011G203100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13  
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3 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 137.0)  
4 z7|gpa3\_orysj : 136.0)  
5 z7|gpa3\_orysj : 136.0)  
6 z7|gpa3\_orysj : 136.0)  
7 z7|gpa3\_orysj : 136.0)  
8 z7|gpa3\_orysj : 136.0)  
9  
10 ing protein 5 OS=Arabidopsis thaliana (sp|q8rwd9|acbp5\_arath : 133.0)  
11 ing protein 5 OS=Arabidopsis thaliana (sp|q8rwd9|acbp5\_arath : 133.0)  
12 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40\_arath : 433.0)  
13 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40\_arath : 433.0)  
14 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40\_arath : 433.0)  
15 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40\_arath : 433.0)  
16 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40\_arath : 433.0)  
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36 annot-version=v2.1) &  
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40 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 265.0)  
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52 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 458.0)  
53 otiana glutinosa (sp|q40392|tmvrn\_nicgu : 238.0)  
54 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 413.0)  
55 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 413.0)  
56 ) &  
57 ) &  
58 ) &  
59 ) &  
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4  $r=v2.1) \&$

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6  $r=v2.1) \&$

7 max (sp|c6tbd0|cspl6\_soybn : 249.0)

8 max (sp|c6tbd0|cspl6\_soybn : 249.0)

9 l.1.v2.1 annot-version=v2.1) &

10 l.1.v2.1 annot-version=v2.1) &

11 not-version=v2.1) &

12  
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16 2.1) &

17 2.1) &

18 in At4g10780 OS=Arabidopsis thaliana (sp|o82484|drl23\_arath : 303.0)

19 in At4g10780 OS=Arabidopsis thaliana (sp|o82484|drl23\_arath : 303.0)

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21  
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23 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 160.0)

24 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 160.0)

25 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 160.0)

26 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 160.0)

27 v2.1 annot-version=v2.1) &

28 in=v2.1) &

29 in=v2.1) &

30 in=v2.1) &

31 in=v2.1) &

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36 \ OS=Arabidopsis thaliana (sp|f4i594|rlm1a\_arath : 191.0)

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46 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 503.0)

47 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 541.0)

48 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 541.0)

49 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 474.0)

50 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 513.0)

51 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 538.0)

52 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 543.0)

53 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 541.0)

54 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 501.0)

55 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 555.0)

56 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 536.0)

57 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 549.0)

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1 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 360.0)  
2 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 483.0)  
3 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 543.0)  
4 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 357.0)  
5 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 565.0)  
6 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 565.0)  
7 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 479.0)  
8 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 479.0)  
9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 483.0)  
10 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 483.0)  
11 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 519.0)  
12 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 519.0)  
13 thaliana (sp|q9fh04|adh17\_arath : 523.0)  
14 thaliana (sp|q9fh04|adh17\_arath : 523.0)  
15 thaliana (sp|q9fh04|adh17\_arath : 523.0)  
16 thaliana (sp|q9fh04|adh17\_arath : 523.0)  
17 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1\_arath : 452.0)  
18 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1\_arath : 452.0)  
19 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1\_arath : 452.0)  
20 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1\_arath : 452.0)  
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39 OS=Arabidopsis thaliana (sp|q680c0|gdl62\_arath : 442.0)  
40 J03G010900.1.v2.1 annot-version=v2.1) &  
41 J03G010900.1.v2.1 annot-version=v2.1) &  
42 annot-version=v2.1) &  
43 annot-version=v2.1) &  
44 &  
45 &  
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48 **!l.003G295800.4.v2.1 annot-version=v2.1) &**  
49 **!l.003G295800.4.v2.1 annot-version=v2.1) &**  
50 **!l.003G295800.4.v2.1 annot-version=v2.1) &**  
51 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
52 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
53 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
54 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
55 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
56 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
57 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
58 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
59 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)  
60 .rabidopsis thaliana (sp|q6tph1|ppa23\_arath : 715.0)

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 2 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 137.0)  
 3 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 137.0)  
 4 =v2.1) &  
 5 =v2.1) &  
 6 =Arabidopsis thaliana (sp|q9lt10|cxe18\_arath : 385.0)  
 7 ing protein At3g49730 OS=Arabidopsis thaliana (sp|p0c8a0|pp275\_arath : 692.0)  
 8 ing protein At3g49730 OS=Arabidopsis thaliana (sp|p0c8a0|pp275\_arath : 692.0)  
 9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 446.0)  
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 15 ;0.2.1 : 182.1) (original description: pacid=37173441 transcript=Phvul.006G180900.1 locus=Phvul.006G180900.1  
 16 ;0.2.1 : 182.1) (original description: pacid=37173441 transcript=Phvul.006G180900.1 locus=Phvul.006G180900.1  
 17  
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 19 ;original description: pacid=37166954 transcript=Phvul.007G096800.1 locus=Phvul.007G096800 ID=Phvul.007G096800  
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 30 t-containing protein At1g19290 OS=Arabidopsis thaliana (sp|q9ln69|ppr50\_arath : 769.0)  
 31 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16\_arath : 573.0)  
 32 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16\_arath : 573.0)  
 33 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16\_arath : 573.0)  
 34 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16\_arath : 573.0)  
 35 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16\_arath : 573.0)  
 36 -like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2\_arath : 498.0)  
 37 -like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2\_arath : 498.0)  
 38 -like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2\_arath : 498.0)  
 39 otiana glutinosa (sp|q40392|tmvrn\_nicgu : 371.0)  
 40 otiana glutinosa (sp|q40392|tmvrn\_nicgu : 371.0)  
 41 ing protein At2g17670 OS=Arabidopsis thaliana (sp|q84j71|pp161\_arath : 496.0)  
 42 ing protein At2g17670 OS=Arabidopsis thaliana (sp|q84j71|pp161\_arath : 496.0)  
 43 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 612.0)  
 44 OS=Lotus japonicus (sp|b5wwz8|fao1\_lotja : 932.0)  
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 56 OS=Arabidopsis thaliana (sp|q9m667|rpp13\_arath : 310.0)  
 57 OS=Arabidopsis thaliana (sp|q9m667|rpp13\_arath : 310.0)  
 58 OS=Arabidopsis thaliana (sp|q9m667|rpp13\_arath : 310.0)  
 59 ; protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1\_arath : 804.0)  
 60 ; protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1\_arath : 804.0)

1 ; protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1\_arath : 804.0)

2 7190 OS=Arabidopsis thaliana (sp|q9t048|drl27\_arath : 177.0)

3 7190 OS=Arabidopsis thaliana (sp|q9t048|drl27\_arath : 177.0)

4 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 540.0)

5 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 542.0)

6 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 545.0)

7 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 525.0)

8 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 424.0)

9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 424.0)

10 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 443.0)

11 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 558.0)

12 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 333.0)

13 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 159.0)

14 3190 OS=Arabidopsis thaliana (sp|q9fhs6|fk119\_arath : 285.0)

15 eracea (sp|o04893|aglu\_spiol : 80.9)

16 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 306.0)

17 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 306.0)

18 OS=Solanum bulbocastanum (sp|q7xbq9|rga2\_solbu : 325.0)

19 OS=Solanum bulbocastanum (sp|q7xbq9|rga2\_solbu : 325.0)

20 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 332.0)

21 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 332.0)

22 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 367.0)

23 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 367.0)

24 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 389.0)

25 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3\_solbu : 389.0)

26 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 379.0)

27 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 379.0)

28 t-version=v2.1) &

29 not-version=v2.1) &

30 donor with incorporation or reduction of molecular oxygen(50.1.13 : 208.0) (original description: p

31 donor with incorporation or reduction of molecular oxygen(50.1.13 : 208.0) (original description: p

32 ated plant protein 36 OS=Arabidopsis thaliana (sp|q84j88|hip36\_arath : 102.0)

33 ated plant protein 36 OS=Arabidopsis thaliana (sp|q84j88|hip36\_arath : 102.0)

34 :Phvul.003G157600.1.v2.1 annot-version=v2.1) &

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6 on=v2.1) &

7 on=v2.1) &

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10 Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 171.0)

11 Arabidopsis thaliana (sp|q9fn03|uvr8\_arath : 171.0)

12 ing protein At1g12300, mitochondrial OS=Arabidopsis thaliana (sp|q0wkv3|ppr36\_arath : 382.0)

13 ing protein At1g12300, mitochondrial OS=Arabidopsis thaliana (sp|q0wkv3|ppr36\_arath : 382.0)

14 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 617.0)

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19 .1.v2.1 annot-version=v2.1) &

20 .5.v2.1 annot-version=v2.1) &

21 .5.v2.1 annot-version=v2.1) &

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23  
24 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 446.0)

25 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 446.0)

26 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 597.0)

27 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 597.0)

28 OS=Arabidopsis thaliana (sp|q9m667|rpp13\_arath : 306.0)

29 OS=Arabidopsis thaliana (sp|q9m667|rpp13\_arath : 306.0)

30 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 171.0)

31 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28\_arath : 171.0)

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51 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 528.0)

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55 helicase 1 homolog OS=Oryza sativa subsp. japonica (sp|a0a0p0v4r0|rtel1\_orysj : 203.0)

56 helicase 1 homolog OS=Oryza sativa subsp. japonica (sp|a0a0p0v4r0|rtel1\_orysj : 203.0)

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59 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 540.0)

60 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 540.0)

61 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 559.0)

1 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 559.0)  
2 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 489.0)  
3 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 489.0)  
4 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 333.0)  
5 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 333.0)  
6 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 159.0)  
7 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 159.0)  
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9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 203.0)  
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11 description: pacid=37163915 transcript=Phvul.L004500.1 locus=Phvul.L004500 ID=Phvul.L004500.1.v2  
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13 description: pacid=37163915 transcript=Phvul.L004500.1 locus=Phvul.L004500 ID=Phvul.L004500.1.v2  
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56 00.3.v2.1 annot-version=v2.1) &  
57 00.3.v2.1 annot-version=v2.1) &  
58 ing protein At2g03380, mitochondrial OS=Arabidopsis thaliana (sp|q9zq74|pp146\_arath : 626.0)  
59 &  
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3 t-containing protein At1g03510 OS=Arabidopsis thaliana (sp|q9lr72|ppr7\_arath : 388.0)  
4 t-containing protein At1g03510 OS=Arabidopsis thaliana (sp|q9lr72|ppr7\_arath : 388.0)  
5  
6 IP98A OS=Arabidopsis thaliana (sp|q8ry25|nu98a\_arath : 109.0)  
7 IP98A OS=Arabidopsis thaliana (sp|q8ry25|nu98a\_arath : 109.0)  
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10 homolog OS=Arabidopsis thaliana (sp|q9fnn2|wdr26\_arath : 697.0)  
11 homolog OS=Arabidopsis thaliana (sp|q9fnn2|wdr26\_arath : 697.0)  
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18 ing protein At3g09060 OS=Arabidopsis thaliana (sp|q9ss81|pp221\_arath : 736.0)  
19 ing protein At3g09060 OS=Arabidopsis thaliana (sp|q9ss81|pp221\_arath : 736.0)  
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23 :0|ops\_arath : 167.0)  
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37 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 541.0)  
38 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 565.0)  
39 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 479.0)  
40 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 483.0)  
41 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1\_arath : 519.0)  
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06G180900 ID=Phvul.006G180900.1.v2.1 annot-version=v2.1) &  
06G180900 ID=Phvul.006G180900.1.v2.1 annot-version=v2.1) &  
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acid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G076900 ID=Phvul.003G076900.1:  
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v2.1 annot-version=v2.1) &  
v2.1 annot-version=v2.1) &

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4	ccgaccuuagcu	Phvul.001G025900.1	3	-1	1	21
5	ccgaccuuagcu	Phvul.002G321900.1	3	-1	1	21
6	ccgaccuuagcu	Phvul.005G110300.3	3	-1	1	21
7	ccgaccuuagcu	Phvul.005G110300.2	3	-1	1	21
8	ccgaccuuagcu	Phvul.005G110300.1	3	-1	1	21
9	ccgaccuuagcu	Phvul.009G128800.1	3	-1	1	21
10	ccgaccuuagcu	Phvul.002G220500.1	3.5	-1	1	21
11	ccgaccuuagcu	Phvul.006G047700.1	3.5	-1	1	21
12	ccgaccuuagcu	Phvul.006G059900.1	3.5	-1	1	21
13	ccgaccuuagcu	Phvul.002G133400.1	4	-1	1	21
14	ccgaccuuagcu	Phvul.002G302600.1	4	-1	1	21
15	ccgaccuuagcu	Phvul.003G263400.1	4	-1	1	21
16	ccgaccuuagcu	Phvul.005G100500.1	4	-1	1	21
17	ccgaccuuagcu	Phvul.006G017100.1	4	-1	1	21
18	ccgaccuuagcu	Phvul.006G199400.1	4	-1	1	21
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20	ccgaccuuagcu	Phvul.001G119000.1	4.5	-1	1	21
21	ccgaccuuagcu	Phvul.001G259300.1	4.5	-1	1	21
22	ccgaccuuagcu	Phvul.002G003000.1	4.5	-1	1	21
23	ccgaccuuagcu	Phvul.002G278800.1	4.5	-1	1	21
24	ccgaccuuagcu	Phvul.003G138382.1	4.5	-1	1	21
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27	ccgaccuuagcu	Phvul.006G015900.1	4.5	-1	1	21
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29	ccgaccuuagcu	Phvul.006G086100.1	4.5	-1	1	21
30	ccgaccuuagcu	Phvul.006G117700.1	4.5	-1	1	21
31	ccgaccuuagcu	Phvul.006G125600.1	4.5	-1	1	21
32	ccgaccuuagcu	Phvul.006G142200.1	4.5	-1	1	21
33	ccgaccuuagcu	Phvul.007G042700.1	4.5	-1	1	21
34	ccgaccuuagcu	Phvul.011G012400.1	4.5	-1	1	21
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36	ccgaccuuagcu	Phvul.001G016500.2	5	-1	1	21
37	ccgaccuuagcu	Phvul.001G016500.1	5	-1	1	21
38	ccgaccuuagcu	Phvul.001G023100.1	5	-1	1	21
39	ccgaccuuagcu	Phvul.002G208300.1	5	-1	1	21
40	ccgaccuuagcu	Phvul.002G267600.2	5	-1	1	21
41	ccgaccuuagcu	Phvul.002G267600.1	5	-1	1	21
42	ccgaccuuagcu	Phvul.003G011400.1	5	-1	1	21
43	ccgaccuuagcu	Phvul.003G031500.1	5	-1	1	21
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45	ccgaccuuagcu	Phvul.004G041500.2	5	-1	1	21
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13					
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16	ccgaccuuagcu Phvul.008G191200.2	5	-1	1	21
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19	ccgaccuuagcu Phvul.008G240000.1	5	-1	1	21
20	ccgaccuuagcu Phvul.008G240300.1	5	-1	1	21
21					
22	ccgaccuuagcu Phvul.008G240500.1	5	-1	1	21
23	ccgaccuuagcu Phvul.009G183600.4	5	-1	1	21
24	ccgaccuuagcu Phvul.009G183600.1	5	-1	1	21
25					
26	ccgaccuuagcu Phvul.009G183600.3	5	-1	1	21
27	ccgaccuuagcu Phvul.009G183600.2	5	-1	1	21
28	ccgaccuuagcu Phvul.009G194700.1	5	-1	1	21
29					
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32	ccgaccuuagcu Phvul.010G112500.1	5	-1	1	21
33					
34	ccgaccuuagcu Phvul.011G077600.1	5	-1	1	21
35	ccgaccuuagcu Phvul.011G158600.1	5	-1	1	21
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3	1676	1696 CCGACCUUAC .....	AGUUAACUC/Cleavage pacid=371543
4	1787	1807 CCGACCUUAC .....	AGUUAACUC/Cleavage pacid=371543
5	2606	2626 CCGACCUUAC:: .....	CAGCAGCUG/Translation pacid=371531
6	2602	2622 CCGACCUUAC .....	AACUGAUUG/Translation pacid=371527
7			
8	530	550 CCGACCUUAC.....	CACUAAUUG/Cleavage pacid=371742
9			
10	1265	1285 CCGACCUUAC.....	CAUUGAUGG/Cleavage pacid=371716
11	1827	1847 CCGACCUUAC .....	AGGGAAUUG.Cleavage pacid=371676
12	2286	2306 CCGACCUUAC:: .....	CAGCUGCUG/Translation pacid=371612
13			
14	2271	2291 CCGACCUUAC:: .....	CAGCUGCUG/Translation pacid=371612
15	517	537 CCGACCUUAC.....	UACCAAUUG/Cleavage pacid=371609
16	1062	1082 CCGACCUUAC .....	GGGAGAUUG.Cleavage pacid=371596
17			
18	1156	1176 CCGACCUUAC .....	GGGAGAUUG.Cleavage pacid=371596
19	238	258 CCGACCUUAC .....	AAUCAAGUG(Cleavage pacid=371605
20	517	537 CCGACCUUAC .....	GAUCAAGUG(Cleavage pacid=371608
21			
22	685	705 CCGACCUUAC .....	GAUCAAGUG(Cleavage pacid=371577
23	75	95 CCGACCUUAC.....	UAUUUACUG.Cleavage pacid=371493
24	75	95 CCGACCUUAC.....	UAUUUACUG.Cleavage pacid=371493
25			
26	75	95 CCGACCUUAC.....	UAUUUACUG.Cleavage pacid=371493
27	75	95 CCGACCUUAC.....	UAUUUACUG.Cleavage pacid=371493
28	1382	1402 CCGACCUUAC.....	UACUAAUCU/Cleavage pacid=371491
29	1526	1546 CCGACCUUAC.....	UACUAAUCU/Cleavage pacid=371491
30			
31	600	620 CCGACCUUAC .....	GAUCAAUGG(Cleavage pacid=371437
32	64	85 CCGACCUUAC.....	UGCCAAGCU/Cleavage pacid=371438
33			
34	2178	2198 CCGACCUUAC:: .....	CAGUAACAAA Cleavage pacid=371546
35	702	722 CCGACCUUAC.....	CACCACUAGA Translation pacid=371558
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	Multiplicity	Target_Acc.	ID	locusName	Pfam
1					
2					
3	1	Phvul.005G179400.1	Phvul.005G179400	Phvul.005G179400	PF01257
4	1	Phvul.001G025900.1	Phvul.001G025900	Phvul.001G025900	PF04788
5	1	Phvul.002G321900.1	Phvul.002G321900	Phvul.002G321900	PF01920
6	1	Phvul.005G110300.3	Phvul.005G110300	Phvul.005G110300	PF08276,PF00
7	1	Phvul.005G110300.2	Phvul.005G110300	Phvul.005G110300	PF08276,PF00
8	1	Phvul.005G110300.1	Phvul.005G110300	Phvul.005G110300	PF08276,PF00
9	1	Phvul.009G128800.1	Phvul.009G128800	Phvul.009G128800	PF01920
10	1	Phvul.002G220500.1	Phvul.002G220500	Phvul.002G220500	PF08276,PF00
11	1	Phvul.006G047700.1	Phvul.006G047700	Phvul.006G047700	PF14432,PF13
12	1	Phvul.006G059900.1	Phvul.006G059900	Phvul.006G059900	PF14432,PF01
13	1	Phvul.002G133400.1	Phvul.002G133400	Phvul.002G133400	PF13855,PF00
14	1	Phvul.002G302600.1	Phvul.002G302600	Phvul.002G302600	PF08263,PF13
15	1	Phvul.003G263400.1	Phvul.003G263400	Phvul.003G263400	PF00314
16	1	Phvul.005G100500.1	Phvul.005G100500	Phvul.005G100500	PF00226,PF01
17	1	Phvul.006G017100.1	Phvul.006G017100	Phvul.006G017100	PF01477,PF00
18	1	Phvul.006G199400.1	Phvul.006G199400	Phvul.006G199400	PF00439,PF17
19	1	Phvul.008G070100.1	Phvul.008G070100	Phvul.008G070100	PF08449
20	1	Phvul.001G119000.1	Phvul.001G119000	Phvul.001G119000	PF07690
21	1	Phvul.001G259300.1	Phvul.001G259300	Phvul.001G259300	PF08418,PF04
22	1	Phvul.002G003000.1	Phvul.002G003000	Phvul.002G003000	PF00169,PF12
23	1	Phvul.002G278800.1	Phvul.002G278800	Phvul.002G278800	0
24	1	Phvul.003G138382.1	Phvul.003G138382	Phvul.003G138382	PF02309
25	1	Phvul.003G155500.1	Phvul.003G155500	Phvul.003G155500	PF02881,PF00
26	1	Phvul.003G185100.1	Phvul.003G185100	Phvul.003G185100	PF12171,PF00
27	1	Phvul.006G015900.1	Phvul.006G015900	Phvul.006G015900	PF00646
28	1	Phvul.006G015900.2	Phvul.006G015900	Phvul.006G015900	PF00646
29	1	Phvul.006G086100.1	Phvul.006G086100	Phvul.006G086100	PF13193,PF00
30	1	Phvul.006G117700.1	Phvul.006G117700	Phvul.006G117700	PF00583
31	1	Phvul.006G125600.1	Phvul.006G125600	Phvul.006G125600	PF08031,PF01
32	1	Phvul.006G142200.1	Phvul.006G142200	Phvul.006G142200	PF04526
33	1	Phvul.007G042700.1	Phvul.007G042700	Phvul.007G042700	PF12854,PF13
34	1	Phvul.011G012400.1	Phvul.011G012400	Phvul.011G012400	PF14226
35	1	Phvul.011G024700.1	Phvul.011G024700	Phvul.011G024700	PF02365
36	1	Phvul.001G016500.2	Phvul.001G016500	Phvul.001G016500	PF07974,PF01
37	1	Phvul.001G016500.1	Phvul.001G016500	Phvul.001G016500	PF07974,PF01
38	1	Phvul.001G023100.1	Phvul.001G023100	Phvul.001G023100	PF13920
39	1	Phvul.002G208300.1	Phvul.002G208300	Phvul.002G208300	PF01535,PF13
40	1	Phvul.002G267600.2	Phvul.002G267600	Phvul.002G267600	PF00443
41	1	Phvul.002G267600.1	Phvul.002G267600	Phvul.002G267600	PF00443
42	1	Phvul.003G011400.1	Phvul.003G011400	Phvul.003G011400	PF00787,PF08
43	1	Phvul.003G031500.1	Phvul.003G031500	Phvul.003G031500	PF10497,PF02
44	1	Phvul.003G216800.1	Phvul.003G216800	Phvul.003G216800	PF08449
45	1	Phvul.004G041500.2	Phvul.004G041500	Phvul.004G041500	PF02005
46	1	Phvul.004G041500.1	Phvul.004G041500	Phvul.004G041500	PF02005
47	1	Phvul.004G106700.1	Phvul.004G106700	Phvul.004G106700	PF11947
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2	1	Phvul.004G170800.1	Phvul.004G170800	Phvul.004G170800	PF00390,PF03
3	1	Phvul.005G003300.2	Phvul.005G003300	Phvul.005G003300	PF07714,PF00
4	1	Phvul.005G003300.1	Phvul.005G003300	Phvul.005G003300	PF07714,PF00
5					
6	1	Phvul.005G084000.1	Phvul.005G084000	Phvul.005G084000	0
7	1	Phvul.005G160700.1	Phvul.005G160700	Phvul.005G160700	PF00069
8	1	Phvul.006G004580.1	Phvul.006G004580	Phvul.006G004580	PF08263
9					
10	1	Phvul.006G135500.1	Phvul.006G135500	Phvul.006G135500	PF05691
11	1	Phvul.007G080800.2	Phvul.007G080800	Phvul.007G080800	PF03033
12	1	Phvul.008G080100.2	Phvul.008G080100	Phvul.008G080100	PF00651,PF03
13	1	Phvul.008G080100.1	Phvul.008G080100	Phvul.008G080100	PF00651,PF03
14	1	Phvul.008G131301.1	Phvul.008G131301	Phvul.008G131301	PF00498
15	1	Phvul.008G191200.2	Phvul.008G191200	Phvul.008G191200	0
16	1	Phvul.008G191200.1	Phvul.008G191200	Phvul.008G191200	0
17					
18	1	Phvul.008G240000.1	Phvul.008G240000	Phvul.008G240000	PF03080
19	1	Phvul.008G240300.1	Phvul.008G240300	Phvul.008G240300	PF14365,PF03
20	1	Phvul.008G240500.1	Phvul.008G240500	Phvul.008G240500	PF14365,PF03
21	1	Phvul.009G183600.4	Phvul.009G183600	Phvul.009G183600	PF00010
22	1	Phvul.009G183600.1	Phvul.009G183600	Phvul.009G183600	PF00010
23	1	Phvul.009G183600.3	Phvul.009G183600	Phvul.009G183600	PF00010
24	1	Phvul.009G183600.2	Phvul.009G183600	Phvul.009G183600	PF00010
25	1	Phvul.009G194700.1	Phvul.009G194700	Phvul.009G194700	PF02881,PF00
26	1	Phvul.009G194700.2	Phvul.009G194700	Phvul.009G194700	PF02881,PF00
27	1	Phvul.010G069638.1	Phvul.010G069638	Phvul.010G069638	PF00225
28	1	Phvul.010G112500.1	Phvul.010G112500	Phvul.010G112500	PF10604
29	1	Phvul.011G077600.1	Phvul.011G077600	Phvul.011G077600	PF02837,PF02
30	1	Phvul.011G158600.1	Phvul.011G158600	Phvul.011G158600	PF02485
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	Panther	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol
1						
2						
3	PTHR10371,P <sup>-</sup>	KOG3196	1.6.99.3,1.6.5	K03943		0 AT4G02580.1 0
4	PTHR31300,P <sup>-</sup>		0	0	0	0 AT3G19540.1 0
5						
6	PTHR21431,P <sup>-</sup>	KOG3478		0 K04798	GO:0051082,C	AT1G29990.1 PFD6
7	PTHR27002,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0006468,C	AT2G19130.1 0
8	PTHR27002,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0006468,C	AT2G19130.1 0
9						
10	PTHR27002,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0006468,C	AT2G19130.1 0
11	PTHR21431,P <sup>-</sup>		0	0 K04798	GO:0051082,C	AT1G29990.1 PFD6
12	PTHR27002,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0048544,C	AT4G21390.1 B120
13						
14	PTHR24015,P <sup>-</sup>		0	0	0	0 AT4G02750.1 0
15	PTHR24015,P <sup>-</sup>		0	0	0	0 AT4G02750.1 0
16	PTHR23155,P <sup>-</sup>	KOG4658		0 K13457	GO:0005515,C	AT3G07040.1 RPM1,RPS3
17	PTHR27008,P <sup>-</sup>	KOG1187	2.7.11.1		0 GO:0005515,C	AT5G35390.1 0
18	PTHR31048,P <sup>-</sup>		0	0	0	0 AT4G38660.1 0
19						
20	PTHR24078,P <sup>-</sup>	KOG0714		0 K09510		0 AT2G20560.1 0
21						
22	PTHR11771,P <sup>-</sup>		0 1.13.11.12	K00454	GO:0005515,C	AT3G45140.1 ATLOX2,LOX2
23	PTHR22880,P <sup>-</sup>	KOG1474		0	0 GO:0005515	AT5G65630.1 GTE7
24	PTHR10778,P <sup>-</sup>	KOG1582		0 K15277	GO:0055085	AT4G23010.3 ATUTR2,UTR2
25						
26	PTHR11654,P <sup>-</sup>		0	0 K14638	GO:0055085,C	AT1G68570.1 0
27	PTHR23061,P <sup>-</sup>	KOG1625	2.7.7.7	K02321	GO:0006260,C	AT1G67630.1 POLA2
28	PTHR16166,P <sup>-</sup>	KOG1809		0	0	0 AT4G17140.3 0
29						
30		0	0	0	0	0 0 0
31	PTHR31734,P <sup>-</sup>		0	0 K14484	GO:0006355,C	AT1G04240.1 IAA3,SHY2
32	<b>PTHR11564,P<sup>-</sup></b>		<b>0</b>	<b>0 K13431</b>	<b>GO:0006614,C</b>	<b>AT4G30600.1 0</b>
33	PTHR24078,P <sup>-</sup>		0	0 K09506		0 AT1G74250.1 0
34						
35	PTHR31482,P <sup>-</sup>		0	0	0 GO:0005515	AT2G32560.1 0
36	PTHR31482,P <sup>-</sup>		0	0	0 GO:0005515	AT2G32560.1 0
37						
38	PTHR24095,P <sup>-</sup>		0	0	0 GO:0008152,C	AT1G65890.1 AAE12
39	PTHR23091,P <sup>-</sup>		0 2.3.1.88		0 GO:0008080	AT2G23060.1 0
40	PTHR32448,P <sup>-</sup>	KOG1231	1.3.3.8		0 GO:0055114,C	AT4G20840.1 0
41						
42	PTHR23130,P <sup>-</sup>		0	0	0	0 AT5G47530.1 0
43	PTHR24015,P <sup>-</sup>		0	0	0	0 AT5G02860.1 0
44	PTHR10209,P <sup>-</sup>		0	0	0	0 AT4G13400.1 0
45	PTHR31989,P <sup>-</sup>		0	0	0 GO:0006355,C	AT2G17040.1 anac036,NAC
46						
47	PTHR10942,P <sup>-</sup>	KOG2556	3.4.24.36		0 GO:0016020,C	AT5G42620.2 0
48	PTHR10942,P <sup>-</sup>	KOG2556	3.4.24.36		0 GO:0016020,C	AT5G42620.2 0
49	PTHR10044,P <sup>-</sup>	KOG1100		0 K19042		0 AT1G45976.1 SBP1
50						
51	PTHR24015,P <sup>-</sup>		0	0	0	0 AT5G18390.1 0
52	PTHR24006,P <sup>-</sup>		0 3.4.19.12		0 GO:0036459,C	AT4G39370.1 UBP27
53	PTHR24006,P <sup>-</sup>		0 3.4.19.12		0 GO:0036459,C	AT4G39370.1 UBP27
54						
55	PTHR22999,P <sup>-</sup>		0	0 K17925	GO:0035091	AT2G15900.1 0
56	PTHR12549,P <sup>-</sup>		0	0 K15601		0 AT1G62310.1 0
57	PTHR11132,P <sup>-</sup>	KOG1441		0	0 GO:0055085	AT1G12500.1 0
58						
59	PTHR10631		0 2.1.1.216	K00555	GO:0008033,C	AT5G15810.1 0
60	PTHR10631		0 2.1.1.216	K00555	GO:0008033,C	AT5G15810.1 0
	PTHR34575,P <sup>-</sup>		0	0	0	0 AT5G52780.1 0





1	arabi-defline	ID	Annot_defline
2	NADH-ubiquinone oxidoreductase 24 kDa subunit, putative	Phvul.005G17K03943	- NAD
3	Protein of unknown function (DUF620)	Phvul.001G02PTHR31300	:SF
4	prefoldin 6	Phvul.002G32K04798	- pref
5	S-locus lectin protein kinase family protein	Phvul.005G11PF00069	//PFC
6	S-locus lectin protein kinase family protein	Phvul.005G11PF00069	//PFC
7	S-locus lectin protein kinase family protein	Phvul.005G11PF00069	//PFC
8	prefoldin 6	Phvul.009G12K04798	- pref
9	S-locus lectin protein kinase family protein	Phvul.002G22PF00954	//PFC
10	Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.006G04PF01535	//PF1
11	Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.006G05PF01535	//PF1
12	NB-ARC domain-containing disease resistance protein	Phvul.002G13PTHR23155	//I
13	Leucine-rich repeat protein kinase family protein	Phvul.002G30PTHR27008	:SF
14	Pathogenesis-related thaumatin superfamily protein	Phvul.003G26PTHR31048	:SF
15	DNAJ heat shock family protein	Phvul.005G10PTHR24078	:SF
16	lipoxygenase 2	Phvul.006G01PTHR11771	:SF
17	global transcription factor group E7	Phvul.006G19PTHR22880	//I
18	UDP-galactose transporter 2	Phvul.008G07K15277	- solut
19	Major facilitator superfamily protein	Phvul.001G11PTHR11654	//I
20	DNA polymerase alpha 2	Phvul.001G25K02321	- DNA
21	pleckstrin homology (PH) domain-containing protein	Phvul.002G00PTHR16166	:SF
22		0	0
23	AUX/IAA transcriptional regulator family protein	Phvul.003G13PTHR31734	:SF
24	signal recognition particle receptor alpha subunit family prot	Phvul.003G15K13431	- signa
25	DNAJ heat shock N-terminal domain-containing protein	Phvul.003G18K09506	- DnaJ
26	F-box family protein	Phvul.006G01PF00646	- F-b
27	F-box family protein	Phvul.006G01PF00646	- F-b
28	acyl activating enzyme 12	Phvul.006G08PF00501	//PF1
29	Acyl-CoA N-acyltransferases (NAT) superfamily protein	Phvul.006G11PTHR23091	:SF
30	FAD-binding Berberine family protein	Phvul.006G12PTHR32448	:SF
31	Auxin-responsive family protein	Phvul.006G14PTHR23130	:SF
32	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G04PF12854	//PF1
33	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.011G01PTHR10209	:SF
34	NAC domain containing protein 36	Phvul.011G02PTHR31989	:SF
35	metalloendopeptidases;zinc ion binding	Phvul.001G013.4.24.36	- Lei
36	metalloendopeptidases;zinc ion binding	Phvul.001G013.4.24.36	- Lei
37	S-ribonuclease binding protein 1	Phvul.001G02PTHR10044	:SF
38	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.002G20PF01535	//PF1
39	ubiquitin-specific protease 27	Phvul.002G26K11851	- ubiq
40	ubiquitin-specific protease 27	Phvul.002G26K11851	- ubiq
41	Phox-associated domain;Phox-like;Sorting nexin, C-terminal	Phvul.003G01K17925	- sorti
42	transcription factor jumonji (jmjC) domain-containing proteir	Phvul.003G03K15601	- lysin
43	Nucleotide-sugar transporter family protein	Phvul.003G21PTHR11132	//I
44	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216	- tRI
45	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216	- tRI
46	Protein of unknown function (DUF3464)	Phvul.004G10PF11947	- Pro

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2	NADP-malic enzyme 4	Phvul.004G17PTHR23406:SI	
3	KCBP-interacting protein kinase	Phvul.005G00PTHR24351//I	
4	KCBP-interacting protein kinase	Phvul.005G00PTHR24351//I	
5	COP1-interacting protein 7	Phvul.005G08PTHR31008:SI	
6	Protein kinase protein with adenine nucleotide alpha hydrolyz	Phvul.005G16PTHR27001:SI	
7	receptor like protein 48	Phvul.006G00PF08263 - Leu	
8	seed imbibition 2	Phvul.006G13PF05691 - Raf	
9	UDP-Glycosyltransferase superfamily protein	Phvul.007G08PTHR11926:SI	
10	Phototropic-responsive NPH3 family protein	Phvul.008G08PF00651//PFC	
11	Phototropic-responsive NPH3 family protein	Phvul.008G08PF00651//PFC	
12	SMAD/FHA domain-containing protein	Phvul.008G13PF00498 - FHA	
13		0	0
14		0	0
15		0	0
16	Protein of Unknown Function (DUF239)	Phvul.008G24PF03080 - Dor	
17	Protein of Unknown Function (DUF239)	Phvul.008G24PF14365 - Dor	
18	Protein of Unknown Function (DUF239)	Phvul.008G24PF14365 - Dor	
19	BIG PETAL P	Phvul.009G18PTHR12565//I	
20	BIG PETAL P	Phvul.009G18PTHR12565//I	
21	BIG PETAL P	Phvul.009G18PTHR12565//I	
22	BIG PETAL P	Phvul.009G18PTHR12565//I	
23	signal recognition particle receptor alpha subunit family prot	Phvul.009G19K13431 - signa	
24	signal recognition particle receptor alpha subunit family prot	Phvul.009G19K13431 - signa	
25	P-loop containing nucleoside triphosphate hydrolases superf	Phvul.010G06PTHR24115:SI	
26	regulatory component of ABA receptor 1	Phvul.010G11PTHR31213:SI	
27	beta-galactosidase 8	Phvul.011G07PF01301//PFC	
28	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.011G15PTHR19297:SI	
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IDENTIFIER	NAME	DESCRIPTION
Phvul.005G17	Cellular respir component	NQO2 of NADH dehydrogenase electron input (module N)
Phvul.001G02	Multi-process	GTPase effector (BDR) (original description: pacid=37169232 transcript=
Phvul.002G32	Cytoskeleton component	PFD6 of Prefoldin co-chaperone complex (original description: pacid=37177113 transcript=
Phvul.005G11	Enzyme classif	G-type lectin S-receptor-like serine/threonine-protein kinase At2g1913
Phvul.005G11	Enzyme classif	G-type lectin S-receptor-like serine/threonine-protein kinase At2g1913
Phvul.005G11	Enzyme classif	G-type lectin S-receptor-like serine/threonine-protein kinase At2g1913
Phvul.009G12	Cytoskeleton component	PFD6 of Prefoldin co-chaperone complex (original description: pacid=37177113 transcript=
Phvul.002G22	Protein modif	protein kinase (SD-1) (original description: pacid=37175156 transcript=
Phvul.006G04	not assigned.	(original description: pacid=37172255 transcript=Phvul.006G047700.1
Phvul.006G05	not assigned.	(original description: pacid=37173205 transcript=Phvul.006G059900.1
Phvul.002G13	not assigned.	(original description: pacid=37177101 transcript=Phvul.002G133400.1
Phvul.002G30	Protein modif	protein kinase (LRR-III) (original description: pacid=37177113 transcript=
Phvul.003G26	not assigned.	(original description: pacid=37147040 transcript=Phvul.003G263400.1
Phvul.005G10	not assigned.	(original description: pacid=37153534 transcript=Phvul.005G100500.1
Phvul.006G01	Phytohormon	13-lipoxygenase (original description: pacid=37174172 transcript=Phvul.006G017700.1
Phvul.006G19	RNA biosynthetranscriptional	co-activator (BET/GTE) (original description: pacid=37177113 transcript=
Phvul.008G07	Solute transp	nucleotide sugar transporter (UTR1 5) (original description: pacid=37177113 transcript=
Phvul.001G11	Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37170064 transcript=
Phvul.001G25	Cell cycle orga	replication fork tethering component POLA2 of DNA polymerase alpha
Phvul.002G00	not assigned.	r no hits & (original description: pacid=37175146 transcript=Phvul.002G007700.1
Phvul.002G27	not assigned.	r no hits & (original description: pacid=37178371 transcript=Phvul.002G277700.1
Phvul.003G13	not assigned.	(original description: pacid=37147466 transcript=Phvul.003G138382.1
Phvul.003G15	Protein transla	component SR-alpha of SRP (signal recognition particle) receptor comp
Phvul.003G18	Protein home	co-chaperone (Jjj1) (original description: pacid=37145570 transcript=Phvul.003G187700.1
Phvul.006G01	Protein home	component FBX of SCF E3 ubiquitin ligase complex (original description: pacid=37177113 transcript=
Phvul.006G01	Protein home	component FBX of SCF E3 ubiquitin ligase complex (original description: pacid=37177113 transcript=
Phvul.006G08	not assigned.	(original description: pacid=37171712 transcript=Phvul.006G086100.1
Phvul.006G11	not assigned.	(original description: pacid=37173640 transcript=Phvul.006G117700.1
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Phvul.006G14	not assigned.	(original description: pacid=37172040 transcript=Phvul.006G142200.1
Phvul.007G04	RNA processir	plastidial mRNA processing factor (PPR10) (original description: pacid=37177113 transcript=
Phvul.011G01	not assigned.	r no hits & (original description: pacid=37154680 transcript=Phvul.011G017700.1
Phvul.011G02	RNA biosynthetranscription	factor (NAC) (original description: pacid=37156658 transcript=Phvul.011G027700.1
Phvul.001G01	Protein home	Leishmanolysin-type protease (original description: pacid=37168734 transcript=
Phvul.001G01	Protein home	Leishmanolysin-type protease (original description: pacid=37168734 transcript=
Phvul.001G02	not assigned.	(original description: pacid=37170145 transcript=Phvul.001G023100.1
Phvul.002G20	not assigned.	(original description: pacid=37178018 transcript=Phvul.002G208300.1
Phvul.002G26	Protein home	deubiquitinase (UBP27) (original description: pacid=37177124 transcript=
Phvul.002G26	Protein home	deubiquitinase (UBP27) (original description: pacid=37177124 transcript=
Phvul.003G01	not assigned.	r no hits & (original description: pacid=37148267 transcript=Phvul.003G017700.1
Phvul.003G03	RNA biosynthetranscription	factor (JUMONJI) (original description: pacid=37147655 transcript=Phvul.003G037700.1
Phvul.003G21	not assigned.	(original description: pacid=37145919 transcript=Phvul.003G216800.1
Phvul.004G04	RNA processir	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37177113 transcript=
Phvul.004G04	RNA processir	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37177113 transcript=
Phvul.004G10	Photosynthesi	PAM68 protein involved in PS-II assembly (original description: pacid=37177113 transcript=

1 Phvul.004G17Lipid metabolic cytosolic NADP-dependent malic enzyme (original description: pacid=3  
2 Phvul.005G00Protein modif protein kinase (AGC-VIII) (original description: pacid=37154375 transcr  
3 Phvul.005G00Protein modif protein kinase (AGC-VIII) (original description: pacid=37154375 transcr  
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6 Phvul.006G00not assigned.ε (original description: pacid=37174231 transcript=Phvul.006G004580.1  
7 Phvul.006G13not assigned.ε (original description: pacid=37171646 transcript=Phvul.006G135500.1  
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12 Phvul.008G19not assigned.r no hits & (original description: pacid=37159620 transcript=Phvul.008G  
13 Phvul.008G19not assigned.r no hits & (original description: pacid=37159620 transcript=Phvul.008G  
14 Phvul.008G24not assigned.r no hits & (original description: pacid=37160578 transcript=Phvul.008G  
15 Phvul.008G24not assigned.r no hits & (original description: pacid=37160890 transcript=Phvul.008G  
16 Phvul.008G24not assigned.r no hits & (original description: pacid=37157759 transcript=Phvul.008G  
17 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr  
18 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr  
19 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr  
20 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr  
21 Phvul.009G19Protein transk component SR-alpha of SRP (signal recognition particle) receptor comp  
22 Phvul.009G19Protein transk component SR-alpha of SRP (signal recognition particle) receptor comp  
23 Phvul.010G06Cytoskeleton motor protein (Kinesin-10) (original description: pacid=37143788 trans  
24 Phvul.010G11Phytohormon receptor component PYL/RCAR of cytoplasm-localized abscisic acid rec  
25 Phvul.011G07Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37154665 trans  
26 Phvul.011G15not assigned.ε (original description: pacid=37155876 transcript=Phvul.011G158600.1  
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(original description: pacid=37153994 transcript=Phvul.005G179400.1 locus=Phvul.005G179400 ID=Phvul.005G179400.1.v2.1 annot-version=v2.1)  
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 ion: pacid=37176929 transcript=Phvul.002G321900.1 locus=Phvul.002G321900 ID=Phvul.002G321900.1.v2.1 annot-version=v2.1) & Enzyme classification.EC\_2 transfer  
 30 OS=Arabidopsis thaliana (sp|o64477|y2913\_arath : 511.0) & Enzyme classification.EC\_2 transfer  
 30 OS=Arabidopsis thaliana (sp|o64477|y2913\_arath : 511.0) & Enzyme classification.EC\_2 transfer  
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 =Phvul.002G220500.1 locus=Phvul.002G220500 ID=Phvul.002G220500.1.v2.1 annot-version=v2.1) &  
 L locus=Phvul.006G047700 ID=Phvul.006G047700.1.v2.1 annot-version=v2.1) & Pentatricopeptide r  
 L locus=Phvul.006G059900 ID=Phvul.006G059900.1.v2.1 annot-version=v2.1) & Pentatricopeptide r  
 L locus=Phvul.002G133400 ID=Phvul.002G133400.1.v2.1 annot-version=v2.1) & Disease resistance p  
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 L locus=Phvul.003G263400 ID=Phvul.003G263400.1.v2.1 annot-version=v2.1) & Thaumatin-like prot  
 L locus=Phvul.005G100500 ID=Phvul.005G100500.1.v2.1 annot-version=v2.1) & DnaJ protein ERDJ3  
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 bbe21\_arath : 580.0) & Enzyme classification.EC\_1 oxidoreductases.EC\_1.1 oxidoreductase acting c  
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 :37165270 transcript=Phvul.007G042700.1 locus=Phvul.007G042700 ID=Phvul.007G042700.1.v2.1 a  
 5012400.1 locus=Phvul.011G012400 ID=Phvul.011G012400.1.v2.1 annot-version=v2.1)  
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 L locus=Phvul.001G023100 ID=Phvul.001G023100.1.v2.1 annot-version=v2.1) & Probable BOI-relate  
 L locus=Phvul.002G208300 ID=Phvul.002G208300.1.v2.1 annot-version=v2.1) & Pentatricopeptide r  
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 L locus=Phvul.003G216800 ID=Phvul.003G216800.1.v2.1 annot-version=v2.1) & Probable sugar pho  
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2 37163561 transcript=Phvul.004G170800.1 locus=Phvul.004G170800 ID=Phvul.004G170800.1.v2.1 ai  
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7 L locus=Phvul.006G004580 ID=Phvul.006G004580.1.v2.1 annot-version=v2.1) & Receptor-like protei  
8 L locus=Phvul.006G135500 ID=Phvul.006G135500.1.v2.1 annot-version=v2.1) & Probable galactinol-  
9 167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 ann  
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13 191200.2 locus=Phvul.008G191200 ID=Phvul.008G191200.2.v2.1 annot-version=v2.1)  
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22 olex (original description: pacid=37149160 transcript=Phvul.009G194700.2 locus=Phvul.009G19470  
23 olex (original description: pacid=37149160 transcript=Phvul.009G194700.2 locus=Phvul.009G19470  
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25 eceptor complex (original description: pacid=37143807 transcript=Phvul.010G112500.1 locus=Phvul.(  
26 ript=Phvul.011G077600.1 locus=Phvul.011G077600 ID=Phvul.011G077600.1.v2.1 annot-version=v  
27 L locus=Phvul.011G158600 ID=Phvul.011G158600.1.v2.1 annot-version=v2.1) & Beta-glucuronosyltr  
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 3 ID=Phvul.005G179400.1.v2.1 annot-version=v2.1) &  
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 6 900.1.v2.1 annot-version=v2.1) &  
 7 ases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript  
 8 ases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript  
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 13 repeat-containing protein At4g02750 OS=Arabidopsis thaliana (sp|q9sy02|pp301\_arath : 429.0)  
 14 repeat-containing protein At4g02750 OS=Arabidopsis thaliana (sp|q9sy02|pp301\_arath : 469.0)  
 15 protein RPM1 OS=Arabidopsis thaliana (sp|q39214|rpm1\_arath : 432.0)  
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 19 B OS=Arabidopsis thaliana (sp|q9lzk5|dnj19\_arath : 137.0)  
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 23 ot-version=v2.1) &  
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 25 in=v2.1) &  
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 27 259300 ID=Phvul.001G259300.1.v2.1 annot-version=v2.1) &  
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 31 ein 22B OS=Vigna radiata var. radiata (sp|p32294|ax22b\_vigrr : 291.0)  
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 35 J.2.v2.1 annot-version=v2.1) &  
 36 J.2.v2.1 annot-version=v2.1) &  
 37 ating enzyme 12, peroxisomal OS=Arabidopsis thaliana (sp|q9ss00|aae12\_arath : 670.0)  
 38 ansferase HLS1-like OS=Arabidopsis thaliana (sp|o64815|hls1\_arath : 254.0)  
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 41 annot-version=v2.1) &  
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 45 2.1) &  
 46 in=v2.1) &  
 47 in=v2.1) &  
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 49 d E3 ubiquitin-protein ligase 3 OS=Arabidopsis thaliana (sp|q9ldd1|brg3\_arath : 117.0)  
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 51 repeat-containing protein At5g18390, mitochondrial OS=Arabidopsis thaliana (sp|q94jx6|pp391\_ar  
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 56 on=v2.1) &  
 57 sphate/phosphate translocator At1g12500 OS=Arabidopsis thaliana (sp|q9ldh3|pt112\_arath : 462.0  
 58 . annot-version=v2.1) &  
 59 . annot-version=v2.1) &  
 60 innot-version=v2.1) &

1 nnot-version=v2.1) &  
2 .1) &  
3 .1) &  
4 protein 7 OS=Arabidopsis thaliana (sp|o80386|cip7\_arath : 505.0)  
5 n=v2.1) &  
6 in EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2\_sollc : 120.0)  
7 --sucrose galactosyltransferase 2 OS=Arabidopsis thaliana (sp|q94a08|rfs2\_arath : 732.0)  
8 not-version=v2.1) &  
9 containing protein At3g08570 OS=Arabidopsis thaliana (sp|q9c9z7|y3857\_arath : 661.0)  
10 containing protein At3g08570 OS=Arabidopsis thaliana (sp|q9c9z7|y3857\_arath : 661.0)  
11 ning protein FHA2 OS=Arabidopsis thaliana (sp|q9sfv2|fha2\_arath : 431.0)  
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26 n=v2.1) &  
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31 v2.1) &  
32 ransferase GlcAT14A OS=Arabidopsis thaliana (sp|q9fld7|gt14a\_arath : 462.0)  
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6G125600.1 locus=Phvul.006G125600 ID=Phvul.006G125600.1.v2.1 annot-version=v2.1) &  
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7 300.3.v2.1 annot-version=v2.1) &  
8 300.3.v2.1 annot-version=v2.1) &  
9 300.3.v2.1 annot-version=v2.1) &  
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Do not distribute

	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
1						
2						
3	gauccccggcaar	Phvul.004G110400.1	3	-1	1	20
4	gauccccggcaar	Phvul.005G120700.1	3	-1	1	20
5	gauccccggcaar	Phvul.005G120700.2	3	-1	1	20
6	gauccccggcaar	Phvul.006G001600.1	3	-1	1	20
7	gauccccggcaar	Phvul.007G023000.1	3.5	-1	1	20
8	gauccccggcaar	Phvul.008G271000.1	3.5	-1	1	20
9	gauccccggcaar	Phvul.008G271000.1	3.5	-1	1	20
10	gauccccggcaar	Phvul.008G271000.1	3.5	-1	1	20
11	gauccccggcaar	Phvul.001G240600.1	4	-1	1	20
12	gauccccggcaar	Phvul.003G220500.1	4	-1	1	20
13	gauccccggcaar	Phvul.003G237300.1	4	-1	1	20
14	gauccccggcaar	Phvul.003G237300.1	4	-1	1	20
15	gauccccggcaar	Phvul.003G285700.1	4	-1	1	20
16	gauccccggcaar	Phvul.004G086300.2	4	-1	1	20
17	gauccccggcaar	Phvul.004G086300.2	4	-1	1	20
18	gauccccggcaar	Phvul.004G086300.1	4	-1	1	20
19	gauccccggcaar	Phvul.006G068400.1	4	-1	1	20
20	gauccccggcaar	Phvul.006G130200.1	4	-1	1	20
21	gauccccggcaar	Phvul.006G130200.1	4	-1	1	20
22	gauccccggcaar	Phvul.007G268300.1	4	-1	1	20
23	gauccccggcaar	Phvul.008G036200.1	4	-1	1	20
24	gauccccggcaar	Phvul.008G290700.1	4	-1	1	20
25	gauccccggcaar	Phvul.008G290700.1	4	-1	1	20
26	gauccccggcaar	Phvul.009G144300.1	4	-1	1	20
27	gauccccggcaar	Phvul.001G028400.1	4.5	-1	1	20
28	gauccccggcaar	Phvul.001G071200.1	4.5	-1	1	20
29	gauccccggcaar	Phvul.001G071200.1	4.5	-1	1	20
30	gauccccggcaar	Phvul.001G146900.1	4.5	-1	1	20
31	gauccccggcaar	Phvul.001G147001.1	4.5	-1	1	20
32	gauccccggcaar	Phvul.001G147001.2	4.5	-1	1	20
33	gauccccggcaar	Phvul.001G147001.2	4.5	-1	1	20
34	gauccccggcaar	Phvul.002G006700.1	4.5	-1	1	20
35	gauccccggcaar	Phvul.002G059000.1	4.5	-1	1	20
36	gauccccggcaar	Phvul.002G092900.2	4.5	-1	1	20
37	gauccccggcaar	Phvul.002G092900.2	4.5	-1	1	20
38	gauccccggcaar	Phvul.002G092900.1	4.5	-1	1	20
39	gauccccggcaar	Phvul.002G274500.1	4.5	-1	1	20
40	gauccccggcaar	Phvul.002G274500.1	4.5	-1	1	20
41	gauccccggcaar	Phvul.002G315300.1	4.5	-1	1	20
42	gauccccggcaar	Phvul.003G076700.2	4.5	-1	1	20
43	gauccccggcaar	Phvul.003G076700.1	4.5	-1	1	20
44	gauccccggcaar	Phvul.003G076700.1	4.5	-1	1	20
45	gauccccggcaar	Phvul.003G099100.1	4.5	-1	1	20
46	gauccccggcaar	Phvul.003G099100.3	4.5	-1	1	20
47	gauccccggcaar	Phvul.003G099100.2	4.5	-1	1	20
48	gauccccggcaar	Phvul.003G099100.2	4.5	-1	1	20
49	gauccccggcaar	Phvul.004G037600.3	4.5	-1	1	20
50	gauccccggcaar	Phvul.004G037600.2	4.5	-1	1	20
51	gauccccggcaar	Phvul.004G049200.1	4.5	-1	1	20
52	gauccccggcaar	Phvul.004G110200.2	4.5	-1	1	20
53	gauccccggcaar	Phvul.004G171500.6	4.5	-1	1	20
54	gauccccggcaar	Phvul.004G171500.6	4.5	-1	1	20
55	gauccccggcaar	Phvul.004G171500.2	4.5	-1	1	20
56	gauccccggcaar	Phvul.004G171500.3	4.5	-1	1	20
57	gauccccggcaar	Phvul.004G171500.3	4.5	-1	1	20
58	gauccccggcaar	Phvul.004G171500.1	4.5	-1	1	20
59	gauccccggcaar	Phvul.004G171500.5	4.5	-1	1	20
60	gauccccggcaar	Phvul.004G171500.4	4.5	-1	1	20
	gauccccggcaar	Phvul.005G022300.1	4.5	-1	1	20



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2	gauccccggcaar	Phvul.005G159600.1	4.5	-1	1	20
3	gauccccggcaar	Phvul.006G049100.1	4.5	-1	1	20
4	gauccccggcaar	Phvul.006G068100.1	4.5	-1	1	20
5	gauccccggcaar	Phvul.006G087700.1	4.5	-1	1	20
6	gauccccggcaar	Phvul.006G087700.1	4.5	-1	1	20
7	gauccccggcaar	Phvul.007G208400.1	4.5	-1	1	20
8	gauccccggcaar	Phvul.008G042900.1	4.5	-1	1	20
9	gauccccggcaar	Phvul.008G124000.2	4.5	-1	1	20
10	gauccccggcaar	Phvul.008G124000.2	4.5	-1	1	20
11	gauccccggcaar	Phvul.008G124000.1	4.5	-1	1	20
12	gauccccggcaar	Phvul.008G233100.1	4.5	-1	1	20
13	gauccccggcaar	Phvul.008G233100.1	4.5	-1	1	20
14	gauccccggcaar	Phvul.009G157200.2	4.5	-1	1	20
15	gauccccggcaar	Phvul.009G157200.1	4.5	-1	1	20
16	gauccccggcaar	Phvul.010G024866.1	4.5	-1	1	20
17	gauccccggcaar	Phvul.010G024866.1	4.5	-1	1	20
18	gauccccggcaar	Phvul.010G082300.1	4.5	-1	1	20
19	gauccccggcaar	Phvul.010G119800.1	4.5	-1	1	20
20	gauccccggcaar	Phvul.011G029450.1	4.5	-1	1	20
21	gauccccggcaar	Phvul.011G029450.1	4.5	-1	1	20
22	gauccccggcaar	Phvul.001G025101.1	5	-1	1	20
23	gauccccggcaar	Phvul.001G183700.1	5	-1	1	20
24	gauccccggcaar	Phvul.001G209500.2	5	-1	1	20
25	gauccccggcaar	Phvul.001G209500.2	5	-1	1	20
26	gauccccggcaar	Phvul.001G209900.2	5	-1	1	20
27	gauccccggcaar	Phvul.001G250100.2	5	-1	1	20
28	gauccccggcaar	Phvul.001G250100.1	5	-1	1	20
29	gauccccggcaar	Phvul.001G250100.1	5	-1	1	20
30	gauccccggcaar	Phvul.002G063100.1	5	-1	1	20
31	gauccccggcaar	Phvul.002G111100.1	5	-1	1	20
32	gauccccggcaar	Phvul.002G132600.2	5	-1	1	20
33	gauccccggcaar	Phvul.002G132600.1	5	-1	1	20
34	gauccccggcaar	Phvul.002G132600.1	5	-1	1	20
35	gauccccggcaar	Phvul.002G188300.1	5	-1	1	20
36	gauccccggcaar	Phvul.002G252700.1	5	-1	1	20
37	gauccccggcaar	Phvul.002G252700.1	5	-1	1	20
38	gauccccggcaar	Phvul.002G324600.1	5	-1	1	20
39	gauccccggcaar	Phvul.002G324600.1	5	-1	1	20
40	gauccccggcaar	Phvul.003G043600.2	5	-1	1	20
41	gauccccggcaar	Phvul.003G064900.1	5	-1	1	20
42	gauccccggcaar	Phvul.003G076900.1	5	-1	1	20
43	gauccccggcaar	Phvul.003G192900.1	5	-1	1	20
44	gauccccggcaar	Phvul.003G192900.2	5	-1	1	20
45	gauccccggcaar	Phvul.003G192900.2	5	-1	1	20
46	gauccccggcaar	Phvul.004G017600.1	5	-1	1	20
47	gauccccggcaar	Phvul.005G035400.1	5	-1	1	20
48	gauccccggcaar	Phvul.005G080800.2	5	-1	1	20
49	gauccccggcaar	Phvul.005G080800.1	5	-1	1	20
50	gauccccggcaar	Phvul.005G080800.1	5	-1	1	20
51	gauccccggcaar	Phvul.005G095300.1	5	-1	1	20
52	gauccccggcaar	Phvul.005G176600.1	5	-1	1	20
53	gauccccggcaar	Phvul.006G034100.1	5	-1	1	20
54	gauccccggcaar	Phvul.006G034100.1	5	-1	1	20
55	gauccccggcaar	Phvul.007G196100.2	5	-1	1	20
56	gauccccggcaar	Phvul.007G196100.1	5	-1	1	20
57	gauccccggcaar	Phvul.007G196100.1	5	-1	1	20
58	gauccccggcaar	Phvul.007G268300.1	5	-1	1	20
59	gauccccggcaar	Phvul.008G015300.3	5	-1	1	20
60	gauccccggcaar	Phvul.008G015300.4	5	-1	1	20
	gauccccggcaar	Phvul.008G015300.2	5	-1	1	20

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2	gaucgccggcaar Phvul.008G015300.5	5	-1	1	20
3	gaucgccggcaar Phvul.008G015300.1	5	-1	1	20
4	gaucgccggcaar Phvul.008G050200.1	5	-1	1	20
5					
6	gaucgccggcaar Phvul.008G092200.2	5	-1	1	20
7	gaucgccggcaar Phvul.008G092200.3	5	-1	1	20
8	gaucgccggcaar Phvul.008G106950.2	5	-1	1	20
9					
10	gaucgccggcaar Phvul.008G106950.1	5	-1	1	20
11	gaucgccggcaar Phvul.008G114300.1	5	-1	1	20
12	gaucgccggcaar Phvul.008G130400.1	5	-1	1	20
13					
14	gaucgccggcaar Phvul.008G203314.1	5	-1	1	20
15	gaucgccggcaar Phvul.009G108800.1	5	-1	1	20
16	gaucgccggcaar Phvul.009G128500.2	5	-1	1	20
17					
18	gaucgccggcaar Phvul.009G128500.3	5	-1	1	20
19	gaucgccggcaar Phvul.009G128500.1	5	-1	1	20
20	gaucgccggcaar Phvul.009G128500.4	5	-1	1	20
21					
22	gaucgccggcaar Phvul.009G255500.1	5	-1	1	20
23	gaucgccggcaar Phvul.009G255500.2	5	-1	1	20
24	gaucgccggcaar Phvul.010G032000.1	5	-1	1	20
25					
26	gaucgccggcaar Phvul.011G062200.1	5	-1	1	20
27	gaucgccggcaar Phvul.011G175000.2	5	-1	1	20
28	gaucgccggcaar Phvul.011G175000.1	5	-1	1	20
29					
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	Target_start	Target_end	miRNA_alignment	Target_alignment	Inhibition	Target_Desc.
1						
2						
3	1053	1072	GAUCCCCGGC	::: ::::: ::	GGGCGCGGUCleavage	pacid=371628
4	222	241	GAUCCCCGGC	::: ::::: ::	CGGCGCCGUL Cleavage	pacid=371525
5	367	386	GAUCCCCGGC	::: ::::: ::	CGGCGCCGUL Cleavage	pacid=371525
6	716	735	GAUCCCCGGC	::: ::: :::::	CGGCGCAGUL Cleavage	pacid=371718
7	559	578	GAUCCCCGGC	::: ::::: ::	CGGCGCCGUL Cleavage	pacid=371640
8						
9						
10	1667	1686	GAUCCCCGGC	::: ::::: ::	AGGCGCCGUC Translation	pacid=371600
11	945	964	GAUCCCCGGC	::: ::::: ::	UGGCGCUGUCleavage	pacid=371707
12	623	642	GAUCCCCGGC	::: ::::: ::	CGGCGCCGAL Cleavage	pacid=371463
13	619	638	GAUCCCCGGC	::: ::::: ::	UGGCGGUGU Cleavage	pacid=371472
14	1454	1473	GAUCCCCGGC	::: ::::: ::	UGGUGCCGUCleavage	pacid=371474
15	1131	1150	GAUCCCCGGC	::: ::::: ::	UGAGGCUGUCleavage	pacid=371618
16	1663	1682	GAUCCCCGGC	::: ::::: ::	UGAGGCUGUCleavage	pacid=371618
17	238	257	GAUCCCCGGC	::: ::::: ::	CGGUGUCGUC Translation	pacid=371737
18	1177	1196	GAUCCCCGGC	::: ::::: ::	CGGUUCUGUCleavage	pacid=371732
19	560	579	GAUCCCCGGC	::: ::::: ::	CCGCGCCGCC Translation	pacid=371658
20	316	335	GAUCCCCGGC	::: ::::: ::	CGGUGCCGUCleavage	pacid=371600
21	221	240	GAUCCCCGGC	::: ::::: ::	AGGCGCGGUCleavage	pacid=371609
22	681	700	GAUCCCCGGC	::: ::::: ::	GGGCGCCUCL Cleavage	pacid=371502
23	596	615	GAUCCCCGGC	::: ::::: ::	AGGAGCUGUCleavage	pacid=371709
24	702	721	GAUCCCCGGC	::: ::::: ::	GGGUGCUGU Cleavage	pacid=371698
25	1160	1179	GAUCCCCGGC	::: ::::: ::	UUGUUCUGU Cleavage	pacid=371680
26	816	835	GAUCCCCGGC	::: ::::: ::	UUGUUCUGU Cleavage	pacid=371704
27	928	947	GAUCCCCGGC	::: ::::: ::	UUGUUCUGU Cleavage	pacid=371704
28	1011	1030	GAUCCCCGGC	::: ::::: ::	UGGUGAAGU Cleavage	pacid=371753
29	680	699	GAUCCCCGGC	::: ::::: ::	CUCCGUCUGUCleavage	pacid=371755
30	5389	5408	GAUCCCCGGC	::: ::::: ::	AUGAGCCGUCleavage	pacid=371766
31	5401	5420	GAUCCCCGGC	::: ::::: ::	AUGAGCCGUCleavage	pacid=371766
32	710	729	GAUCCCCGGC	::: ::::: ::	GGGCACCGUCleavage	pacid=371760
33	1178	1197	GAUCCCCGGC	::: ::::: ::	UGGGGUUGU Cleavage	pacid=371744
34	247	266	GAUCCCCGGC	::: ::::: ::	UGGCGAUGUCleavage	pacid=371472
35	247	266	GAUCCCCGGC	::: ::::: ::	UGGCGAUGUCleavage	pacid=371472
36	2013	2032	GAUCCCCGGC	::: ::::: ::	AGGCGCAGUCleavage	pacid=371449
37	2411	2430	GAUCCCCGGC	::: ::::: ::	AGGCGCAGUCleavage	pacid=371449
38	2449	2468	GAUCCCCGGC	::: ::::: ::	AGGCGCAGUCleavage	pacid=371449
39	1246	1265	GAUCCCCGGC	::: ::::: ::	UGGGGAUGU Cleavage	pacid=371632
40	1246	1265	GAUCCCCGGC	::: ::::: ::	UGGGGAUGU Cleavage	pacid=371632
41	1075	1094	GAUCCCCGGC	::: ::::: ::	UGUUGGUGU Cleavage	pacid=371636
42	705	724	GAUCCCCGGC	::: ::: :::::	GGGCGCGGUC Translation	pacid=371636
43	463	482	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
44	472	491	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
45	463	482	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
46	472	491	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
47	463	482	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
48	472	491	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
49	463	482	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
50	472	491	GAUCCCCGGC	::: ::::: ::	UGGUGCUGU Cleavage	pacid=371623
51	998	1017	GAUCCCCGGC	::: ::::: ::	GGGUGUUGU Cleavage	pacid=371537

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2	513	532 GAUCCCCGGC	::: : ::: ::::: AGGUGGCCUI	Cleavage	pacid=371545
3	1225	1244 GAUCCCCGGC	::: ::::: : ::: UGGUGCCGUI	Cleavage	pacid=371719
4	511	530 GAUCCCCGGC	::: ::::: : ::: GGGUGUUGU	Cleavage	pacid=371741
5	861	880 GAUCCCCGGC	:: : ::::: : GGGGGCUGU	Cleavage	pacid=371738
6	576	595 GAUCCCCGGC	::: : ::::: : CGGCACAGU	Cleavage	pacid=371665
7	432	451 GAUCCCCGGC	: : ::::: : UCCCACUGU	Cleavage	pacid=371596
8	773	792 GAUCCCCGGC	::: ::::: : AAGUGCUGU	Cleavage	pacid=371580
9	1132	1151 GAUCCCCGGC	::: ::::: : AAGUGCUGU	Cleavage	pacid=371580
10	516	535 GAUCCCCGGC	::: : ::::: : UGGUGUAGU	Cleavage	pacid=371605
11	1341	1360 GAUCCCCGGC	::: : ::::: : UGGUUCUGU	Cleavage	pacid=371499
12	1368	1387 GAUCCCCGGC	::: : ::::: : UGGUUCUGU	Cleavage	pacid=371499
13	154	173 GAUCCCCGGC	::: : ::::: : UGGUGUAGU	Cleavage	pacid=371422
14	1652	1671 GAUCCCCGGC	::: ::::: : ::: UGGCACCGU	Cleavage	pacid=371438
15	597	616 GAUCCCCGGC	::: : ::::: : UGUCGCUGU	Translation	pacid=371439
16	2765	2784 GAUCCCCGGC	: : ::::: : GGCUGCUGU	Cleavage	pacid=371573
17	276	295 GAUCCCCGGC	::: : ::::: : AGGUGGCGU	Cleavage	pacid=371681
18	871	890 GAUCCCCGGC	::: : ::::: : UGGCGGCGU	Cleavage	pacid=371692
19	1254	1273 GAUCCCCGGC	::: ::::: : : GGGUGCCGU	Cleavage	pacid=371677
20	1156	1175 GAUCCCCGGC	::: : ::::: : UGGCGAAGU	Cleavage	pacid=371689
21	48	67 GAUCCCCGGC	::: : ::::: : : UGGAGCUGU	Cleavage	pacid=371707
22	57	76 GAUCCCCGGC	::: : ::::: : : UGGAGCUGU	Cleavage	pacid=371707
23	707	726 GAUCCCCGGC	::: : ::::: : CUGCCCAAL	Cleavage	pacid=371743
24	1118	1137 GAUCCCCGGC	::: : ::::: : ACGCGCCGUC	Translation	pacid=371761
25	1742	1761 GAUCCCCGGC	::: ::::: : : AGGUGCUGU	Cleavage	pacid=371787
26	1708	1727 GAUCCCCGGC	::: ::::: : : AGGUGCUGU	Cleavage	pacid=371787
27	624	643 GAUCCCCGGC	::: : ::::: : UGUCACUGU	Translation	pacid=371749
28	896	915 GAUCCCCGGC	::: : ::::: : CGGUGCUGU	Translation	pacid=371746
29	1576	1595 GAUCCCCGGC	::: : ::::: : UGUUGUUGU	Cleavage	pacid=371755
30	89	108 GAUCCCCGGC	::: : ::::: : UGGUGAUGU	Cleavage	pacid=371474
31	900	919 GAUCCCCGGC	::: ::::: : GGGCGCUGU	Cleavage	pacid=371461
32	1207	1227 GAUCC-CCGG	::: : ::::: : CGGCGUGGU	Cleavage	pacid=371478
33	81	100 GAUCCCCGGC	::: ::::: : UCUCGUCGU	Cleavage	pacid=371457
34	81	100 GAUCCCCGGC	::: ::::: : UCUCGUCGU	Cleavage	pacid=371457
35	3869	3888 GAUCCCCGGC	::: : ::::: : UCGUGUUGU	Translation	pacid=371629
36	842	861 GAUCCCCGGC	::: ::::: : : AGGCGCUGU	Cleavage	pacid=371525
37	860	879 GAUCCCCGGC	::: : ::::: : UGGUUCUGU	Cleavage	pacid=371543
38	863	882 GAUCCCCGGC	::: : ::::: : UGGUUCUGU	Cleavage	pacid=371543
39	542	561 GAUCCCCGGC	::: : ::::: : UGGUCUUGA	Cleavage	pacid=371545
40	1260	1279 GAUCCCCGGC	: : ::::: : AGUUGUCGU	Cleavage	pacid=371526
41	472	491 GAUCCCCGGC	::: : ::::: : UGGUGUUGG	Cleavage	pacid=371721
42	1295	1314 GAUCCCCGGC	::: : ::::: : UGGUGCCGG	Cleavage	pacid=371642
43	1580	1599 GAUCCCCGGC	::: : ::::: : UGGUGCCGG	Cleavage	pacid=371642
44	293	312 GAUCCCCGGC	::: : ::::: : CGGCACUGU	Cleavage	pacid=371658
45	876	895 GAUCCCCGGC	::: : ::::: : UGAUGCUGU	Cleavage	pacid=371611
46	876	895 GAUCCCCGGC	::: : ::::: : UGAUGCUGU	Cleavage	pacid=371611
47	875	894 GAUCCCCGGC	::: : ::::: : UGAUGCUGU	Cleavage	pacid=371611



Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.004G110400.1	Phvul.004G110400	Phvul.004G110400	PF00168
1	Phvul.005G120700.1	Phvul.005G120700	Phvul.005G120700	PF00069
1	Phvul.005G120700.2	Phvul.005G120700	Phvul.005G120700	PF00069
1	Phvul.006G001600.1	Phvul.006G001600	Phvul.006G001600	PF00012
1	Phvul.007G023000.1	Phvul.007G023000	Phvul.007G023000	PF01814
1	Phvul.008G271000.1	Phvul.008G271000	Phvul.008G271000	PF07983,PF00
1	Phvul.001G240600.1	Phvul.001G240600	Phvul.001G240600	PF00168
1	Phvul.003G220500.1	Phvul.003G220500	Phvul.003G220500	PF01095
1	Phvul.003G237300.1	Phvul.003G237300	Phvul.003G237300	PF05922,PF02
1	Phvul.003G285700.1	Phvul.003G285700	Phvul.003G285700	PF00010,PF14
1	Phvul.004G086300.2	Phvul.004G086300	Phvul.004G086300	PF00069
1	Phvul.004G086300.1	Phvul.004G086300	Phvul.004G086300	PF00069
1	Phvul.006G068400.1	Phvul.006G068400	Phvul.006G068400	PF13540,PF00
1	Phvul.006G130200.1	Phvul.006G130200	Phvul.006G130200	PF04146
2	Phvul.007G268300.1	Phvul.007G268300	Phvul.007G268300	0
1	Phvul.008G036200.1	Phvul.008G036200	Phvul.008G036200	PF00520
1	Phvul.008G290700.1	Phvul.008G290700	Phvul.008G290700	PF05678
1	Phvul.009G144300.1	Phvul.009G144300	Phvul.009G144300	PF03479
1	Phvul.001G028400.1	Phvul.001G028400	Phvul.001G028400	PF03081
1	Phvul.001G071200.1	Phvul.001G071200	Phvul.001G071200	PF00069
1	Phvul.001G146900.1	Phvul.001G146900	Phvul.001G146900	PF00069
1	Phvul.001G147001.1	Phvul.001G147001	Phvul.001G147001	PF07714
1	Phvul.001G147001.2	Phvul.001G147001	Phvul.001G147001	PF07714
1	Phvul.002G006700.1	Phvul.002G006700	Phvul.002G006700	PF03479
1	Phvul.002G059000.1	Phvul.002G059000	Phvul.002G059000	0
1	Phvul.002G092900.2	Phvul.002G092900	Phvul.002G092900	PF00118,PF01
1	Phvul.002G092900.1	Phvul.002G092900	Phvul.002G092900	PF00118,PF01
1	Phvul.002G274500.1	Phvul.002G274500	Phvul.002G274500	PF01764
1	Phvul.002G315300.1	Phvul.002G315300	Phvul.002G315300	PF03456,PF00
1	Phvul.003G076700.2	Phvul.003G076700	Phvul.003G076700	PF00232
1	Phvul.003G076700.1	Phvul.003G076700	Phvul.003G076700	PF00232
1	Phvul.003G099100.1	Phvul.003G099100	Phvul.003G099100	PF01156
1	Phvul.003G099100.3	Phvul.003G099100	Phvul.003G099100	PF01156
1	Phvul.003G099100.2	Phvul.003G099100	Phvul.003G099100	PF01156
1	Phvul.004G037600.3	Phvul.004G037600	Phvul.004G037600	PF00560,PF00
1	Phvul.004G037600.2	Phvul.004G037600	Phvul.004G037600	PF00560,PF00
1	Phvul.004G049200.1	Phvul.004G049200	Phvul.004G049200	PF03639
1	Phvul.004G110200.2	Phvul.004G110200	Phvul.004G110200	PF00168
1	Phvul.004G171500.6	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.2	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.3	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.1	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.5	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.4	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.005G022300.1	Phvul.005G022300	Phvul.005G022300	PF03151



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2	1	Phvul.005G159600.1	Phvul.005G159600	Phvul.005G159600	PF05879
3	1	Phvul.006G049100.1	Phvul.006G049100	Phvul.006G049100	PF12327,PF00
4	1	Phvul.006G068100.1	Phvul.006G068100	Phvul.006G068100	PF01713,PF08
5	1	Phvul.006G087700.1	Phvul.006G087700	Phvul.006G087700	PF00069,PF00
6	1	Phvul.007G208400.1	Phvul.007G208400	Phvul.007G208400	PF00249
7	1	Phvul.008G042900.1	Phvul.008G042900	Phvul.008G042900	PF13360
8	1	Phvul.008G124000.2	Phvul.008G124000	Phvul.008G124000	PF12452
9	1	Phvul.008G124000.1	Phvul.008G124000	Phvul.008G124000	PF12452
10	1	Phvul.008G233100.1	Phvul.008G233100	Phvul.008G233100	PF01841,PF10
11	1	Phvul.009G157200.2	Phvul.009G157200	Phvul.009G157200	PF02493,PF01
12	1	Phvul.009G157200.1	Phvul.009G157200	Phvul.009G157200	PF02493,PF01
13	1	Phvul.010G024866.1	Phvul.010G024866	Phvul.010G024866	PF10404,PF10
14	1	Phvul.010G082300.1	Phvul.010G082300	Phvul.010G082300	PF01073
15	1	Phvul.010G119800.1	Phvul.010G119800	Phvul.010G119800	PF03168
16	1	Phvul.011G029450.1	Phvul.011G029450	Phvul.011G029450	PF04818,PF00
17	1	Phvul.001G025101.1	Phvul.001G025101	Phvul.001G025101	PF03629
18	1	Phvul.001G183700.1	Phvul.001G183700	Phvul.001G183700	PF03465,PF03
19	1	Phvul.001G209500.2	Phvul.001G209500	Phvul.001G209500	PF00759
20	1	Phvul.001G209900.2	Phvul.001G209900	Phvul.001G209900	PF01966,PF04
21	1	Phvul.001G250100.2	Phvul.001G250100	Phvul.001G250100	PF00168,PF00
22	1	Phvul.001G250100.1	Phvul.001G250100	Phvul.001G250100	PF00168,PF00
23	1	Phvul.002G063100.1	Phvul.002G063100	Phvul.002G063100	PF01095
24	1	Phvul.002G111100.1	Phvul.002G111100	Phvul.002G111100	PF08263,PF07
25	1	Phvul.002G132600.2	Phvul.002G132600	Phvul.002G132600	0
26	1	Phvul.002G132600.1	Phvul.002G132600	Phvul.002G132600	0
27	1	Phvul.002G188300.1	Phvul.002G188300	Phvul.002G188300	PF00646
28	1	Phvul.002G252700.1	Phvul.002G252700	Phvul.002G252700	PF00400
29	1	Phvul.002G324600.1	Phvul.002G324600	Phvul.002G324600	PF08263,PF13
30	1	Phvul.003G043600.2	Phvul.003G043600	Phvul.003G043600	PF00232
31	1	Phvul.003G064900.1	Phvul.003G064900	Phvul.003G064900	PF01384
32	1	Phvul.003G076900.1	Phvul.003G076900	Phvul.003G076900	PF00067
33	1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G192900	PF02183,PF00
34	1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G192900	PF02183,PF00
35	1	Phvul.004G017600.1	Phvul.004G017600	Phvul.004G017600	PF15612,PF01
36	1	Phvul.005G035400.1	Phvul.005G035400	Phvul.005G035400	PF08799,PF02
37	1	Phvul.005G080800.2	Phvul.005G080800	Phvul.005G080800	PF09507
38	1	Phvul.005G080800.1	Phvul.005G080800	Phvul.005G080800	PF09507
39	1	Phvul.005G095300.1	Phvul.005G095300	Phvul.005G095300	PF00311
40	1	Phvul.005G176600.1	Phvul.005G176600	Phvul.005G176600	PF13041
41	1	Phvul.006G034100.1	Phvul.006G034100	Phvul.006G034100	PF01501
42	1	Phvul.007G196100.2	Phvul.007G196100	Phvul.007G196100	0
43	1	Phvul.007G196100.1	Phvul.007G196100	Phvul.007G196100	0
44	2	Phvul.007G268300.1	Phvul.007G268300	Phvul.007G268300	0
45	1	Phvul.008G015300.3	Phvul.008G015300	Phvul.008G015300	0
46	1	Phvul.008G015300.4	Phvul.008G015300	Phvul.008G015300	0
47	1	Phvul.008G015300.2	Phvul.008G015300	Phvul.008G015300	0

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2	1	Phvul.008G015300.5	Phvul.008G015300	Phvul.008G015300	0
3	1	Phvul.008G015300.1	Phvul.008G015300	Phvul.008G015300	0
4	1	Phvul.008G050200.1	Phvul.008G050200	Phvul.008G050200	0
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6	1	Phvul.008G092200.2	Phvul.008G092200	Phvul.008G092200	0
7	1	Phvul.008G092200.3	Phvul.008G092200	Phvul.008G092200	0
8	1	Phvul.008G106950.2	Phvul.008G106950	Phvul.008G106950	PF02207
9					
10	1	Phvul.008G106950.1	Phvul.008G106950	Phvul.008G106950	PF02207
11	1	Phvul.008G114300.1	Phvul.008G114300	Phvul.008G114300	PF05920,PF07
12	1	Phvul.008G130400.1	Phvul.008G130400	Phvul.008G130400	PF10510
13					
14	1	Phvul.008G203314.1	Phvul.008G203314	Phvul.008G203314	PF02298
15	1	Phvul.009G108800.1	Phvul.009G108800	Phvul.009G108800	PF00230
16	1	Phvul.009G128500.2	Phvul.009G128500	Phvul.009G128500	PF01490
17					
18	1	Phvul.009G128500.3	Phvul.009G128500	Phvul.009G128500	PF01490
19	1	Phvul.009G128500.1	Phvul.009G128500	Phvul.009G128500	PF01490
20	1	Phvul.009G128500.4	Phvul.009G128500	Phvul.009G128500	PF01490
21					
22	1	Phvul.009G255500.1	Phvul.009G255500	Phvul.009G255500	0
23	1	Phvul.009G255500.2	Phvul.009G255500	Phvul.009G255500	0
24	1	Phvul.010G032000.1	Phvul.010G032000	Phvul.010G032000	PF01453,PF00
25					
26	1	Phvul.011G062200.1	Phvul.011G062200	Phvul.011G062200	PF00806,PF07
27	1	Phvul.011G175000.2	Phvul.011G175000	Phvul.011G175000	PF08276,PF07
28	1	Phvul.011G175000.1	Phvul.011G175000	Phvul.011G175000	PF08276,PF07
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	Panther	KOG	KEGG	KOG	GO	Best-hit-arabi
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2	PTHR11649,P <sup>-</sup>	0	0	0	0 AT1G72960.1
3	PTHR30314,P <sup>-</sup>	0 3.6.5.6	K03531	GO:0003924	AT5G55280.1
4	PTHR13308,P <sup>-</sup> KOG2401		0	0	0 AT5G58720.1
5					
6	PTHR27007,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,(	AT3G53380.1
7	PTHR10641,P <sup>-</sup> KOG0048		0 K09422		0 AT4G01680.1
8	PTHR32303,P <sup>-</sup>	0 1.1.2.6		0	0 0
9					
10	PTHR36807,P <sup>-</sup>	0	0	0	0 AT5G48830.1
11	PTHR36807,P <sup>-</sup>	0	0	0	0 AT5G48830.1
12	PTHR12135,P <sup>-</sup> KOG2179		0 K10838	GO:0003677,(	AT5G16630.1
13					
14	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(	AT1G21980.1
15	PTHR23086,P <sup>-</sup>	0 2.7.1.68	K00889	GO:0046488,(	AT1G21980.1
16	PTHR12135,P <sup>-</sup> KOG2179		0 K10838	GO:0003677,(	AT5G16630.1
17					
18	<b>PTHR10366,P<sup>-</sup> KOG1371</b>	<b>5.1.3.6</b>	<b>K08679</b>	<b>GO:0055114,(</b>	<b>AT4G00110.1</b>
19	PTHR31415,P <sup>-</sup>	0	0	0	0 AT4G01410.1
20	PTHR12550,P <sup>-</sup>	0	0	0	0 AT5G08230.1
21					
22	PTHR31988	0 3.1.1.73		0	0 AT4G34215.1
23	PTHR10853 KOG2869		0 K06965	GO:0071025,(	AT4G27650.1
24	PTHR22298,P <sup>-</sup>	0 3.2.1.4		0 GO:0005975,(	AT4G02290.1
25					
26	PTHR21262,P <sup>-</sup>	0 2.7.6.5		0 GO:0015969	AT4G02260.2
27	PTHR23315,P <sup>-</sup> KOG2160,KOG		0	0 GO:0005515	AT2G22125.1
28	PTHR23315,P <sup>-</sup> KOG2160,KOG		0	0 GO:0005515	AT2G22125.1
29					
30	PTHR31321,P <sup>-</sup>	0 3.1.1.11		0 GO:0042545,(	AT5G47500.1
31	PTHR27000,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,(	AT4G36180.1
32					
33	PTHR37891,P <sup>-</sup>	0	0	0	0 0
34	PTHR37891,P <sup>-</sup>	0	0	0	0 0
35	PTHR32133,P <sup>-</sup>	0	0	0 GO:0005515	AT1G30950.1
36	PTHR22844,P <sup>-</sup> KOG0645	2.7.11.7		0 GO:0005515	AT1G24530.1
37	PTHR27001,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0005515,(	AT1G66150.1
38					
39	PTHR10353,P <sup>-</sup>	0 3.2.1.21	K01188	GO:0005975,(	AT1G26560.1
40	PTHR11101 KOG2493		0 K14640	GO:0016020,(	AT3G26570.2
41	PTHR24298,P <sup>-</sup> KOG0156		0	0 GO:0055114,(	AT1G11600.1
42					
43	PTHR24326,P <sup>-</sup>	0	0	0 GO:0043565,(	AT3G01470.1
44	PTHR24326,P <sup>-</sup>	0	0	0 GO:0043565,(	AT3G01470.1
45	PTHR14140,P <sup>-</sup>	0 2.3.1.48		0 GO:0005634,(	AT3G01460.1
46					
47	<b>PTHR13007,P<sup>-</sup> KOG2808</b>		<b>0 K12817</b>	<b>GO:0008380,(</b>	<b>AT1G03140.1</b>
48	PTHR17598	0	0 K03504	GO:0006260,(	AT1G78650.1
49	PTHR17598	0	0 K03504	GO:0006260,(	AT1G78650.1
50					
51	PTHR30523,P <sup>-</sup>	0 4.1.1.31	K01595	GO:0015977,(	AT2G42600.2
52	PTHR24015,P <sup>-</sup>	0	0	0	0 AT1G52620.1
53	PTHR32116,P <sup>-</sup>	0 2.4.1.43	K13648	GO:0016757,(	AT3G58790.1
54					
55	PTHR10593,P <sup>-</sup>	0	0	0	0 AT3G50700.1
56	PTHR10593,P <sup>-</sup>	0	0	0	0 AT3G50700.1
57	PTHR36351,P <sup>-</sup>	0	0	0	0 0
58					
59	PTHR10159,P <sup>-</sup>	0 3.1.3.48		0	0 AT3G55270.1
60	PTHR10159,P <sup>-</sup>	0 3.1.3.48		0	0 AT3G55270.1
	PTHR10159,P <sup>-</sup>	0 3.1.3.48		0	0 AT3G55270.1

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2	PTHR10159,P <sup>-</sup>	0	3.1.3.48	0	0 AT3G55270.1
3	PTHR10159,P <sup>-</sup>	0	3.1.3.48	0	0 AT3G55270.1
4	PTHR12655,P <sup>-</sup> KOG2763		3.1.2.2,3.1.2.2K17361		0 AT5G48370.1
5					
6	PTHR20938,P <sup>-</sup>	0	0 K13141		0 AT3G08800.1
7	PTHR20938,P <sup>-</sup>	0	0 K13141		0 AT3G08800.1
8	PTHR21497,P <sup>-</sup> KOG1139		3.4.17.20	0	GO:0008270 AT5G02310.1
9					
10	PTHR21497,P <sup>-</sup> KOG1139		3.4.17.20	0	GO:0008270 AT5G02310.1
11	PTHR11850,P <sup>-</sup> KOG0773		0	0	GO:0006355,C AT5G02030.1
12	PTHR21072 KOG2459		0 K05291		GO:0042765,C AT3G07180.1
13					
14	PTHR33021,P <sup>-</sup>	0	0	0	GO:0009055 AT1G08500.1
15	PTHR19139 KOG0223		0 K09873		GO:0016020,C AT2G25810.1
16	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G77380.1
17					
18	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G77380.1
19	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G77380.1
20	PTHR22950,P <sup>-</sup> KOG1303		0	0	0 AT1G77380.1
21					
22	0	0	0	0	0 0
23	0	0	0	0	0 0
24	PTHR27002,P <sup>-</sup> KOG1187		2.7.11.1	0	GO:0006468,C AT5G60900.1
25					
26	PTHR12537,P <sup>-</sup>	0	0 K17943		GO:0003723 AT2G29190.2
27	PTHR27002,P <sup>-</sup>	0	2.7.11.1	0	GO:0006468,C AT1G67520.1
28	PTHR27002,P <sup>-</sup>	0	2.7.11.1	0	GO:0006468,C AT1G67520.1
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arabi-symbol	arabi-defline	ID
	0 Calcium-dependent lipid-binding (CaLB domain) family	Phvul.004G11
ATNEK6,IBO1,NEK6	NIMA (never in mitosis, gene A)-related 6	Phvul.005G12
ATNEK6,IBO1,NEK6	NIMA (never in mitosis, gene A)-related 6	Phvul.005G12
	0 heat shock protein 70 (Hsp 70) family protein	Phvul.006G00
	0	0 Phvul.007G02
	0 O-Glycosyl hydrolases family 17 protein	Phvul.008G27
	0 Calcium-dependent lipid-binding (CaLB domain) family	Phvul.001G24
	0 Pectin lyase-like superfamily protein	Phvul.003G22
ARA12	Subtilase family protein	Phvul.003G23
ATMYC2,JAI1,JIN1,M	Basic helix-loop-helix (bHLH) DNA-binding family protei	Phvul.003G28
ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1	Phvul.004G08
ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1	Phvul.004G08
ATCRR3,CCR3	CRINKLY4 related 3	Phvul.006G06
ATCPSF30,CPSF30	cleavage and polyadenylation specificity factor 30	Phvul.006G13
	0	0 Phvul.007G26
ATCNGC2,CNGC2,DN	Cyclic nucleotide-regulated ion channel family protein	Phvul.008G03
	0 VQ motif-containing protein	Phvul.008G29
	0 Predicted AT-hook DNA-binding family protein	Phvul.009G14
ATEXO70G1,EXO70G	exocyst subunit exo70 family protein G1	Phvul.001G02
	0 Protein kinase superfamily protein	Phvul.001G07
RKF3	receptor-like kinase in in flowers 3	Phvul.001G14
RKF3	receptor-like kinase in in flowers 3	Phvul.001G14
RKF3	receptor-like kinase in in flowers 3	Phvul.001G14
	0 AT hook motif DNA-binding family protein	Phvul.002G00
	0 alpha/beta-Hydrolases superfamily protein	Phvul.002G05
FAB1C	FORMS APLOID AND BINUCLEATE CELLS 1C	Phvul.002G09
FAB1C	FORMS APLOID AND BINUCLEATE CELLS 1C	Phvul.002G09
ATPAD4,PAD4	alpha/beta-Hydrolases superfamily protein	Phvul.002G27
SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	Phvul.002G31
BGLU46	beta glucosidase 46	Phvul.003G07
BGLU46	beta glucosidase 46	Phvul.003G07
	0 inosine-uridine preferring nucleoside hydrolase family	Phvul.003G09
	0 inosine-uridine preferring nucleoside hydrolase family	Phvul.003G09
	0 inosine-uridine preferring nucleoside hydrolase family	Phvul.003G09
RPK2,TOAD2	receptor-like protein kinase 2	Phvul.004G03
RPK2,TOAD2	receptor-like protein kinase 2	Phvul.004G03
	0 glycosyl hydrolase family 81 protein	Phvul.004G04
	0 Calcium-dependent lipid-binding (CaLB domain) family	Phvul.004G11
	0 bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
	0 bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
	0 bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
	0 bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
	0 bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
	0 bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
	0 Nucleotide/sugar transporter family protein	Phvul.005G02



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2		0 Root hair defective 3 GTP-binding protein (RHD3)	Phvul.005G15
3	ATFTSZ1-1,CPFTSZ,FT	homolog of bacterial cytokinesis Z-ring protein FTSZ 1-	Phvul.006G04
4		0 smr (Small MutS Related) domain-containing protein	Phvul.006G06
5		0 Concanavalin A-like lectin protein kinase family protein	Phvul.006G08
6			
7	AtMYB55,MYB55	myb domain protein 55	Phvul.007G20
8		0	0 Phvul.008G04
9		0	0 Phvul.008G12
10		0	0 Phvul.008G12
11			
12	ATRAD4,RAD4	DNA repair protein Rad4 family	Phvul.008G23
13			
14	ATPIP5K1,ATPIP1K,PI	phosphatidylinositol-4-phosphate 5-kinase 1	Phvul.009G15
15	ATPIP5K1,ATPIP1K,PI	phosphatidylinositol-4-phosphate 5-kinase 1	Phvul.009G15
16	ATRAD4,RAD4	DNA repair protein Rad4 family	Phvul.010G02
17			
18	<b>GAE3</b>	<b>UDP-D-glucuronate 4-epimerase 3</b>	<b>Phvul.010G08</b>
19		0 Late embryogenesis abundant (LEA) hydroxyproline-ric	Phvul.010G11
20		0 Tudor/PWWP/MBT domain-containing protein	Phvul.011G02
21		0 Domain of unknown function (DUF303)	Phvul.001G02
22			
23	PEL1	Eukaryotic release factor 1 (eRF1) family protein	Phvul.001G18
24	AtGH9B13,GH9B13	glycosyl hydrolase 9B13	Phvul.001G20
25			
26	AT-RSH1,ATRSH1,RSR	RELA/SPOT homolog 1	Phvul.001G20
27	CSI1	binding	Phvul.001G25
28	CSI1	binding	Phvul.001G25
29		0 Pectin lyase-like superfamily protein	Phvul.002G06
30		0 Leucine-rich receptor-like protein kinase family protein	Phvul.002G11
31		0	0 0
32		0	0 0
33		0	0 0
34			
35	UFO	F-box family protein	Phvul.002G18
36		0 Transducin/WD40 repeat-like superfamily protein	Phvul.002G25
37			
38	TMK1	transmembrane kinase 1	Phvul.002G32
39	BGLU40	beta glucosidase 40	Phvul.003G04
40	ORF02,PHT2;1	phosphate transporter 2;1	Phvul.003G06
41	CYP77B1	cytochrome P450, family 77, subfamily B, polypeptide	Phvul.003G07
42			
43	ATHB-1,ATHB1,HAT5	homeobox 1	Phvul.003G19
44	ATHB-1,ATHB1,HAT5	homeobox 1	Phvul.003G19
45	ATMBD9,MBD9	methyl-CPG-binding domain 9	Phvul.004G01
46			
47		<b>0 splicing factor Prp18 family protein</b>	<b>Phvul.005G03</b>
48	POLD3	DNA-directed DNA polymerases	Phvul.005G08
49	POLD3	DNA-directed DNA polymerases	Phvul.005G08
50			
51	ATPPC2,PPC2	phosphoenolpyruvate carboxylase 2	Phvul.005G09
52		0 Pentatricopeptide repeat (PPR) superfamily protein	Phvul.005G17
53			
54	GAUT15	galacturonosyltransferase 15	Phvul.006G03
55	AtIDD2,IDD2	indeterminate(ID)-domain 2	Phvul.007G19
56	AtIDD2,IDD2	indeterminate(ID)-domain 2	Phvul.007G19
57		0	0 Phvul.007G26
58			
59	ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
60	ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
	ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01

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2	ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
3	ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
4		0 Thioesterase/thiol ester dehydrase-isomerase superfar	Phvul.008G05
5			
6		0 ARM repeat superfamily protein	Phvul.008G09
7		0 ARM repeat superfamily protein	Phvul.008G09
8	PRT6	proteolysis 6	Phvul.008G10
9	PRT6	proteolysis 6	Phvul.008G10
10	PRT6	proteolysis 6	Phvul.008G10
11	BLH9,BLR,HB-6,LSN,P	POX (plant homeobox) family protein	Phvul.008G11
12		0 GPI transamidase component PIG-S-related	Phvul.008G13
13			
14	AtENODL18,ENODL18	early nodulin-like protein 18	Phvul.008G20
15	TIP4;1	tonoplast intrinsic protein 4;1	Phvul.009G10
16	AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
17	AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
18	AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
19	AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
20	AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
21			
22		0	0 0
23		0	0 0
24	RLK1	receptor-like protein kinase 1	Phvul.010G03
25	APUM2,PUM2	pumilio 2	Phvul.011G06
26			
27		0 lectin protein kinase family protein	Phvul.011G17
28		0 lectin protein kinase family protein	Phvul.011G17
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Annot_defline	IDENTIFIER	NAME	DESCRIPTION
	PF00168 - C2	Phvul.004G11	not assigned.r no hits & (original description: pacid=37162836 transcri
	PTHR24362:SI	Phvul.005G12	Protein modif protein kinase (NEK) (original description: pacid=371525
	PTHR24362:SI	Phvul.005G12	Protein modif protein kinase (NEK) (original description: pacid=371525
	K09486 - hyc	Phvul.006G00	Protein home nucleotide exchange factor (Grp170) (original descriptio
	PF01814 - Her	Phvul.007G02	not assigned.r no hits & (original description: pacid=37164059 transcri
	PTHR32227:SI	Phvul.008G27	Enzyme classii Glucan endo-1,3-beta-glucosidase 12 OS=Arabidopsis th
	PTHR32246:SI	Phvul.001G24	not assigned.r no hits & (original description: pacid=37170768 transcri
	PTHR31321:SI	Phvul.003G22	Cell wall orgar pectin methylesterase (original description: pacid=37146
	PTHR10795://I	Phvul.003G23	Protein home protease (SBT1) (original description: pacid=37147285 tr
	K13422 - tran	Phvul.003G28	RNA biosynthi transcription factor (bHLH) (original description: pacid=3
	K13418 - som	Phvul.004G08	Protein modif protein kinase (LRR-II) (original description: pacid=37161
	K13418 - som	Phvul.004G08	Protein modif protein kinase (LRR-II) (original description: pacid=37161
	PF00069://PF1	Phvul.006G06	Protein modif protein kinase (Crinkly-like) (original description: pacid=3
	PTHR12357:SI	Phvul.006G13	RNA processir component CPSF30/Yth1 of Cleavage and Polyadenylatic
	PTHR36351:SI	Phvul.007G26	not assigned.r no hits & (original description: pacid=37165888 transcri
	PTHR10217:SI	Phvul.008G03	External stimu temperature sensor protein (CNGC2) (original descriptio
	PTHR33179:SI	Phvul.008G29	not assigned.r no hits & (original description: pacid=37160918 transcri
	PTHR31100:SI	Phvul.009G14	not assigned.r (original description: pacid=37150218 transcript=Phvul.(
	PTHR12542://I	Phvul.001G02	Vesicle trafficl component EXO70 of Exocyst complex (original descripti
	2.7.11.1 - Non	Phvul.001G07	Protein modif protein kinase (RKF3) (original description: pacid=371698
	PTHR27006:SI	Phvul.001G14	Protein modif protein kinase (RKF3) (original description: pacid=371680
	PTHR27006:SI	Phvul.001G14	Enzyme classii Probable LRR receptor-like serine/threonine-protein kin
	PTHR27006:SI	Phvul.001G14	Enzyme classii Probable LRR receptor-like serine/threonine-protein kin
	PTHR31500:SI	Phvul.002G00	not assigned.r (original description: pacid=37175392 transcript=Phvul.(
	3.1.1.3//3.1.1	Phvul.002G05	not assigned.r no hits & (original description: pacid=37175506 transcri
	PTHR11353:SI	Phvul.002G09	Multi-process phosphatidylinositol 3-phosphate 5-kinase (FAB1) (origir
	PTHR11353:SI	Phvul.002G09	Multi-process phosphatidylinositol 3-phosphate 5-kinase (FAB1) (origir
	PTHR21493://I	Phvul.002G27	External stimu PAD4 effector-triggered immunity co-regulator (original
	PTHR22844:SI	Phvul.002G31	Vesicle trafficl SCD1 component of post-Golgi trafficking SCD complex (
	PTHR10353:SI	Phvul.003G07	Enzyme classii Beta-glucosidase 46 OS=Arabidopsis thaliana (sp o80690
	PTHR10353:SI	Phvul.003G07	Enzyme classii Beta-glucosidase 46 OS=Arabidopsis thaliana (sp o80690
	PTHR12304:SI	Phvul.003G09	Nucleotide mε nucleoside hydrolase (original description: pacid=371449
	PTHR12304:SI	Phvul.003G09	Nucleotide mε nucleoside hydrolase (original description: pacid=371449
	PTHR12304:SI	Phvul.003G09	Nucleotide mε nucleoside hydrolase (original description: pacid=371449
	PTHR27000:SI	Phvul.004G03	Protein modif protein kinase (LRR-XV) (original description: pacid=3716
	PTHR27000:SI	Phvul.004G03	Protein modif protein kinase (LRR-XV) (original description: pacid=3716
	K01180 - endc	Phvul.004G04	not assigned.r no hits & (original description: pacid=37163654 transcri
	PF00168 - C2	Phvul.004G11	not assigned.r no hits & (original description: pacid=37163692 transcri
	2.3.1.129 - Ac	Phvul.004G17	Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
	2.3.1.129 - Ac	Phvul.004G17	Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
	2.3.1.129 - Ac	Phvul.004G17	Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
	2.3.1.129 - Ac	Phvul.004G17	Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
	2.3.1.129 - Ac	Phvul.004G17	Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
	2.3.1.129 - Ac	Phvul.004G17	Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
	PTHR11132:SI	Phvul.005G02	Solute transpc phosphometabolite transporter (TPT PPT GPT XPT) (ori

1 PTHR11649:SlPhvul.005G15Cell cycle orgaER tubulae formation factor (RHD3/RL) (original descript  
 2 PTHR30314:SlPhvul.006G04Cell cycle orgacomponent FtsZ1 of plastid division FtsZ prokaryotic-tub  
 3 KOG2401 - PrPhvul.006G06not assigned.ε (original description: pacid=37174192 transcript=Phvul.  
 4 PTHR27007:SlPhvul.006G08Protein modif protein kinase (L-lectin) (original description: pacid=3717  
 5 PTHR10641:SlPhvul.007G20RNA biosynthtranscription factor (MYB) (original description: pacid=37  
 6 1.1.2.6 - PolyvPhvul.008G04not assigned.r no hits & (original description: pacid=37159669 transcri  
 7 PF12452 - ProPhvul.008G12not assigned.r no hits & (original description: pacid=37158036 transcri  
 8 PF12452 - ProPhvul.008G12not assigned.r no hits & (original description: pacid=37158036 transcri  
 9 K10838 - xeroPhvul.008G23DNA damage DNA repair protein (XPC) (original description: pacid=37:  
 10 PTHR23086:SlPhvul.009G15Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (origi  
 11 PTHR23086:SlPhvul.009G15Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (origi  
 12 K10838 - xeroPhvul.010G02DNA damage DNA repair protein (XPC) (original description: pacid=37:  
 13 **PTHR10366:SlPhvul.010G08Carbohydrate UDP-D-glucuronic acid 4-epimerase (original description:**  
 14 PF03168 - LatPhvul.010G11not assigned.ε (original description: pacid=37143932 transcript=Phvul.  
 15 PTHR12550:SlPhvul.011G02RNA biosynthtranscription factor (HUA2) (original description: pacid=ε  
 16 3.1.1.73 - FeruPhvul.001G02not assigned.ε (original description: pacid=37168114 transcript=Phvul.  
 17 K06965 - protPhvul.001G18Protein biosyr component DOM34 of DOM34-HBS1 aberrant mRNA del  
 18 PTHR22298:SlPhvul.001G20not assigned.ε (original description: pacid=37167724 transcript=Phvul.  
 19 PTHR21262:SlPhvul.001G20not assigned.ε (original description: pacid=37168990 transcript=Phvul.  
 20 KOG2160//KCPPhvul.001G25Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (origi  
 21 KOG2160//KCPPhvul.001G25Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (origi  
 22 PTHR31321:SlPhvul.002G06Cell wall orgar pectin methylesterase (original description: pacid=37174  
 23 PTHR27000:SlPhvul.002G11Protein modif protein kinase (LRR-VII) (original description: pacid=3717  
 24 O Phvul.002G13not assigned.r no hits & (original description: pacid=37178726 transcri  
 25 O Phvul.002G13not assigned.r no hits & (original description: pacid=37178726 transcri  
 26 PTHR32133:SlPhvul.002G18Protein home component UFO of SCF E3 ubiquitin ligase complex (orig  
 27 PTHR22844:SlPhvul.002G25not assigned.ε (original description: pacid=37174658 transcript=Phvul.  
 28 PTHR27001:SlPhvul.002G32Protein modif protein kinase (LRR-IX) (original description: pacid=3717:  
 29 PTHR10353:SlPhvul.003G04Enzyme classiiBeta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0  
 30 K14640 - soluiPhvul.003G06Solute transpc phosphate transporter (PHT2) (original description: pacid  
 31 PTHR24298:SlPhvul.003G07Enzyme classiiCytochrome P450 77A1 (Fragment) OS=Solanum melong  
 32 KOG0483 - TrPhvul.003G19RNA biosynthtranscription factor (HD-ZIP I/II) (original description: pac  
 33 KOG0483 - TrPhvul.003G19RNA biosynthtranscription factor (HD-ZIP I/II) (original description: pac  
 34 PTHR14140:SlPhvul.004G01not assigned.ε (original description: pacid=37162939 transcript=Phvul.  
 35 **K12817 - pre-iPhvul.005G03not assigned.r no hits & (original description: pacid=37152518 transcri**  
 36 K03504 - DNAPhvul.005G08Cell cycle orgacomponent POLD3 of DNA polymerase delta complex (oi  
 37 K03504 - DNAPhvul.005G08Cell cycle orgacomponent POLD3 of DNA polymerase delta complex (oi  
 38 K01595 - phosPhvul.005G09PhotosynthesiPEP carboxylase (original description: pacid=37154500 tr  
 39 PF13041 - PPFPhvul.005G17not assigned.ε (original description: pacid=37152686 transcript=Phvul.  
 40 PTHR32116:SlPhvul.006G03not assigned.ε (original description: pacid=37172111 transcript=Phvul.  
 41 PTHR10593:SlPhvul.007G19RNA biosynthC2H2 zinc finger transcription factor (original description  
 42 PTHR10593:SlPhvul.007G19RNA biosynthC2H2 zinc finger transcription factor (original description  
 43 PTHR36351:SlPhvul.007G26not assigned.r no hits & (original description: pacid=37165888 transcri  
 44 PTHR10159:SlPhvul.008G01not assigned.ε (original description: pacid=37161122 transcript=Phvul.  
 45 PTHR10159:SlPhvul.008G01not assigned.ε (original description: pacid=37161122 transcript=Phvul.  
 46 PTHR10159:SlPhvul.008G01not assigned.ε (original description: pacid=37161122 transcript=Phvul.

1 PTHR10159:SlPhvul.008G01 not assigned.ε (original description: pacid=37161122 transcript=Phvul.0  
2 PTHR10159:SlPhvul.008G01 not assigned.ε (original description: pacid=37161122 transcript=Phvul.0  
3 3.1.2.2//3.1.2 Phvul.008G05 not assigned.r no hits & (original description: pacid=37160794 transcri  
4 K13141 - inteḡPhvul.008G09 Protein transi SIEL plasmodesmata intercellular trafficking regulator pr  
5 K13141 - inteḡPhvul.008G09 Protein transi SIEL plasmodesmata intercellular trafficking regulator pr  
6 3.4.17.20 - CaPhvul.008G10 Protein home type-I-residues E3 ubiquitin ligase (PRT6) (original descri  
7 3.4.17.20 - CaPhvul.008G10 Protein home type-I-residues E3 ubiquitin ligase (PRT6) (original descri  
8 PTHR11850:SlPhvul.008G11 RNA biosynth transcription factor (BEL) (original description: pacid=371  
9 K05291 - phosPhvul.008G13 Protein modif component PIG-S of GPI transamidase complex (original  
10 PTHR33021:SlPhvul.008G20 not assigned.r no hits & (original description: pacid=37161432 transcri  
11 K09873 - aquaPhvul.009G10 Solute transp tonoplast intrinsic protein (TIP) (original description: pac  
12 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid  
13 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid  
14 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid  
15 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid  
16 0 Phvul.009G25 not assigned.r no hits & (original description: pacid=37149126 transcri  
17 0 Phvul.009G25 not assigned.r no hits & (original description: pacid=37149126 transcri  
18 PF00069//PF0Phvul.010G03 Enzyme classii G-type lectin S-receptor-like serine/threonine-protein kin  
19 PTHR12537:SlPhvul.011G06 not assigned.ε (original description: pacid=37156482 transcript=Phvul.0  
20 PF01453//PF0Phvul.011G17 Enzyme classii G-type lectin S-receptor-like serine/threonine-protein kin  
21 PF01453//PF0Phvul.011G17 Enzyme classii G-type lectin S-receptor-like serine/threonine-protein kin  
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pt=Phvul.004G110400.1 locus=Phvul.004G110400 ID=Phvul.004G110400.1.v2.1 annot-version=v2.1  
 59 transcript=Phvul.005G120700.3 locus=Phvul.005G120700 ID=Phvul.005G120700.3.v2.1 annot-v  
 59 transcript=Phvul.005G120700.3 locus=Phvul.005G120700 ID=Phvul.005G120700.3.v2.1 annot-v  
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 ranscript=Phvul.003G237300.1 locus=Phvul.003G237300 ID=Phvul.003G237300.1.v2.1 annot-versio  
 37147468 transcript=Phvul.003G285700.1 locus=Phvul.003G285700 ID=Phvul.003G285700.1.v2.1 ar  
 L848 transcript=Phvul.004G086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-  
 L848 transcript=Phvul.004G086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-  
 37173758 transcript=Phvul.006G068400.1 locus=Phvul.006G068400 ID=Phvul.006G068400.1.v2.1 a  
 on Specificity Factor (CPSF) complex (original description: pacid=37173223 transcript=Phvul.006G13  
 pt=Phvul.007G268300.1 locus=Phvul.007G268300 ID=Phvul.007G268300.1.v2.1 annot-version=v2.1  
 n: pacid=37160007 transcript=Phvul.008G036200.1 locus=Phvul.008G036200 ID=Phvul.008G03620  
 pt=Phvul.008G290700.1 locus=Phvul.008G290700 ID=Phvul.008G290700.1.v2.1 annot-version=v2.1  
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 019 transcript=Phvul.001G146900.1 locus=Phvul.001G146900 ID=Phvul.001G146900.1.v2.1 annot-  
 ase RKF3 OS=Arabidopsis thaliana (sp|p93050|rkf3\_arath : 454.0) & Enzyme classification.EC\_2 trar  
 ase RKF3 OS=Arabidopsis thaliana (sp|p93050|rkf3\_arath : 454.0) & Enzyme classification.EC\_2 trar  
 002G006700.1 locus=Phvul.002G006700 ID=Phvul.002G006700.1.v2.1 annot-version=v2.1) & AT-hc  
 pt=Phvul.002G059000.1 locus=Phvul.002G059000 ID=Phvul.002G059000.1.v2.1 annot-version=v2.1  
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 0|bgl46\_arath : 462.0) & Enzyme classification.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 272.9) (c  
 0|bgl46\_arath : 462.0) & Enzyme classification.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 272.9) (c  
 950 transcript=Phvul.003G099100.3 locus=Phvul.003G099100 ID=Phvul.003G099100.3.v2.1 annot-  
 950 transcript=Phvul.003G099100.3 locus=Phvul.003G099100 ID=Phvul.003G099100.3.v2.1 annot-  
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 53248 transcript=Phvul.004G037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 anno  
 53248 transcript=Phvul.004G037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 anno  
 pt=Phvul.004G049200.1 locus=Phvul.004G049200 ID=Phvul.004G049200.1.v2.1 annot-version=v2.1  
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 inal description: pacid=37153709 transcript=Phvul.005G022300.1 locus=Phvul.005G022300 ID=Ph





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2 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote  
3 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote  
4 pt=Phvul.008G050200.1 locus=Phvul.008G050200 ID=Phvul.008G050200.1.v2.1 annot-version=v2.1  
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6 protein (original description: pacid=37159576 transcript=Phvul.008G092200.3 locus=Phvul.008G0922  
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8 protein (original description: pacid=37159576 transcript=Phvul.008G092200.3 locus=Phvul.008G0922  
9  
10 ption: pacid=37159444 transcript=Phvul.008G106950.2 locus=Phvul.008G106950 ID=Phvul.008G10  
11  
12 ption: pacid=37159444 transcript=Phvul.008G106950.2 locus=Phvul.008G106950 ID=Phvul.008G10  
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14 159820 transcript=Phvul.008G114300.1 locus=Phvul.008G114300 ID=Phvul.008G114300.1.v2.1 ann  
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16 description: pacid=37158932 transcript=Phvul.008G130400.1 locus=Phvul.008G130400 ID=Phvul.0  
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18 pt=Phvul.008G203314.1 locus=Phvul.008G203314 ID=Phvul.008G203314.1.v2.1 annot-version=v2.1  
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22 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1  
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24 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1  
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26 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1  
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28 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1  
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33  
34 nase RLK1 OS=Arabidopsis thaliana (sp|q39202|rlk1\_arath : 652.0) & Enzyme classification.EC\_2 tra  
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36 011G062200.1 locus=Phvul.011G062200 ID=Phvul.011G062200.1.v2.1 annot-version=v2.1) & Pumil  
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38 nase At1g67520 OS=Arabidopsis thaliana (sp|o64793|y1675\_arath : 249.0) & Enzyme classification  
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40 nase At1g67520 OS=Arabidopsis thaliana (sp|o64793|y1675\_arath : 249.0) & Enzyme classification  
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9 e(50.3.2 : 323.5) (original description: pacid=37160089 transcript=Phvul.008G271000.1 locus=Phvul  
10 1)  
11 -version=v2.1) &  
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13 nnot-version=v2.1) &  
14 -version=v2.1) &  
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16 ersion=v2.1) &  
17 0200.1 locus=Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &  
18 1)  
19 0.1.v2.1 annot-version=v2.1) &  
20 1)  
21 ook motif nuclear-localized protein 17 OS=Arabidopsis thaliana (sp|q9lta2|ahl17\_arath : 179.0)  
22 0.1.v2.1 annot-version=v2.1) &  
23 version=v2.1) &  
24 version=v2.1) &  
25 nsferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 109.2) (original des  
26 nsferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 109.2) (original des  
27 ook motif nuclear-localized protein 13 OS=Arabidopsis thaliana (sp|q940i0|ahl13\_arath : 144.0)  
28 1)  
29 il.002G092900.2.v2.1 annot-version=v2.1) &  
30 il.002G092900.2.v2.1 annot-version=v2.1) &  
31 02G274500.1.v2.1 annot-version=v2.1) &  
32 =Phvul.002G315300.1.v2.1 annot-version=v2.1) &  
33 original description: pacid=37147256 transcript=Phvul.003G076700.2 locus=Phvul.003G076700 ID=  
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35 version=v2.1) &  
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42 vul.004G171500.6.v2.1 annot-version=v2.1) &  
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1 600.1.v2.1 annot-version=v2.1) &  
2 06G049100 ID=Phvul.006G049100.1.v2.1 annot-version=v2.1) &  
3 domain-containing protein At5g58720 OS=Arabidopsis thaliana (sp|o65573|y5872\_arath : 334.0)  
4 nt-version=v2.1) &  
5 annot-version=v2.1) &  
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2 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1\_arath : 348.0)  
3 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1\_arath : 348.0)  
4 1)  
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6 200 ID=Phvul.008G092200.3.v2.1 annot-version=v2.1) &  
7 200 ID=Phvul.008G092200.3.v2.1 annot-version=v2.1) &  
8 )6950.2.v2.1 annot-version=v2.1) &  
9 )6950.2.v2.1 annot-version=v2.1) &  
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12 08G130400.1.v2.1 annot-version=v2.1) &  
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21 1)  
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24 ansferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 103.4) (original de  
25 lio homolog 2 OS=Arabidopsis thaliana (sp|q9zw06|pum2\_arath : 992.0)  
26  
27 i.EC\_2 transferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 57.7) (orig  
28 i.EC\_2 transferases.EC\_2.7 transferase transferring phosphorus-containing group(50.2.7 : 57.7) (orig  
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31 ;cription: pacid=37170420 transcript=Phvul.001G147001.2 locus=Phvul.001G147001 ID=Phvul.001G  
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41 =Phvul.003G076700.2.v2.1 annot-version=v2.1) &  
42 =Phvul.003G076700.2.v2.1 annot-version=v2.1) &  
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Phvul.003G043600.2.v2.1 annot-version=v2.1) &

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description: pacid=37142844 transcript=Phvul.010G032000.1 locus=Phvul.010G032000 ID=Phvul.010

ginal description: pacid=37155309 transcript=Phvul.011G175000.2 locus=Phvul.011G175000 ID=Phv

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ld	H42_1	H42_2	H42_3	X42_1	X42_2	
cfa-miR-31	13		0	2	17	3
cpo-miR-31-5p	13		0	2	17	3
dno-miR-31-5p	13		0	2	17	3
ocu-miR-31-5p	13		0	2	17	3
aly-miR164a-5p	477	598		177	50	83
aly-miR164b-5p	477	598		177	50	83
aof-miR164	477	598		177	50	83
ata-miR164b-5p	477	598		177	50	83
ata-miR164c-5p	477	598		177	50	83
ath-miR164a	477	598		177	50	83
ath-miR164b-5p	477	598		177	50	83
atr-miR164a	477	598		177	50	83
atr-miR164b	477	598		177	50	83
bdi-miR164a-5p	477	598		177	50	83
bdi-miR164b	477	598		177	50	83
bdi-miR164e	477	598		177	50	83
bna-miR164a	477	598		177	50	83
bra-miR164a	477	598		177	50	83
cas-miR164	477	598		177	50	83
cme-miR164c	477	598		177	50	83
cme-miR164d	477	598		177	50	83
cpa-miR164a	477	598		177	50	83
cpa-miR164b	477	598		177	50	83
cpa-miR164c	477	598		177	50	83
csi-miR164a-5p	477	598		177	50	83
csi-miR164b-5p	477	598		177	50	83
csi-miR164c-5p	477	598		177	50	83
csi-miR164d-5p	477	598		177	50	83
ctr-miR164	477	598		177	50	83
fve-miR164a-5p	477	598		177	50	83
fve-miR164b	477	598		177	50	83
ghr-miR164	477	598		177	50	83
gma-miR164a	477	598		177	50	83
gma-miR164e	477	598		177	50	83
gma-miR164f	477	598		177	50	83
gma-miR164g	477	598		177	50	83
gma-miR164h	477	598		177	50	83
gma-miR164i	477	598		177	50	83
gma-miR164j	477	598		177	50	83
gma-miR164k	477	598		177	50	83
lus-miR164a	477	598		177	50	83
lus-miR164b	477	598		177	50	83



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3	lus-miR164c	477	598	177	50	83
4	lus-miR164d	477	598	177	50	83
5	lus-miR164e	477	598	177	50	83
6	mdm-miR164b	477	598	177	50	83
7	mdm-miR164c	477	598	177	50	83
8	mdm-miR164d	477	598	177	50	83
9	mdm-miR164e	477	598	177	50	83
10	mdm-miR164f	477	598	177	50	83
11	mes-miR164a	477	598	177	50	83
12	mes-miR164b	477	598	177	50	83
13	mes-miR164c	477	598	177	50	83
14	mtr-miR164a	477	598	177	50	83
15	mtr-miR164b	477	598	177	50	83
16	mtr-miR164c	477	598	177	50	83
17	nta-miR164a	477	598	177	50	83
18	nta-miR164b	477	598	177	50	83
19	osa-miR164a	477	598	177	50	83
20	osa-miR164b	477	598	177	50	83
21	osa-miR164f	477	598	177	50	83
22	ppe-miR164a	477	598	177	50	83
23	ppe-miR164b	477	598	177	50	83
24	ppe-miR164c	477	598	177	50	83
25	ptc-miR164a	477	598	177	50	83
26	ptc-miR164b	477	598	177	50	83
27	ptc-miR164c	477	598	177	50	83
28	ptc-miR164d	477	598	177	50	83
29	ptc-miR164e	477	598	177	50	83
30	rco-miR164a	477	598	177	50	83
31	rco-miR164b	477	598	177	50	83
32	rco-miR164c	477	598	177	50	83
33	sbi-miR164a	477	598	177	50	83
34	sbi-miR164d	477	598	177	50	83
35	sbi-miR164e	477	598	177	50	83
36	sly-miR164a-5p	477	598	177	50	83
37	sly-miR164b-5p	477	598	177	50	83
38	ssl-miR164a	477	598	177	50	83
39	ssl-miR164b	477	598	177	50	83
40	tae-miR164	477	598	177	50	83
41	tcc-miR164a	477	598	177	50	83
42	tcc-miR164b	477	598	177	50	83
43	vvi-miR164a	477	598	177	50	83
44	vvi-miR164c	477	598	177	50	83
45	vvi-miR164d	477	598	177	50	83
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3	zma-miR164a-5p	477	598	177	50	83
4	zma-miR164b-5p	477	598	177	50	83
5	zma-miR164c-5p	477	598	177	50	83
6	zma-miR164d-5p	477	598	177	50	83
7	zma-miR164e-5p	477	598	177	50	83
8	zma-miR164g-5p	477	598	177	50	83
9	bra-miR164e-5p	482	598	180	50	83
10	bta-miR-451	86	276	3131	81	55
11	cja-miR-451	86	276	3131	81	55
12	cpo-miR-451-5p	86	276	3131	81	55
13	dno-miR-451-5p	86	276	3131	81	55
14	gga-miR-451	86	276	3131	81	55
15	oan-miR-451	86	276	3131	81	55
16	ocu-miR-451-5p	86	276	3131	81	55
17	oha-miR-451-??	86	276	3131	81	55
18	tgu-miR-451	86	276	3131	81	55
19	aca-miR-451-5p	33	261	1822	29	15
20	cfa-miR-451	33	261	1822	29	15
21	cgr-miR-451a	33	261	1822	29	15
22	dre-miR-451	33	261	1822	29	15
23	hsa-miR-451a	33	261	1822	29	15
24	mml-miR-451	33	261	1822	29	15
25	mmu-miR-451a	33	261	1822	29	15
26	ppy-miR-451	33	261	1822	29	15
27	ptr-miR-451	33	261	1822	29	15
28	rno-miR-451-5p	33	261	1822	29	15
29	ssc-miR-451	33	261	1822	29	15
30	xtr-miR-451	33	261	1822	29	15
31	ebv-miR-BART8-3p	0	0	1	0	0
32	ebv-miR-BART1-3p	0	0	1	0	0
33	ebv-miR-BART1-5p	0	0	1	0	0
34	ebv-miR-BART17-5p	0	0	0	0	0
35	ebv-miR-BART6-3p	0	0	0	0	0
36	ebv-miR-BART17-3p	0	0	0	0	0
37	ebv-miR-BART6-5p	0	0	1	0	0
38	ebv-miR-BART7-5p	0	0	0	0	0
39	ebv-miR-BART19-3p	0	0	0	0	0
40	ebv-miR-BART14-5p	0	0	0	0	0
41	ebv-miR-BART2-5p	0	0	1	0	0
42	ebv-miR-BART5-5p	0	0	1	0	0
43	ebv-miR-BART9-3p	0	0	2	0	0
44	ebv-miR-BART22	0	0	5	0	0
45	rlcv-miR-rL1-6-3p	0	0	11	0	0
46	ebv-miR-BART10-3p	0	0	2	0	0
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3	ebv-miR-BART7-3p	0	0	2	0	0
4	ebv-miR-BART11-5p	0	0	2	0	0
5	ebv-miR-BART8-5p	0	0	3	0	0
6	efu-miR-192	3	5	9	5	2
7	cfa-miR-192	0	2	3	2	1
8	chi-miR-192-5p	0	2	3	2	1
9	cpo-miR-192-5p	0	2	3	2	1
10	eca-miR-192	0	2	3	2	1
11	ggo-miR-192	0	2	3	2	1
12	hsa-miR-192-5p	0	2	3	2	1
13	mml-miR-192-5p	0	2	3	2	1
14	mmu-miR-192-5p	0	2	3	2	1
15	nle-miR-192	0	2	3	2	1
16	oan-miR-192-5p	0	2	3	2	1
17	oga-miR-192	0	2	3	2	1
18	ppa-miR-192	0	2	3	2	1
19	ppy-miR-192	0	2	3	2	1
20	ptr-miR-192	0	2	3	2	1
21	rno-miR-192-5p	0	2	3	2	1
22	ssc-miR-192	0	2	3	2	1
23	tch-miR-192-5p	0	2	3	2	1
24	bta-miR-192	3	5	5	4	2
25	cgr-miR-192	2	4	4	3	2
26	oar-miR-127	5	2	39	5	6
27	age-miR-127	5	2	39	5	6
28	bta-miR-127	5	2	39	5	6
29	cfa-miR-127	5	2	39	5	6
30	cgr-miR-127	5	2	39	5	6
31	cpo-miR-127-3p	5	2	39	5	6
32	dma-miR-127	5	2	39	5	6
33	dno-miR-127-3p	5	2	39	5	6
34	eca-miR-127	5	2	39	5	6
35	hsa-miR-127-3p	5	2	39	5	6
36	lla-miR-127	5	2	39	5	6
37	mml-miR-127-3p	5	2	39	5	6
38	mmu-miR-127-3p	5	2	39	5	6
39	mne-miR-127	5	2	39	5	6
40	nle-miR-127	5	2	39	5	6
41	ocu-miR-127-3p	5	2	39	5	6
42	oga-miR-127	5	2	39	5	6
43	pal-miR-127-3p	5	2	39	5	6
44	pha-miR-127	5	2	39	5	6
45	ppa-miR-127	5	2	39	5	6
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3	ppy-miR-127	5	2	39	5	6
4	ptr-miR-127	5	2	39	5	6
5	rno-miR-127-3p	5	2	39	5	6
6	sbo-miR-127	5	2	39	5	6
7	sla-miR-127	5	2	39	5	6
8	sla-miR-127	5	2	39	5	6
9	ssc-miR-127	5	2	39	5	6
10	ssc-miR-127	5	2	39	5	6
11	tch-miR-127-3p	5	2	39	5	6
12	efu-miR-127	5	2	40	5	6
13	efu-miR-127	5	2	40	5	6
14	ola-miR-7	14	28	15	9	6
15	aae-miR-7	14	28	15	9	6
16	abu-miR-7	14	28	15	9	6
17	abu-miR-7	14	28	15	9	6
18	aca-miR-7-5p	14	28	15	9	6
19	aga-miR-7	14	28	15	9	6
20	ame-miR-7-5p	14	28	15	9	6
21	ame-miR-7-5p	14	28	15	9	6
22	ami-miR-7a-5p	14	28	15	9	6
23	bbe-miR-7-5p	14	28	15	9	6
24	bfl-miR-7	14	28	15	9	6
25	bfl-miR-7	14	28	15	9	6
26	bmo-miR-7-5p	14	28	15	9	6
27	cfa-miR-7	14	28	15	9	6
28	cgr-miR-7a	14	28	15	9	6
29	cgr-miR-7a	14	28	15	9	6
30	cqu-miR-7	14	28	15	9	6
31	csa-miR-7	14	28	15	9	6
32	csa-miR-7	14	28	15	9	6
33	dan-miR-7	14	28	15	9	6
34	der-miR-7	14	28	15	9	6
35	dgr-miR-7	14	28	15	9	6
36	dme-miR-7-5p	14	28	15	9	6
37	dme-miR-7-5p	14	28	15	9	6
38	dmo-miR-7	14	28	15	9	6
39	dpe-miR-7	14	28	15	9	6
40	dps-miR-7	14	28	15	9	6
41	dps-miR-7	14	28	15	9	6
42	dpu-miR-7	14	28	15	9	6
43	dre-miR-7a	14	28	15	9	6
44	dse-miR-7	14	28	15	9	6
45	dse-miR-7	14	28	15	9	6
46	dsi-miR-7	14	28	15	9	6
47	dwi-miR-7	14	28	15	9	6
48	dya-miR-7	14	28	15	9	6
49	dya-miR-7	14	28	15	9	6
50	eca-miR-7	14	28	15	9	6
51	gmo-miR-7c-5p	14	28	15	9	6
52	ipu-miR-7a	14	28	15	9	6
53	ipu-miR-7a	14	28	15	9	6
54	isc-miR-7	14	28	15	9	6
55	lva-miR-7-5p	14	28	15	9	6
56	mml-miR-7	14	28	15	9	6
57	mml-miR-7	14	28	15	9	6
58	mmu-miR-7a-5p	14	28	15	9	6
59	mze-miR-7b	14	28	15	9	6
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3	nbr-miR-7	14	28	15	9	6
4	nlo-miR-7	14	28	15	9	6
5	nvi-miR-7	14	28	15	9	6
6	oan-miR-7-5p	14	28	15	9	6
7	oni-miR-7	14	28	15	9	6
8	pma-miR-7a-5p	14	28	15	9	6
9	pmi-miR-7-5p	14	28	15	9	6
10	pony-miR-7	14	28	15	9	6
11	ptr-miR-7	14	28	15	9	6
12	rno-miR-7a-5p	14	28	15	9	6
13	sko-miR-7-5p	14	28	15	9	6
14	spu-miR-7	14	28	15	9	6
15	ssa-miR-7a-5p	14	28	15	9	6
16	tgu-miR-7-5p	14	28	15	9	6
17	tni-miR-7	14	28	15	9	6
18	bta-miR-411a	6	1	21	8	2
19	cfa-miR-411	6	1	21	8	2
20	ggo-miR-411	6	1	21	8	2
21	oar-miR-411a-5p	6	1	21	8	2
22	cja-miR-411	6	1	14	6	1
23	cpo-miR-411-5p	6	1	14	6	1
24	dno-miR-411-5p	6	1	14	6	1
25	eca-miR-411	6	1	14	6	1
26	hsa-miR-411-5p	6	1	14	6	1
27	mml-miR-411-5p	6	1	14	6	1
28	mmr-miR-411a	6	1	14	6	1
29	mmu-miR-411-5p	6	1	14	6	1
30	ocu-miR-411-5p	6	1	14	6	1
31	oga-miR-411a	6	1	14	6	1
32	pha-miR-411a	6	1	14	6	1
33	ppa-miR-411a	6	1	14	6	1
34	ppy-miR-411	6	1	14	6	1
35	ptr-miR-411	6	1	14	6	1
36	rno-miR-411-5p	6	1	14	6	1
37	tch-miR-411-5p	6	1	14	6	1
38	aca-miR-10a-5p	8	5	15	4	5
39	age-miR-10a	8	5	15	4	5
40	ami-miR-10a-5p	8	5	15	4	5
41	bfl-miR-10a-5p	8	5	15	4	5
42	bta-miR-10a	8	5	15	4	5
43	cli-miR-10a-5p	8	5	15	4	5
44	dno-miR-10a-5p	8	5	15	4	5
45	eca-miR-10a	8	5	15	4	5
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3	ggo-miR-10a	8	5	15	4	5
4	hsa-miR-10a-5p	8	5	15	4	5
5	mdo-miR-10a-5p	8	5	15	4	5
6	mml-miR-10a-5p	8	5	15	4	5
7	mmu-miR-10a-5p	8	5	15	4	5
8	oha-miR-10a-5p	8	5	15	4	5
9	oha-miR-10a-5p	8	5	15	4	5
10	oha-miR-10a-5p	8	5	15	4	5
11	pbv-miR-10a-5p	8	5	15	4	5
12	ppa-miR-10a	8	5	15	4	5
13	ppy-miR-10a	8	5	15	4	5
14	ptr-miR-10a	8	5	15	4	5
15	rno-miR-10a-5p	8	5	15	4	5
16	rno-miR-10a-5p	8	5	15	4	5
17	rno-miR-10a-5p	8	5	15	4	5
18	ska-miR-10a	8	5	15	4	5
19	sla-miR-10a	8	5	15	4	5
20	xtr-miR-10a	8	5	15	4	5
21	xtr-miR-10a	8	5	15	4	5
22	xla-miR-10a-5p	8	5	16	4	5
23	api-miR-7	97	187	35	103	49
24	bdo-miR-7	97	187	35	103	49
25	bdo-miR-7	97	187	35	103	49
26	bta-miR-7	97	187	35	103	49
27	ccr-miR-7a	97	187	35	103	49
28	chi-miR-7-5p	97	187	35	103	49
29	chi-miR-7-5p	97	187	35	103	49
30	cja-miR-7	97	187	35	103	49
31	cli-miR-7a-5p	97	187	35	103	49
32	cli-miR-7a-5p	97	187	35	103	49
33	cpo-miR-7-5p	97	187	35	103	49
34	dno-miR-7-5p	97	187	35	103	49
35	dqu-miR-7-5p	97	187	35	103	49
36	dvi-miR-7-5p	97	187	35	103	49
37	dvi-miR-7-5p	97	187	35	103	49
38	efu-miR-7a	97	187	35	103	49
39	efu-miR-7b	97	187	35	103	49
40	efu-miR-7c	97	187	35	103	49
41	efu-miR-7c	97	187	35	103	49
42	gmo-miR-7a-5p	97	187	35	103	49
43	hsa-miR-7-5p	97	187	35	103	49
44	lgi-miR-7	97	187	35	103	49
45	lgi-miR-7	97	187	35	103	49
46	mse-miR-7	97	187	35	103	49
47	mze-miR-7a	97	187	35	103	49
48	ocu-miR-7a-5p	97	187	35	103	49
49	ocu-miR-7a-5p	97	187	35	103	49
50	oha-miR-7-5p	97	187	35	103	49
51	pal-miR-7b-5p	97	187	35	103	49
52	pbv-miR-7-5p	97	187	35	103	49
53	pbv-miR-7-5p	97	187	35	103	49
54	pca-miR-7-5p	97	187	35	103	49
55	ssc-miR-7-5p	97	187	35	103	49
56	tca-miR-7-5p	97	187	35	103	49
57	tca-miR-7-5p	97	187	35	103	49
58	tcf-miR-7	97	187	35	103	49
59	tch-miR-7-5p	97	187	35	103	49
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3	tur-miR-7-5p	97	187	35	103	49
4	abu-let-7a	261	217	212	242	138
5	aca-let-7a-5p	261	217	212	242	138
6	ami-let-7a-5p	261	217	212	242	138
7	asu-let-7-5p	261	217	212	242	138
8	bbe-let-7a-5p	261	217	212	242	138
9	bfl-let-7a-5p	261	217	212	242	138
10	bma-let-7	261	217	212	242	138
11	bta-let-7a-5p	261	217	212	242	138
12	cbn-let-7	261	217	212	242	138
13	cbr-let-7	261	217	212	242	138
14	ccr-let-7a	261	217	212	242	138
15	cel-let-7-5p	261	217	212	242	138
16	cfa-let-7a	261	217	212	242	138
17	cgr-let-7a	261	217	212	242	138
18	chi-let-7a-5p	261	217	212	242	138
19	cja-let-7a	261	217	212	242	138
20	cli-let-7a-5p	261	217	212	242	138
21	cpi-let-7a-5p	261	217	212	242	138
22	cpo-let-7a-5p	261	217	212	242	138
23	crm-let-7	261	217	212	242	138
24	dma-let-7a	261	217	212	242	138
25	dno-let-7a-5p	261	217	212	242	138
26	dre-let-7a	261	217	212	242	138
27	eca-let-7a	261	217	212	242	138
28	fru-let-7a	261	217	212	242	138
29	gga-let-7a-5p	261	217	212	242	138
30	gga-let-7j-5p	261	217	212	242	138
31	gmo-let-7a-5p	261	217	212	242	138
32	hpo-let-7-5p	261	217	212	242	138
33	hsa-let-7a-5p	261	217	212	242	138
34	ipu-let-7a	261	217	212	242	138
35	lgi-let-7	261	217	212	242	138
36	mdo-let-7a-5p	261	217	212	242	138
37	mml-let-7a-5p	261	217	212	242	138
38	mmr-let-7a	261	217	212	242	138
39	mmu-let-7a-5p	261	217	212	242	138
40	mze-let-7a	261	217	212	242	138
41	nbr-let-7a	261	217	212	242	138
42	nle-let-7a	261	217	212	242	138
43	oar-let-7a	261	217	212	242	138
44	ocu-let-7a-5p	261	217	212	242	138
45	oga-let-7a	261	217	212	242	138
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3	oha-let-7a	261	217	212	242	138
4	oha-let-7a-5p	261	217	212	242	138
5	ola-let-7a	261	217	212	242	138
6	oni-let-7a	261	217	212	242	138
7	oni-let-7a	261	217	212	242	138
8	pal-let-7a-5p	261	217	212	242	138
9	pal-let-7a-5p	261	217	212	242	138
10	pbv-let-7a-5p	261	217	212	242	138
11	pha-let-7a	261	217	212	242	138
12	pha-let-7a	261	217	212	242	138
13	pma-let-7a	261	217	212	242	138
14	ppy-let-7a	261	217	212	242	138
15	ppa-let-7a	261	217	212	242	138
16	ppc-let-7	261	217	212	242	138
17	ppc-let-7	261	217	212	242	138
18	ppy-let-7a	261	217	212	242	138
19	pte-let-7-5p	261	217	212	242	138
20	ptr-let-7a	261	217	212	242	138
21	ptr-let-7a	261	217	212	242	138
22	rno-let-7a-5p	261	217	212	242	138
23	sbo-let-7a	261	217	212	242	138
24	sbo-let-7a	261	217	212	242	138
25	sbo-let-7a	261	217	212	242	138
26	ssa-let-7a-5p	261	217	212	242	138
27	ssc-let-7a	261	217	212	242	138
28	tgu-let-7a-5p	261	217	212	242	138
29	tgu-let-7a-5p	261	217	212	242	138
30	tni-let-7a	261	217	212	242	138
31	xla-let-7a-5p	261	217	212	242	138
32	xtr-let-7a	261	217	212	242	138
33	xtr-let-7a	261	217	212	242	138
34	prd-let-7-5p	264	220	219	248	141
35	cgr-miR-196b	39	3	4	18	27
36	cja-miR-196b	39	3	4	18	27
37	cja-miR-196b	39	3	4	18	27
38	eca-miR-196b	39	3	4	18	27
39	ggo-miR-196b	39	3	4	18	27
40	ggo-miR-196b	39	3	4	18	27
41	hsa-miR-196b-5p	39	3	4	18	27
42	mdo-miR-196a-5p	39	3	4	18	27
43	mml-miR-196b-5p	39	3	4	18	27
44	mml-miR-196b-5p	39	3	4	18	27
45	mmr-miR-196b	39	3	4	18	27
46	mmu-miR-196b-5p	39	3	4	18	27
47	nle-miR-196b	39	3	4	18	27
48	oga-miR-196b	39	3	4	18	27
49	oga-miR-196b	39	3	4	18	27
50	pal-miR-196b-5p	39	3	4	18	27
51	ppy-miR-196b	39	3	4	18	27
52	ppy-miR-196b	39	3	4	18	27
53	ptr-miR-196b	39	3	4	18	27
54	rno-miR-196b-5p	39	3	4	18	27
55	ssc-miR-196b-5p	39	3	4	18	27
56	efu-miR-34a	69	10	99	57	33
57	ami-miR-34a-5p	69	10	99	57	33
58	ami-miR-34a-5p	69	10	99	57	33
59	cja-miR-34a	69	10	99	57	33
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2						
3	gga-miR-34a-5p	69	10	99	57	33
4	mdo-miR-34a-5p	69	10	99	57	33
5	oha-miR-34a-5p	69	10	99	57	33
6	tch-miR-34a-5p	69	10	99	57	33
7	tch-miR-34a-5p	69	10	99	57	33
8	xtr-miR-34a	69	10	99	57	33
9	xtr-miR-34a	69	10	99	57	33
10	bta-miR-196b	45	4	4	26	31
11	cfa-miR-196b	45	4	4	26	31
12	cpo-miR-196b-5p	45	4	4	26	31
13	cpo-miR-196b-5p	45	4	4	26	31
14	dno-miR-196b-5p	45	4	4	26	31
15	ocu-miR-196b-5p	45	4	4	26	31
16	abu-let-7b	262	161	189	198	135
17	abu-let-7b	262	161	189	198	135
18	ami-let-7b-5p	262	161	189	198	135
19	bta-let-7b	262	161	189	198	135
20	ccb-let-7b	262	161	189	198	135
21	ccb-let-7b	262	161	189	198	135
22	cfa-let-7b	262	161	189	198	135
23	cgr-let-7b	262	161	189	198	135
24	chi-let-7b-5p	262	161	189	198	135
25	chi-let-7b-5p	262	161	189	198	135
26	cja-let-7b	262	161	189	198	135
27	cpi-let-7b-5p	262	161	189	198	135
28	cpo-let-7b-5p	262	161	189	198	135
29	cpo-let-7b-5p	262	161	189	198	135
30	dma-let-7b	262	161	189	198	135
31	dno-let-7b-5p	262	161	189	198	135
32	dno-let-7b-5p	262	161	189	198	135
33	dre-let-7b	262	161	189	198	135
34	fru-let-7b	262	161	189	198	135
35	gga-let-7b	262	161	189	198	135
36	hsa-let-7b-5p	262	161	189	198	135
37	hsa-let-7b-5p	262	161	189	198	135
38	mdo-let-7b	262	161	189	198	135
39	mml-let-7b-5p	262	161	189	198	135
40	mmr-let-7b	262	161	189	198	135
41	mmr-let-7b	262	161	189	198	135
42	mmu-let-7b-5p	262	161	189	198	135
43	mze-let-7b	262	161	189	198	135
44	nbr-let-7b	262	161	189	198	135
45	nbr-let-7b	262	161	189	198	135
46	oan-let-7b-5p	262	161	189	198	135
47	ocu-let-7b-5p	262	161	189	198	135
48	oga-let-7b	262	161	189	198	135
49	oga-let-7b	262	161	189	198	135
50	oha-let-7b-5p	262	161	189	198	135
51	oni-let-7b	262	161	189	198	135
52	pbv-let-7b-5p	262	161	189	198	135
53	pha-let-7b	262	161	189	198	135
54	pha-let-7b	262	161	189	198	135
55	ppy-let-7b	262	161	189	198	135
56	pol-let-7b-5p	262	161	189	198	135
57	ppa-let-7b	262	161	189	198	135
58	ppa-let-7b	262	161	189	198	135
59	ppy-let-7b	262	161	189	198	135
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2						
3	ptr-let-7b	262	161	189	198	135
4	rno-let-7b-5p	262	161	189	198	135
5	sbo-let-7b	262	161	189	198	135
6	ssa-let-7b-5p	262	161	189	198	135
7	tgu-let-7b-5p	262	161	189	198	135
8	tni-let-7b	262	161	189	198	135
9						
10	abu-miR-34	58	9	85	42	29
11	age-miR-34a	58	9	85	42	29
12	bta-miR-34a	58	9	85	42	29
13	ccb-miR-34	58	9	85	42	29
14	cfa-miR-34a	58	9	85	42	29
15	cgr-miR-34a	58	9	85	42	29
16	chi-miR-34a	58	9	85	42	29
17	cli-miR-34a-5p	58	9	85	42	29
18	cpi-miR-34a-5p	58	9	85	42	29
19	cpo-miR-34a-5p	58	9	85	42	29
20	dno-miR-34a-5p	58	9	85	42	29
21	dre-miR-34a	58	9	85	42	29
22	eca-miR-34a	58	9	85	42	29
23	ggo-miR-34a	58	9	85	42	29
24	gmo-miR-34-5p	58	9	85	42	29
25	hsa-miR-34a-5p	58	9	85	42	29
26	ipu-miR-34a	58	9	85	42	29
27	lla-miR-34a	58	9	85	42	29
28	mml-miR-34a-5p	58	9	85	42	29
29	mmr-miR-34a	58	9	85	42	29
30	mmu-miR-34a-5p	58	9	85	42	29
31	mne-miR-34a	58	9	85	42	29
32	mze-miR-34	58	9	85	42	29
33	nbr-miR-34	58	9	85	42	29
34	nle-miR-34a	58	9	85	42	29
35	ocu-miR-34a-5p	58	9	85	42	29
36	oga-miR-34a	58	9	85	42	29
37	oni-miR-34	58	9	85	42	29
38	pal-miR-34a-5p	58	9	85	42	29
39	pbv-miR-34a-5p	58	9	85	42	29
40	pony-miR-34	58	9	85	42	29
41	ppa-miR-34a	58	9	85	42	29
42	ppy-miR-34a	58	9	85	42	29
43	ptr-miR-34a	58	9	85	42	29
44	rno-miR-34a-5p	58	9	85	42	29
45	sla-miR-34a	58	9	85	42	29
46	ssc-miR-34a	58	9	85	42	29
47						
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2						
3	tgu-miR-34a	58	9	85	42	29
4	cja-miR-222	28	20	33	32	14
5	cpi-miR-222a-3p	28	20	33	32	14
6	gmo-miR-222-3p	28	20	33	32	14
7	gmo-miR-222-3p	28	20	33	32	14
8	mmu-miR-222-3p	28	20	33	32	14
9	mmu-miR-222-3p	28	20	33	32	14
10	pal-miR-222-3p	28	20	33	32	14
11	xla-miR-222-3p	28	20	33	32	14
12	xla-miR-222-3p	28	20	33	32	14
13	ccr-miR-100	31	0	40	10	8
14	cgr-miR-100-5p	31	0	40	10	8
15	chi-miR-100-5p	31	0	40	10	8
16	cpi-miR-100-5p	31	0	40	10	8
17	cpi-miR-100-5p	31	0	40	10	8
18	dma-miR-100	31	0	40	10	8
19	mdo-miR-100-5p	31	0	40	10	8
20	mdo-miR-100-5p	31	0	40	10	8
21	pmi-miR-100-5p	31	0	40	10	8
22	sbo-miR-100	31	0	40	10	8
23	sha-miR-100	31	0	40	10	8
24	sha-miR-100	31	0	40	10	8
25	tgu-miR-100-5p	31	0	40	10	8
26	hme-let-7	86	41	76	62	44
27	pca-let-7-5p	86	41	76	62	44
28	ame-let-7-5p	86	41	76	62	43
29	ame-let-7-5p	86	41	76	62	43
30	bdo-let-7	86	41	76	62	43
31	bmo-let-7-5p	86	41	76	62	43
32	bmo-let-7-5p	86	41	76	62	43
33	cte-let-7	86	41	76	62	43
34	dan-let-7	86	41	76	62	43
35	der-let-7	86	41	76	62	43
36	dgr-let-7	86	41	76	62	43
37	dgr-let-7	86	41	76	62	43
38	dme-let-7-5p	86	41	76	62	43
39	dmo-let-7	86	41	76	62	43
40	dpe-let-7	86	41	76	62	43
41	dpe-let-7	86	41	76	62	43
42	dps-let-7	86	41	76	62	43
43	dqu-let-7-5p	86	41	76	62	43
44	dse-let-7	86	41	76	62	43
45	dse-let-7	86	41	76	62	43
46	dsi-let-7	86	41	76	62	43
47	dvi-let-7	86	41	76	62	43
48	dwi-let-7	86	41	76	62	43
49	dwi-let-7	86	41	76	62	43
50	dya-let-7	86	41	76	62	43
51	ggo-let-7a	86	41	76	62	43
52	isc-let-7	86	41	76	62	43
53	isc-let-7	86	41	76	62	43
54	ngi-let-7	86	41	76	62	43
55	nvi-let-7	86	41	76	62	43
56	ola-let-7a-5p	86	41	76	62	43
57	ola-let-7a-5p	86	41	76	62	43
58	sha-let-7a	86	41	76	62	43
59	abu-miR-222	123	106	185	150	53
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2						
3	age-miR-222	123	106	185	150	53
4	ami-miR-222a-3p	123	106	185	150	53
5	cgr-miR-222-3p	123	106	185	150	53
6	chi-miR-222-3p	123	106	185	150	53
7	cli-miR-222a-3p	123	106	185	150	53
8	cli-miR-222a-3p	123	106	185	150	53
9	cli-miR-222a-3p	123	106	185	150	53
10	cpo-miR-222-3p	123	106	185	150	53
11	dma-miR-222	123	106	185	150	53
12	dno-miR-222-3p	123	106	185	150	53
13	dno-miR-222-3p	123	106	185	150	53
14	dre-miR-222a-3p	123	106	185	150	53
15	fru-miR-222	123	106	185	150	53
16	gga-miR-222a	123	106	185	150	53
17	gga-miR-222a	123	106	185	150	53
18	mdo-miR-222a	123	106	185	150	53
19	mmr-miR-222	123	106	185	150	53
20	mze-miR-222	123	106	185	150	53
21	mze-miR-222	123	106	185	150	53
22	nbr-miR-222	123	106	185	150	53
23	nle-miR-222	123	106	185	150	53
24	ocu-miR-222-3p	123	106	185	150	53
25	ocu-miR-222-3p	123	106	185	150	53
26	oga-miR-222	123	106	185	150	53
27	oha-miR-222a-3p	123	106	185	150	53
28	oni-miR-222	123	106	185	150	53
29	oni-miR-222	123	106	185	150	53
30	pbv-miR-222a-3p	123	106	185	150	53
31	pha-miR-222	123	106	185	150	53
32	pha-miR-222	123	106	185	150	53
33	ppy-miR-222	123	106	185	150	53
34	ppa-miR-222	123	106	185	150	53
35	ssa-miR-222a-3p	123	106	185	150	53
36	ssc-miR-222	123	106	185	150	53
37	ssc-miR-222	123	106	185	150	53
38	tgu-miR-222-3p	123	106	185	150	53
39	tni-miR-222	123	106	185	150	53
40	xtr-miR-222	123	106	185	150	53
41	xtr-miR-222	123	106	185	150	53
42	efu-let-7f	201	112	115	183	125
43	aca-let-7f-5p	199	112	115	182	125
44	bta-let-7f	199	112	115	182	125
45	bta-let-7f	199	112	115	182	125
46	cfa-let-7f	199	112	115	182	125
47	cgr-let-7f	199	112	115	182	125
48	chi-let-7f-5p	199	112	115	182	125
49	chi-let-7f-5p	199	112	115	182	125
50	cja-let-7f	199	112	115	182	125
51	cli-let-7f-5p	199	112	115	182	125
52	cpi-let-7f-5p	199	112	115	182	125
53	cpi-let-7f-5p	199	112	115	182	125
54	cpo-let-7f-5p	199	112	115	182	125
55	dma-let-7f	199	112	115	182	125
56	dno-let-7f-5p	199	112	115	182	125
57	dno-let-7f-5p	199	112	115	182	125
58	dre-let-7f	199	112	115	182	125
59	eca-let-7f	199	112	115	182	125
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3	gga-let-7f-5p	199	112	115	182	125
4	gmo-let-7f-5p	199	112	115	182	125
5	gmo-let-7f-5p	199	112	115	182	125
6	hsa-let-7f-5p	199	112	115	182	125
7	ipu-let-7f	199	112	115	182	125
8	mdo-let-7f-5p	199	112	115	182	125
9	mml-let-7f-5p	199	112	115	182	125
10	mml-let-7f-5p	199	112	115	182	125
11	mmr-let-7f	199	112	115	182	125
12	mmu-let-7f-5p	199	112	115	182	125
13	mmu-let-7f-5p	199	112	115	182	125
14	nle-let-7f	199	112	115	182	125
15	oan-let-7f-5p	199	112	115	182	125
16	ocu-let-7f-5p	199	112	115	182	125
17	ocu-let-7f-5p	199	112	115	182	125
18	oga-let-7f	199	112	115	182	125
19	oha-let-7f-5p	199	112	115	182	125
20	oni-let-7f	199	112	115	182	125
21	oni-let-7f	199	112	115	182	125
22	pal-let-7f-5p	199	112	115	182	125
23	pal-let-7f-5p	199	112	115	182	125
24	pbv-let-7f-5p	199	112	115	182	125
25	pha-let-7f	199	112	115	182	125
26	ppa-let-7f	199	112	115	182	125
27	ppy-let-7f	199	112	115	182	125
28	ptr-let-7f	199	112	115	182	125
29	ptr-let-7f	199	112	115	182	125
30	rno-let-7f-5p	199	112	115	182	125
31	sbo-let-7f	199	112	115	182	125
32	ssc-let-7f-5p	199	112	115	182	125
33	ssc-let-7f-5p	199	112	115	182	125
34	tch-let-7f-5p	199	112	115	182	125
35	tgu-let-7f-5p	199	112	115	182	125
36	xla-let-7f-5p	199	112	115	182	125
37	xla-let-7f-5p	199	112	115	182	125
38	xtr-let-7f	199	112	115	182	125
39	bfl-miR-100-5p	57	2	301	35	20
40	dpu-miR-100	57	2	301	35	20
41	dpu-miR-100	57	2	301	35	20
42	hpo-miR-100-5p	57	2	301	35	20
43	isc-miR-100	57	2	301	35	20
44	abu-let-7i	305	162	122	253	165
45	aca-let-7i-5p	305	162	122	253	165
46	aca-let-7i-5p	305	162	122	253	165
47	bta-let-7i	305	162	122	253	165
48	chi-let-7i-5p	305	162	122	253	165
49	chi-let-7i-5p	305	162	122	253	165
50	cja-let-7i	305	162	122	253	165
51	cpi-let-7i-5p	305	162	122	253	165
52	cpi-let-7i-5p	305	162	122	253	165
53	cpo-let-7i-5p	305	162	122	253	165
54	dno-let-7i-5p	305	162	122	253	165
55	dre-let-7i	305	162	122	253	165
56	fru-let-7i	305	162	122	253	165
57	fru-let-7i	305	162	122	253	165
58	gmo-let-7i-5p	305	162	122	253	165
59	hsa-let-7i-5p	305	162	122	253	165
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2						
3	ipu-let-7i	305	162	122	253	165
4	mml-let-7i-5p	305	162	122	253	165
5	mmu-let-7i-5p	305	162	122	253	165
6	mze-let-7i	305	162	122	253	165
7	nbr-let-7i	305	162	122	253	165
8	nle-let-7i	305	162	122	253	165
9	oar-let-7i	305	162	122	253	165
10	ocu-let-7i-5p	305	162	122	253	165
11	oga-let-7i	305	162	122	253	165
12	oha-let-7i-5p	305	162	122	253	165
13	oni-let-7i	305	162	122	253	165
14	pal-let-7i-5p	305	162	122	253	165
15	pbv-let-7i-5p	305	162	122	253	165
16	pha-let-7i	305	162	122	253	165
17	ppy-let-7i	305	162	122	253	165
18	ppa-let-7i	305	162	122	253	165
19	ppy-let-7i	305	162	122	253	165
20	ptr-let-7i	305	162	122	253	165
21	rno-let-7i-5p	305	162	122	253	165
22	ssa-let-7i-5p	305	162	122	253	165
23	tch-let-7i-5p	305	162	122	253	165
24	tgu-let-7i-5p	305	162	122	253	165
25	tni-let-7i	305	162	122	253	165
26	cli-let-7i-5p	309	162	123	256	165
27	asu-miR-100a-5p	57	3	311	35	20
28	prd-miR-100-5p	57	3	311	35	20
29	oha-miR-100-5p	47	2	288	32	16
30	aae-miR-100	47	2	288	31	16
31	abu-miR-100	47	2	288	31	16
32	aca-miR-100	47	2	288	31	16
33	aga-miR-100	47	2	288	31	16
34	age-miR-100	47	2	288	31	16
35	ame-miR-100-5p	47	2	288	31	16
36	ami-miR-100-5p	47	2	288	31	16
37	bbe-miR-100-5p	47	2	288	31	16
38	bma-miR-100b	47	2	288	31	16
39	bmo-miR-100	47	2	288	31	16
40	bta-miR-100	47	2	288	31	16
41	cja-miR-100	47	2	288	31	16
42	cli-miR-100-5p	47	2	288	31	16
43	cpo-miR-100-5p	47	2	288	31	16
44	cqu-miR-100-5p	47	2	288	31	16
45	dno-miR-100-5p	47	2	288	31	16
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2						
3	dre-miR-100-5p	47	2	288	31	16
4	eca-miR-100	47	2	288	31	16
5	fru-miR-100	47	2	288	31	16
6	gga-miR-100-5p	47	2	288	31	16
7	ggo-miR-100	47	2	288	31	16
8	gmo-miR-100a-5p	47	2	288	31	16
9	gmo-miR-100a-5p	47	2	288	31	16
10	gmo-miR-100a-5p	47	2	288	31	16
11	hsa-miR-100-5p	47	2	288	31	16
12	ipu-miR-100	47	2	288	31	16
13	ipu-miR-100	47	2	288	31	16
14	lgi-miR-100	47	2	288	31	16
15	lla-miR-100	47	2	288	31	16
16	mml-miR-100-5p	47	2	288	31	16
17	mml-miR-100-5p	47	2	288	31	16
18	mmr-miR-100	47	2	288	31	16
19	mmu-miR-100-5p	47	2	288	31	16
20	mse-miR-100	47	2	288	31	16
21	mse-miR-100	47	2	288	31	16
22	mze-miR-100	47	2	288	31	16
23	nbr-miR-100	47	2	288	31	16
24	nle-miR-100	47	2	288	31	16
25	nle-miR-100	47	2	288	31	16
26	nvi-miR-100	47	2	288	31	16
27	oan-miR-100-5p	47	2	288	31	16
28	ocu-miR-100-5p	47	2	288	31	16
29	ocu-miR-100-5p	47	2	288	31	16
30	oga-miR-100	47	2	288	31	16
31	oni-miR-100	47	2	288	31	16
32	oni-miR-100	47	2	288	31	16
33	pal-miR-100-5p	47	2	288	31	16
34	pbv-miR-100-5p	47	2	288	31	16
35	pha-miR-100	47	2	288	31	16
36	pma-miR-100a-5p	47	2	288	31	16
37	pma-miR-100a-5p	47	2	288	31	16
38	pny-miR-100	47	2	288	31	16
39	ppa-miR-100	47	2	288	31	16
40	ppy-miR-100	47	2	288	31	16
41	ppy-miR-100	47	2	288	31	16
42	pte-miR-100b-5p	47	2	288	31	16
43	ptr-miR-100	47	2	288	31	16
44	rno-miR-100-5p	47	2	288	31	16
45	rno-miR-100-5p	47	2	288	31	16
46	sko-miR-100	47	2	288	31	16
47	sla-miR-100	47	2	288	31	16
48	ssa-miR-100a-5p	47	2	288	31	16
49	ssc-miR-100	47	2	288	31	16
50	ssc-miR-100	47	2	288	31	16
51	tcf-miR-100	47	2	288	31	16
52	tch-miR-100-5p	47	2	288	31	16
53	tni-miR-100	47	2	288	31	16
54	tni-miR-100	47	2	288	31	16
55	xla-miR-100-5p	47	2	288	31	16
56	xtr-miR-100	47	2	288	31	16
57	tca-miR-100-5p	47	2	290	31	16
58	tca-miR-100-5p	47	2	290	31	16
59	ami-let-7f-5p	54	16	39	51	36
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3	ggo-let-7f	54	16	39	51	36
4	oar-let-7f	54	16	39	51	36
5	cli-miR-199-3p	450	16	114	402	242
6	efu-miR-199	450	16	114	402	242
7	dre-miR-199-3p	426	15	111	375	227
8	oha-miR-199c-3p	426	15	111	375	227
9	ssc-miR-199b-3p	426	15	111	375	227
10	xtr-miR-199a-3p	426	15	111	375	227
11	xla-miR-199-3p	379	12	105	334	200
12	ami-miR-199-3p	379	12	105	334	200
13	bta-miR-199a-3p	379	12	105	334	200
14	cpi-miR-199-3p	379	12	105	334	200
15	cpo-miR-199-3p	379	12	105	334	200
16	dno-miR-199-3p	379	12	105	334	200
17	eca-miR-199a-3p	379	12	105	334	200
18	eca-miR-199b-3p	379	12	105	334	200
19	gmo-miR-199-3p	379	12	105	334	200
20	hsa-miR-199a-3p	379	12	105	334	200
21	hsa-miR-199b-3p	379	12	105	334	200
22	mml-miR-199a-3p	379	12	105	334	200
23	mmu-miR-199a-3p	379	12	105	334	200
24	mmu-miR-199b-3p	379	12	105	334	200
25	ocu-miR-199a-3p	379	12	105	334	200
26	oha-miR-199a-3p	379	12	105	334	200
27	ola-miR-199a-3p	379	12	105	334	200
28	pol-miR-199a-3p	379	12	105	334	200
29	ptr-miR-199a-3p	379	12	105	334	200
30	ptr-miR-199b	379	12	105	334	200
31	rno-miR-199a-3p	379	12	105	334	200
32	ssc-miR-199a-3p	379	12	105	334	200
33	abu-miR-199-3p	358	11	102	309	185
34	ccr-miR-199-3p	358	11	102	309	185
35	cfa-miR-199	358	11	102	309	185
36	cgr-miR-199a-3p	358	11	102	309	185
37	chi-miR-199a-3p	358	11	102	309	185
38	chi-miR-199b-3p	358	11	102	309	185
39	chi-miR-199c-3p	358	11	102	309	185
40	cja-miR-199	358	11	102	309	185
41	dma-miR-199	358	11	102	309	185
42	gmo-miR-199-4-3p	358	11	102	309	185
43	ipu-miR-199a-3p	358	11	102	309	185
44	mdo-miR-199b-3p	358	11	102	309	185
45	mmr-miR-199	358	11	102	309	185
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3	mze-miR-199	358	11	102	309	185
4	nbr-miR-199	358	11	102	309	185
5	nle-miR-199a	358	11	102	309	185
6	nle-miR-199b	358	11	102	309	185
7	oan-miR-199-3p	358	11	102	309	185
8	oar-miR-199a-3p	358	11	102	309	185
9	oga-miR-199	358	11	102	309	185
10	oni-miR-199a	358	11	102	309	185
11	pal-miR-199-3p	358	11	102	309	185
12	pbv-miR-199-3p	358	11	102	309	185
13	pha-miR-199	358	11	102	309	185
14	ppy-miR-199	358	11	102	309	185
15	ppa-miR-199b	358	11	102	309	185
16	sbo-miR-199	358	11	102	309	185
17	sha-miR-199a	358	11	102	309	185
18	ssa-miR-199a-3p	358	11	102	309	185
19	tch-miR-199a-3p	358	11	102	309	185
20	tch-miR-199b-3p	358	11	102	309	185
21	tgu-miR-199-3p	358	11	102	309	185
22	aae-miR-125-5p	75	5	62	39	22
23	abu-miR-125b	75	5	62	39	22
24	aca-miR-125b	75	5	62	39	22
25	aga-miR-125	75	5	62	39	22
26	age-miR-125b	75	5	62	39	22
27	ami-miR-125b-5p	75	5	62	39	22
28	bbe-miR-125a-5p	75	5	62	39	22
29	bdo-miR-125	75	5	62	39	22
30	bfl-miR-125a-5p	75	5	62	39	22
31	bta-miR-125b	75	5	62	39	22
32	ccr-miR-125b	75	5	62	39	22
33	cfa-miR-125b	75	5	62	39	22
34	cgr-miR-125b-5p	75	5	62	39	22
35	cja-miR-125	75	5	62	39	22
36	cja-miR-125b	75	5	62	39	22
37	cli-miR-125-5p	75	5	62	39	22
38	cpi-miR-125b-5p	75	5	62	39	22
39	cpo-miR-125b-5p	75	5	62	39	22
40	cqu-miR-125-5p	75	5	62	39	22
41	cte-miR-125	75	5	62	39	22
42	dan-miR-125	75	5	62	39	22
43	der-miR-125	75	5	62	39	22
44	dgr-miR-125	75	5	62	39	22
45	dma-miR-125b	75	5	62	39	22
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3	dme-miR-125-5p	75	5	62	39	22
4	dmo-miR-125	75	5	62	39	22
5	dno-miR-125b-5p	75	5	62	39	22
6	dpe-miR-125	75	5	62	39	22
7	dps-miR-125	75	5	62	39	22
8	dps-miR-125	75	5	62	39	22
9	dps-miR-125	75	5	62	39	22
10	dqu-miR-125-5p	75	5	62	39	22
11	dre-miR-125b-5p	75	5	62	39	22
12	dse-miR-125	75	5	62	39	22
13	dse-miR-125	75	5	62	39	22
14	dsi-miR-125	75	5	62	39	22
15	dwi-miR-125	75	5	62	39	22
16	dya-miR-125	75	5	62	39	22
17	dya-miR-125	75	5	62	39	22
18	eca-miR-125b-5p	75	5	62	39	22
19	efu-miR-125b	75	5	62	39	22
20	fru-miR-125b	75	5	62	39	22
21	fru-miR-125b	75	5	62	39	22
22	gga-miR-125b-5p	75	5	62	39	22
23	ggo-miR-125b	75	5	62	39	22
24	ggo-miR-125b	75	5	62	39	22
25	gmo-miR-125b-5p	75	5	62	39	22
26	hsa-miR-125b-5p	75	5	62	39	22
27	ipu-miR-125b	75	5	62	39	22
28	lca-miR-125b	75	5	62	39	22
29	lca-miR-125b	75	5	62	39	22
30	lla-miR-125b	75	5	62	39	22
31	lva-miR-125-5p	75	5	62	39	22
32	mdo-miR-125b-5p	75	5	62	39	22
33	mdo-miR-125b-5p	75	5	62	39	22
34	mml-miR-125b-5p	75	5	62	39	22
35	mmr-miR-125a	75	5	62	39	22
36	mmu-miR-125b-5p	75	5	62	39	22
37	mmu-miR-125b-5p	75	5	62	39	22
38	mne-miR-125b	75	5	62	39	22
39	mze-miR-125b	75	5	62	39	22
40	nbr-miR-125b	75	5	62	39	22
41	nbr-miR-125b	75	5	62	39	22
42	nle-miR-125b	75	5	62	39	22
43	nlo-miR-125	75	5	62	39	22
44	nvi-miR-125	75	5	62	39	22
45	nvi-miR-125	75	5	62	39	22
46	oan-miR-125-5p	75	5	62	39	22
47	ocu-miR-125b-5p	75	5	62	39	22
48	oga-miR-125b	75	5	62	39	22
49	oga-miR-125b	75	5	62	39	22
50	oha-miR-125b-5p	75	5	62	39	22
51	ola-miR-125b	75	5	62	39	22
52	ola-miR-125c	75	5	62	39	22
53	oni-miR-125b	75	5	62	39	22
54	oni-miR-125b	75	5	62	39	22
55	pal-miR-125b-5p	75	5	62	39	22
56	pbv-miR-125b-5p	75	5	62	39	22
57	pbv-miR-125b-5p	75	5	62	39	22
58	pha-miR-125b	75	5	62	39	22
59	pma-miR-125-5p	75	5	62	39	22
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3	pmi-miR-125-5p	75	5	62	39	22
4	pony-miR-125b	75	5	62	39	22
5	ppa-miR-125b	75	5	62	39	22
6	ppy-miR-125b	75	5	62	39	22
7	ptr-miR-125b	75	5	62	39	22
8	rno-miR-125b-5p	75	5	62	39	22
9	sha-miR-125a	75	5	62	39	22
10	sko-miR-125a	75	5	62	39	22
11	sla-miR-125b	75	5	62	39	22
12	spu-miR-125-5p	75	5	62	39	22
13	ssa-miR-125a-5p	75	5	62	39	22
14	ssc-miR-125b	75	5	62	39	22
15	tca-miR-125-5p	75	5	62	39	22
16	tcf-miR-125	75	5	62	39	22
17	tch-miR-125b-5p	75	5	62	39	22
18	tgu-miR-125-5p	75	5	62	39	22
19	tni-miR-125b	75	5	62	39	22
20	xla-miR-125b-5p	75	5	62	39	22
21	xtr-miR-125b	75	5	62	39	22
22	aca-let-7b-5p	66	35	74	42	30
23	ggo-let-7b	66	35	74	42	30
24	ipu-let-7b	66	35	74	42	30
25	oar-let-7b	66	35	74	42	30
26	ola-let-7b	66	35	74	42	30
27	cgr-miR-125a-5p	43	2	23	26	18
28	cpo-miR-125a-5p	43	2	23	26	18
29	eca-miR-125a-5p	43	2	23	26	18
30	hsa-miR-125a-5p	43	2	23	26	18
31	mml-miR-125a-5p	43	2	23	26	18
32	mmu-miR-125a-5p	43	2	23	26	18
33	oga-miR-125a	43	2	23	26	18
34	ppy-miR-125a-5p	43	2	23	26	18
35	rno-miR-125a-5p	43	2	23	26	18
36	sbo-miR-125a	43	2	23	26	18
37	efu-miR-99b	42	1	76	17	18
38	bta-miR-99b	42	1	76	17	18
39	cfa-miR-99b	42	1	76	17	18
40	chi-miR-99b-5p	42	1	76	17	18
41	cpo-miR-99b-5p	42	1	76	17	18
42	eca-miR-99b	42	1	76	17	18
43	hsa-miR-99b-5p	42	1	76	17	18
44	mml-miR-99b-5p	42	1	76	17	18
45	mmu-miR-99b-5p	42	1	76	17	18
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3	oga-miR-99b	42	1	76	17	18
4	pal-miR-99b-5p	42	1	76	17	18
5	ptr-miR-99b	42	1	76	17	18
6	rno-miR-99b-5p	42	1	76	17	18
7	ssc-miR-99b	42	1	76	17	18
8	tch-miR-99b-5p	42	1	76	17	18
9	abu-miR-26a	615	49	348	440	277
10	aca-miR-26-3-5p	615	49	348	440	277
11	ami-miR-26-5p	615	49	348	440	277
12	bta-miR-26a	615	49	348	440	277
13	cca-miR-26a	615	49	348	440	277
14	cfa-miR-26a	615	49	348	440	277
15	chi-miR-26a-5p	615	49	348	440	277
16	cja-miR-26a	615	49	348	440	277
17	cli-miR-26-5p	615	49	348	440	277
18	cpi-miR-26-5p	615	49	348	440	277
19	cpo-miR-26a-5p	615	49	348	440	277
20	dma-miR-26a	615	49	348	440	277
21	dno-miR-26a-5p	615	49	348	440	277
22	dre-miR-26a-5p	615	49	348	440	277
23	eca-miR-26a	615	49	348	440	277
24	fru-miR-26	615	49	348	440	277
25	gga-miR-26a-2-5p	615	49	348	440	277
26	ggo-miR-26a	615	49	348	440	277
27	gmo-miR-26a-5p	615	49	348	440	277
28	hsa-miR-26a-5p	615	49	348	440	277
29	ipu-miR-26a	615	49	348	440	277
30	lla-miR-26a	615	49	348	440	277
31	mml-miR-26a-5p	615	49	348	440	277
32	mmr-miR-26a	615	49	348	440	277
33	mmu-miR-26a-5p	615	49	348	440	277
34	mne-miR-26a	615	49	348	440	277
35	mze-miR-26a	615	49	348	440	277
36	nbr-miR-26a	615	49	348	440	277
37	nle-miR-26a	615	49	348	440	277
38	oan-miR-26-5p	615	49	348	440	277
39	oar-miR-26a	615	49	348	440	277
40	ocu-miR-26a-5p	615	49	348	440	277
41	oga-miR-26a	615	49	348	440	277
42	oha-miR-26-5p	615	49	348	440	277
43	oni-miR-26a	615	49	348	440	277
44	pal-miR-26a-5p	615	49	348	440	277
45	pav-miR-26-5p	615	49	348	440	277
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3	pha-miR-26a	615	49	348	440	277
4	pma-miR-26a-5p	615	49	348	440	277
5	ppy-miR-26a	615	49	348	440	277
6	ppa-miR-26a	615	49	348	440	277
7	ppa-miR-26a	615	49	348	440	277
8	ppa-miR-26a	615	49	348	440	277
9	ppa-miR-26a	615	49	348	440	277
10	ptr-miR-26a	615	49	348	440	277
11	rno-miR-26a-5p	615	49	348	440	277
12	sbo-miR-26a	615	49	348	440	277
13	ssa-miR-26a-5p	615	49	348	440	277
14	ssa-miR-26a-5p	615	49	348	440	277
15	ssc-miR-26a	615	49	348	440	277
16	tch-miR-26a-5p	615	49	348	440	277
17	tch-miR-26a-5p	615	49	348	440	277
18	tgu-miR-26-5p	615	49	348	440	277
19	tni-miR-26	615	49	348	440	277
20	xla-miR-26-5p	615	49	348	440	277
21	xla-miR-26-5p	615	49	348	440	277
22	efu-miR-26a	618	49	351	447	278
23	efu-miR-26c	618	49	351	447	278
24	bta-miR-21-5p	2370	1990	2099	2260	1180
25	bta-miR-21-5p	2370	1990	2099	2260	1180
26	cpo-miR-21-5p	2370	1990	2099	2260	1180
27	dno-miR-21-5p	2370	1990	2099	2260	1180
28	ocu-miR-21-5p	2370	1990	2099	2260	1180
29	ocu-miR-21-5p	2370	1990	2099	2260	1180
30	sha-miR-21	2370	1990	2099	2260	1180
31	ami-miR-21-5p	2354	1975	2085	2242	1167
32	chi-miR-21-5p	2354	1975	2085	2242	1167
33	chi-miR-21-5p	2354	1975	2085	2242	1167
34	dma-miR-21	2354	1975	2085	2242	1167
35	mmr-miR-21	2354	1975	2085	2242	1167
36	nle-miR-21	2354	1975	2085	2242	1167
37	nle-miR-21	2354	1975	2085	2242	1167
38	oar-miR-21	2354	1975	2085	2242	1167
39	oga-miR-21	2354	1975	2085	2242	1167
40	pbv-miR-21-5p	2354	1975	2085	2242	1167
41	pbv-miR-21-5p	2354	1975	2085	2242	1167
42	pha-miR-21	2354	1975	2085	2242	1167
43	sbo-miR-21	2354	1975	2085	2242	1167
44	aca-miR-181a	530	24	204	364	281
45	ami-miR-181a-5p	530	24	204	364	281
46	ami-miR-181a-5p	530	24	204	364	281
47	cgr-miR-181a-5p	530	24	204	364	281
48	cja-miR-181a	530	24	204	364	281
49	cja-miR-181a	530	24	204	364	281
50	cpi-miR-181a-5p	530	24	204	364	281
51	dma-miR-181a	530	24	204	364	281
52	dre-miR-181a-5p	530	24	204	364	281
53	dre-miR-181a-5p	530	24	204	364	281
54	eca-miR-181a	530	24	204	364	281
55	fru-miR-181a-5p	530	24	204	364	281
56	gga-miR-181a-5p	530	24	204	364	281
57	gga-miR-181a-5p	530	24	204	364	281
58	ggo-miR-181a-5p	530	24	204	364	281
59	gmo-miR-181a-5p	530	24	204	364	281
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3	hsa-miR-181a-5p	530	24	204	364	281
4	lla-miR-181a-5p	530	24	204	364	281
5	mdo-miR-181a-5p	530	24	204	364	281
6	mml-miR-181a-5p	530	24	204	364	281
7	mmu-miR-181a-5p	530	24	204	364	281
8	mne-miR-181a-5p	530	24	204	364	281
9	nle-miR-181a	530	24	204	364	281
10	oan-miR-181a-5p	530	24	204	364	281
11	oar-miR-181a	530	24	204	364	281
12	oga-miR-181a	530	24	204	364	281
13	pha-miR-181a	530	24	204	364	281
14	pma-miR-181a-5p	530	24	204	364	281
15	ppa-miR-181a-5p	530	24	204	364	281
16	ppy-miR-181a-5p	530	24	204	364	281
17	ptr-miR-181a-5p	530	24	204	364	281
18	rno-miR-181a-5p	530	24	204	364	281
19	sla-miR-181a	530	24	204	364	281
20	ssa-miR-181a-5p	530	24	204	364	281
21	tch-miR-181a-5p	530	24	204	364	281
22	tgu-miR-181a-5p	530	24	204	364	281
23	tni-miR-181a-5p	530	24	204	364	281
24	xtr-miR-181a-5p	530	24	204	364	281
25	gma-miR169k	4455	4521	1104	4737	10493
26	gma-miR169l-5p	4455	4521	1104	4737	10493
27	mes-miR169l	4455	4521	1104	4737	10493
28	mes-miR169m	4455	4521	1104	4737	10493
29	bta-miR-181a	573	27	235	389	301
30	cli-miR-181a-5p	573	27	235	389	301
31	cpo-miR-181a-5p	573	27	235	389	301
32	dno-miR-181a-5p	573	27	235	389	301
33	ocu-miR-181a-5p	573	27	235	389	301
34	oha-miR-181a-5p	573	27	235	389	301
35	pal-miR-181a-5p	573	27	235	389	301
36	pbv-miR-181a-5p	573	27	235	389	301
37	ssc-miR-181a	573	27	235	389	301
38	ami-let-7i-5p	41	17	46	40	27
39	ccr-let-7i	41	17	46	40	27
40	gga-let-7i	41	17	46	40	27
41	ggo-let-7i	41	17	46	40	27
42	mdo-let-7i-5p	41	17	46	40	27
43	sha-let-7i	41	17	46	40	27
44	xla-let-7i-5p	41	17	46	40	27
45	xtr-let-7i	41	17	46	40	27
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3	bta-miR-26b	46	28	38	40	14
4	cfa-miR-26b	46	28	38	40	14
5	cgr-miR-26b-5p	46	28	38	40	14
6	chi-miR-26b-5p	46	28	38	40	14
7	chi-miR-26b-5p	46	28	38	40	14
8	cja-miR-26b	46	28	38	40	14
9	cja-miR-26b	46	28	38	40	14
10	cpo-miR-26b-5p	46	28	38	40	14
11	dma-miR-26b	46	28	38	40	14
12	dma-miR-26b	46	28	38	40	14
13	dno-miR-26b-5p	46	28	38	40	14
14	dno-miR-26b-5p	46	28	38	40	14
15	mmr-miR-26b	46	28	38	40	14
16	ocu-miR-26b-5p	46	28	38	40	14
17	pal-miR-26b-5p	46	28	38	40	14
18	pha-miR-26b	46	28	38	40	14
19	pha-miR-26b	46	28	38	40	14
20	ppa-miR-26b	46	28	38	40	14
21	ssc-miR-26b-5p	46	28	38	40	14
22	tch-miR-26b-5p	46	28	38	40	14
23	efu-miR-26b	47	30	39	41	14
24	cfa-miR-24	507	314	364	538	238
25	cfa-miR-24	507	314	364	538	238
26	cgr-miR-24-3p	507	314	364	538	238
27	ipu-miR-24	507	314	364	538	238
28	ipu-miR-24	507	314	364	538	238
29	oga-miR-24	507	314	364	538	238
30	oha-miR-24-3p	507	314	364	538	238
31	abu-miR-24b-3p	505	314	364	538	237
32	aca-miR-24-3p	505	314	364	538	237
33	aca-miR-24-3p	505	314	364	538	237
34	ami-miR-24-3p	505	314	364	538	237
35	bta-miR-24-3p	505	314	364	538	237
36	ccb-miR-24	505	314	364	538	237
37	ccb-miR-24	505	314	364	538	237
38	cja-miR-24	505	314	364	538	237
39	cpo-miR-24-3p	505	314	364	538	237
40	dno-miR-24a-3p	505	314	364	538	237
41	dno-miR-24a-3p	505	314	364	538	237
42	dre-miR-24	505	314	364	538	237
43	eca-miR-24	505	314	364	538	237
44	fru-miR-24-3p	505	314	364	538	237
45	fru-miR-24-3p	505	314	364	538	237
46	gga-miR-24-3p	505	314	364	538	237
47	ggo-miR-24	505	314	364	538	237
48	ggo-miR-24	505	314	364	538	237
49	hsa-miR-24-3p	505	314	364	538	237
50	mml-miR-24-3p	505	314	364	538	237
51	mmu-miR-24-3p	505	314	364	538	237
52	mne-miR-24-3p	505	314	364	538	237
53	nbr-miR-24a	505	314	364	538	237
54	nbr-miR-24a	505	314	364	538	237
55	oan-miR-24-3p	505	314	364	538	237
56	ocu-miR-24-3p	505	314	364	538	237
57	ocu-miR-24-3p	505	314	364	538	237
58	ola-miR-24a	505	314	364	538	237
59	oni-miR-24a	505	314	364	538	237
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3	pbv-miR-24-3p	505	314	364	538	237
4	pma-miR-24	505	314	364	538	237
5	ppy-miR-24a	505	314	364	538	237
6	ppa-miR-24-3p	505	314	364	538	237
7	ppa-miR-24-3p	505	314	364	538	237
8	ppp-miR-24-3p	505	314	364	538	237
9	ptr-miR-24	505	314	364	538	237
10	ptr-miR-24	505	314	364	538	237
11	rno-miR-24-3p	505	314	364	538	237
12	ssc-miR-24-3p	505	314	364	538	237
13	ssc-miR-24-3p	505	314	364	538	237
14	tgu-miR-24-3p	505	314	364	538	237
15	tni-miR-24	505	314	364	538	237
16	xla-miR-24a-3p	505	314	364	538	237
17	xtr-miR-24a-3p	505	314	364	538	237
18	xtr-miR-24a-3p	505	314	364	538	237
19	abu-miR-181c	64	15	28	42	45
20	chi-miR-181b-5p	64	15	28	42	45
21	chi-miR-181b-5p	64	15	28	42	45
22	eca-miR-181b	64	15	28	42	45
23	eca-miR-181b	64	15	28	42	45
24	hsa-miR-181b-5p	64	15	28	42	45
25	mdo-miR-181b-5p	64	15	28	42	45
26	oha-miR-181b-5p	64	15	28	42	45
27	ppy-miR-181b	64	15	28	42	45
28	ppy-miR-181b	64	15	28	42	45
29	ptr-miR-181b	64	15	28	42	45
30	rno-miR-181b-5p	64	15	28	42	45
31	tch-miR-181b-5p	64	15	28	42	45
32	tch-miR-181b-5p	64	15	28	42	45
33	pde-miR159	342	153	44	381	330
34	ssa-miR-23b-3p	153	17	36	119	64
35	bta-miR-10174-3p	155	17	35	118	64
36	oga-miR-23b	155	17	35	118	64
37	oga-miR-23b	155	17	35	118	64
38	tch-miR-23b-3p	155	17	35	118	64
39	cpi-miR-93-5p	11	10	75	9	5
40	sha-miR-93	11	10	75	9	5
41	sha-miR-93	11	10	75	9	5
42	gga-let-7g-5p	33	17	56	30	20
43	ggo-let-7g	33	17	56	30	20
44	ggo-let-7g	33	17	56	30	20
45	mdo-let-7g-5p	33	17	56	30	20
46	oar-let-7g	33	17	56	30	20
47	sha-let-7g	33	17	56	30	20
48	sha-let-7g	33	17	56	30	20
49	cli-miR-23b-3p	155	18	35	119	63
50	efu-miR-23b	156	17	36	118	65
51	aca-let-7g	99	80	152	91	48
52	ami-let-7g-5p	99	80	152	91	48
53	ami-let-7g-5p	99	80	152	91	48
54	bta-let-7g	99	80	152	91	48
55	cfa-let-7g	99	80	152	91	48
56	cgr-let-7g-5p	99	80	152	91	48
57	chi-let-7g-5p	99	80	152	91	48
58	chi-let-7g-5p	99	80	152	91	48
59	cja-let-7g	99	80	152	91	48
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3	cli-let-7g-5p	99	80	152	91	48
4	cpi-let-7g-5p	99	80	152	91	48
5	cpo-let-7g-5p	99	80	152	91	48
6	dma-let-7g	99	80	152	91	48
7	dno-let-7g-5p	99	80	152	91	48
8	eca-let-7g	99	80	152	91	48
9	hsa-let-7g-5p	99	80	152	91	48
10	mml-let-7g-5p	99	80	152	91	48
11	mmr-let-7g	99	80	152	91	48
12	mmu-let-7g-5p	99	80	152	91	48
13	nle-let-7g	99	80	152	91	48
14	oan-let-7g-5p	99	80	152	91	48
15	ocu-let-7g-5p	99	80	152	91	48
16	oga-let-7g	99	80	152	91	48
17	oha-let-7g-5p	99	80	152	91	48
18	pal-let-7g-5p	99	80	152	91	48
19	pbv-let-7g-5p	99	80	152	91	48
20	pha-let-7g	99	80	152	91	48
21	ppa-let-7g	99	80	152	91	48
22	ppy-let-7g	99	80	152	91	48
23	ptr-let-7g	99	80	152	91	48
24	rno-let-7g-5p	99	80	152	91	48
25	ssc-let-7g	99	80	152	91	48
26	tch-let-7g-5p	99	80	152	91	48
27	tgu-let-7g-5p	99	80	152	91	48
28	ami-miR-23b-3p	153	17	35	116	63
29	bta-miR-23b-3p	153	17	35	116	63
30	cpo-miR-23b-3p	153	17	35	116	63
31	dno-miR-23b-3p	153	17	35	116	63
32	dre-miR-23b-3p	153	17	35	116	63
33	hsa-miR-23b-3p	153	17	35	116	63
34	ocu-miR-23b-3p	153	17	35	116	63
35	oha-miR-23b-3p	153	17	35	116	63
36	ola-miR-23b	153	17	35	116	63
37	pbv-miR-23b-3p	153	17	35	116	63
38	pma-miR-23b	153	17	35	116	63
39	ppa-miR-23b	153	17	35	116	63
40	ppy-miR-23b	153	17	35	116	63
41	ptr-miR-23b	153	17	35	116	63
42	aca-miR-23a-3p	403	112	128	342	207
43	age-miR-23a	403	112	128	342	207
44	ccr-miR-23a	403	112	128	342	207
45	cgr-miR-23a-3p	403	112	128	342	207
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3	chi-miR-23a	403	112	128	342	207
4	cpi-miR-23a-3p	403	112	128	342	207
5	eca-miR-23a	403	112	128	342	207
6	ggo-miR-23a	403	112	128	342	207
7	ggo-miR-23a	403	112	128	342	207
8	hsa-miR-23a-3p	403	112	128	342	207
9	ipu-miR-23a	403	112	128	342	207
10	ipu-miR-23a	403	112	128	342	207
11	lca-miR-23a	403	112	128	342	207
12	lca-miR-23a	403	112	128	342	207
13	mml-miR-23a-3p	403	112	128	342	207
14	mmu-miR-23a-3p	403	112	128	342	207
15	mne-miR-23a	403	112	128	342	207
16	pbv-miR-23a-3p	403	112	128	342	207
17	pbv-miR-23a-3p	403	112	128	342	207
18	pha-miR-23a	403	112	128	342	207
19	phn-miR-23a	403	112	128	342	207
20	ppy-miR-23a	403	112	128	342	207
21	ppa-miR-23a	403	112	128	342	207
22	ppy-miR-23a	403	112	128	342	207
23	ptr-miR-23a	403	112	128	342	207
24	ptr-miR-23a	403	112	128	342	207
25	rno-miR-23a-3p	403	112	128	342	207
26	sla-miR-23a	403	112	128	342	207
27	ssa-miR-23a-3p	403	112	128	342	207
28	ssc-miR-23a	403	112	128	342	207
29	ssc-miR-23a	403	112	128	342	207
30	xla-miR-23a	403	112	128	342	207
31	xtr-miR-23a	403	112	128	342	207
32	xtr-miR-23a	403	112	128	342	207
33	bta-miR-93	14	16	76	13	8
34	cpo-miR-151-5p	38	45	24	48	27
35	dno-miR-151-5p	38	45	24	48	27
36	ami-miR-181b-5p	95	27	50	66	59
37	ami-miR-181b-5p	95	27	50	66	59
38	bta-miR-181b	95	27	50	66	59
39	cli-miR-181b-5p	95	27	50	66	59
40	cpi-miR-181b-5p	95	27	50	66	59
41	cpi-miR-181b-5p	95	27	50	66	59
42	cpo-miR-181b-5p	95	27	50	66	59
43	dno-miR-181b-5p	95	27	50	66	59
44	efu-miR-181e	95	27	50	66	59
45	efu-miR-181e	95	27	50	66	59
46	ggo-miR-181b	95	27	50	66	59
47	gmo-miR-181b-5p	95	27	50	66	59
48	hhi-miR-181b	95	27	50	66	59
49	hhi-miR-181b	95	27	50	66	59
50	lla-miR-181b	95	27	50	66	59
51	mml-miR-181b-5p	95	27	50	66	59
52	mmu-miR-181b-5p	95	27	50	66	59
53	mmu-miR-181b-5p	95	27	50	66	59
54	mne-miR-181b	95	27	50	66	59
55	ocu-miR-181b-5p	95	27	50	66	59
56	ola-miR-181b-5p	95	27	50	66	59
57	ola-miR-181b-5p	95	27	50	66	59
58	pal-miR-181b-5p	95	27	50	66	59
59	ppa-miR-181b	95	27	50	66	59
60	ppa-miR-181b	95	27	50	66	59

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3	ssc-miR-181b	95	27	50	66	59
4	tgu-miR-181b-5p	95	27	50	66	59
5	abu-miR-221	34	21	39	23	11
6	ami-miR-221-3p	34	21	39	23	11
7	ami-miR-221-3p	34	21	39	23	11
8	cgr-miR-221-3p	34	21	39	23	11
9	cgr-miR-221-3p	34	21	39	23	11
10	cpo-miR-221-3p	34	21	39	23	11
11	dma-miR-221	34	21	39	23	11
12	dno-miR-221-3p	34	21	39	23	11
13	dno-miR-221-3p	34	21	39	23	11
14	dre-miR-221-3p	34	21	39	23	11
15	eca-miR-221	34	21	39	23	11
16	fru-miR-221	34	21	39	23	11
17	fru-miR-221	34	21	39	23	11
18	gga-miR-221-3p	34	21	39	23	11
19	ggo-miR-221	34	21	39	23	11
20	ggo-miR-221	34	21	39	23	11
21	hsa-miR-221-3p	34	21	39	23	11
22	mdo-miR-221-3p	34	21	39	23	11
23	mml-miR-221-3p	34	21	39	23	11
24	mml-miR-221-3p	34	21	39	23	11
25	mmr-miR-221	34	21	39	23	11
26	mmu-miR-221-3p	34	21	39	23	11
27	mze-miR-221	34	21	39	23	11
28	nbr-miR-221	34	21	39	23	11
29	nbr-miR-221	34	21	39	23	11
30	nle-miR-221	34	21	39	23	11
31	ocu-miR-221-3p	34	21	39	23	11
32	oga-miR-221	34	21	39	23	11
33	oga-miR-221	34	21	39	23	11
34	oha-miR-221-3p	34	21	39	23	11
35	ola-miR-221	34	21	39	23	11
36	oni-miR-221	34	21	39	23	11
37	oni-miR-221	34	21	39	23	11
38	pha-miR-221	34	21	39	23	11
39	phn-miR-221	34	21	39	23	11
40	ppy-miR-221	34	21	39	23	11
41	ppa-miR-221	34	21	39	23	11
42	ppy-miR-221	34	21	39	23	11
43	ptr-miR-221	34	21	39	23	11
44	rno-miR-221-3p	34	21	39	23	11
45	rno-miR-221-3p	34	21	39	23	11
46	sbo-miR-221	34	21	39	23	11
47	tgu-miR-221-3p	34	21	39	23	11
48	tni-miR-221	34	21	39	23	11
49	tni-miR-221	34	21	39	23	11
50	xtr-miR-221	34	21	39	23	11
51	abu-miR-23b	106	6	23	67	42
52	aca-miR-23b-3p	106	6	23	67	42
53	aca-miR-23b-3p	106	6	23	67	42
54	cca-miR-23b	106	6	23	67	42
55	cgr-miR-23b-3p	106	6	23	67	42
56	chi-miR-23b-3p	106	6	23	67	42
57	chi-miR-23b-3p	106	6	23	67	42
58	cja-miR-23b	106	6	23	67	42
59	cpi-miR-23b-3p	106	6	23	67	42
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3	dma-miR-23b	106	6	23	67	42
4	eca-miR-23b	106	6	23	67	42
5	gga-miR-23b-3p	106	6	23	67	42
6	ipu-miR-23b	106	6	23	67	42
7	mdo-miR-23b-3p	106	6	23	67	42
8	mml-miR-23b-3p	106	6	23	67	42
9	mmr-miR-23b	106	6	23	67	42
10	mmu-miR-23b-3p	106	6	23	67	42
11	mze-miR-23b	106	6	23	67	42
12	nbr-miR-23b	106	6	23	67	42
13	nle-miR-23b	106	6	23	67	42
14	oni-miR-23b	106	6	23	67	42
15	pha-miR-23b	106	6	23	67	42
16	pma-miR-23a-3p	106	6	23	67	42
17	ppy-miR-23b	106	6	23	67	42
18	rno-miR-23b-3p	106	6	23	67	42
19	tgu-miR-23-3p	106	6	23	67	42
20	xla-miR-23b-3p	106	6	23	67	42
21	xtr-miR-23b	106	6	23	67	42
22	efu-miR-23a	692	247	187	626	335
23	ami-miR-30d-5p	57	28	69	62	22
24	bta-miR-30d	57	28	69	62	22
25	cfa-miR-30d	57	28	69	62	22
26	cli-miR-30d-5p	57	28	69	62	22
27	cpo-miR-30d-5p	57	28	69	62	22
28	dno-miR-30d-5p	57	28	69	62	22
29	gmo-miR-30a-5p	57	28	69	62	22
30	nle-miR-30d	57	28	69	62	22
31	ocu-miR-30d-5p	57	28	69	62	22
32	oga-miR-30d	57	28	69	62	22
33	oha-miR-30d-5p	57	28	69	62	22
34	pal-miR-30d-5p	57	28	69	62	22
35	pbv-miR-30d-5p	57	28	69	62	22
36	pha-miR-30d	57	28	69	62	22
37	ssa-miR-30b-5p	57	28	69	62	22
38	ssc-miR-30d	57	28	69	62	22
39	tgu-miR-30d-5p	57	28	69	62	22
40	xla-miR-30d-5p	57	28	69	62	22
41	abu-miR-24a	90	32	44	67	41
42	chi-miR-24-3p	90	32	44	67	41
43	dma-miR-24	90	32	44	67	41
44	dre-miR-24b-3p	90	32	44	67	41
45	gmo-miR-24a-3p	90	32	44	67	41
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3	ipu-miR-24b	90	32	44	67	41
4	mnr-miR-24	90	32	44	67	41
5	mze-miR-24a	90	32	44	67	41
6	nbr-miR-24c	90	32	44	67	41
7	nle-miR-24	90	32	44	67	41
8	oni-miR-24a-3	90	32	44	67	41
9	oni-miR-24a-4	90	32	44	67	41
10	oni-miR-24b-3p	90	32	44	67	41
11	pha-miR-24	90	32	44	67	41
12	ppy-miR-24a-3	90	32	44	67	41
13	ppy-miR-24a-4	90	32	44	67	41
14	ssa-miR-24a-3p	90	32	44	67	41
15	dre-miR-23b	138	9	32	97	54
16	fru-miR-23b	138	9	32	97	54
17	ggo-miR-23b	138	9	32	97	54
18	gmo-miR-23b-3p	138	9	32	97	54
19	pal-miR-23b-3p	138	9	32	97	54
20	ssc-miR-23b	138	9	32	97	54
21	tni-miR-23b	138	9	32	97	54
22	cpo-miR-23a-3p	672	228	184	607	324
23	dno-miR-23a-3p	672	228	184	607	324
24	bta-miR-423-3p	130	129	28	140	71
25	sbo-miR-423	130	129	28	140	71
26	dno-miR-24b-3p	91	32	44	67	42
27	efu-miR-92a	967	1113	97	1161	475
28	abu-miR-92a	967	1113	97	1161	475
29	aca-miR-92a	967	1113	97	1161	475
30	age-miR-92	967	1113	97	1161	475
31	ami-miR-92a-3p	967	1113	97	1161	475
32	bta-miR-92a	967	1113	97	1161	475
33	ccr-miR-92a	967	1113	97	1161	475
34	cfa-miR-92a	967	1113	97	1161	475
35	cgr-miR-92a-3p	967	1113	97	1161	475
36	chi-miR-92a-3p	967	1113	97	1161	475
37	chi-miR-92b	967	1113	97	1161	475
38	cja-miR-92a	967	1113	97	1161	475
39	cli-miR-92-3p	967	1113	97	1161	475
40	cpo-miR-92a-3p	967	1113	97	1161	475
41	dma-miR-92a	967	1113	97	1161	475
42	dno-miR-92a-3p	967	1113	97	1161	475
43	dre-miR-92a-3p	967	1113	97	1161	475
44	eca-miR-92a	967	1113	97	1161	475
45	fru-miR-92	967	1113	97	1161	475
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3	ggo-miR-92	967	1113	97	1161	475
4	hsa-miR-92a-3p	967	1113	97	1161	475
5	ipu-miR-92a	967	1113	97	1161	475
6	lca-miR-92	967	1113	97	1161	475
7	lla-miR-92	967	1113	97	1161	475
8	lla-miR-92	967	1113	97	1161	475
9	lla-miR-92	967	1113	97	1161	475
10	mdo-miR-92a-3p	967	1113	97	1161	475
11	mml-miR-92a-3p	967	1113	97	1161	475
12	mmr-miR-92a	967	1113	97	1161	475
13	mmr-miR-92a	967	1113	97	1161	475
14	mmr-miR-92b	967	1113	97	1161	475
15	mne-miR-92	967	1113	97	1161	475
16	mze-miR-92a	967	1113	97	1161	475
17	mze-miR-92a	967	1113	97	1161	475
18	nbr-miR-92a	967	1113	97	1161	475
19	nle-miR-92a	967	1113	97	1161	475
20	oan-miR-92a-3p	967	1113	97	1161	475
21	oan-miR-92a-3p	967	1113	97	1161	475
22	ocu-miR-92a-3p	967	1113	97	1161	475
23	oga-miR-92a	967	1113	97	1161	475
24	oha-miR-92a	967	1113	97	1161	475
25	oha-miR-92a	967	1113	97	1161	475
26	oha-miR-92a-3p	967	1113	97	1161	475
27	oni-miR-92a	967	1113	97	1161	475
28	pal-miR-92a-3p	967	1113	97	1161	475
29	pal-miR-92a-3p	967	1113	97	1161	475
30	pbv-miR-92a-3p	967	1113	97	1161	475
31	pha-miR-92a	967	1113	97	1161	475
32	pha-miR-92a	967	1113	97	1161	475
33	ppy-miR-92	967	1113	97	1161	475
34	ppa-miR-92a	967	1113	97	1161	475
35	ppy-miR-92	967	1113	97	1161	475
36	ptr-miR-92	967	1113	97	1161	475
37	ptr-miR-92	967	1113	97	1161	475
38	sbo-miR-92a	967	1113	97	1161	475
39	sla-miR-92	967	1113	97	1161	475
40	ssa-miR-92a-3p	967	1113	97	1161	475
41	ssa-miR-92a-3p	967	1113	97	1161	475
42	ssc-miR-92a	967	1113	97	1161	475
43	tch-miR-92a-3p	967	1113	97	1161	475
44	tgu-miR-92-3p	967	1113	97	1161	475
45	tgu-miR-92-3p	967	1113	97	1161	475
46	tni-miR-92	967	1113	97	1161	475
47	xla-miR-92a-3p	967	1113	97	1161	475
48	abu-miR-23a	651	218	181	584	309
49	ami-miR-23a-3p	651	218	181	584	309
50	ami-miR-23a-3p	651	218	181	584	309
51	bta-miR-23a	651	218	181	584	309
52	cja-miR-23a	651	218	181	584	309
53	cja-miR-23a	651	218	181	584	309
54	dre-miR-23a-3p	651	218	181	584	309
55	fru-miR-23a	651	218	181	584	309
56	gmo-miR-23a-3p	651	218	181	584	309
57	gmo-miR-23a-3p	651	218	181	584	309
58	hhi-miR-23a	651	218	181	584	309
59	mze-miR-23a	651	218	181	584	309
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3	nbr-miR-23a	651	218	181	584	309
4	oan-miR-23a-3p	651	218	181	584	309
5	oar-miR-23a	651	218	181	584	309
6	oga-miR-23a	651	218	181	584	309
7	oha-miR-23a-3p	651	218	181	584	309
8	ola-miR-23a	651	218	181	584	309
9	oni-miR-23a	651	218	181	584	309
10	pal-miR-23a-3p	651	218	181	584	309
11	tni-miR-23a	651	218	181	584	309
12	xla-miR-23a-3p	651	218	181	584	309
13	gma-miR396e	610	282	349	380	635
14	aau-miR396	610	282	348	380	635
15	aly-miR396a-5p	610	282	348	380	635
16	amg-miR396	610	282	348	380	635
17	aof-miR396b	610	282	348	380	635
18	aqc-miR396a	610	282	348	380	635
19	ata-miR396e-5p	610	282	348	380	635
20	ath-miR396a-5p	610	282	348	380	635
21	bcy-miR396a	610	282	348	380	635
22	bdi-miR396c-5p	610	282	348	380	635
23	bdi-miR396d-5p	610	282	348	380	635
24	bgv-miR396a	610	282	348	380	635
25	cas-miR396a	610	282	348	380	635
26	cme-miR396b	610	282	348	380	635
27	cpa-miR396	610	282	348	380	635
28	csi-miR396a-5p	610	282	348	380	635
29	csi-miR396b-5p	610	282	348	380	635
30	dpr-miR396	610	282	348	380	635
31	eun-miR396b-5p	610	282	348	380	635
32	fve-miR396a-5p	610	282	348	380	635
33	fve-miR396c-5p	610	282	348	380	635
34	fve-miR396d	610	282	348	380	635
35	ghr-miR396a	610	282	348	380	635
36	ghr-miR396b	610	282	348	380	635
37	gma-miR396a-5p	610	282	348	380	635
38	gma-miR396i-5p	610	282	348	380	635
39	hbr-miR396b	610	282	348	380	635
40	lja-miR396	610	282	348	380	635
41	lus-miR396a	610	282	348	380	635
42	lus-miR396c	610	282	348	380	635
43	mdm-miR396b	610	282	348	380	635
44	mes-miR396a	610	282	348	380	635
45	mes-miR396b	610	282	348	380	635
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3	mtr-miR396b-5p	610	282	348	380	635
4	nta-miR396a	610	282	348	380	635
5	osa-miR396a-5p	610	282	348	380	635
6	osa-miR396b-5p	610	282	348	380	635
7	osa-miR396b-5p	610	282	348	380	635
8	ptc-miR396a	610	282	348	380	635
9	ptc-miR396b	610	282	348	380	635
10	ptc-miR396b	610	282	348	380	635
11	sbi-miR396a	610	282	348	380	635
12	sbi-miR396b	610	282	348	380	635
13	sbi-miR396b	610	282	348	380	635
14	sly-miR396a-5p	610	282	348	380	635
15	sof-miR396	610	282	348	380	635
16	ssl-miR396	610	282	348	380	635
17	ssl-miR396	610	282	348	380	635
18	ssp-miR396	610	282	348	380	635
19	tcc-miR396a	610	282	348	380	635
20	tcc-miR396b	610	282	348	380	635
21	tcc-miR396b	610	282	348	380	635
22	vvi-miR396c	610	282	348	380	635
23	vvi-miR396d	610	282	348	380	635
24	vvi-miR396d	610	282	348	380	635
25	zma-miR396a-5p	610	282	348	380	635
26	zma-miR396b-5p	610	282	348	380	635
27	ami-miR-140-5p	150	17	4	108	74
28	ami-miR-140-5p	150	17	4	108	74
29	ami-miR-140-5p	150	17	4	108	74
30	ami-miR-140-5p	150	17	4	108	74
31	ami-miR-140-5p	150	17	4	108	74
32	ami-miR-140-5p	150	17	4	108	74
33	ami-miR-140-5p	150	17	4	108	74
34	ami-miR-140-5p	150	17	4	108	74
35	ami-miR-140-5p	150	17	4	108	74
36	ami-miR-140-5p	150	17	4	108	74
37	ami-miR-140-5p	150	17	4	108	74
38	ami-miR-140-5p	150	17	4	108	74
39	ami-miR-140-5p	150	17	4	108	74
40	ami-miR-140	150	17	4	108	74
41	ami-miR-140	150	17	4	108	74
42	ami-miR-140	150	17	4	108	74
43	ami-miR-140-5p	150	17	4	108	74
44	ami-miR-140-5p	150	17	4	108	74
45	ami-miR-140-5p	150	17	4	108	74
46	ami-miR-140-5p	150	17	4	108	74
47	ami-miR-140-5p	150	17	4	108	74
48	ami-miR-140-5p	150	17	4	108	74
49	ami-miR-140-5p	150	17	4	108	74
50	ami-miR-140-5p	150	17	4	108	74
51	ami-miR-140-5p	150	17	4	108	74
52	ami-miR-140-5p	150	17	4	108	74
53	ami-miR-140	150	17	4	108	74
54	ami-miR-140	150	17	4	108	74
55	ami-miR-140-5p	150	17	4	108	74
56	ami-miR-140-5p	150	17	4	108	74
57	ami-miR-140-5p	150	17	4	108	74
58	ami-miR-140-5p	150	17	4	108	74
59	ami-miR-140-5p	150	17	4	108	74
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3	tgu-miR-140-5p	150	17	4	108	74
4	tni-miR-140	150	17	4	108	74
5	xla-miR-140-5p	152	18	4	110	74
6	cgr-miR-423-3p	123	121	27	134	63
7	chi-miR-423-3p	123	121	27	134	63
8	cja-miR-423-3p	123	121	27	134	63
9	cpo-miR-423-3p	123	121	27	134	63
10	dma-miR-423	123	121	27	134	63
11	dno-miR-423-3p	123	121	27	134	63
12	eca-miR-423-3p	123	121	27	134	63
13	hsa-miR-423-3p	123	121	27	134	63
14	mml-miR-423-3p	123	121	27	134	63
15	mmu-miR-423-3p	123	121	27	134	63
16	nle-miR-423	123	121	27	134	63
17	ocu-miR-423-3p	123	121	27	134	63
18	oga-miR-423	123	121	27	134	63
19	pal-miR-423-3p	123	121	27	134	63
20	ppa-miR-423	123	121	27	134	63
21	ppy-miR-423-3p	123	121	27	134	63
22	ptr-miR-423	123	121	27	134	63
23	rno-miR-423-3p	123	121	27	134	63
24	ssc-miR-423-3p	123	121	27	134	63
25	tch-miR-423-3p	123	121	27	134	63
26	ahy-miR408-3p	38	40	43	72	52
27	aly-miR408-3p	38	40	43	72	52
28	ath-miR408-3p	38	40	43	72	52
29	cas-miR408	38	40	43	72	52
30	cme-miR408	38	40	43	72	52
31	csi-miR408-3p	38	40	43	72	52
32	gma-miR408a-3p	38	40	43	72	52
33	gma-miR408b-3p	38	40	43	72	52
34	gma-miR408c-3p	38	40	43	72	52
35	lus-miR408a	38	40	43	72	52
36	mdm-miR408a	38	40	43	72	52
37	mes-miR408	38	40	43	72	52
38	mtr-miR408-3p	38	40	43	72	52
39	pta-miR408	38	40	43	72	52
40	ptc-miR408-3p	38	40	43	72	52
41	vun-miR408	38	40	43	72	52
42	vvi-miR408	38	40	43	72	52
43	dre-miR-27a-3p	526	304	354	521	256
44	ipu-miR-27a	526	304	354	521	256
45	ssa-miR-27a-3p	526	304	354	521	256
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3	aly-miR396a-3p	127	102	90	94	201
4	ath-miR396a-3p	127	102	90	94	201
5	csi-miR396b-3p	127	102	90	94	201
6	eun-miR396a-3p	127	102	90	94	201
7	fve-miR396a-3p	127	102	90	94	201
8	fve-miR396c-3p	127	102	90	94	201
9	gma-miR396i-3p	127	102	90	94	201
10	mtr-miR396b-3p	127	102	90	94	201
11	sly-miR396a-3p	127	102	90	94	201
12	abu-miR-27a	466	289	340	482	226
13	aca-miR-27a-3p	466	289	340	482	226
14	ami-miR-27a-3p	466	289	340	482	226
15	ccr-miR-27a	466	289	340	482	226
16	cgr-miR-27a-3p	466	289	340	482	226
17	cja-miR-27a	466	289	340	482	226
18	cpi-miR-27a-3p	466	289	340	482	226
19	dno-miR-27a-3p	466	289	340	482	226
20	eca-miR-27a	466	289	340	482	226
21	hsa-miR-27a-3p	466	289	340	482	226
22	mdo-miR-27a-3p	466	289	340	482	226
23	mmu-miR-27a-3p	466	289	340	482	226
24	mze-miR-27a	466	289	340	482	226
25	nbr-miR-27a	466	289	340	482	226
26	oan-miR-27a-3p	466	289	340	482	226
27	oar-miR-27a	466	289	340	482	226
28	oni-miR-27a	466	289	340	482	226
29	pbv-miR-27a-3p	466	289	340	482	226
30	ppy-miR-27a	466	289	340	482	226
31	rno-miR-27a-3p	466	289	340	482	226
32	sbo-miR-27a	466	289	340	482	226
33	ssc-miR-27a	466	289	340	482	226
34	xtr-miR-27a	466	289	340	482	226
35	age-miR-27a	466	290	340	483	226
36	ggo-miR-27a	466	290	340	483	226
37	lca-miR-27a	466	290	340	483	226
38	mml-miR-27a-3p	466	290	340	483	226
39	mne-miR-27a	466	290	340	483	226
40	oha-miR-27a-3p	466	290	340	483	226
41	ppa-miR-27a	466	290	340	483	226
42	ppy-miR-27a	466	290	340	483	226
43	ptr-miR-27a	466	290	340	483	226
44	sla-miR-27a	466	290	340	483	226
45	cpo-miR-27a-3p	178	92	314	181	109
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3	tch-miR-27a-3p	178	92	314	181	109
4	efu-miR-93	52	85	87	71	35
5	ami-miR-93-5p	48	75	85	63	28
6	cfa-miR-93	48	75	85	63	28
7	cgr-miR-93-5p	48	75	85	63	28
8	chi-miR-93-5p	48	75	85	63	28
9	chi-miR-93-5p	48	75	85	63	28
10	chi-miR-93-5p	48	75	85	63	28
11	cja-miR-93	48	75	85	63	28
12	cpo-miR-93-5p	48	75	85	63	28
13	cpo-miR-93-5p	48	75	85	63	28
14	dma-miR-93	48	75	85	63	28
15	dno-miR-93-5p	48	75	85	63	28
16	eca-miR-93	48	75	85	63	28
17	eca-miR-93	48	75	85	63	28
18	hsa-miR-93-5p	48	75	85	63	28
19	mmu-miR-93-5p	48	75	85	63	28
20	nle-miR-93	48	75	85	63	28
21	nle-miR-93	48	75	85	63	28
22	ocu-miR-93-5p	48	75	85	63	28
23	oga-miR-93	48	75	85	63	28
24	pal-miR-93-5p	48	75	85	63	28
25	pal-miR-93-5p	48	75	85	63	28
26	pha-miR-93	48	75	85	63	28
27	rno-miR-93-5p	48	75	85	63	28
28	tch-miR-93-5p	48	75	85	63	28
29	tch-miR-93-5p	48	75	85	63	28
30	xla-miR-93-5p	48	75	85	63	28
31	ptc-miR6478	2152	3721	7602	2350	8982
32	pvu-miR482-5p	4383	5090	697	3076	6462
33	pvu-miR482-5p	4383	5090	697	3076	6462
34	aca-miR-27b-3p	213	40	135	172	87
35	dre-miR-27b-3p	213	40	135	172	87
36	fru-miR-27b	213	40	135	172	87
37	fru-miR-27b	213	40	135	172	87
38	oha-miR-27b-3p	213	40	135	172	87
39	tni-miR-27b	213	40	135	172	87
40	xla-miR-27b-3p	213	40	135	172	87
41	xla-miR-27b-3p	213	40	135	172	87
42	abu-miR-27b	171	33	131	134	76
43	bta-miR-27b	171	33	131	134	76
44	bta-miR-27b	171	33	131	134	76
45	cfa-miR-27b	171	33	131	134	76
46	cgr-miR-27b-3p	171	33	131	134	76
47	chi-miR-27b-3p	171	33	131	134	76
48	chi-miR-27b-3p	171	33	131	134	76
49	cja-miR-27b	171	33	131	134	76
50	cli-miR-27b-3p	171	33	131	134	76
51	cpi-miR-27b-3p	171	33	131	134	76
52	cpo-miR-27b-3p	171	33	131	134	76
53	cpo-miR-27b-3p	171	33	131	134	76
54	dno-miR-27b-3p	171	33	131	134	76
55	eca-miR-27b	171	33	131	134	76
56	gga-miR-27b-3p	171	33	131	134	76
57	ggo-miR-27b	171	33	131	134	76
58	ggo-miR-27b	171	33	131	134	76
59	hsa-miR-27b-3p	171	33	131	134	76
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3	ipu-miR-27b	171	33	131	134	76
4	mdo-miR-27b-3p	171	33	131	134	76
5	mml-miR-27b-3p	171	33	131	134	76
6	mmr-miR-27b	171	33	131	134	76
7	mmu-miR-27b-3p	171	33	131	134	76
8	mze-miR-27b	171	33	131	134	76
9	nbr-miR-27b	171	33	131	134	76
10	oan-miR-27b-3p	171	33	131	134	76
11	ocu-miR-27b-3p	171	33	131	134	76
12	oni-miR-27b	171	33	131	134	76
13	pal-miR-27b-3p	171	33	131	134	76
14	pbv-miR-27b-3p	171	33	131	134	76
15	pma-miR-27b-3p	171	33	131	134	76
16	ppy-miR-27b	171	33	131	134	76
17	ppa-miR-27b	171	33	131	134	76
18	ppp-miR-27b	171	33	131	134	76
19	ptr-miR-27b	171	33	131	134	76
20	rno-miR-27b-3p	171	33	131	134	76
21	sbo-miR-27b	171	33	131	134	76
22	sha-miR-27b	171	33	131	134	76
23	ssa-miR-27b-3p	171	33	131	134	76
24	ssc-miR-27b-3p	171	33	131	134	76
25	tch-miR-27b-3p	171	33	131	134	76
26	tgu-miR-27-3p	171	33	131	134	76
27	xtr-miR-27b	171	33	131	134	76
28	efu-miR-27b	217	42	137	172	87
29	ggo-let-7c	95	32	29	90	55
30	ola-let-7c	95	32	29	90	55
31	cpi-miR-24-3p	202	107	198	200	94
32	sbo-miR-24	202	107	198	200	94
33	bcy-miR156	497	289	178	259	317
34	bgp-miR156	497	289	178	259	317
35	ahy-miR156b-5p	497	289	177	259	317
36	aly-miR157a-5p	497	289	177	259	317
37	aly-miR157b-5p	497	289	177	259	317
38	aly-miR157c-5p	497	289	177	259	317
39	aof-miR156b	497	289	177	259	317
40	ath-miR157a-5p	497	289	177	259	317
41	ath-miR157b-5p	497	289	177	259	317
42	ath-miR157c-5p	497	289	177	259	317
43	atr-miR156a	497	289	177	259	317
44	atr-miR156c	497	289	177	259	317
45	bnm-miR156b	497	289	177	259	317
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3	bna-miR156c	497	289	177	259	317
4	bna-miR156g	497	289	177	259	317
5	bol-miR157a	497	289	177	259	317
6	bol-miR157a	497	289	177	259	317
7	bra-miR157a	497	289	177	259	317
8	cca-miR156c	497	289	177	259	317
9	cme-miR156b	497	289	177	259	317
10	cme-miR156b	497	289	177	259	317
11	cpa-miR156e	497	289	177	259	317
12	cpa-miR156f	497	289	177	259	317
13	cpa-miR156f	497	289	177	259	317
14	fve-miR156f	497	289	177	259	317
15	fve-miR156g-5p	497	289	177	259	317
16	gma-miR156c	497	289	177	259	317
17	gma-miR156c	497	289	177	259	317
18	gma-miR156d	497	289	177	259	317
19	gma-miR156i	497	289	177	259	317
20	gma-miR156j	497	289	177	259	317
21	gma-miR156j	497	289	177	259	317
22	gma-miR156l	497	289	177	259	317
23	gma-miR156l	497	289	177	259	317
24	gma-miR156m	497	289	177	259	317
25	gra-miR157a	497	289	177	259	317
26	gra-miR157b	497	289	177	259	317
27	han-miR156c	497	289	177	259	317
28	lus-miR156b	497	289	177	259	317
29	lus-miR156b	497	289	177	259	317
30	lus-miR156c	497	289	177	259	317
31	lus-miR156e	497	289	177	259	317
32	lus-miR156e	497	289	177	259	317
33	lus-miR156f	497	289	177	259	317
34	lus-miR156h	497	289	177	259	317
35	lus-miR156i	497	289	177	259	317
36	mdm-miR156ab	497	289	177	259	317
37	mdm-miR156ab	497	289	177	259	317
38	mdm-miR156ac	497	289	177	259	317
39	mes-miR156h	497	289	177	259	317
40	mes-miR156i	497	289	177	259	317
41	mes-miR156i	497	289	177	259	317
42	mes-miR156j	497	289	177	259	317
43	mtr-miR156e	497	289	177	259	317
44	mtr-miR156f	497	289	177	259	317
45	mtr-miR156f	497	289	177	259	317
46	mtr-miR156h-5p	497	289	177	259	317
47	ppe-miR156g	497	289	177	259	317
48	ppe-miR156h	497	289	177	259	317
49	ppe-miR156h	497	289	177	259	317
50	ppe-miR156i	497	289	177	259	317
51	ptc-miR156g	497	289	177	259	317
52	ptc-miR156g	497	289	177	259	317
53	ptc-miR156h	497	289	177	259	317
54	ptc-miR156i	497	289	177	259	317
55	ptc-miR156j	497	289	177	259	317
56	rco-miR156f	497	289	177	259	317
57	rco-miR156g	497	289	177	259	317
58	rco-miR156g	497	289	177	259	317
59	rco-miR156h	497	289	177	259	317
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3	sly-miR156a	497	289	177	259	317
4	sly-miR156b	497	289	177	259	317
5	sly-miR156c	497	289	177	259	317
6	stu-miR156a	497	289	177	259	317
7	stu-miR156b	497	289	177	259	317
8	stu-miR156c	497	289	177	259	317
9	stu-miR156d-5p	497	289	177	259	317
10	tcc-miR156e	497	289	177	259	317
11	tcc-miR156f	497	289	177	259	317
12	vca-miR156b-5p	497	289	177	259	317
13	vun-miR156b	497	289	177	259	317
14	vvi-miR156f	497	289	177	259	317
15	vvi-miR156g	497	289	177	259	317
16	vvi-miR156i	497	289	177	259	317
17	pta-miR159a	214	147	5	235	134
18	osa-miR159c	221	151	6	236	138
19	aof-miR319b	4361	1697	3131	4130	2409
20	atr-miR319b	4361	1697	3131	4130	2409
21	atr-miR319d	4361	1697	3131	4130	2409
22	atr-miR319e	4361	1697	3131	4130	2409
23	cas-miR319c	4361	1697	3131	4130	2409
24	csi-miR159d	4361	1697	3131	4130	2409
25	fve-miR319	4361	1697	3131	4130	2409
26	tcc-miR319	4361	1697	3131	4130	2409
27	vvi-miR319e	4361	1697	3131	4130	2409
28	abu-let-7c	435	201	101	374	235
29	aca-let-7c-5p	435	201	101	374	235
30	ami-let-7c-5p	435	201	101	374	235
31	bta-let-7c	435	201	101	374	235
32	cfa-let-7c	435	201	101	374	235
33	chi-let-7c-5p	435	201	101	374	235
34	cja-let-7c	435	201	101	374	235
35	cli-let-7c-5p	435	201	101	374	235
36	cpi-let-7c-5p	435	201	101	374	235
37	cpo-let-7c-5p	435	201	101	374	235
38	dma-let-7c	435	201	101	374	235
39	dno-let-7c-5p	435	201	101	374	235
40	dre-let-7c-5p	435	201	101	374	235
41	eca-let-7c	435	201	101	374	235
42	gga-let-7c-5p	435	201	101	374	235
43	gmo-let-7c-5p	435	201	101	374	235
44	hhi-let-7c	435	201	101	374	235
45	hsa-let-7c-5p	435	201	101	374	235
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3	ipu-let-7c	435	201	101	374	235
4	mml-let-7c-5p	435	201	101	374	235
5	mmr-let-7c	435	201	101	374	235
6	mmu-let-7c-5p	435	201	101	374	235
7	mze-let-7c	435	201	101	374	235
8	nbr-let-7c	435	201	101	374	235
9	nle-let-7c	435	201	101	374	235
10	oan-let-7c-5p	435	201	101	374	235
11	oar-let-7c	435	201	101	374	235
12	ocu-let-7c-5p	435	201	101	374	235
13	oga-let-7c	435	201	101	374	235
14	oha-let-7c-5p	435	201	101	374	235
15	oni-let-7c	435	201	101	374	235
16	pal-let-7c-5p	435	201	101	374	235
17	pbv-let-7c-5p	435	201	101	374	235
18	pha-let-7c	435	201	101	374	235
19	ppy-let-7c	435	201	101	374	235
20	pol-let-7a-5p	435	201	101	374	235
21	ppa-let-7c	435	201	101	374	235
22	ppy-let-7c	435	201	101	374	235
23	ptr-let-7c	435	201	101	374	235
24	rno-let-7c-5p	435	201	101	374	235
25	ssa-let-7c-5p	435	201	101	374	235
26	ssc-let-7c	435	201	101	374	235
27	tcf-let-7-5p	435	201	101	374	235
28	tgu-let-7c-5p	435	201	101	374	235
29	xla-let-7c-5p	435	201	101	374	235
30	xtr-let-7c	435	201	101	374	235
31	efu-let-7c	448	209	111	385	247
32	abu-miR-143	115	4	328	51	30
33	aca-miR-143-3p	115	4	328	51	30
34	aja-miR-143	115	4	328	51	30
35	ami-miR-143-3p	115	4	328	51	30
36	bta-miR-143	115	4	328	51	30
37	cfa-miR-143	115	4	328	51	30
38	cgr-miR-143	115	4	328	51	30
39	chi-miR-143-3p	115	4	328	51	30
40	cli-miR-143-3p	115	4	328	51	30
41	cpi-miR-143-3p	115	4	328	51	30
42	cpo-miR-143-3p	115	4	328	51	30
43	dno-miR-143-3p	115	4	328	51	30
44	dre-miR-143	115	4	328	51	30
45	eca-miR-143	115	4	328	51	30
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3	gga-miR-143-3p	115	4	328	51	30
4	hsa-miR-143-3p	115	4	328	51	30
5	ipu-miR-143	115	4	328	51	30
6	mdo-miR-143-3p	115	4	328	51	30
7	mml-miR-143-3p	115	4	328	51	30
8	mmu-miR-143-3p	115	4	328	51	30
9	nle-miR-143	115	4	328	51	30
10	oan-miR-143-3p	115	4	328	51	30
11	oar-miR-143	115	4	328	51	30
12	ocu-miR-143-3p	115	4	328	51	30
13	oga-miR-143	115	4	328	51	30
14	oni-miR-143	115	4	328	51	30
15	pal-miR-143-3p	115	4	328	51	30
16	pbv-miR-143-3p	115	4	328	51	30
17	pha-miR-143	115	4	328	51	30
18	ssa-miR-143-3p	115	4	328	51	30
19	ssc-miR-143-3p	115	4	328	51	30
20	tch-miR-143-3p	115	4	328	51	30
21	xla-miR-143-3p	115	4	328	51	30
22	xtr-miR-143	115	4	328	51	30
23	efu-miR-143	115	4	329	51	30
24	mes-miR319h	237	83	202	210	130
25	vun-miR319b	237	83	202	210	130
26	cme-miR319c	218	77	198	201	122
27	cme-miR319d	218	77	198	201	122
28	gma-miR319c	218	77	198	201	122
29	ptc-miR319e	218	77	198	201	122
30	ptc-miR319f	218	77	198	201	122
31	ptc-miR319g	218	77	198	201	122
32	ptc-miR319h	218	77	198	201	122
33	stu-miR319b	218	77	198	201	122
34	ipu-miR-99b	629	10	298	423	321
35	efu-miR-99a	615	9	287	415	310
36	gma-miR169n-5p	703	297	415	379	640
37	mtr-miR169c	703	297	415	379	640
38	oga-miR-99a	585	9	284	397	295
39	pbv-miR-99a-5p	585	9	284	397	295
40	pha-miR-99a	585	9	284	397	295
41	aca-miR-99a-5p	585	9	284	396	294
42	ami-miR-99a-5p	585	9	284	396	294
43	cli-miR-99-5p	585	9	284	396	294
44	cpi-miR-99a-5p	585	9	284	396	294
45	cpo-miR-99a-5p	585	9	284	396	294
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3	dno-miR-99a-5p	585	9	284	396	294
4	dre-miR-99	585	9	284	396	294
5	eca-miR-99a	585	9	284	396	294
6	gga-miR-99a-5p	585	9	284	396	294
7	ggo-miR-99a	585	9	284	396	294
8	gmo-miR-99-5p	585	9	284	396	294
9	gmo-miR-99-5p	585	9	284	396	294
10	gmo-miR-99-5p	585	9	284	396	294
11	hsa-miR-99a-5p	585	9	284	396	294
12	ipu-miR-99a	585	9	284	396	294
13	ipu-miR-99a	585	9	284	396	294
14	lla-miR-99a	585	9	284	396	294
15	mml-miR-99a-5p	585	9	284	396	294
16	mmr-miR-99a	585	9	284	396	294
17	mmr-miR-99a	585	9	284	396	294
18	mmu-miR-99a-5p	585	9	284	396	294
19	mne-miR-99a	585	9	284	396	294
20	mze-miR-99b	585	9	284	396	294
21	mze-miR-99b	585	9	284	396	294
22	nbr-miR-99b	585	9	284	396	294
23	ocu-miR-99a-5p	585	9	284	396	294
24	oha-miR-99a-5p	585	9	284	396	294
25	oha-miR-99a-5p	585	9	284	396	294
26	oni-miR-99b	585	9	284	396	294
27	ony-miR-99b	585	9	284	396	294
28	ppa-miR-99a	585	9	284	396	294
29	ppa-miR-99a	585	9	284	396	294
30	ppy-miR-99a	585	9	284	396	294
31	ptr-miR-99a	585	9	284	396	294
32	ptr-miR-99a	585	9	284	396	294
33	rno-miR-99a-5p	585	9	284	396	294
34	ssa-miR-99-5p	585	9	284	396	294
35	ssc-miR-99a-5p	585	9	284	396	294
36	tch-miR-99a-5p	585	9	284	396	294
37	tch-miR-99a-5p	585	9	284	396	294
38	xtr-miR-99	585	9	284	396	294
39	gma-miR171n	100	118	70	64	161
40	gma-miR171p	100	118	70	64	161
41	gma-miR171p	100	118	70	64	161
42	aly-miR319c-3p	246	84	228	218	126
43	aly-miR319d-3p	246	84	228	218	126
44	ath-miR319c	246	84	228	218	126
45	ath-miR319c	246	84	228	218	126
46	mes-miR319g	246	84	228	218	126
47	pvu-miR319c	246	84	228	218	126
48	rco-miR319d	246	84	228	218	126
49	rco-miR319d	246	84	228	218	126
50	sly-miR319c-3p	246	84	228	218	126
51	dma-miR-143	122	6	361	56	36
52	ggo-miR-143	122	6	361	56	36
53	ggo-miR-143	122	6	361	56	36
54	lla-miR-143	122	6	361	56	36
55	oha-miR-143-3p	122	6	361	56	36
56	ppa-miR-143	122	6	361	56	36
57	ppy-miR-143	122	6	361	56	36
58	ppy-miR-143	122	6	361	56	36
59	ptr-miR-143	122	6	361	56	36
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3	rno-miR-143-3p	122	6	361	56	36
4	bta-miR-27a-3p	136	65	270	137	76
5	cfa-miR-27a	136	65	270	137	76
6	chi-miR-27a-3p	136	65	270	137	76
7	gmo-miR-27d-3p	136	65	270	137	76
8	oga-miR-27a	136	65	270	137	76
9	ola-miR-27a	136	65	270	137	76
10	pal-miR-27a-3p	136	65	270	137	76
11	xla-miR-27a-3p	136	65	270	137	76
12	cfa-miR-181a	163	6	105	105	85
13	ipu-miR-181a	163	6	105	105	85
14	mmr-miR-181a	163	6	105	105	85
15	oni-miR-181c	163	6	105	105	85
16	sbo-miR-181a	163	6	105	105	85
17	bta-miR-29a	105	39	119	96	50
18	ssc-miR-29a-3p	105	39	119	96	50
19	efu-miR-29a	109	41	122	97	52
20	age-miR-29a	65	23	96	58	29
21	ggo-miR-29a	65	23	96	58	29
22	lla-miR-29a	65	23	96	58	29
23	mml-miR-29a-3p	65	23	96	58	29
24	mne-miR-29a	65	23	96	58	29
25	ppa-miR-29a	65	23	96	58	29
26	ppy-miR-29a	65	23	96	58	29
27	ptr-miR-29a	65	23	96	58	29
28	sbo-miR-29a	65	23	96	58	29
29	sla-miR-29a	65	23	96	58	29
30	abu-miR-99b	366	1	184	239	176
31	bta-miR-99a-5p	366	1	184	239	176
32	ccr-miR-99	366	1	184	239	176
33	cfa-miR-99a	366	1	184	239	176
34	cgr-miR-99a-5p	366	1	184	239	176
35	chi-miR-99a-5p	366	1	184	239	176
36	cja-miR-99	366	1	184	239	176
37	nle-miR-99a	366	1	184	239	176
38	oan-miR-99-5p	366	1	184	239	176
39	pal-miR-99a-5p	366	1	184	239	176
40	sbo-miR-99a	366	1	184	239	176
41	tgu-miR-99-5p	366	1	184	239	176
42	xla-miR-99-5p	366	1	184	239	176
43	cpo-miR-652-3p	101	100	36	158	64
44	vca-miR396-5p	82	71	127	54	97
45	vvi-miR396b	82	71	127	54	97
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3	bta-let-7d	116	139	52	122	61
4	cgr-let-7d-5p	116	139	52	122	61
5	chi-let-7d-5p	116	139	52	122	61
6	chi-let-7d-5p	116	139	52	122	61
7	cja-let-7d	116	139	52	122	61
8	cli-let-7d-5p	116	139	52	122	61
9	cli-let-7d-5p	116	139	52	122	61
10	cpi-let-7d-5p	116	139	52	122	61
11	cpo-let-7d-5p	116	139	52	122	61
12	dno-let-7d-5p	116	139	52	122	61
13	dno-let-7d-5p	116	139	52	122	61
14	eca-let-7d	116	139	52	122	61
15	hsa-let-7d-5p	116	139	52	122	61
16	mml-let-7d	116	139	52	122	61
17	mml-let-7d	116	139	52	122	61
18	mmu-let-7d-5p	116	139	52	122	61
19	oan-let-7d-5p	116	139	52	122	61
20	ocu-let-7d-5p	116	139	52	122	61
21	ocu-let-7d-5p	116	139	52	122	61
22	oha-let-7d-5p	116	139	52	122	61
23	pbv-let-7d-5p	116	139	52	122	61
24	ppy-let-7d	116	139	52	122	61
25	ppy-let-7d	116	139	52	122	61
26	ptr-let-7d	116	139	52	122	61
27	rno-let-7d-5p	116	139	52	122	61
28	ssc-let-7d-5p	116	139	52	122	61
29	ssc-let-7d-5p	116	139	52	122	61
30	tgu-let-7d-5p	116	139	52	122	61
31	efu-let-7d	119	140	55	124	63
32	pab-miR396a-5p	84	74	132	57	101
33	pab-miR396a-5p	84	74	132	57	101
34	vvi-miR396a	84	74	132	57	101
35	pvu-miR159a.2	382	199	126	276	252
36	gma-miR319p	306	182	302	270	172
37	gma-miR319p	306	182	302	270	172
38	cfa-let-7d	75	62	14	75	34
39	cpo-miR-16b-5p	580	450	216	583	251
40	dno-miR-16b-5p	580	450	216	583	251
41	dno-miR-16b-5p	580	450	216	583	251
42	efu-miR-16	580	450	216	583	251
43	ocu-miR-16b-5p	580	450	216	583	251
44	ocu-miR-16b-5p	580	450	216	583	251
45	ccr-miR-181a	114	4	73	73	54
46	xla-miR-181a-5p	114	4	73	73	54
47	ahy-miR159	1399117	1317402	284674	1510032	995210
48	aly-miR159a-3p	1399117	1317402	284674	1510032	995210
49	aly-miR159a-3p	1399117	1317402	284674	1510032	995210
50	aof-miR159	1399117	1317402	284674	1510032	995210
51	ath-miR159a	1399117	1317402	284674	1510032	995210
52	atr-miR159	1399117	1317402	284674	1510032	995210
53	atr-miR159	1399117	1317402	284674	1510032	995210
54	bna-miR159	1399117	1317402	284674	1510032	995210
55	bra-miR159a	1399117	1317402	284674	1510032	995210
56	bra-miR159a	1399117	1317402	284674	1510032	995210
57	cme-miR159a	1399117	1317402	284674	1510032	995210
58	cpa-miR159a	1399117	1317402	284674	1510032	995210
59	csi-miR159a-3p	1399117	1317402	284674	1510032	995210
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3	fve-miR159a-3p	1399117	1317402	284674	1510032	995210
4	gma-miR159a-3p	1399117	1317402	284674	1510032	995210
5	gma-miR159e-3p	1399117	1317402	284674	1510032	995210
6	gma-miR159e-3p	1399117	1317402	284674	1510032	995210
7	hbr-miR159a	1399117	1317402	284674	1510032	995210
8	htu-miR159a	1399117	1317402	284674	1510032	995210
9	htu-miR159a	1399117	1317402	284674	1510032	995210
10	mdm-miR159d	1399117	1317402	284674	1510032	995210
11	mdm-miR159e	1399117	1317402	284674	1510032	995210
12	mdm-miR159e	1399117	1317402	284674	1510032	995210
13	mdm-miR159f	1399117	1317402	284674	1510032	995210
14	mes-miR159a-3p	1399117	1317402	284674	1510032	995210
15	mes-miR159b	1399117	1317402	284674	1510032	995210
16	mes-miR159b	1399117	1317402	284674	1510032	995210
17	mtr-miR159a	1399117	1317402	284674	1510032	995210
18	nta-miR159	1399117	1317402	284674	1510032	995210
19	ppe-miR159	1399117	1317402	284674	1510032	995210
20	ptc-miR159a	1399117	1317402	284674	1510032	995210
21	ptc-miR159a	1399117	1317402	284674	1510032	995210
22	ptc-miR159b	1399117	1317402	284674	1510032	995210
23	pvu-miR159a.1	1399117	1317402	284674	1510032	995210
24	rco-miR159	1399117	1317402	284674	1510032	995210
25	rco-miR159	1399117	1317402	284674	1510032	995210
26	sly-miR159	1399117	1317402	284674	1510032	995210
27	vca-miR159-3p	1399117	1317402	284674	1510032	995210
28	vvi-miR159c	1399117	1317402	284674	1510032	995210
29	vvi-miR159c	1399117	1317402	284674	1510032	995210
30	osa-miR159f	21111	20133	10743	24199	16704
31	cgr-let-7d-3p	74	62	14	74	34
32	cgr-let-7d-3p	74	62	14	74	34
33	cpo-let-7d-3p	74	62	14	74	34
34	dno-let-7d-3p	74	62	14	74	34
35	hsa-let-7d-3p	74	62	14	74	34
36	mmu-let-7d-3p	74	62	14	74	34
37	mmu-let-7d-3p	74	62	14	74	34
38	ocu-let-7d-3p	74	62	14	74	34
39	rno-let-7d-3p	74	62	14	74	34
40	rno-let-7d-3p	74	62	14	74	34
41	ssc-let-7d-3p	74	62	14	74	34
42	bdi-miR159b-3p.1	43621	42808	14189	43362	35789
43	far-miR159	43621	42808	14189	43362	35789
44	far-miR159	43621	42808	14189	43362	35789
45	hvu-miR159a	43621	42808	14189	43362	35789
46	hvu-miR159b	43621	42808	14189	43362	35789
47	hvu-miR159b	43621	42808	14189	43362	35789
48	osa-miR159a.1	43621	42808	14189	43362	35789
49	osa-miR159b	43621	42808	14189	43362	35789
50	osa-miR159b	43621	42808	14189	43362	35789
51	sbi-miR159a	43621	42808	14189	43362	35789
52	sof-miR159a	43621	42808	14189	43362	35789
53	sof-miR159a	43621	42808	14189	43362	35789
54	sof-miR159b	43621	42808	14189	43362	35789
55	sof-miR159d	43621	42808	14189	43362	35789
56	ssp-miR159a	43621	42808	14189	43362	35789
57	ssp-miR159a	43621	42808	14189	43362	35789
58	tae-miR159a	43621	42808	14189	43362	35789
59	tae-miR159b	43621	42808	14189	43362	35789
60	zma-miR159a-3p	43621	42808	14189	43362	35789

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3	zma-miR159b-3p	43621	42808	14189	43362	35789
4	zma-miR159f-3p	43621	42808	14189	43362	35789
5	zma-miR159j-3p	43621	42808	14189	43362	35789
6	zma-miR159k-3p	43621	42808	14189	43362	35789
7	zma-miR159k-3p	43621	42808	14189	43362	35789
8	cas-miR394	6054	4250	7309	3694	7125
9	cas-miR394	6054	4250	7309	3694	7125
10	ahy-miR394	6029	4235	7280	3673	7098
11	aly-miR394a-5p	6029	4235	7280	3673	7098
12	aly-miR394b-5p	6029	4235	7280	3673	7098
13	aly-miR394b-5p	6029	4235	7280	3673	7098
14	aof-miR394	6029	4235	7280	3673	7098
15	ata-miR394-5p	6029	4235	7280	3673	7098
16	ata-miR394-5p	6029	4235	7280	3673	7098
17	ath-miR394a	6029	4235	7280	3673	7098
18	ath-miR394b-5p	6029	4235	7280	3673	7098
19	atr-miR394	6029	4235	7280	3673	7098
20	atr-miR394	6029	4235	7280	3673	7098
21	bdi-miR394	6029	4235	7280	3673	7098
22	bdi-miR394	6029	4235	7280	3673	7098
23	bna-miR394a	6029	4235	7280	3673	7098
24	bna-miR394a	6029	4235	7280	3673	7098
25	bna-miR394b	6029	4235	7280	3673	7098
26	bna-miR394b	6029	4235	7280	3673	7098
27	cca-miR394	6029	4235	7280	3673	7098
28	cca-miR394	6029	4235	7280	3673	7098
29	cme-miR394a	6029	4235	7280	3673	7098
30	cme-miR394a	6029	4235	7280	3673	7098
31	cme-miR394b	6029	4235	7280	3673	7098
32	cme-miR394b	6029	4235	7280	3673	7098
33	cpa-miR394a	6029	4235	7280	3673	7098
34	cpa-miR394a	6029	4235	7280	3673	7098
35	cpa-miR394b	6029	4235	7280	3673	7098
36	cpa-miR394b	6029	4235	7280	3673	7098
37	csi-miR394a	6029	4235	7280	3673	7098
38	csi-miR394a	6029	4235	7280	3673	7098
39	csi-miR394b-5p	6029	4235	7280	3673	7098
40	csi-miR394b-5p	6029	4235	7280	3673	7098
41	fve-miR394	6029	4235	7280	3673	7098
42	fve-miR394	6029	4235	7280	3673	7098
43	ghr-miR394a	6029	4235	7280	3673	7098
44	ghr-miR394a	6029	4235	7280	3673	7098
45	ghr-miR394b	6029	4235	7280	3673	7098
46	ghr-miR394b	6029	4235	7280	3673	7098
47	gma-miR394a-5p	6029	4235	7280	3673	7098
48	gma-miR394a-5p	6029	4235	7280	3673	7098
49	gma-miR394b-5p	6029	4235	7280	3673	7098
50	gma-miR394b-5p	6029	4235	7280	3673	7098
51	gma-miR394c-5p	6029	4235	7280	3673	7098
52	gma-miR394c-5p	6029	4235	7280	3673	7098
53	gma-miR394d	6029	4235	7280	3673	7098
54	gma-miR394d	6029	4235	7280	3673	7098
55	gma-miR394e	6029	4235	7280	3673	7098
56	gma-miR394e	6029	4235	7280	3673	7098
57	gma-miR394f	6029	4235	7280	3673	7098
58	gma-miR394f	6029	4235	7280	3673	7098
59	gma-miR394g	6029	4235	7280	3673	7098
60	gma-miR394g	6029	4235	7280	3673	7098
61	lus-miR394a	6029	4235	7280	3673	7098
62	lus-miR394a	6029	4235	7280	3673	7098
63	lus-miR394b	6029	4235	7280	3673	7098
64	lus-miR394b	6029	4235	7280	3673	7098
65	mdm-miR394a	6029	4235	7280	3673	7098
66	mdm-miR394a	6029	4235	7280	3673	7098
67	mdm-miR394b	6029	4235	7280	3673	7098
68	mdm-miR394b	6029	4235	7280	3673	7098
69	mes-miR394a	6029	4235	7280	3673	7098
70	mes-miR394a	6029	4235	7280	3673	7098
71	mes-miR394b	6029	4235	7280	3673	7098
72	mes-miR394b	6029	4235	7280	3673	7098
73	nta-miR394	6029	4235	7280	3673	7098
74	nta-miR394	6029	4235	7280	3673	7098
75	osa-miR394	6029	4235	7280	3673	7098
76	osa-miR394	6029	4235	7280	3673	7098
77	pab-miR394c	6029	4235	7280	3673	7098
78	pab-miR394c	6029	4235	7280	3673	7098
79	ppe-miR394a	6029	4235	7280	3673	7098
80	ppe-miR394a	6029	4235	7280	3673	7098

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3	ppe-miR394b	6029	4235	7280	3673	7098
4	ptc-miR394a-5p	6029	4235	7280	3673	7098
5	ptc-miR394b-5p	6029	4235	7280	3673	7098
6	sbi-miR394a	6029	4235	7280	3673	7098
7	sbi-miR394b	6029	4235	7280	3673	7098
8	sly-miR394-5p	6029	4235	7280	3673	7098
9	ssl-miR394	6029	4235	7280	3673	7098
10	stu-miR384-5p	6029	4235	7280	3673	7098
11	tcc-miR394a	6029	4235	7280	3673	7098
12	tcc-miR394b	6029	4235	7280	3673	7098
13	vvi-miR394b	6029	4235	7280	3673	7098
14	zma-miR394a-5p	6029	4235	7280	3673	7098
15	zma-miR394b-5p	6029	4235	7280	3673	7098
16	mes-miR394c	6040	4241	7286	3676	7110
17	vvi-miR394a	6040	4241	7286	3676	7110
18	vvi-miR394c	6040	4241	7286	3676	7110
19	lus-miR159b	43789	43024	14233	43434	35919
20	aly-miR159b-3p	51628	50239	15411	50307	41274
21	ath-miR159b-3p	51628	50239	15411	50307	41274
22	cas-miR159b-3p	51628	50239	15411	50307	41274
23	cas-miR159c-3p	51628	50239	15411	50307	41274
24	lus-miR159c	51628	50239	15411	50307	41274
25	aca-miR-21-5p	481	200	352	368	215
26	age-miR-21	481	200	352	368	215
27	cfa-miR-21	481	200	352	368	215
28	cgr-miR-21-5p	481	200	352	368	215
29	cja-miR-21	481	200	352	368	215
30	cli-miR-21-5p	481	200	352	368	215
31	cpi-miR-21-5p	481	200	352	368	215
32	eca-miR-21	481	200	352	368	215
33	gga-miR-21-5p	481	200	352	368	215
34	ggo-miR-21	481	200	352	368	215
35	hsa-miR-21-5p	481	200	352	368	215
36	mdo-miR-21-5p	481	200	352	368	215
37	mml-miR-21-5p	481	200	352	368	215
38	mmu-miR-21a-5p	481	200	352	368	215
39	mne-miR-21	481	200	352	368	215
40	oan-miR-21-5p	481	200	352	368	215
41	oha-miR-21-5p	481	200	352	368	215
42	pal-miR-21-5p	481	200	352	368	215
43	ppa-miR-21	481	200	352	368	215
44	ppy-miR-21	481	200	352	368	215
45	ptr-miR-21	481	200	352	368	215
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3	rno-miR-21-5p	481	200	352	368	215
4	ssc-miR-21-5p	481	200	352	368	215
5	tch-miR-21-5p	481	200	352	368	215
6	tgu-miR-21-5p	481	200	352	368	215
7	age-miR-16	415	332	171	423	173
8	cfa-miR-16	415	332	171	423	173
9	cgr-miR-16-5p	415	332	171	423	173
10	cja-miR-16	415	332	171	423	173
11	cpi-miR-16a-5p	415	332	171	423	173
12	dma-miR-16	415	332	171	423	173
13	eca-miR-16	415	332	171	423	173
14	ggo-miR-16	415	332	171	423	173
15	hsa-miR-16-5p	415	332	171	423	173
16	lla-miR-16	415	332	171	423	173
17	mdo-miR-16-5p	415	332	171	423	173
18	mml-miR-16-5p	415	332	171	423	173
19	mmu-miR-16-5p	415	332	171	423	173
20	mne-miR-16	415	332	171	423	173
21	mze-miR-16a	415	332	171	423	173
22	nle-miR-16	415	332	171	423	173
23	oan-miR-16a-5p	415	332	171	423	173
24	oga-miR-16	415	332	171	423	173
25	oni-miR-16a	415	332	171	423	173
26	pal-miR-16-5p	415	332	171	423	173
27	pha-miR-16	415	332	171	423	173
28	ppa-miR-16	415	332	171	423	173
29	ptr-miR-16	415	332	171	423	173
30	rno-miR-16-5p	415	332	171	423	173
31	sbo-miR-16	415	332	171	423	173
32	sla-miR-16	415	332	171	423	173
33	ssa-miR-16c-5p	415	332	171	423	173
34	ssc-miR-16	415	332	171	423	173
35	gma-miR482c-3p	115	195	343	188	202
36	aof-miR171a	18981	26336	17317	24117	23314
37	aqc-miR171a	18981	26336	17317	24117	23314
38	aqc-miR171b	18981	26336	17317	24117	23314
39	aqc-miR171d	18981	26336	17317	24117	23314
40	ata-miR171b-3p	18981	26336	17317	24117	23314
41	ata-miR171d-3p	18981	26336	17317	24117	23314
42	bdi-miR171b	18981	26336	17317	24117	23314
43	bdi-miR171c-3p	18981	26336	17317	24117	23314
44	bdi-miR171d-3p	18981	26336	17317	24117	23314
45	bdi-miR171e	18981	26336	17317	24117	23314
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3	cme-miR171c	18981	26336	17317	24117	23314
4	cme-miR171f	18981	26336	17317	24117	23314
5	cpa-miR171a	18981	26336	17317	24117	23314
6	cpa-miR171b	18981	26336	17317	24117	23314
7	cpa-miR171c	18981	26336	17317	24117	23314
8	cpa-miR171d	18981	26336	17317	24117	23314
9	crt-miR171	18981	26336	17317	24117	23314
10	csi-miR171c-3p	18981	26336	17317	24117	23314
11	csi-miR171d-3p	18981	26336	17317	24117	23314
12	csi-miR171f-3p	18981	26336	17317	24117	23314
13	csi-miR171h-3p	18981	26336	17317	24117	23314
14	csi-miR171i-3p	18981	26336	17317	24117	23314
15	far-miR171	18981	26336	17317	24117	23314
16	fve-miR171a	18981	26336	17317	24117	23314
17	fve-miR171c-3p	18981	26336	17317	24117	23314
18	fve-miR171d	18981	26336	17317	24117	23314
19	fve-miR171e	18981	26336	17317	24117	23314
20	fve-miR171g	18981	26336	17317	24117	23314
21	gma-miR171e	18981	26336	17317	24117	23314
22	gma-miR171f	18981	26336	17317	24117	23314
23	gma-miR171g	18981	26336	17317	24117	23314
24	gma-miR171j-3p	18981	26336	17317	24117	23314
25	gma-miR171u	18981	26336	17317	24117	23314
26	hpa-miR171a	18981	26336	17317	24117	23314
27	htu-miR171b	18981	26336	17317	24117	23314
28	htu-miR171c	18981	26336	17317	24117	23314
29	hvu-miR171-3p	18981	26336	17317	24117	23314
30	lja-miR171a	18981	26336	17317	24117	23314
31	lus-miR171b	18981	26336	17317	24117	23314
32	lus-miR171c	18981	26336	17317	24117	23314
33	lus-miR171e	18981	26336	17317	24117	23314
34	mdm-miR171g	18981	26336	17317	24117	23314
35	mdm-miR171h	18981	26336	17317	24117	23314
36	mes-miR171g	18981	26336	17317	24117	23314
37	mes-miR171h	18981	26336	17317	24117	23314
38	mes-miR171i	18981	26336	17317	24117	23314
39	mes-miR171j	18981	26336	17317	24117	23314
40	mes-miR171k	18981	26336	17317	24117	23314
41	mtr-miR171d	18981	26336	17317	24117	23314
42	nta-miR171c	18981	26336	17317	24117	23314
43	osa-miR171b	18981	26336	17317	24117	23314
44	osa-miR171c-3p	18981	26336	17317	24117	23314
45	osa-miR171d-3p	18981	26336	17317	24117	23314
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3	osa-miR171e-3p	18981	26336	17317	24117	23314
4	osa-miR171f-3p	18981	26336	17317	24117	23314
5	pde-miR171	18981	26336	17317	24117	23314
6	ppe-miR171a	18981	26336	17317	24117	23314
7	ppe-miR171c	18981	26336	17317	24117	23314
8	ppe-miR171f	18981	26336	17317	24117	23314
9	ppe-miR171g	18981	26336	17317	24117	23314
10	ptc-miR171e	18981	26336	17317	24117	23314
11	ptc-miR171f	18981	26336	17317	24117	23314
12	ptc-miR171g-3p	18981	26336	17317	24117	23314
13	ptc-miR171h-3p	18981	26336	17317	24117	23314
14	ptc-miR171i	18981	26336	17317	24117	23314
15	rco-miR171c	18981	26336	17317	24117	23314
16	rco-miR171d	18981	26336	17317	24117	23314
17	rco-miR171e	18981	26336	17317	24117	23314
18	rco-miR171f	18981	26336	17317	24117	23314
19	sbi-miR171a	18981	26336	17317	24117	23314
20	sbi-miR171b	18981	26336	17317	24117	23314
21	sbi-miR171d	18981	26336	17317	24117	23314
22	sbi-miR171i	18981	26336	17317	24117	23314
23	sbi-miR171k	18981	26336	17317	24117	23314
24	sly-miR171a	18981	26336	17317	24117	23314
25	stu-miR171a-3p	18981	26336	17317	24117	23314
26	stu-miR171e	18981	26336	17317	24117	23314
27	tae-miR171a	18981	26336	17317	24117	23314
28	tcc-miR171d	18981	26336	17317	24117	23314
29	tcc-miR171e	18981	26336	17317	24117	23314
30	tcc-miR171f	18981	26336	17317	24117	23314
31	tcc-miR171g	18981	26336	17317	24117	23314
32	tcc-miR171h	18981	26336	17317	24117	23314
33	vvi-miR171a	18981	26336	17317	24117	23314
34	vvi-miR171c	18981	26336	17317	24117	23314
35	vvi-miR171d	18981	26336	17317	24117	23314
36	vvi-miR171i	18981	26336	17317	24117	23314
37	vvi-miR171j	18981	26336	17317	24117	23314
38	zma-miR171d-3p	18981	26336	17317	24117	23314
39	zma-miR171e-3p	18981	26336	17317	24117	23314
40	zma-miR171i-3p	18981	26336	17317	24117	23314
41	zma-miR171j-3p	18981	26336	17317	24117	23314
42	aly-miR159c-3p	143	159	52	148	104
43	ath-miR159c	143	159	52	148	104
44	cas-miR159a	143	159	52	148	104
45	zma-miR169a-3p	3225	6734	3860	4745	5231
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3	zma-miR169b-3p	3225	6734	3860	4745	5231
4	gma-miR482a-3p	6550	10477	13426	7472	7453
5	vun-miR482	6550	10477	13426	7472	7453
6	atr-miR171b	355	690	319	428	500
7	atr-miR171b	355	690	319	428	500
8	gma-miR171c-3p	355	690	319	428	500
9	gma-miR171c-3p	355	690	319	428	500
10	gma-miR171o-3p	355	690	319	428	500
11	gma-miR171q	355	690	319	428	500
12	gma-miR171q	355	690	319	428	500
13	mdm-miR171m	355	690	319	428	500
14	mdm-miR171n	355	690	319	428	500
15	zma-miR171f-3p	355	690	319	428	500
16	aca-miR-191-5p	477	428	181	576	207
17	aca-miR-191-5p	477	428	181	576	207
18	bta-miR-191	477	428	181	576	207
19	cgr-miR-191-5p	477	428	181	576	207
20	cja-miR-191	477	428	181	576	207
21	cja-miR-191	477	428	181	576	207
22	cpo-miR-191-5p	477	428	181	576	207
23	dma-miR-191	477	428	181	576	207
24	dno-miR-191-5p	477	428	181	576	207
25	dno-miR-191-5p	477	428	181	576	207
26	eca-miR-191a	477	428	181	576	207
27	gga-miR-191-5p	477	428	181	576	207
28	hsa-miR-191-5p	477	428	181	576	207
29	hsa-miR-191-5p	477	428	181	576	207
30	mml-miR-191-5p	477	428	181	576	207
31	mmr-miR-191	477	428	181	576	207
32	mmr-miR-191	477	428	181	576	207
33	mmu-miR-191-5p	477	428	181	576	207
34	nle-miR-191	477	428	181	576	207
35	ocu-miR-191-5p	477	428	181	576	207
36	oga-miR-191	477	428	181	576	207
37	oga-miR-191	477	428	181	576	207
38	oha-miR-191-5p	477	428	181	576	207
39	pbv-miR-191-5p	477	428	181	576	207
40	pha-miR-191	477	428	181	576	207
41	pha-miR-191	477	428	181	576	207
42	ppa-miR-191	477	428	181	576	207
43	ppy-miR-191	477	428	181	576	207
44	ptr-miR-191	477	428	181	576	207
45	ptr-miR-191	477	428	181	576	207
46	rno-miR-191a-5p	477	428	181	576	207
47	sbo-miR-191	477	428	181	576	207
48	ssc-miR-191	477	428	181	576	207
49	ssc-miR-191	477	428	181	576	207
50	gma-miR171o-5p	84	80	19	34	90
51	cfa-miR-29a	75	30	84	70	34
52	cja-miR-29a	75	30	84	70	34
53	cja-miR-29a	75	30	84	70	34
54	cpo-miR-29a-3p	75	30	84	70	34
55	dma-miR-29a	75	30	84	70	34
56	dno-miR-29a-3p	75	30	84	70	34
57	dno-miR-29a-3p	75	30	84	70	34
58	eca-miR-29a	75	30	84	70	34
59	hsa-miR-29a-3p	75	30	84	70	34
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3	mmr-miR-29a	75	30	84	70	34
4	mmu-miR-29a-3p	75	30	84	70	34
5	nle-miR-29a	75	30	84	70	34
6	ocu-miR-29a-3p	75	30	84	70	34
7	oga-miR-29a	75	30	84	70	34
8	pal-miR-29a-3p	75	30	84	70	34
9	pha-miR-29a	75	30	84	70	34
10	rno-miR-29a-3p	75	30	84	70	34
11	csi-miR393b-5p	724	322	100	306	461
12	gma-miR393h	724	322	100	306	461
13	gma-miR393i	724	322	100	306	461
14	gma-miR393j	724	322	100	306	461
15	gma-miR393k	724	322	100	306	461
16	ami-miR-191-5p	194	181	119	234	96
17	cfa-miR-191	194	181	119	234	96
18	chi-miR-191-5p	194	181	119	234	96
19	cpi-miR-191-5p	194	181	119	234	96
20	mdo-miR-191-5p	194	181	119	234	96
21	oan-miR-191-5p	194	181	119	234	96
22	oar-miR-191	194	181	119	234	96
23	pal-miR-191-5p	194	181	119	234	96
24	tch-miR-191-5p	194	181	119	234	96
25	xla-miR-191-5p	194	181	119	234	96
26	xtr-miR-191	194	181	119	234	96
27	aly-miR169b-5p	146961	237557	30977	164185	155727
28	aly-miR169c-5p	146961	237557	30977	164185	155727
29	aqc-miR169c	146961	237557	30977	164185	155727
30	ata-miR169d-5p	146961	237557	30977	164185	155727
31	ath-miR169b-5p	146961	237557	30977	164185	155727
32	ath-miR169c	146961	237557	30977	164185	155727
33	bdi-miR169c-5p	146961	237557	30977	164185	155727
34	bdi-miR169f	146961	237557	30977	164185	155727
35	bna-miR169n	146961	237557	30977	164185	155727
36	cas-miR169b	146961	237557	30977	164185	155727
37	cme-miR169f	146961	237557	30977	164185	155727
38	cme-miR169h	146961	237557	30977	164185	155727
39	csi-miR169g-5p	146961	237557	30977	164185	155727
40	csi-miR169k-5p	146961	237557	30977	164185	155727
41	csi-miR169m-5p	146961	237557	30977	164185	155727
42	csi-miR169n-5p	146961	237557	30977	164185	155727
43	csi-miR169o-5p	146961	237557	30977	164185	155727
44	csi-miR169r-5p	146961	237557	30977	164185	155727
45	gma-miR169a	146961	237557	30977	164185	155727
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3	gma-miR169f	146961	237557	30977	164185	155727
4	gma-miR169g	146961	237557	30977	164185	155727
5	gma-miR169m	146961	237557	30977	164185	155727
6	gma-miR169m	146961	237557	30977	164185	155727
7	lus-miR169f	146961	237557	30977	164185	155727
8	lus-miR169h	146961	237557	30977	164185	155727
9	lus-miR169j	146961	237557	30977	164185	155727
10	lus-miR169j	146961	237557	30977	164185	155727
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12	mdm-miR169g	146961	237557	30977	164185	155727
13	mdm-miR169g	146961	237557	30977	164185	155727
14	mdm-miR169h	146961	237557	30977	164185	155727
15	mdm-miR169i	146961	237557	30977	164185	155727
16	mdm-miR169j	146961	237557	30977	164185	155727
17	mdm-miR169j	146961	237557	30977	164185	155727
18	mes-miR169a	146961	237557	30977	164185	155727
19	mes-miR169b	146961	237557	30977	164185	155727
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21	mes-miR169c	146961	237557	30977	164185	155727
22	mes-miR169d	146961	237557	30977	164185	155727
23	mes-miR169e	146961	237557	30977	164185	155727
24	mes-miR169e	146961	237557	30977	164185	155727
25	mtr-miR169b	146961	237557	30977	164185	155727
26	mtr-miR169g	146961	237557	30977	164185	155727
27	mtr-miR169l-5p	146961	237557	30977	164185	155727
28	nta-miR169q	146961	237557	30977	164185	155727
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30	nta-miR169r	146961	237557	30977	164185	155727
31	nta-miR169s	146961	237557	30977	164185	155727
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33	osa-miR169b	146961	237557	30977	164185	155727
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35	ppe-miR169a	146961	237557	30977	164185	155727
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38	ppe-miR169c	146961	237557	30977	164185	155727
39	ptc-miR169d	146961	237557	30977	164185	155727
40	ptc-miR169d	146961	237557	30977	164185	155727
41	ptc-miR169e	146961	237557	30977	164185	155727
42	ptc-miR169f	146961	237557	30977	164185	155727
43	ptc-miR169g	146961	237557	30977	164185	155727
44	ptc-miR169g	146961	237557	30977	164185	155727
45	ptc-miR169h	146961	237557	30977	164185	155727
46	ptc-miR169p	146961	237557	30977	164185	155727
47	rco-miR169a	146961	237557	30977	164185	155727
48	rco-miR169b	146961	237557	30977	164185	155727
49	rco-miR169b	146961	237557	30977	164185	155727
50	sbi-miR169b	146961	237557	30977	164185	155727
51	sbi-miR169k	146961	237557	30977	164185	155727
52	sbi-miR169k	146961	237557	30977	164185	155727
53	sly-miR169a	146961	237557	30977	164185	155727
54	tcc-miR169b	146961	237557	30977	164185	155727
55	tcc-miR169k	146961	237557	30977	164185	155727
56	tcc-miR169l	146961	237557	30977	164185	155727
57	tcc-miR169l	146961	237557	30977	164185	155727
58	vun-miR169	146961	237557	30977	164185	155727
59	vvi-miR169a	146961	237557	30977	164185	155727
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3	vvi-miR169c	146961	237557	30977	164185	155727
4	vvi-miR169j	146961	237557	30977	164185	155727
5	vvi-miR169k	146961	237557	30977	164185	155727
6	vvi-miR169s	146961	237557	30977	164185	155727
7	vvi-miR169w	146961	237557	30977	164185	155727
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10	zma-miR169c-5p	146961	237557	30977	164185	155727
11	zma-miR169r-5p	146961	237557	30977	164185	155727
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13	aly-miR170-3p	15308	25886	3466	19075	16163
14	ath-miR170-3p	15308	25886	3466	19075	16163
15	stu-miR171c-3p	15308	25886	3466	19075	16163
16						
17	cli-miR-146a-5p	343	393	170	459	165
18	cpo-miR-146a-5p	343	393	170	459	165
19	ocu-miR-146a-5p	343	393	170	459	165
20						
21	dno-miR-146a-5p	390	443	190	506	189
22	gma-miR319d	4472	2104	493	3426	1420
23	gma-miR319o	4472	2104	493	3426	1420
24	gma-miR319i	4536	2115	515	3463	1429
25						
26	cfa-miR-146a	341	392	170	457	164
27	cgr-miR-146a	341	392	170	457	164
28	cja-miR-146a	341	392	170	457	164
29						
30	eca-miR-146a	341	392	170	457	164
31	gga-miR-146a-5p	341	392	170	457	164
32	hsa-miR-146a-5p	341	392	170	457	164
33						
34	mdo-miR-146a-5p	341	392	170	457	164
35	mml-miR-146a-5p	341	392	170	457	164
36	mmr-miR-146a	341	392	170	457	164
37						
38	mmu-miR-146a-5p	341	392	170	457	164
39	nle-miR-146a	341	392	170	457	164
40	pal-miR-146a-5p	341	392	170	457	164
41						
42	pha-miR-146a	341	392	170	457	164
43	ppy-miR-146a	341	392	170	457	164
44	ptr-miR-146a	341	392	170	457	164
45						
46	rno-miR-146a-5p	341	392	170	457	164
47	ssc-miR-146a-5p	341	392	170	457	164
48	tch-miR-146a-5p	341	392	170	457	164
49						
50	tgu-miR-146c	341	392	170	457	164
51	efu-miR-22	731	372	963	618	328
52	xla-miR-22-3p	731	372	963	618	328
53						
54	aly-miR171b-3p	424	544	1350	408	747
55	aly-miR171c-3p	424	544	1350	408	747
56	ata-miR171c-3p	424	544	1350	408	747
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58	ath-miR171b-3p	424	544	1350	408	747
59	ath-miR171c-3p	424	544	1350	408	747
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3	bna-miR171a	424	544	1350	408	747
4	bna-miR171b	424	544	1350	408	747
5	bna-miR171c	424	544	1350	408	747
6	bna-miR171d	424	544	1350	408	747
7	bna-miR171e	424	544	1350	408	747
8	bol-miR171a	424	544	1350	408	747
9	bra-miR171a	424	544	1350	408	747
10	bra-miR171b	424	544	1350	408	747
11	bra-miR171c	424	544	1350	408	747
12	bra-miR171d	424	544	1350	408	747
13	cas-miR171b	424	544	1350	408	747
14	cas-miR171c-3p	424	544	1350	408	747
15	cme-miR171b	424	544	1350	408	747
16	cme-miR171d	424	544	1350	408	747
17	gma-miR171i-3p	424	544	1350	408	747
18	lus-miR171i	424	544	1350	408	747
19	mdm-miR171f-3p	424	544	1350	408	747
20	mes-miR171b	424	544	1350	408	747
21	mes-miR171c	424	544	1350	408	747
22	mtr-miR171f	424	544	1350	408	747
23	ptc-miR171a-3p	424	544	1350	408	747
24	ptc-miR171b	424	544	1350	408	747
25	rco-miR171a	424	544	1350	408	747
26	rco-miR171b	424	544	1350	408	747
27	sly-miR171b-3p	424	544	1350	408	747
28	ssl-miR171a	424	544	1350	408	747
29	stu-miR171d-3p	424	544	1350	408	747
30	tae-miR171b	424	544	1350	408	747
31	age-miR-22	709	369	937	608	319
32	aja-miR-22	709	369	937	608	319
33	cfa-miR-22	709	369	937	608	319
34	cgr-miR-22-3p	709	369	937	608	319
35	cja-miR-22	709	369	937	608	319
36	cli-miR-22-3p	709	369	937	608	319
37	cpi-miR-22-3p	709	369	937	608	319
38	cpo-miR-22-3p	709	369	937	608	319
39	dma-miR-22	709	369	937	608	319
40	dno-miR-22-3p	709	369	937	608	319
41	eca-miR-22	709	369	937	608	319
42	gga-miR-22-3p	709	369	937	608	319
43	hsa-miR-22-3p	709	369	937	608	319
44	lca-miR-22	709	369	937	608	319
45	lla-miR-22	709	369	937	608	319
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3	mml-miR-22	709	369	937	608	319
4	mmr-miR-22	709	369	937	608	319
5	mmu-miR-22-3p	709	369	937	608	319
6	mne-miR-22	709	369	937	608	319
7	nle-miR-22	709	369	937	608	319
8	oan-miR-22-3p	709	369	937	608	319
9	ocu-miR-22-3p	709	369	937	608	319
10	oga-miR-22	709	369	937	608	319
11	oha-miR-22a	709	369	937	608	319
12	pal-miR-22-3p	709	369	937	608	319
13	pbv-miR-22-3p	709	369	937	608	319
14	pha-miR-22	709	369	937	608	319
15	ppa-miR-22	709	369	937	608	319
16	ppy-miR-22	709	369	937	608	319
17	ptr-miR-22	709	369	937	608	319
18	rno-miR-22-3p	709	369	937	608	319
19	sbo-miR-22	709	369	937	608	319
20	sla-miR-22	709	369	937	608	319
21	ssc-miR-22-3p	709	369	937	608	319
22	tch-miR-22-3p	709	369	937	608	319
23	xtr-miR-22-3p	709	369	937	608	319
24	gma-miR319g	72394	42723	7142	58789	26709
25	gma-miR319l	72394	42723	7142	58789	26709
26	gma-miR319q	71606	42408	6869	58263	26449
27	aly-miR393a-5p	306	138	44	193	134
28	aly-miR393b-5p	306	138	44	193	134
29	ath-miR393a-5p	306	138	44	193	134
30	ath-miR393b-5p	306	138	44	193	134
31	atr-miR393	306	138	44	193	134
32	cas-miR393-5p	306	138	44	193	134
33	cpa-miR393	306	138	44	193	134
34	gma-miR393c-5p	306	138	44	193	134
35	gma-miR393d	306	138	44	193	134
36	gma-miR393e	306	138	44	193	134
37	gma-miR393f	306	138	44	193	134
38	gma-miR393g	306	138	44	193	134
39	htu-miR393a	306	138	44	193	134
40	htu-miR393b	306	138	44	193	134
41	htu-miR393c	306	138	44	193	134
42	mes-miR393b	306	138	44	193	134
43	stu-miR393-5p	306	138	44	193	134
44	tcc-miR393a	306	138	44	193	134
45	zma-miR393b-5p	306	138	44	193	134
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3	aof-miR393b	174	86	26	102	86
4	fve-miR393b	174	86	26	102	86
5	ghr-miR393	174	86	26	102	86
6	mdm-miR393a	174	86	26	102	86
7	mdm-miR393b	174	86	26	102	86
8	mdm-miR393c	174	86	26	102	86
9	mes-miR393c	174	86	26	102	86
10	mes-miR393d	174	86	26	102	86
11	osa-miR393b-5p	174	86	26	102	86
12	zma-miR393a-5p	174	86	26	102	86
13	zma-miR393c-5p	174	86	26	102	86
14	zma-miR393d-5p	174	86	26	102	86
15	smo-miR171a	54	99	106	64	80
16	atr-miR319a	10552	5675	5926	6787	3696
17	atr-miR319c	10552	5675	5926	6787	3696
18	cme-miR319a	10552	5675	5926	6787	3696
19	cme-miR319b	10552	5675	5926	6787	3696
20	ctr-miR319	10552	5675	5926	6787	3696
21	gma-miR319a	10552	5675	5926	6787	3696
22	gma-miR319b	10552	5675	5926	6787	3696
23	gma-miR319e	10552	5675	5926	6787	3696
24	lus-miR319b	10552	5675	5926	6787	3696
25	mtr-miR319a-3p	10552	5675	5926	6787	3696
26	mtr-miR319b-3p	10552	5675	5926	6787	3696
27	pab-miR319a	10552	5675	5926	6787	3696
28	pab-miR319b	10552	5675	5926	6787	3696
29	pab-miR319c	10552	5675	5926	6787	3696
30	pab-miR319f	10552	5675	5926	6787	3696
31	pab-miR319g	10552	5675	5926	6787	3696
32	pab-miR319i	10552	5675	5926	6787	3696
33	pab-miR319k	10552	5675	5926	6787	3696
34	pab-miR319l	10552	5675	5926	6787	3696
35	pab-miR319m	10552	5675	5926	6787	3696
36	pab-miR319n	10552	5675	5926	6787	3696
37	ppe-miR319a	10552	5675	5926	6787	3696
38	ptc-miR319a	10552	5675	5926	6787	3696
39	ptc-miR319b	10552	5675	5926	6787	3696
40	ptc-miR319c	10552	5675	5926	6787	3696
41	ptc-miR319d	10552	5675	5926	6787	3696
42	mtr-miR319c-3p	10669	5711	5950	6835	3724
43	vvi-miR319g	10669	5711	5950	6835	3724
44	csi-miR159c-3p	10896	5940	5944	7003	3829
45	ppt-miR319c	10896	5940	5944	7003	3829
46	ppt-miR319d-3p	10896	5940	5944	7003	3829
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3	ppt-miR319e	10896	5940	5944	7003	3829
4	ath-miR8175	15	20	96	15	27
5	abu-miR-200a	0	2	202	0	0
6	bta-miR-200a	0	2	202	0	0
7	cgr-miR-200a	0	2	202	0	0
8	cli-miR-200a-3p	0	2	202	0	0
9	cpi-miR-200a-3p	0	2	202	0	0
10	cpo-miR-200a-3p	0	2	202	0	0
11	efu-miR-200a	0	2	202	0	0
12	mze-miR-200a	0	2	202	0	0
13	nbr-miR-200a	0	2	202	0	0
14	oan-miR-200a-3p	0	2	202	0	0
15	oha-miR-200a	0	2	202	0	0
16	oni-miR-200a	0	2	202	0	0
17	pal-miR-200a-3p	0	2	202	0	0
18	pbv-miR-200a-3p	0	2	202	0	0
19	pny-miR-200a	0	2	202	0	0
20	ssa-miR-200b-3p	0	2	202	0	0
21	tch-miR-200a-3p	0	2	202	0	0
22	tgu-miR-200a-3p	0	2	202	0	0
23	xla-miR-200a-3p	0	2	202	0	0
24	aa-miR162	2516	1966	8709	2401	1344
25	aly-miR162a-3p	2516	1966	8709	2401	1344
26	aly-miR162b-3p	2516	1966	8709	2401	1344
27	ath-miR162a-3p	2516	1966	8709	2401	1344
28	ath-miR162b-3p	2516	1966	8709	2401	1344
29	bra-miR162-3p	2516	1966	8709	2401	1344
30	cme-miR162	2516	1966	8709	2401	1344
31	cpa-miR162a	2516	1966	8709	2401	1344
32	csi-miR162-3p	2516	1966	8709	2401	1344
33	eun-miR162-3p	2516	1966	8709	2401	1344
34	fve-miR162-3p	2516	1966	8709	2401	1344
35	ghr-miR162a	2516	1966	8709	2401	1344
36	gma-miR162b	2516	1966	8709	2401	1344
37	gma-miR162c	2516	1966	8709	2401	1344
38	hpe-miR162a	2516	1966	8709	2401	1344
39	htu-miR162a	2516	1966	8709	2401	1344
40	lus-miR162a	2516	1966	8709	2401	1344
41	lus-miR162b	2516	1966	8709	2401	1344
42	mdm-miR162a	2516	1966	8709	2401	1344
43	mdm-miR162b	2516	1966	8709	2401	1344
44	mes-miR162	2516	1966	8709	2401	1344
45	mtr-miR162	2516	1966	8709	2401	1344
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3	nta-miR162a	2516	1966	8709	2401	1344
4	nta-miR162b	2516	1966	8709	2401	1344
5	osa-miR162a	2516	1966	8709	2401	1344
6	osa-miR162a	2516	1966	8709	2401	1344
7	pde-miR162	2516	1966	8709	2401	1344
8	pde-miR162	2516	1966	8709	2401	1344
9	ppe-miR162	2516	1966	8709	2401	1344
10	ptc-miR162a	2516	1966	8709	2401	1344
11	ptc-miR162b	2516	1966	8709	2401	1344
12	ptc-miR162b	2516	1966	8709	2401	1344
13	rco-miR162	2516	1966	8709	2401	1344
14	sbi-miR162	2516	1966	8709	2401	1344
15	sly-miR162	2516	1966	8709	2401	1344
16	stu-miR162a-3p	2516	1966	8709	2401	1344
17	stu-miR162a-3p	2516	1966	8709	2401	1344
18	stu-miR162b-3p	2516	1966	8709	2401	1344
19	tcc-miR162	2516	1966	8709	2401	1344
20	vun-miR162	2516	1966	8709	2401	1344
21	vun-miR162	2516	1966	8709	2401	1344
22	vvi-miR162	2516	1966	8709	2401	1344
23	gma-miR169s-5p	3996	5895	1244	4675	3356
24	mtr-miR169d-5p	3996	5895	1244	4675	3356
25	mtr-miR169d-5p	3996	5895	1244	4675	3356
26	gma-miR169d	3762	5773	1252	4542	3103
27	aau-miR319	15967	7907	7713	9478	4930
28	aly-miR319a-3p	15967	7907	7713	9478	4930
29	aly-miR319a-3p	15967	7907	7713	9478	4930
30	aly-miR319b-3p	15967	7907	7713	9478	4930
31	amg-miR319	15967	7907	7713	9478	4930
32	aof-miR319a	15967	7907	7713	9478	4930
33	aof-miR319a	15967	7907	7713	9478	4930
34	aqc-miR319	15967	7907	7713	9478	4930
35	ath-miR319a	15967	7907	7713	9478	4930
36	ath-miR319a	15967	7907	7713	9478	4930
37	ath-miR319b	15967	7907	7713	9478	4930
38	bra-miR319-3p	15967	7907	7713	9478	4930
39	cca-miR319	15967	7907	7713	9478	4930
40	gma-miR319h	15967	7907	7713	9478	4930
41	gma-miR319h	15967	7907	7713	9478	4930
42	gma-miR319j	15967	7907	7713	9478	4930
43	gma-miR319k	15967	7907	7713	9478	4930
44	gma-miR319k	15967	7907	7713	9478	4930
45	gma-miR319m	15967	7907	7713	9478	4930
46	hbr-miR319	15967	7907	7713	9478	4930
47	lus-miR319a	15967	7907	7713	9478	4930
48	mdm-miR319a	15967	7907	7713	9478	4930
49	mdm-miR319a	15967	7907	7713	9478	4930
50	mdm-miR319b-3p	15967	7907	7713	9478	4930
51	mes-miR319a	15967	7907	7713	9478	4930
52	mes-miR319a	15967	7907	7713	9478	4930
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54	mes-miR319c	15967	7907	7713	9478	4930
55	mes-miR319d	15967	7907	7713	9478	4930
56	mes-miR319e	15967	7907	7713	9478	4930
57	mes-miR319e	15967	7907	7713	9478	4930
58	mtr-miR319d-3p	15967	7907	7713	9478	4930
59	nta-miR319a	15967	7907	7713	9478	4930
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3	nta-miR319b	15967	7907	7713	9478	4930
4	rco-miR319a	15967	7907	7713	9478	4930
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6	rco-miR319c	15967	7907	7713	9478	4930
7	rco-miR319c	15967	7907	7713	9478	4930
8	sly-miR319b	15967	7907	7713	9478	4930
9	sly-miR319b	15967	7907	7713	9478	4930
10	stu-miR319a-3p	15967	7907	7713	9478	4930
11	tae-miR319	15967	7907	7713	9478	4930
12	tae-miR319	15967	7907	7713	9478	4930
13	vun-miR319a	15967	7907	7713	9478	4930
14	vvi-miR319b	15967	7907	7713	9478	4930
15	vvi-miR319c	15967	7907	7713	9478	4930
16	vvi-miR319c	15967	7907	7713	9478	4930
17	vvi-miR319f	15967	7907	7713	9478	4930
18	mtr-miR169e-5p	3708	5721	1198	4514	3024
19	vvi-miR169m	3708	5721	1198	4514	3024
20	vvi-miR169n	3708	5721	1198	4514	3024
21	vvi-miR169n	3708	5721	1198	4514	3024
22	vvi-miR169p	3708	5721	1198	4514	3024
23	vvi-miR169q	3708	5721	1198	4514	3024
24	vvi-miR169q	3708	5721	1198	4514	3024
25	csi-miR171a	52	95	103	56	74
26	zma-miR171b-3p	52	95	103	56	74
27	gma-miR166u	1208	580	1158	920	659
28	ami-miR-27b-3p	74	16	91	56	31
29	ami-miR-27b-3p	74	16	91	56	31
30	dma-miR-27b	74	16	91	56	31
31	gmo-miR-27b-3p	74	16	91	56	31
32	nle-miR-27b	74	16	91	56	31
33	nle-miR-27b	74	16	91	56	31
34	oga-miR-27b	74	16	91	56	31
35	pha-miR-27b	74	16	91	56	31
36	cme-miR156j	21180	34742	3642	21446	16004
37	cme-miR156j	21180	34742	3642	21446	16004
38	fve-miR156a	21179	34742	3642	21446	16004
39	fve-miR156b	21179	34742	3642	21446	16004
40	fve-miR156c	21179	34742	3642	21446	16004
41	fve-miR156c	21179	34742	3642	21446	16004
42	fve-miR156e	21179	34742	3642	21446	16004
43	gma-miR156k	21179	34742	3642	21446	16004
44	gma-miR156n	21179	34742	3642	21446	16004
45	gma-miR156n	21179	34742	3642	21446	16004
46	gma-miR156o	21179	34742	3642	21446	16004
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48	aly-miR156b-5p	20768	34227	3548	21110	15698
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51	aly-miR156d-5p	20768	34227	3548	21110	15698
52	aly-miR156e-5p	20768	34227	3548	21110	15698
53	aly-miR156e-5p	20768	34227	3548	21110	15698
54	aly-miR156f-5p	20768	34227	3548	21110	15698
55	aof-miR156a	20768	34227	3548	21110	15698
56	ata-miR156a-5p	20768	34227	3548	21110	15698
57	ata-miR156a-5p	20768	34227	3548	21110	15698
58	ata-miR156b-5p	20768	34227	3548	21110	15698
59	ata-miR156c-5p	20768	34227	3548	21110	15698
60	ata-miR156c-5p	20768	34227	3548	21110	15698

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ata-miR156e-5p	20768	34227	3548	21110	15698
ath-miR156a-5p	20768	34227	3548	21110	15698
ath-miR156b-5p	20768	34227	3548	21110	15698
ath-miR156c-5p	20768	34227	3548	21110	15698
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ath-miR156e	20768	34227	3548	21110	15698
ath-miR156f-5p	20768	34227	3548	21110	15698
atr-miR156b	20768	34227	3548	21110	15698
atr-miR156d	20768	34227	3548	21110	15698
bdi-miR156b-5p	20768	34227	3548	21110	15698
bdi-miR156c	20768	34227	3548	21110	15698
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bdi-miR156e-5p	20768	34227	3548	21110	15698
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bdi-miR156g-5p	20768	34227	3548	21110	15698
bdi-miR156h-5p	20768	34227	3548	21110	15698
bdi-miR156i-5p	20768	34227	3548	21110	15698
bna-miR156d	20768	34227	3548	21110	15698
bna-miR156e	20768	34227	3548	21110	15698
bna-miR156f	20768	34227	3548	21110	15698
bra-miR156a-5p	20768	34227	3548	21110	15698
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bra-miR156c-5p	20768	34227	3548	21110	15698
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bra-miR156f-5p	20768	34227	3548	21110	15698
bra-miR156g-5p	20768	34227	3548	21110	15698
cas-miR156a	20768	34227	3548	21110	15698
cas-miR156b-5p	20768	34227	3548	21110	15698
cas-miR156c-5p	20768	34227	3548	21110	15698
cas-miR156d-5p	20768	34227	3548	21110	15698
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cca-miR156a	20768	34227	3548	21110	15698
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cme-miR156d	20768	34227	3548	21110	15698
cme-miR156i	20768	34227	3548	21110	15698
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cpa-miR156b	20768	34227	3548	21110	15698
cpa-miR156c	20768	34227	3548	21110	15698



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4	csi-miR156a-5p	20768	34227	3548	21110	15698
5	csi-miR156b-5p	20768	34227	3548	21110	15698
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7	csi-miR156c-5p	20768	34227	3548	21110	15698
8	ctr-miR156	20768	34227	3548	21110	15698
9	ctr-miR156	20768	34227	3548	21110	15698
10	dpr-miR156b	20768	34227	3548	21110	15698
11	fve-miR156d	20768	34227	3548	21110	15698
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13	ghr-miR156a	20768	34227	3548	21110	15698
14	ghr-miR156b	20768	34227	3548	21110	15698
15	ghr-miR156d	20768	34227	3548	21110	15698
16	ghr-miR156d	20768	34227	3548	21110	15698
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18	gma-miR156h	20768	34227	3548	21110	15698
19	gma-miR156u	20768	34227	3548	21110	15698
20	gma-miR156v	20768	34227	3548	21110	15698
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22	gma-miR156w	20768	34227	3548	21110	15698
23	gma-miR156x	20768	34227	3548	21110	15698
24	gma-miR156y	20768	34227	3548	21110	15698
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26	han-miR156a	20768	34227	3548	21110	15698
27	han-miR156b	20768	34227	3548	21110	15698
28	han-miR156b	20768	34227	3548	21110	15698
29	har-miR156a	20768	34227	3548	21110	15698
30	htu-miR156a	20768	34227	3548	21110	15698
31	htu-miR156a	20768	34227	3548	21110	15698
32	lus-miR156a	20768	34227	3548	21110	15698
33	lus-miR156g	20768	34227	3548	21110	15698
34	mdm-miR156a	20768	34227	3548	21110	15698
35	mdm-miR156b	20768	34227	3548	21110	15698
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38	mdm-miR156d	20768	34227	3548	21110	15698
39	mdm-miR156e	20768	34227	3548	21110	15698
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41	mdm-miR156f	20768	34227	3548	21110	15698
42	mdm-miR156g	20768	34227	3548	21110	15698
43	mdm-miR156h	20768	34227	3548	21110	15698
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45	mdm-miR156i	20768	34227	3548	21110	15698
46	mdm-miR156j	20768	34227	3548	21110	15698
47	mdm-miR156k	20768	34227	3548	21110	15698
48	mdm-miR156k	20768	34227	3548	21110	15698
49	mdm-miR156l	20768	34227	3548	21110	15698
50	mdm-miR156m	20768	34227	3548	21110	15698
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56	mes-miR156b	20768	34227	3548	21110	15698
57	mes-miR156c	20768	34227	3548	21110	15698
58	mes-miR156d	20768	34227	3548	21110	15698
59	mes-miR156e	20768	34227	3548	21110	15698
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mes-miR156f	20768	34227	3548	21110	15698
mes-miR156g	20768	34227	3548	21110	15698
mtr-miR156b-5p	20768	34227	3548	21110	15698
mtr-miR156c-5p	20768	34227	3548	21110	15698
mtr-miR156d-5p	20768	34227	3548	21110	15698
mtr-miR156i-5p	20768	34227	3548	21110	15698
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nta-miR156c	20768	34227	3548	21110	15698
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nta-miR156e	20768	34227	3548	21110	15698
osa-miR156a	20768	34227	3548	21110	15698
osa-miR156b-5p	20768	34227	3548	21110	15698
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osa-miR156g-5p	20768	34227	3548	21110	15698
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osa-miR156i	20768	34227	3548	21110	15698
osa-miR156j-5p	20768	34227	3548	21110	15698
pab-miR156a	20768	34227	3548	21110	15698
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ppe-miR156e	20768	34227	3548	21110	15698
ppt-miR156a	20768	34227	3548	21110	15698
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ppt-miR156c	20768	34227	3548	21110	15698
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ptc-miR156f	20768	34227	3548	21110	15698
sbi-miR156a	20768	34227	3548	21110	15698
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sbi-miR156c	20768	34227	3548	21110	15698
sbi-miR156f	20768	34227	3548	21110	15698
sbi-miR156g	20768	34227	3548	21110	15698
sbi-miR156h	20768	34227	3548	21110	15698
sbi-miR156i	20768	34227	3548	21110	15698
sly-miR156d-5p	20768	34227	3548	21110	15698

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3	sof-miR156	20768	34227	3548	21110	15698
4	stu-miR156e	20768	34227	3548	21110	15698
5	stu-miR156g-5p	20768	34227	3548	21110	15698
6	stu-miR156h-5p	20768	34227	3548	21110	15698
7	stu-miR156i-5p	20768	34227	3548	21110	15698
8	stu-miR156j-5p	20768	34227	3548	21110	15698
9	stu-miR156k-5p	20768	34227	3548	21110	15698
10	tcc-miR156b	20768	34227	3548	21110	15698
11	tcc-miR156c	20768	34227	3548	21110	15698
12	tcc-miR156d	20768	34227	3548	21110	15698
13	tcc-miR156g	20768	34227	3548	21110	15698
14	vca-miR156a-5p	20768	34227	3548	21110	15698
15	vun-miR156a	20768	34227	3548	21110	15698
16	vvi-miR156b	20768	34227	3548	21110	15698
17	vvi-miR156c	20768	34227	3548	21110	15698
18	vvi-miR156d	20768	34227	3548	21110	15698
19	zma-miR156a-5p	20768	34227	3548	21110	15698
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21	zma-miR156c	20768	34227	3548	21110	15698
22	zma-miR156d-5p	20768	34227	3548	21110	15698
23	zma-miR156e-5p	20768	34227	3548	21110	15698
24	zma-miR156f-5p	20768	34227	3548	21110	15698
25	zma-miR156g-5p	20768	34227	3548	21110	15698
26	zma-miR156h-5p	20768	34227	3548	21110	15698
27	zma-miR156i-5p	20768	34227	3548	21110	15698
28	zma-miR156l-5p	20768	34227	3548	21110	15698
29	ama-miR156	20779	34249	3551	21127	15700
30	gma-miR169e	3672	5706	1196	4464	2983
31	gma-miR156q	20887	34400	3565	21195	15776
32	gma-miR156s	20887	34400	3565	21195	15776
33	ata-miR169h-5p	3720	5831	1223	4517	3047
34	bdi-miR169b	3720	5831	1223	4517	3047
35	mes-miR169f	3720	5831	1223	4517	3047
36	osa-miR169e	3720	5831	1223	4517	3047
37	sbi-miR169e	3720	5831	1223	4517	3047
38	sbi-miR169j	3720	5831	1223	4517	3047
39	ssp-miR169	3720	5831	1223	4517	3047
40	zma-miR169p-5p	3720	5831	1223	4517	3047
41	bna-miR156a	20891	34481	3564	21215	15781
42	hvu-miR156a	20891	34481	3564	21215	15781
43	hvu-miR156b	20891	34481	3564	21215	15781
44	rco-miR156a	20891	34481	3564	21215	15781
45	rco-miR156b	20891	34481	3564	21215	15781
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rco-miR156c	20891	34481	3564	21215	15781
rco-miR156d	20891	34481	3564	21215	15781
ssl-miR156	20891	34481	3564	21215	15781
ssp-miR156	20891	34481	3564	21215	15781
tae-miR156	20891	34481	3564	21215	15781
gso-miR2218	212283	470943	271083	300516	243499
pvu-miR2118	212283	470943	271083	300516	243499
vun-miR2118	212283	470943	271083	300516	243499
aof-miR166b	1357	657	1354	1043	722
ahy-miR156a	187	211	101	167	113
aof-miR156c	187	211	101	167	113
ath-miR156j	187	211	101	167	113
bdi-miR156j	187	211	101	167	113
cas-miR156j	187	211	101	167	113
hpa-miR156a	187	211	101	167	113
ahy-miR167-3p	4463	5492	1307	2236	4610
ptc-miR167f-3p	4463	5492	1307	2236	4610
ptc-miR167g-3p	4463	5492	1307	2236	4610
ptc-miR167h-3p	4463	5492	1307	2236	4610
bdi-miR156a	193	211	103	169	114
far-miR156a	193	211	103	169	114
gma-miR156b	193	211	103	169	114
mtr-miR156a	193	211	103	169	114
osa-miR156k	193	211	103	169	114
rco-miR156e	193	211	103	169	114
sbi-miR156d	193	211	103	169	114
tcc-miR156a	193	211	103	169	114
zma-miR156j-5p	193	211	103	169	114
gma-miR2118a-3p	2919	4326	7841	4325	3577
gma-miR2118b-3p	2919	4326	7841	4325	3577
aqc-miR159	110	106	100	90	52
mtr-miR2118	77	252	70	111	89
gma-miR1515a	6869	8641	20282	4539	11745
gma-miR1515b	6869	8641	20282	4539	11745
aof-miR166a	15790	7474	18107	11179	9533
atr-miR166b	15790	7474	18107	11179	9533
bdi-miR166f	15790	7474	18107	11179	9533
csi-miR166b-3p	15790	7474	18107	11179	9533
csi-miR166d-3p	15790	7474	18107	11179	9533
csi-miR166g-3p	15790	7474	18107	11179	9533
gma-miR166h-3p	15790	7474	18107	11179	9533
gma-miR166k	15790	7474	18107	11179	9533
pab-miR166e	15790	7474	18107	11179	9533

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3	sly-miR156e-3p	9056	10012	17656	9528	9902
4	stu-miR156g-3p	9056	10012	17656	9528	9902
5	cas-miR156k-3p	9076	10019	17678	9536	9910
6	mtr-miR156c-3p	9076	10019	17678	9536	9910
7						
8	pvu-miR1514a	13941	9159	16954	12770	7637
9						
10	aly-miR397a-5p	13	14	140	50	28
11	aly-miR397b-5p	13	14	140	50	28
12						
13	ath-miR397a	13	14	140	50	28
14	bdi-miR397a	13	14	140	50	28
15	bna-miR397a	13	14	140	50	28
16	bna-miR397b	13	14	140	50	28
17						
18	cas-miR397	13	14	140	50	28
19	cme-miR397	13	14	140	50	28
20	csi-miR397-5p	13	14	140	50	28
21						
22	fve-miR397	13	14	140	50	28
23	gma-miR397a	13	14	140	50	28
24	gma-miR397b-5p	13	14	140	50	28
25						
26	lus-miR397b	13	14	140	50	28
27	mes-miR397b	13	14	140	50	28
28	mtr-miR397-5p	13	14	140	50	28
29						
30	osa-miR397a	13	14	140	50	28
31	ppe-miR397	13	14	140	50	28
32	ptc-miR397a	13	14	140	50	28
33						
34	rco-miR397	13	14	140	50	28
35	sbi-miR397-5p	13	14	140	50	28
36	ssl-miR397	13	14	140	50	28
37						
38	tcc-miR397	13	14	140	50	28
39	vca-miR397-5p	13	14	140	50	28
40	vvi-miR397a	13	14	140	50	28
41						
42	pvu-miR482-3p	53	84	281	74	63
43	bdi-miR393a	133	78	12	81	58
44	bdi-miR393b-5p	133	78	12	81	58
45						
46	bna-miR393	133	78	12	81	58
47	cme-miR393a	133	78	12	81	58
48	cme-miR393b	133	78	12	81	58
49						
50	cme-miR393c	133	78	12	81	58
51	csi-miR393c-5p	133	78	12	81	58
52	fve-miR393a	133	78	12	81	58
53						
54	gma-miR393a	133	78	12	81	58
55	lus-miR393a	133	78	12	81	58
56	lus-miR393b	133	78	12	81	58
57						
58	lus-miR393c	133	78	12	81	58
59	lus-miR393d	133	78	12	81	58
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3	mes-miR393a	133	78	12	81	58
4	mtr-miR393a	133	78	12	81	58
5	mtr-miR393b-5p	133	78	12	81	58
6	osa-miR393a	133	78	12	81	58
7	ppe-miR393b	133	78	12	81	58
8	ptc-miR393a-5p	133	78	12	81	58
9	ptc-miR393b-5p	133	78	12	81	58
10	ptc-miR393c	133	78	12	81	58
11	rco-miR393	133	78	12	81	58
12	sbi-miR393a	133	78	12	81	58
13	sbi-miR393b	133	78	12	81	58
14	tcc-miR393b	133	78	12	81	58
15	vca-miR393-5p	133	78	12	81	58
16	vvi-miR393a	133	78	12	81	58
17	vvi-miR393b	133	78	12	81	58
18	sly-miR171e	218	358	269	153	276
19	stu-miR171b-3p	218	358	269	153	276
20	aof-miR171c	212	347	248	146	267
21	csi-miR171e-3p	212	347	248	146	267
22	csi-miR171g-3p	212	347	248	146	267
23	ctr-miR171	212	347	248	146	267
24	fve-miR171h	212	347	248	146	267
25	mdm-miR171a	212	347	248	146	267
26	mdm-miR171b	212	347	248	146	267
27	mdm-miR171p	212	347	248	146	267
28	mes-miR171a	212	347	248	146	267
29	ppe-miR171h	212	347	248	146	267
30	efu-miR-126	173	35	497	123	79
31	bdi-miR160f	269	267	351	221	234
32	cas-miR160a	269	267	351	221	234
33	cas-miR160b-5p	269	267	351	221	234
34	gma-miR160b	269	267	351	221	234
35	gma-miR160c	269	267	351	221	234
36	gma-miR160d	269	267	351	221	234
37	gma-miR160e	269	267	351	221	234
38	htu-miR160a	269	267	351	221	234
39	pab-miR160c	269	267	351	221	234
40	pab-miR160e	269	267	351	221	234
41	pab-miR160f	269	267	351	221	234
42	gma-miR159e-5p	1346	1115	1126	751	1072
43	aca-miR-126-3p	165	35	490	120	78
44	ami-miR-126-3p	165	35	490	120	78
45	cgr-miR-126a	165	35	490	120	78
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3	cja-miR-126	165	35	490	120	78
4	cli-miR-126-3p	165	35	490	120	78
5	cpi-miR-126-3p	165	35	490	120	78
6	cpi-miR-126-3p	165	35	490	120	78
7	cpo-miR-126-3p	165	35	490	120	78
8	dno-miR-126-3p	165	35	490	120	78
9	dno-miR-126-3p	165	35	490	120	78
10	eca-miR-126-3p	165	35	490	120	78
11	gga-miR-126-3p	165	35	490	120	78
12	gga-miR-126-3p	165	35	490	120	78
13	hsa-miR-126-3p	165	35	490	120	78
14	mdo-miR-126-3p	165	35	490	120	78
15	mml-miR-126	165	35	490	120	78
16	mmu-miR-126a-3p	165	35	490	120	78
17	mmu-miR-126a-3p	165	35	490	120	78
18	oan-miR-126-3p	165	35	490	120	78
19	pbv-miR-126-3p	165	35	490	120	78
20	ppy-miR-126	165	35	490	120	78
21	ppy-miR-126	165	35	490	120	78
22	ptr-miR-126	165	35	490	120	78
23	rno-miR-126a-3p	165	35	490	120	78
24	ssc-miR-126-3p	165	35	490	120	78
25	ssc-miR-126-3p	165	35	490	120	78
26	tgu-miR-126-3p	165	35	490	120	78
27	cme-miR168	1102	1956	779	1355	812
28	bra-miR168b-5p	1151	2054	812	1449	839
29	bra-miR168b-5p	1151	2054	812	1449	839
30	bra-miR168c-5p	1151	2054	812	1449	839
31	nta-miR168a	1151	2054	812	1449	839
32	nta-miR168b	1151	2054	812	1449	839
33	nta-miR168b	1151	2054	812	1449	839
34	nta-miR168c	1151	2054	812	1449	839
35	sly-miR168a-5p	1151	2054	812	1449	839
36	sly-miR168b-5p	1151	2054	812	1449	839
37	sly-miR168b-5p	1151	2054	812	1449	839
38	csi-miR160b-5p	270	268	359	222	234
39	mes-miR160c	270	268	359	222	234
40	osa-miR160e-5p	270	268	359	222	234
41	osa-miR160e-5p	270	268	359	222	234
42	zma-miR160f-5p	270	268	359	222	234
43	aly-miR167d-5p	52986	43732	40946	44083	24763
44	ath-miR167d	52986	43732	40946	44083	24763
45	ath-miR167d	52986	43732	40946	44083	24763
46	cca-miR167	52986	43732	40946	44083	24763
47	eun-miR167b-5p	52986	43732	40946	44083	24763
48	nta-miR167a	52986	43732	40946	44083	24763
49	nta-miR167a	52986	43732	40946	44083	24763
50	nta-miR167b	52986	43732	40946	44083	24763
51	nta-miR167c	52986	43732	40946	44083	24763
52	pab-miR167b	52986	43732	40946	44083	24763
53	pab-miR167b	52986	43732	40946	44083	24763
54	rco-miR167c	52986	43732	40946	44083	24763
55	csi-miR393a	135	83	12	81	58
56	ghr-miR169b	72	100	50	52	73
57	aly-miR170-5p	6950	14810	10511	9105	8883
58	aly-miR170-5p	6950	14810	10511	9105	8883
59	aly-miR171a-5p	6950	14810	10511	9105	8883
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3	ath-miR170-5p	6950	14810	10511	9105	8883
4	ath-miR171a-5p	6950	14810	10511	9105	8883
5	cas-miR170	6950	14810	10511	9105	8883
6	cas-miR171a-5p	6950	14810	10511	9105	8883
7	csi-miR171f-5p	6950	14810	10511	9105	8883
8	gma-miR171j-5p	6950	14810	10511	9105	8883
9	sly-miR171f	6950	14810	10511	9105	8883
10	stu-miR171a-5p	6950	14810	10511	9105	8883
11	stu-miR171c-5p	6950	14810	10511	9105	8883
12	gma-miR482b-3p	2853	6453	1543	3760	1637
13	gma-miR482d-3p	2853	6453	1543	3760	1637
14	gma-miR159a-5p	1844	1295	2005	1030	1335
15	ptc-miR396e-3p	432	620	184	245	397
16	gma-miR319f	103	34	139	68	43
17	age-miR-19b	57	49	84	90	22
18	bta-miR-19b	57	49	84	90	22
19	cgr-miR-19b-3p	57	49	84	90	22
20	chi-miR-19b-3p	57	49	84	90	22
21	cja-miR-19b	57	49	84	90	22
22	cli-miR-19b-3p	57	49	84	90	22
23	cpo-miR-19b-3p	57	49	84	90	22
24	dno-miR-19b-3p	57	49	84	90	22
25	dre-miR-19b-3p	57	49	84	90	22
26	eca-miR-19b	57	49	84	90	22
27	fru-miR-19b	57	49	84	90	22
28	gga-miR-19b-3p	57	49	84	90	22
29	ggo-miR-19b	57	49	84	90	22
30	gmo-miR-19b-3p	57	49	84	90	22
31	hsa-miR-19b-3p	57	49	84	90	22
32	lca-miR-19b	57	49	84	90	22
33	lla-miR-19b	57	49	84	90	22
34	mdo-miR-19b-3p	57	49	84	90	22
35	mml-miR-19b	57	49	84	90	22
36	mmu-miR-19b-3p	57	49	84	90	22
37	mne-miR-19b	57	49	84	90	22
38	oan-miR-19b-3p	57	49	84	90	22
39	oar-miR-19b	57	49	84	90	22
40	ocu-miR-19b-3p	57	49	84	90	22
41	oha-miR-19b-3p	57	49	84	90	22
42	pal-miR-19-3p	57	49	84	90	22
43	pma-miR-19b-3p	57	49	84	90	22
44	ppa-miR-19b	57	49	84	90	22
45	ppy-miR-19b	57	49	84	90	22
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3	ptr-miR-19b	57	49	84	90	22
4	rno-miR-19b-3p	57	49	84	90	22
5	sha-miR-19b	57	49	84	90	22
6	sla-miR-19b	57	49	84	90	22
7	ssa-miR-19b	57	49	84	90	22
8	ssc-miR-19b	57	49	84	90	22
9	tch-miR-19b-3p	57	49	84	90	22
10	tgu-miR-19b-3p	57	49	84	90	22
11	tni-miR-19b	57	49	84	90	22
12	xla-miR-19b	57	49	84	90	22
13	xtr-miR-19b	57	49	84	90	22
14	efu-miR-378	200	224	143	216	102
15	ggo-miR-378a	199	224	143	216	102
16	bta-miR-378	195	224	143	215	102
17	cfa-miR-378	195	224	143	215	102
18	cgr-miR-378-3p	195	224	143	215	102
19	chi-miR-378-3p	195	224	143	215	102
20	cja-miR-378	195	224	143	215	102
21	cpo-miR-378-3p	195	224	143	215	102
22	dno-miR-378-3p	195	224	143	215	102
23	hsa-miR-378a-3p	195	224	143	215	102
24	nle-miR-378a	195	224	143	215	102
25	ocu-miR-378-3p	195	224	143	215	102
26	oga-miR-378	195	224	143	215	102
27	pal-miR-378-3p	195	224	143	215	102
28	pha-miR-378	195	224	143	215	102
29	ppa-miR-378a	195	224	143	215	102
30	ssc-miR-378	195	224	143	215	102
31	tch-miR-378a-3p	195	224	143	215	102
32	efu-miR-19	58	50	84	91	22
33	xla-miR-19b-3p	58	50	84	91	22
34	gma-miR156f	12431	14883	2848	9875	6181
35	ahy-miR156c	12339	14785	2836	9790	6132
36	far-miR156b	12339	14785	2836	9790	6132
37	mdm-miR156t	12339	14785	2836	9790	6132
38	mdm-miR156u	12339	14785	2836	9790	6132
39	mdm-miR156v	12339	14785	2836	9790	6132
40	mdm-miR156w	12339	14785	2836	9790	6132
41	mes-miR156k	12339	14785	2836	9790	6132
42	gma-miR390b-5p	304	338	292	199	164
43	gma-miR390d	304	338	292	199	164
44	nta-miR390a	304	338	292	199	164
45	sly-miR390a-5p	304	338	292	199	164
46	stu-miR390-5p	304	338	292	199	164
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3	csi-miR396f-3p	468	659	204	252	413
4	gma-miR396b-3p	468	659	204	252	413
5	gma-miR396k-3p	468	659	204	252	413
6	mtr-miR396a-3p	468	659	204	252	413
7	ahy-miR160-5p	95	80	217	96	42
8	aof-miR160a	95	80	217	96	42
9	bdi-miR160e-5p	95	80	217	96	42
10	cme-miR160d	95	80	217	96	42
11	cpa-miR160d	95	80	217	96	42
12	mes-miR160e	95	80	217	96	42
13	mes-miR160f	95	80	217	96	42
14	mtr-miR160c	95	80	217	96	42
15	osa-miR160f-5p	95	80	217	96	42
16	ptc-miR160e-5p	95	80	217	96	42
17	ptc-miR160f	95	80	217	96	42
18	rco-miR160c	95	80	217	96	42
19	sbi-miR160f	95	80	217	96	42
20	tcc-miR160a	95	80	217	96	42
21	vca-miR160-5p	95	80	217	96	42
22	vvi-miR160a	95	80	217	96	42
23	vvi-miR160b	95	80	217	96	42
24	lja-miR166-3p	41108	35806	93852	26586	32868
25	aly-miR166a-3p	39290	34477	91739	25385	31490
26	aly-miR166b-3p	39290	34477	91739	25385	31490
27	aly-miR166c-3p	39290	34477	91739	25385	31490
28	aly-miR166d-3p	39290	34477	91739	25385	31490
29	aly-miR166e-3p	39290	34477	91739	25385	31490
30	aly-miR166f-3p	39290	34477	91739	25385	31490
31	aly-miR166g-3p	39290	34477	91739	25385	31490
32	aly-miR166h-3p	39290	34477	91739	25385	31490
33	aof-miR166d	39290	34477	91739	25385	31490
34	aqc-miR166b	39290	34477	91739	25385	31490
35	aqc-miR166e	39290	34477	91739	25385	31490
36	ata-miR166a-3p	39290	34477	91739	25385	31490
37	ata-miR166b-3p	39290	34477	91739	25385	31490
38	ata-miR166d-3p	39290	34477	91739	25385	31490
39	ata-miR166e-3p	39290	34477	91739	25385	31490
40	ath-miR166a-3p	39290	34477	91739	25385	31490
41	ath-miR166b-3p	39290	34477	91739	25385	31490
42	ath-miR166c	39290	34477	91739	25385	31490
43	ath-miR166d	39290	34477	91739	25385	31490
44	ath-miR166e-3p	39290	34477	91739	25385	31490
45	ath-miR166f	39290	34477	91739	25385	31490
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3	ath-miR166g	39290	34477	91739	25385	31490
4	atr-miR166a	39290	34477	91739	25385	31490
5	atr-miR166c	39290	34477	91739	25385	31490
6	atr-miR166d	39290	34477	91739	25385	31490
7	atr-miR166d	39290	34477	91739	25385	31490
8	bdi-miR166a-3p	39290	34477	91739	25385	31490
9	bdi-miR166b-3p	39290	34477	91739	25385	31490
10	bdi-miR166c-3p	39290	34477	91739	25385	31490
11	bdi-miR166c-3p	39290	34477	91739	25385	31490
12	bdi-miR166d-3p	39290	34477	91739	25385	31490
13	bdi-miR166d-3p	39290	34477	91739	25385	31490
14	bdi-miR166i-3p	39290	34477	91739	25385	31490
15	bna-miR166a	39290	34477	91739	25385	31490
16	bna-miR166b	39290	34477	91739	25385	31490
17	bna-miR166c	39290	34477	91739	25385	31490
18	bna-miR166c	39290	34477	91739	25385	31490
19	bna-miR166d	39290	34477	91739	25385	31490
20	bna-miR166e	39290	34477	91739	25385	31490
21	bna-miR166e	39290	34477	91739	25385	31490
22	cme-miR166a	39290	34477	91739	25385	31490
23	cme-miR166b	39290	34477	91739	25385	31490
24	cme-miR166c	39290	34477	91739	25385	31490
25	cme-miR166c	39290	34477	91739	25385	31490
26	cme-miR166d	39290	34477	91739	25385	31490
27	cme-miR166d	39290	34477	91739	25385	31490
28	cme-miR166f	39290	34477	91739	25385	31490
29	cme-miR166h	39290	34477	91739	25385	31490
30	cpa-miR166a	39290	34477	91739	25385	31490
31	cpa-miR166b	39290	34477	91739	25385	31490
32	cpa-miR166b	39290	34477	91739	25385	31490
33	cpa-miR166c	39290	34477	91739	25385	31490
34	csi-miR166e-3p	39290	34477	91739	25385	31490
35	dpr-miR166b	39290	34477	91739	25385	31490
36	eun-miR166-3p	39290	34477	91739	25385	31490
37	eun-miR166-3p	39290	34477	91739	25385	31490
38	fve-miR166a	39290	34477	91739	25385	31490
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40	fve-miR166c	39290	34477	91739	25385	31490
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42	fve-miR166d-3p	39290	34477	91739	25385	31490
43	fve-miR166e	39290	34477	91739	25385	31490
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45	fve-miR166f	39290	34477	91739	25385	31490
46	ghr-miR166b	39290	34477	91739	25385	31490
47	gma-miR166a-3p	39290	34477	91739	25385	31490
48	gma-miR166b	39290	34477	91739	25385	31490
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51	gma-miR166d	39290	34477	91739	25385	31490
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56	gma-miR166g	39290	34477	91739	25385	31490
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58	gma-miR166i-3p	39290	34477	91739	25385	31490
59	gma-miR166n	39290	34477	91739	25385	31490
60	gma-miR166o	39290	34477	91739	25385	31490

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3	hpa-miR166a	39290	34477	91739	25385	31490
4	hpe-miR166a	39290	34477	91739	25385	31490
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6	hvu-miR166b	39290	34477	91739	25385	31490
7	hvu-miR166c	39290	34477	91739	25385	31490
8	lus-miR166a	39290	34477	91739	25385	31490
9	lus-miR166c	39290	34477	91739	25385	31490
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11	lus-miR166g	39290	34477	91739	25385	31490
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18	mdm-miR166e	39290	34477	91739	25385	31490
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22	mdm-miR166i	39290	34477	91739	25385	31490
23	mdm-miR166j	39290	34477	91739	25385	31490
24	mes-miR166a	39290	34477	91739	25385	31490
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42	osa-miR166a-3p	39290	34477	91739	25385	31490
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45	osa-miR166d-3p	39290	34477	91739	25385	31490
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4	osa-miR166j-3p	39290	34477	91739	25385	31490
5	pab-miR166f	39290	34477	91739	25385	31490
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7	pab-miR166h	39290	34477	91739	25385	31490
8	pab-miR166i	39290	34477	91739	25385	31490
9	ppe-miR166a	39290	34477	91739	25385	31490
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18	ppt-miR166e	39290	34477	91739	25385	31490
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38	pvu-miR166a	39290	34477	91739	25385	31490
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44	sly-miR166a	39290	34477	91739	25385	31490
45	sly-miR166b	39290	34477	91739	25385	31490
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4	smo-miR166b	39290	34477	91739	25385	31490
5	smo-miR166c	39290	34477	91739	25385	31490
6	ssl-miR166b	39290	34477	91739	25385	31490
7	ssp-miR166	39290	34477	91739	25385	31490
8	stu-miR166a-3p	39290	34477	91739	25385	31490
9	stu-miR166c-3p	39290	34477	91739	25385	31490
10	stu-miR166d-3p	39290	34477	91739	25385	31490
11	tcc-miR166a	39290	34477	91739	25385	31490
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14	vca-miR166b-3p	39290	34477	91739	25385	31490
15	vca-miR166c-3p	39290	34477	91739	25385	31490
16	vvi-miR166c	39290	34477	91739	25385	31490
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18	vvi-miR166e	39290	34477	91739	25385	31490
19	vvi-miR166f	39290	34477	91739	25385	31490
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21	vvi-miR166h	39290	34477	91739	25385	31490
22	zma-miR166a-3p	39290	34477	91739	25385	31490
23	csi-miR166a-3p	39295	34481	91787	25387	31492
24	ctr-miR166	39295	34481	91787	25387	31492
25	hbr-miR166b	39295	34481	91787	25387	31492
26	lus-miR166i	39295	34481	91787	25387	31492
27	lus-miR166k	39295	34481	91787	25387	31492
28	cas-miR166c-3p	39375	34575	92370	25450	31533
29	cas-miR166d	39375	34575	92370	25450	31533
30	cas-miR166f-3p	39375	34575	92370	25450	31533
31	lja-miR168-5p	64684	135916	28128	81069	38549
32	aly-miR168a-5p	64535	135686	28082	80905	38434
33	aly-miR168b-5p	64535	135686	28082	80905	38434
34	aof-miR168a	64535	135686	28082	80905	38434
35	ath-miR168a-5p	64535	135686	28082	80905	38434
36	ath-miR168b-5p	64535	135686	28082	80905	38434
37	atr-miR168	64535	135686	28082	80905	38434
38	bna-miR168a	64535	135686	28082	80905	38434
39	bra-miR168a-5p	64535	135686	28082	80905	38434
40	cca-miR168a	64535	135686	28082	80905	38434
41	ccl-miR168	64535	135686	28082	80905	38434
42	crt-miR168	64535	135686	28082	80905	38434
43	csi-miR168-5p	64535	135686	28082	80905	38434
44	fve-miR168-5p	64535	135686	28082	80905	38434
45	gma-miR168a	64535	135686	28082	80905	38434
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3	lus-miR168a	64535	135686	28082	80905	38434
4	lus-miR168b	64535	135686	28082	80905	38434
5	mdm-miR168a	64535	135686	28082	80905	38434
6	mdm-miR168b	64535	135686	28082	80905	38434
7	mes-miR168a	64535	135686	28082	80905	38434
8	mes-miR168b	64535	135686	28082	80905	38434
9	mtr-miR168b	64535	135686	28082	80905	38434
10	mtr-miR168c-5p	64535	135686	28082	80905	38434
11	nta-miR168d	64535	135686	28082	80905	38434
12	nta-miR168e	64535	135686	28082	80905	38434
13	pab-miR168a	64535	135686	28082	80905	38434
14	ppe-miR168	64535	135686	28082	80905	38434
15	ptc-miR168a-5p	64535	135686	28082	80905	38434
16	ptc-miR168b-5p	64535	135686	28082	80905	38434
17	rco-miR168	64535	135686	28082	80905	38434
18	tcc-miR168	64535	135686	28082	80905	38434
19	vca-miR168a-5p	64535	135686	28082	80905	38434
20	vca-miR168b-5p	64535	135686	28082	80905	38434
21	vun-miR168	64535	135686	28082	80905	38434
22	vvi-miR168	64535	135686	28082	80905	38434
23	ahy-miR167-5p	32592	40851	39761	19815	28085
24	cme-miR167c	32592	40851	39761	19815	28085
25	cpa-miR167c	32592	40851	39761	19815	28085
26	csi-miR167b-5p	32592	40851	39761	19815	28085
27	gma-miR167e	32592	40851	39761	19815	28085
28	gma-miR167f	32592	40851	39761	19815	28085
29	lus-miR167b	32592	40851	39761	19815	28085
30	mes-miR167g	32592	40851	39761	19815	28085
31	mes-miR167h	32592	40851	39761	19815	28085
32	ptc-miR167f-5p	32592	40851	39761	19815	28085
33	ptc-miR167g-5p	32592	40851	39761	19815	28085
34	tcc-miR167c	32592	40851	39761	19815	28085
35	gma-miR403a	5565	3750	30300	4887	2458
36	gma-miR403b	5565	3750	30300	4887	2458
37	aly-miR396b-5p	1143	1233	2696	688	841
38	ama-miR396-5p	1143	1233	2696	688	841
39	aqc-miR396b	1143	1233	2696	688	841
40	ata-miR396c-5p	1143	1233	2696	688	841
41	ath-miR396b-5p	1143	1233	2696	688	841
42	atr-miR396b	1143	1233	2696	688	841
43	atr-miR396c	1143	1233	2696	688	841
44	atr-miR396e	1143	1233	2696	688	841
45	bcy-miR396b	1143	1233	2696	688	841
46	bdi-miR396e-5p	1143	1233	2696	688	841
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3	bgm-miR396b	1143	1233	2696	688	841
4	bnm-miR396a	1143	1233	2696	688	841
5	brm-miR396-5p	1143	1233	2696	688	841
6	cas-miR396b	1143	1233	2696	688	841
7	cca-miR396a-5p	1143	1233	2696	688	841
8	ccl-miR396	1143	1233	2696	688	841
9	cme-miR396a	1143	1233	2696	688	841
10	cme-miR396c	1143	1233	2696	688	841
11	cme-miR396d	1143	1233	2696	688	841
12	csi-miR396f-5p	1143	1233	2696	688	841
13	fve-miR396b-5p	1143	1233	2696	688	841
14	gma-miR396b-5p	1143	1233	2696	688	841
15	gma-miR396c	1143	1233	2696	688	841
16	gma-miR396k-5p	1143	1233	2696	688	841
17	lus-miR396b	1143	1233	2696	688	841
18	lus-miR396e	1143	1233	2696	688	841
19	mdm-miR396c	1143	1233	2696	688	841
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21	mdm-miR396e	1143	1233	2696	688	841
22	mes-miR396c	1143	1233	2696	688	841
23	mes-miR396d	1143	1233	2696	688	841
24	mes-miR396e	1143	1233	2696	688	841
25	mes-miR396f	1143	1233	2696	688	841
26	mtr-miR396a-5p	1143	1233	2696	688	841
27	nta-miR396b	1143	1233	2696	688	841
28	nta-miR396c	1143	1233	2696	688	841
29	osa-miR396c-5p	1143	1233	2696	688	841
30	pab-miR396g	1143	1233	2696	688	841
31	pab-miR396h	1143	1233	2696	688	841
32	ppe-miR396b	1143	1233	2696	688	841
33	pta-miR396	1143	1233	2696	688	841
34	ptc-miR396c	1143	1233	2696	688	841
35	ptc-miR396d	1143	1233	2696	688	841
36	ptc-miR396e-5p	1143	1233	2696	688	841
37	rco-miR396	1143	1233	2696	688	841
38	sbi-miR396c	1143	1233	2696	688	841
39	sly-miR396b	1143	1233	2696	688	841
40	stu-miR396-5p	1143	1233	2696	688	841
41	tcc-miR396c	1143	1233	2696	688	841
42	tcc-miR396e	1143	1233	2696	688	841
43	zma-miR396e-5p	1143	1233	2696	688	841
44	zma-miR396f-5p	1143	1233	2696	688	841
45	gma-miR1511	1103	618	4493	521	1150
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3	gma-miR5374-5p	554	502	295	428	210
4	mtr-miR171c	28	60	103	47	25
5	aly-miR166a-5p	15363	15709	1648	5141	10013
6	aly-miR166c-5p	15363	15709	1648	5141	10013
7	aly-miR166d-5p	15363	15709	1648	5141	10013
8	bdi-miR166e-5p	15363	15709	1648	5141	10013
9	cas-miR166a	15363	15709	1648	5141	10013
10	csi-miR166a-5p	15363	15709	1648	5141	10013
11	csi-miR166e-5p	15363	15709	1648	5141	10013
12	eun-miR166-5p	15363	15709	1648	5141	10013
13	gma-miR166a-5p	15363	15709	1648	5141	10013
14	gma-miR166c-5p	15363	15709	1648	5141	10013
15	gma-miR166l	15363	15709	1648	5141	10013
16	mtr-miR166g-5p	15363	15709	1648	5141	10013
17	osa-miR166d-5p	15363	15709	1648	5141	10013
18	stu-miR166a-5p	15363	15709	1648	5141	10013
19	vca-miR166b-5p	15363	15709	1648	5141	10013
20	zma-miR166c-5p	15363	15709	1648	5141	10013
21	gma-miR391-5p	85	61	167	59	39
22	gma-miR171m	9514	18038	18276	8015	9536
23	gma-miR171t	9514	18038	18276	8015	9536
24	aly-miR169a-5p	491	981	621	460	423
25	ata-miR169e-5p	491	981	621	460	423
26	ata-miR169f-5p	491	981	621	460	423
27	ata-miR169g-5p	491	981	621	460	423
28	ath-miR169a-5p	491	981	621	460	423
29	bdi-miR169a-5p	491	981	621	460	423
30	bna-miR169a	491	981	621	460	423
31	bna-miR169b	491	981	621	460	423
32	cas-miR169a	491	981	621	460	423
33	gma-miR169b	491	981	621	460	423
34	lus-miR169g	491	981	621	460	423
35	lus-miR169l	491	981	621	460	423
36	mes-miR169g	491	981	621	460	423
37	mtr-miR169a	491	981	621	460	423
38	nta-miR169a	491	981	621	460	423
39	nta-miR169b	491	981	621	460	423
40	nta-miR169c	491	981	621	460	423
41	nta-miR169d	491	981	621	460	423
42	nta-miR169e	491	981	621	460	423
43	nta-miR169f	491	981	621	460	423
44	nta-miR169g	491	981	621	460	423
45	nta-miR169h	491	981	621	460	423
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3	nta-miR169i	491	981	621	460	423
4	nta-miR169j	491	981	621	460	423
5	nta-miR169k	491	981	621	460	423
6	nta-miR169l	491	981	621	460	423
7	nta-miR169m	491	981	621	460	423
8	nta-miR169n	491	981	621	460	423
9	nta-miR169o	491	981	621	460	423
10	nta-miR169p	491	981	621	460	423
11	osa-miR169a	491	981	621	460	423
12	ptc-miR169a	491	981	621	460	423
13	ptc-miR169b-5p	491	981	621	460	423
14	ptc-miR169c	491	981	621	460	423
15	sbi-miR169a	491	981	621	460	423
16	sly-miR169c	491	981	621	460	423
17	tcc-miR169a	491	981	621	460	423
18	tcc-miR169c	491	981	621	460	423
19	tcc-miR169e	491	981	621	460	423
20	vvi-miR169f	491	981	621	460	423
21	vvi-miR169g	491	981	621	460	423
22	zma-miR169a-5p	491	981	621	460	423
23	zma-miR169b-5p	491	981	621	460	423
24	gma-miR169u	487	966	649	440	429
25	mdm-miR167h	68755	87811	93911	40687	54233
26	mdm-miR167i	68755	87811	93911	40687	54233
27	mdm-miR167j	68755	87811	93911	40687	54233
28	ppe-miR167d	68755	87811	93911	40687	54233
29	ppe-miR398b	60	51	339	61	58
30	bna-miR167a	5635	8853	15331	4957	5190
31	bna-miR167b	5635	8853	15331	4957	5190
32	aly-miR167a-5p	5632	8844	15323	4951	5186
33	aly-miR167b-5p	5632	8844	15323	4951	5186
34	aof-miR167a	5632	8844	15323	4951	5186
35	ata-miR167a-5p	5632	8844	15323	4951	5186
36	ata-miR167c-5p	5632	8844	15323	4951	5186
37	ata-miR167e-5p	5632	8844	15323	4951	5186
38	ath-miR167a-5p	5632	8844	15323	4951	5186
39	ath-miR167b	5632	8844	15323	4951	5186
40	bdi-miR167a	5632	8844	15323	4951	5186
41	bdi-miR167b	5632	8844	15323	4951	5186
42	bdi-miR167f	5632	8844	15323	4951	5186
43	bna-miR167c	5632	8844	15323	4951	5186
44	bra-miR167a	5632	8844	15323	4951	5186
45	bra-miR167b	5632	8844	15323	4951	5186
46	bra-miR167c	5632	8844	15323	4951	5186
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3	bra-miR167d	5632	8844	15323	4951	5186
4	cme-miR167a	5632	8844	15323	4951	5186
5	cme-miR167b	5632	8844	15323	4951	5186
6	cpa-miR167a	5632	8844	15323	4951	5186
7	cpa-miR167b	5632	8844	15323	4951	5186
8	csi-miR167d-5p	5632	8844	15323	4951	5186
9	csi-miR167e-5p	5632	8844	15323	4951	5186
10	dpr-miR167a	5632	8844	15323	4951	5186
11	dpr-miR167b	5632	8844	15323	4951	5186
12	ghr-miR167a	5632	8844	15323	4951	5186
13	ghr-miR167b	5632	8844	15323	4951	5186
14	gma-miR167a	5632	8844	15323	4951	5186
15	gma-miR167b	5632	8844	15323	4951	5186
16	gma-miR167d	5632	8844	15323	4951	5186
17	lus-miR167c	5632	8844	15323	4951	5186
18	lus-miR167d	5632	8844	15323	4951	5186
19	lus-miR167e	5632	8844	15323	4951	5186
20	lus-miR167h	5632	8844	15323	4951	5186
21	mdm-miR167b	5632	8844	15323	4951	5186
22	mdm-miR167c	5632	8844	15323	4951	5186
23	mdm-miR167d	5632	8844	15323	4951	5186
24	mdm-miR167e	5632	8844	15323	4951	5186
25	mdm-miR167f	5632	8844	15323	4951	5186
26	mdm-miR167g	5632	8844	15323	4951	5186
27	mes-miR167c	5632	8844	15323	4951	5186
28	mtr-miR167a	5632	8844	15323	4951	5186
29	nta-miR167d	5632	8844	15323	4951	5186
30	nta-miR167e	5632	8844	15323	4951	5186
31	osa-miR167a-5p	5632	8844	15323	4951	5186
32	osa-miR167b	5632	8844	15323	4951	5186
33	osa-miR167c-5p	5632	8844	15323	4951	5186
34	ppe-miR167a	5632	8844	15323	4951	5186
35	ppe-miR167b	5632	8844	15323	4951	5186
36	ptc-miR167a	5632	8844	15323	4951	5186
37	ptc-miR167b	5632	8844	15323	4951	5186
38	ptc-miR167c	5632	8844	15323	4951	5186
39	ptc-miR167d	5632	8844	15323	4951	5186
40	rco-miR167a	5632	8844	15323	4951	5186
41	rco-miR167b	5632	8844	15323	4951	5186
42	sbi-miR167a	5632	8844	15323	4951	5186
43	sbi-miR167b	5632	8844	15323	4951	5186
44	sbi-miR167i	5632	8844	15323	4951	5186
45	sly-miR167a	5632	8844	15323	4951	5186
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3	stu-miR167a-5p	5632	8844	15323	4951	5186
4	stu-miR167b-5p	5632	8844	15323	4951	5186
5	stu-miR167c-5p	5632	8844	15323	4951	5186
6	stu-miR167d-5p	5632	8844	15323	4951	5186
7	tae-miR167a	5632	8844	15323	4951	5186
8	tcc-miR167a	5632	8844	15323	4951	5186
9	tcc-miR167b	5632	8844	15323	4951	5186
10	vvi-miR167b	5632	8844	15323	4951	5186
11	vvi-miR167d	5632	8844	15323	4951	5186
12	vvi-miR167e	5632	8844	15323	4951	5186
13	zma-miR167a-5p	5632	8844	15323	4951	5186
14	zma-miR167b-5p	5632	8844	15323	4951	5186
15	zma-miR167c-5p	5632	8844	15323	4951	5186
16	zma-miR167d-5p	5632	8844	15323	4951	5186
17	ppt-miR160b	33	24	341	30	17
18	ppt-miR160i	33	24	341	30	17
19	lus-miR398f	59	52	334	59	55
20	gma-miR159d	3954	2175	751	1985	1102
21	aof-miR398	6176	8152	22550	5826	6562
22	aqc-miR398b	6176	8152	22550	5826	6562
23	bdi-miR398a	6176	8152	22550	5826	6562
24	cca-miR398	6176	8152	22550	5826	6562
25	cme-miR398a	6176	8152	22550	5826	6562
26	csi-miR398b-3p	6176	8152	22550	5826	6562
27	gma-miR398c	6176	8152	22550	5826	6562
28	gma-miR398d	6176	8152	22550	5826	6562
29	lus-miR398a	6176	8152	22550	5826	6562
30	mdm-miR398b	6176	8152	22550	5826	6562
31	mdm-miR398c	6176	8152	22550	5826	6562
32	mes-miR398	6176	8152	22550	5826	6562
33	mtr-miR398b	6176	8152	22550	5826	6562
34	mtr-miR398c	6176	8152	22550	5826	6562
35	nta-miR398	6176	8152	22550	5826	6562
36	osa-miR398b	6176	8152	22550	5826	6562
37	ppe-miR398a-3p	6176	8152	22550	5826	6562
38	ptc-miR398b	6176	8152	22550	5826	6562
39	ptc-miR398c-3p	6176	8152	22550	5826	6562
40	rco-miR398b	6176	8152	22550	5826	6562
41	tcc-miR398a	6176	8152	22550	5826	6562
42	vvi-miR398b	6176	8152	22550	5826	6562
43	vvi-miR398c	6176	8152	22550	5826	6562
44	bdi-miR166e-3p	380	323	1408	247	290
45	ptc-miR169s	400	865	603	371	338
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3	aof-miR171b	202	402	561	162	158
4	fve-miR171f-3p	202	402	561	162	158
5	gma-miR171k-3p	202	402	561	162	158
6	lja-miR171d-5p	202	402	561	162	158
7	mdm-miR171j	202	402	561	162	158
8	mdm-miR171k	202	402	561	162	158
9	mdm-miR171l	202	402	561	162	158
10	mes-miR171e	202	402	561	162	158
11	nta-miR171b	202	402	561	162	158
12	pab-miR171b	202	402	561	162	158
13	pab-miR171c	202	402	561	162	158
14	ppe-miR171b	202	402	561	162	158
15	ssl-miR171b	202	402	561	162	158
16	vvi-miR171f	202	402	561	162	158
17	lja-miR1511-3p	12708	10343	28977	6523	8375
18	htu-miR171a	21	50	99	36	17
19	fve-miR167d	1734	2867	4223	1487	1553
20	lus-miR167a	1609	2734	4204	1417	1469
21	vvi-miR167c	1609	2734	4204	1417	1469
22	bna-miR167d	1547	2691	4152	1384	1420
23	fve-miR167a	1547	2691	4152	1384	1420
24	fve-miR167b	1547	2691	4152	1384	1420
25	fve-miR167c	1547	2691	4152	1384	1420
26	gma-miR167l	1547	2691	4152	1384	1420
27	lja-miR167a	1547	2691	4152	1384	1420
28	lja-miR167b	1547	2691	4152	1384	1420
29	lja-miR167c	1547	2691	4152	1384	1420
30	mes-miR167b	1547	2691	4152	1384	1420
31	ptc-miR390d-3p	69	72	127	26	49
32	sly-miR390a-3p	69	72	127	26	49
33	cme-miR166g	322	277	935	199	221
34	csi-miR166c-3p	322	277	935	199	221
35	gma-miR166p	322	277	935	199	221
36	gma-miR166q	322	277	935	199	221
37	gma-miR166r	322	277	935	199	221
38	gma-miR166s	322	277	935	199	221
39	gma-miR166t	322	277	935	199	221
40	sbi-miR166a	322	277	935	199	221
41	sbi-miR166b	322	277	935	199	221
42	sbi-miR166c	322	277	935	199	221
43	sbi-miR166d	322	277	935	199	221
44	sbi-miR166h	322	277	935	199	221
45	sbi-miR166i	322	277	935	199	221
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3	sbi-miR166j	322	277	935	199	221
4	tcc-miR166b	322	277	935	199	221
5	zma-miR166b-3p	322	277	935	199	221
6	zma-miR166c-3p	322	277	935	199	221
7	zma-miR166d-3p	322	277	935	199	221
8	zma-miR166e	322	277	935	199	221
9	zma-miR166f	322	277	935	199	221
10	zma-miR166g-3p	322	277	935	199	221
11	zma-miR166h-3p	322	277	935	199	221
12	zma-miR166i-3p	322	277	935	199	221
13	eun-miR167b-3p	464	825	474	344	315
14	csi-miR167c-3p	2180	2342	4079	1257	1598
15	ppt-miR390c-5p	244	380	768	230	183
16	csi-miR390b-5p	244	380	767	230	183
17	gma-miR390e	244	380	767	230	183
18	eca-miR-378	53	77	105	70	35
19	mml-miR-378a	53	77	105	70	35
20	mmu-miR-378a-3p	53	77	105	70	35
21	ptr-miR-378a	53	77	105	70	35
22	rno-miR-378a-3p	53	77	105	70	35
23	aof-miR167b	4141	6388	13239	3318	3696
24	ata-miR167b-5p	4141	6388	13239	3318	3696
25	ata-miR167d-5p	4141	6388	13239	3318	3696
26	bdi-miR167c-5p	4141	6388	13239	3318	3696
27	bdi-miR167d-5p	4141	6388	13239	3318	3696
28	bdi-miR167e-5p	4141	6388	13239	3318	3696
29	bdi-miR167g	4141	6388	13239	3318	3696
30	ccl-miR167a	4141	6388	13239	3318	3696
31	ccl-miR167b	4141	6388	13239	3318	3696
32	cpa-miR167d	4141	6388	13239	3318	3696
33	ctr-miR167	4141	6388	13239	3318	3696
34	eun-miR167a-5p	4141	6388	13239	3318	3696
35	gma-miR167g	4141	6388	13239	3318	3696
36	mes-miR167d	4141	6388	13239	3318	3696
37	mes-miR167e	4141	6388	13239	3318	3696
38	mes-miR167f	4141	6388	13239	3318	3696
39	ppe-miR167c	4141	6388	13239	3318	3696
40	vca-miR167a-5p	4141	6388	13239	3318	3696
41	vca-miR167b-5p	4141	6388	13239	3318	3696
42	cpa-miR166d	2329	1741	8028	1495	1533
43	gma-miR166j-3p	2329	1741	8028	1495	1533
44	mes-miR160h	8719	7677	23410	5160	4684
45	crt-miR166a	2333	1741	8038	1495	1535
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3	mes-miR166h	2333	1741	8038	1495	1535
4	gma-miR390a-3p	3229	3523	12001	2369	3052
5	gma-miR390c	3229	3523	12001	2369	3052
6	mes-miR390	3229	3523	12001	2369	3052
7	aly-miR390a-3p	3489	3760	12662	2457	3259
8	ath-miR390a-3p	3489	3760	12662	2457	3259
9	cas-miR390a-3p	3489	3760	12662	2457	3259
10	csi-miR390a-3p	3489	3760	12662	2457	3259
11	lja-miR390a-3p	3489	3760	12662	2457	3259
12	lja-miR390b-3p	3489	3760	12662	2457	3259
13	sly-miR390b-3p	3489	3760	12662	2457	3259
14	aly-miR160a-5p	8586	7490	23233	5057	4547
15	aly-miR160b-5p	8586	7490	23233	5057	4547
16	aly-miR160c-5p	8586	7490	23233	5057	4547
17	aof-miR160c	8586	7490	23233	5057	4547
18	aqc-miR160b	8586	7490	23233	5057	4547
19	ata-miR160a-5p	8586	7490	23233	5057	4547
20	ata-miR160b-5p	8586	7490	23233	5057	4547
21	ata-miR160c-5p	8586	7490	23233	5057	4547
22	ath-miR160a-5p	8586	7490	23233	5057	4547
23	ath-miR160b	8586	7490	23233	5057	4547
24	ath-miR160c-5p	8586	7490	23233	5057	4547
25	atr-miR160	8586	7490	23233	5057	4547
26	bdi-miR160a-5p	8586	7490	23233	5057	4547
27	bdi-miR160b-5p	8586	7490	23233	5057	4547
28	bdi-miR160c-5p	8586	7490	23233	5057	4547
29	bdi-miR160d-5p	8586	7490	23233	5057	4547
30	bna-miR160a	8586	7490	23233	5057	4547
31	bna-miR160b	8586	7490	23233	5057	4547
32	bna-miR160c	8586	7490	23233	5057	4547
33	bna-miR160d	8586	7490	23233	5057	4547
34	bra-miR160a-5p	8586	7490	23233	5057	4547
35	cca-miR160b	8586	7490	23233	5057	4547
36	cme-miR160a	8586	7490	23233	5057	4547
37	cme-miR160b	8586	7490	23233	5057	4547
38	cme-miR160c	8586	7490	23233	5057	4547
39	cpa-miR160a	8586	7490	23233	5057	4547
40	cpa-miR160b	8586	7490	23233	5057	4547
41	cpa-miR160c-5p	8586	7490	23233	5057	4547
42	cpa-miR160e	8586	7490	23233	5057	4547
43	cpa-miR160f-5p	8586	7490	23233	5057	4547
44	eun-miR160-5p	8586	7490	23233	5057	4547
45	far-miR160	8586	7490	23233	5057	4547
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3	fve-miR160a	8586	7490	23233	5057	4547
4	fve-miR160b	8586	7490	23233	5057	4547
5	gma-miR160a-5p	8586	7490	23233	5057	4547
6	gma-miR160f	8586	7490	23233	5057	4547
7	lus-miR160a	8586	7490	23233	5057	4547
8	lus-miR160b	8586	7490	23233	5057	4547
9	lus-miR160d	8586	7490	23233	5057	4547
10	lus-miR160e	8586	7490	23233	5057	4547
11	lus-miR160f	8586	7490	23233	5057	4547
12	lus-miR160h	8586	7490	23233	5057	4547
13	lus-miR160i	8586	7490	23233	5057	4547
14	lus-miR160j	8586	7490	23233	5057	4547
15	mdm-miR160a	8586	7490	23233	5057	4547
16	mdm-miR160b	8586	7490	23233	5057	4547
17	mdm-miR160c	8586	7490	23233	5057	4547
18	mdm-miR160d	8586	7490	23233	5057	4547
19	mdm-miR160e	8586	7490	23233	5057	4547
20	mes-miR160a	8586	7490	23233	5057	4547
21	mes-miR160b	8586	7490	23233	5057	4547
22	mes-miR160d	8586	7490	23233	5057	4547
23	mtr-miR160a	8586	7490	23233	5057	4547
24	mtr-miR160b	8586	7490	23233	5057	4547
25	mtr-miR160d	8586	7490	23233	5057	4547
26	mtr-miR160e	8586	7490	23233	5057	4547
27	nta-miR160a	8586	7490	23233	5057	4547
28	nta-miR160b	8586	7490	23233	5057	4547
29	nta-miR160c	8586	7490	23233	5057	4547
30	osa-miR160a-5p	8586	7490	23233	5057	4547
31	osa-miR160b-5p	8586	7490	23233	5057	4547
32	osa-miR160c-5p	8586	7490	23233	5057	4547
33	osa-miR160d-5p	8586	7490	23233	5057	4547
34	pab-miR160a	8586	7490	23233	5057	4547
35	pab-miR160b	8586	7490	23233	5057	4547
36	pab-miR160d	8586	7490	23233	5057	4547
37	ppe-miR160a	8586	7490	23233	5057	4547
38	ppe-miR160b	8586	7490	23233	5057	4547
39	ppt-miR160a	8586	7490	23233	5057	4547
40	ppt-miR160e	8586	7490	23233	5057	4547
41	ppt-miR160f	8586	7490	23233	5057	4547
42	ptc-miR160a	8586	7490	23233	5057	4547
43	ptc-miR160b-5p	8586	7490	23233	5057	4547
44	ptc-miR160c-5p	8586	7490	23233	5057	4547
45	ptc-miR160d	8586	7490	23233	5057	4547
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3	rco-miR160a	8586	7490	23233	5057	4547
4	rco-miR160b	8586	7490	23233	5057	4547
5	sbi-miR160a	8586	7490	23233	5057	4547
6	sbi-miR160b	8586	7490	23233	5057	4547
7	sbi-miR160c	8586	7490	23233	5057	4547
8	sbi-miR160d	8586	7490	23233	5057	4547
9	sbi-miR160e	8586	7490	23233	5057	4547
10	sly-miR160a	8586	7490	23233	5057	4547
11	smo-miR160a	8586	7490	23233	5057	4547
12	smo-miR160b	8586	7490	23233	5057	4547
13	stu-miR160a-5p	8586	7490	23233	5057	4547
14	stu-miR160b	8586	7490	23233	5057	4547
15	tae-miR160	8586	7490	23233	5057	4547
16	tcc-miR160b	8586	7490	23233	5057	4547
17	ttu-miR160	8586	7490	23233	5057	4547
18	vun-miR160	8586	7490	23233	5057	4547
19	vvi-miR160c	8586	7490	23233	5057	4547
20	vvi-miR160d	8586	7490	23233	5057	4547
21	vvi-miR160e	8586	7490	23233	5057	4547
22	zma-miR160a-5p	8586	7490	23233	5057	4547
23	zma-miR160b-5p	8586	7490	23233	5057	4547
24	zma-miR160c-5p	8586	7490	23233	5057	4547
25	zma-miR160d-5p	8586	7490	23233	5057	4547
26	zma-miR160e	8586	7490	23233	5057	4547
27	zma-miR160g-5p	8586	7490	23233	5057	4547
28	mes-miR160g	8613	7512	23314	5065	4566
29	cas-miR166e	450	435	1699	337	287
30	csi-miR166f-3p	450	435	1699	337	287
31	osa-miR166m	450	435	1699	337	287
32	crt-miR166b	450	439	1702	337	288
33	ata-miR167f-5p	3638	5641	12623	2961	3288
34	tae-miR167c-5p	3638	5641	12623	2961	3288
35	aof-miR167c	3574	5613	12595	2914	3256
36	atr-miR167	3574	5613	12595	2914	3256
37	cme-miR167d	3574	5613	12595	2914	3256
38	cme-miR167f	3574	5613	12595	2914	3256
39	csi-miR167a-5p	3574	5613	12595	2914	3256
40	csi-miR167c-5p	3574	5613	12595	2914	3256
41	dpr-miR167c	3574	5613	12595	2914	3256
42	gma-miR167c	3574	5613	12595	2914	3256
43	gma-miR167j	3574	5613	12595	2914	3256
44	gso-miR167a	3574	5613	12595	2914	3256
45	lja-miR167	3574	5613	12595	2914	3256
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3	lus-miR167f	3574	5613	12595	2914	3256
4	lus-miR167g	3574	5613	12595	2914	3256
5	lus-miR167i	3574	5613	12595	2914	3256
6	mes-miR167a	3574	5613	12595	2914	3256
7	mes-miR167a	3574	5613	12595	2914	3256
8	mtr-miR167b-5p	3574	5613	12595	2914	3256
9	mtr-miR167b-5p	3574	5613	12595	2914	3256
10	osa-miR167d-5p	3574	5613	12595	2914	3256
11	osa-miR167e-5p	3574	5613	12595	2914	3256
12	osa-miR167e-5p	3574	5613	12595	2914	3256
13	osa-miR167f	3574	5613	12595	2914	3256
14	osa-miR167g	3574	5613	12595	2914	3256
15	osa-miR167h-5p	3574	5613	12595	2914	3256
16	osa-miR167i-5p	3574	5613	12595	2914	3256
17	osa-miR167i-5p	3574	5613	12595	2914	3256
18	osa-miR167j	3574	5613	12595	2914	3256
19	ptc-miR167e	3574	5613	12595	2914	3256
20	ptc-miR167e	3574	5613	12595	2914	3256
21	sbi-miR167c	3574	5613	12595	2914	3256
22	sbi-miR167d	3574	5613	12595	2914	3256
23	sbi-miR167e	3574	5613	12595	2914	3256
24	sbi-miR167e	3574	5613	12595	2914	3256
25	sbi-miR167f	3574	5613	12595	2914	3256
26	sbi-miR167g	3574	5613	12595	2914	3256
27	sbi-miR167g	3574	5613	12595	2914	3256
28	sbi-miR167h	3574	5613	12595	2914	3256
29	sof-miR167a	3574	5613	12595	2914	3256
30	sof-miR167b	3574	5613	12595	2914	3256
31	sof-miR167b	3574	5613	12595	2914	3256
32	ssp-miR167b	3574	5613	12595	2914	3256
33	vvi-miR167a	3574	5613	12595	2914	3256
34	zma-miR167e-5p	3574	5613	12595	2914	3256
35	zma-miR167f-5p	3574	5613	12595	2914	3256
36	zma-miR167g-5p	3574	5613	12595	2914	3256
37	zma-miR167g-5p	3574	5613	12595	2914	3256
38	zma-miR167h-5p	3574	5613	12595	2914	3256
39	zma-miR167i-5p	3574	5613	12595	2914	3256
40	zma-miR167j-5p	3574	5613	12595	2914	3256
41	zma-miR167j-5p	3574	5613	12595	2914	3256
42	aly-miR166g-5p	700	800	69	148	435
43	cas-miR166f-5p	700	800	69	148	435
44	cas-miR166f-5p	700	800	69	148	435
45	csi-miR166b-5p	700	800	69	148	435
46	gma-miR166h-5p	700	800	69	148	435
47	gma-miR166j-5p	700	800	69	148	435
48	gma-miR166j-5p	700	800	69	148	435
49	stu-miR166c-5p	700	800	69	148	435
50	aly-miR390a-5p	1490	1960	3675	965	866
51	aly-miR390b-5p	1490	1960	3675	965	866
52	aof-miR390	1490	1960	3675	965	866
53	ata-miR390-5p	1490	1960	3675	965	866
54	ata-miR390-5p	1490	1960	3675	965	866
55	ath-miR390a-5p	1490	1960	3675	965	866
56	ath-miR390b-5p	1490	1960	3675	965	866
57	ath-miR390b-5p	1490	1960	3675	965	866
58	atr-miR390.2	1490	1960	3675	965	866
59	bdi-miR390a-5p	1490	1960	3675	965	866
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3	bna-miR390a	1490	1960	3675	965	866
4	bna-miR390b	1490	1960	3675	965	866
5	bna-miR390c	1490	1960	3675	965	866
6	bra-miR390-5p	1490	1960	3675	965	866
7	cas-miR390a-5p	1490	1960	3675	965	866
8	cas-miR390b	1490	1960	3675	965	866
9	cme-miR390a	1490	1960	3675	965	866
10	cme-miR390b	1490	1960	3675	965	866
11	cme-miR390c	1490	1960	3675	965	866
12	cme-miR390d	1490	1960	3675	965	866
13	cpa-miR390a	1490	1960	3675	965	866
14	cpa-miR390b	1490	1960	3675	965	866
15	csi-miR390a-5p	1490	1960	3675	965	866
16	fve-miR390a	1490	1960	3675	965	866
17	fve-miR390b	1490	1960	3675	965	866
18	ghr-miR390a	1490	1960	3675	965	866
19	ghr-miR390b	1490	1960	3675	965	866
20	ghr-miR390c	1490	1960	3675	965	866
21	gma-miR390a-5p	1490	1960	3675	965	866
22	gma-miR390f	1490	1960	3675	965	866
23	gma-miR390g	1490	1960	3675	965	866
24	hex-miR390a	1490	1960	3675	965	866
25	hex-miR390b	1490	1960	3675	965	866
26	lja-miR390a-5p	1490	1960	3675	965	866
27	lja-miR390b-5p	1490	1960	3675	965	866
28	lus-miR390a	1490	1960	3675	965	866
29	lus-miR390b	1490	1960	3675	965	866
30	lus-miR390c	1490	1960	3675	965	866
31	lus-miR390d	1490	1960	3675	965	866
32	mdm-miR390a	1490	1960	3675	965	866
33	mdm-miR390b	1490	1960	3675	965	866
34	mdm-miR390c	1490	1960	3675	965	866
35	mdm-miR390d	1490	1960	3675	965	866
36	mdm-miR390e	1490	1960	3675	965	866
37	mdm-miR390f	1490	1960	3675	965	866
38	mes-miR390b	1490	1960	3675	965	866
39	mtr-miR390	1490	1960	3675	965	866
40	nta-miR390b	1490	1960	3675	965	866
41	nta-miR390c	1490	1960	3675	965	866
42	osa-miR390-5p	1490	1960	3675	965	866
43	pab-miR390a	1490	1960	3675	965	866
44	pab-miR390b	1490	1960	3675	965	866
45	ppe-miR390	1490	1960	3675	965	866
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3	ppt-miR390a	1490	1960	3675	965	866
4	ppt-miR390b	1490	1960	3675	965	866
5	ptc-miR390a	1490	1960	3675	965	866
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7	ptc-miR390c	1490	1960	3675	965	866
8	ptc-miR390d-5p	1490	1960	3675	965	866
9	rco-miR390a	1490	1960	3675	965	866
10	rco-miR390b	1490	1960	3675	965	866
11	sbi-miR390	1490	1960	3675	965	866
12	sly-miR390b-5p	1490	1960	3675	965	866
13	tcc-miR390a	1490	1960	3675	965	866
14	tcc-miR390b	1490	1960	3675	965	866
15	vvi-miR390	1490	1960	3675	965	866
16	zma-miR390a-5p	1490	1960	3675	965	866
17	zma-miR390b-5p	1490	1960	3675	965	866
18	csi-miR160a-5p	35	24	336	24	15
19	pab-miR166j	76	50	1329	38	57
20	mes-miR166i	15	10	174	5	15
21	gma-miR166m	69	36	1299	29	44
22	mtr-miR166e-5p	206	672	52	93	201
23	osa-miR166h-5p	206	672	52	93	201
24	zma-miR166m-5p	206	672	52	93	201
25	aly-miR168a-3p	434	484	5046	334	647
26	ath-miR168a-3p	434	484	5046	334	647
27	bra-miR168b-3p	434	484	5046	334	647
28	bra-miR168c-3p	434	484	5046	334	647
29	cas-miR168	434	484	5046	334	647
30	csi-miR168-3p	434	484	5046	334	647
31	fve-miR168-3p	434	484	5046	334	647
32	mtr-miR168c-3p	434	484	5046	334	647
33	ptc-miR168a-3p	434	484	5046	334	647
34	ptc-miR168b-3p	434	484	5046	334	647
35	sly-miR168b-3p	434	484	5046	334	647
36	lja-miR168-3p	436	488	5067	335	648
37	aof-miR166c	5	6	1623	3	11
38	ath-miR165a-3p	5	6	1623	3	11
39	ath-miR165b	5	6	1623	3	11
40	bna-miR166f	5	6	1623	3	11
41	cas-miR165a	5	6	1623	3	11
42	lus-miR166b	5	6	1623	3	11
43	gmo-miR-451-5p	12	192	761	11	7
44	cfa-miR-375	0	0	477	0	0
45	cpo-miR-375-3p	0	0	477	0	0
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3	dno-miR-375-3p	0	0	477	0	0
4	ggo-miR-375	0	0	477	0	0
5	hsa-miR-375-3p	0	0	477	0	0
6	mml-miR-375	0	0	477	0	0
7	mmu-miR-375-3p	0	0	477	0	0
8	ocu-miR-375-3p	0	0	477	0	0
9	pal-miR-375-3p	0	0	477	0	0
10	ppy-miR-375	0	0	477	0	0
11	ptr-miR-375	0	0	477	0	0
12	rno-miR-375-3p	0	0	477	0	0
13	ssc-miR-375	0	0	477	0	0
14	bta-miR-375	0	0	486	0	0
15	efu-miR-375	0	0	486	0	0
16	mdo-miR-375	0	0	486	0	0
17	aae-miR-184	1	352	0	0	1
18	abu-miR-184a	1	352	0	0	1
19	ame-miR-184-3p	1	352	0	0	1
20	api-miR-184a	1	352	0	0	1
21	bbe-miR-184-3p	1	352	0	0	1
22	bdo-miR-184	1	352	0	0	1
23	bmo-miR-184-3p	1	352	0	0	1
24	ccr-miR-184	1	352	0	0	1
25	cin-miR-184	1	352	0	0	1
26	cqu-miR-184	1	352	0	0	1
27	cte-miR-184a	1	352	0	0	1
28	dan-miR-184-3p	1	352	0	0	1
29	der-miR-184-3p	1	352	0	0	1
30	dgr-miR-184-3p	1	352	0	0	1
31	dme-miR-184-3p	1	352	0	0	1
32	dmo-miR-184-3p	1	352	0	0	1
33	dpe-miR-184-3p	1	352	0	0	1
34	dps-miR-184	1	352	0	0	1
35	dre-miR-184	1	352	0	0	1
36	dse-miR-184-3p	1	352	0	0	1
37	dsi-miR-184-3p	1	352	0	0	1
38	dvi-miR-184-3p	1	352	0	0	1
39	dwi-miR-184-3p	1	352	0	0	1
40	dya-miR-184-3p	1	352	0	0	1
41	hme-miR-184	1	352	0	0	1
42	ipu-miR-184	1	352	0	0	1
43	isc-miR-184	1	352	0	0	1
44	lgi-miR-184	1	352	0	0	1
45	lva-miR-184-3p	1	352	0	0	1
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mle-miR-184-3p	1	352	0	0	1
mse-miR-184	1	352	0	0	1
mze-miR-184a	1	352	0	0	1
nbr-miR-184a	1	352	0	0	1
ngi-miR-184	1	352	0	0	1
nlo-miR-184	1	352	0	0	1
nvi-miR-184	1	352	0	0	1
oni-miR-184a	1	352	0	0	1
pca-miR-184-3p	1	352	0	0	1
pmi-miR-184-3p	1	352	0	0	1
pony-miR-184a	1	352	0	0	1
pte-miR-184-3p	1	352	0	0	1
sko-miR-184-3p	1	352	0	0	1
spu-miR-184	1	352	0	0	1
tca-miR-184-3p	1	352	0	0	1
tcf-miR-184-3p	1	352	0	0	1
tur-miR-184-3p	1	352	0	0	1
aae-miR-2940-3p	0	673	2	0	0

Do not distribute





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3	390	430	793	198	53	135	184
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13	779	77	366	3498	86	89	367
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17	779	77	366	3498	86	89	367
18	779	77	366	3498	86	89	367
19	779	77	366	3498	86	89	367
20	779	77	366	3498	86	89	367
21	779	77	366	3498	86	89	367
22	779	77	366	3498	86	89	367
23	574	30	346	2036	31	24	271
24	574	30	346	2036	31	24	271
25	574	30	346	2036	31	24	271
26	574	30	346	2036	31	24	271
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37	574	30	346	2036	31	24	271
38	574	30	346	2036	31	24	271
39	5568	0	0	1	0	0	2627
40	5136	0	0	1	0	0	2423
41	2181	0	0	1	0	0	1029
42	1803	0	0	0	0	0	850
43	1599	0	0	0	0	0	754
44	1591	0	0	0	0	0	750
45	1294	0	0	1	0	0	610
46	1102	0	0	0	0	0	520
47	396	0	0	0	0	0	187
48	393	0	0	0	0	0	185
49	336	0	0	1	0	0	158
50	308	0	0	1	0	0	145
51	9770	0	0	2	0	0	4609
52	16301	0	0	6	0	0	7689
53	26912	0	0	12	0	0	12695
54	6438	0	0	2	0	0	3037
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3	4629	0	0	2	0	0	2184
4	3487	0	0	2	0	0	1645
5	1308	0	0	3	0	0	617
6	1809	3	7	10	5	3	853
7	422	0	3	3	2	2	199
8	422	0	3	3	2	2	199
9	422	0	3	3	2	2	199
10	422	0	3	3	2	2	199
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27	422	0	3	3	2	2	199
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25	139	14	13	194	5	24	66
26	1135	62	48	1451	31	72	535
27	80	186	891	58	98	327	38
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41	171.65	0	343	1.186	#DIV/0!	2.521	NA
42	141.75	0	283	3691349.76	#DIV/0!	5.902	NA
43	125.71	0	251	4829582.72	#DIV/0!	6.007	NA
44	125.08	0	250	4228034	#DIV/0!	5.955	NA
45	101.92	0	203	1.108	#DIV/0!	2.328	NA
46	86.64	0	173	3621108.59	#DIV/0!	5.894	NA
47	31.13	0	62	1416934	#DIV/0!	5.529	NA
48	30.9	0	62	1402888.26	#DIV/0!	5.525	NA
49	26.6	0	53	1.276	#DIV/0!	2.901	NA
50	24.4	0	48	1.229	#DIV/0!	2.845	NA
51	768.48	1	1536	1.526	10.5849625	2.851	NA
52	1282.5	2	2563	1.369	10.3236178	2.758	NA
53	2117.84	4	4232	1.273	10.0471239	2.67	NA
54	506.52	1	1012	1.311	9.98299357	2.696	NA
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27	41.74	10	73	1.009	2.86789646	1.857 NA
28	29.04	7	51	1.008	2.86507042	1.766 NA
29	29.04	7	51	1.008	2.86507042	1.766 NA
30	29.04	7	51	1.008	2.86507042	1.766 NA
31	29.04	7	51	1.008	2.86507042	1.766 NA
32	29.04	7	51	1.008	2.86507042	1.766 NA
33	29.04	7	51	1.008	2.86507042	1.766 NA
34	29.04	7	51	1.008	2.86507042	1.766 NA
35	29.04	7	51	1.008	2.86507042	1.766 NA
36	29.04	7	51	1.008	2.86507042	1.766 NA
37	29.04	7	51	1.008	2.86507042	1.766 NA
38	29.04	7	51	1.008	2.86507042	1.766 NA
39	29.04	7	51	1.008	2.86507042	1.766 NA
40	29.04	7	51	1.008	2.86507042	1.766 NA
41	29.04	7	51	1.008	2.86507042	1.766 NA
42	29.04	7	51	1.008	2.86507042	1.766 NA
43	29.04	7	51	1.008	2.86507042	1.766 NA
44	29.04	7	51	1.008	2.86507042	1.766 NA
45	29.04	7	51	1.008	2.86507042	1.766 NA
46	29.04	7	51	1.008	2.86507042	1.766 NA
47	29.04	7	51	1.008	2.86507042	1.766 NA
48	29.04	7	51	1.008	2.86507042	1.766 NA
49	38.69	10	67	1.01	2.7441611	1.925 NA
50	38.69	10	67	1.01	2.7441611	1.925 NA
51	38.69	10	67	1.01	2.7441611	1.925 NA
52	38.69	10	67	1.01	2.7441611	1.925 NA
53	38.69	10	67	1.01	2.7441611	1.925 NA
54	38.69	10	67	1.01	2.7441611	1.925 NA
55	38.69	10	67	1.01	2.7441611	1.925 NA
56	38.69	10	67	1.01	2.7441611	1.925 NA
57	38.69	10	67	1.01	2.7441611	1.925 NA
58	38.69	10	67	1.01	2.7441611	1.925 NA
59	38.69	10	67	1.01	2.7441611	1.925 NA
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8	38.69	10	67	1.01	2.7441611	1.925 NA
9	38.69	10	67	1.01	2.7441611	1.925 NA
10	38.69	10	67	1.01	2.7441611	1.925 NA
11	38.69	10	67	1.01	2.7441611	1.925 NA
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14	38.69	10	67	1.01	2.7441611	1.925 NA
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16	38.69	10	67	1.01	2.7441611	1.925 NA
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18	38.69	10	67	1.01	2.7441611	1.925 NA
19	38.69	10	67	1.01	2.7441611	1.925 NA
20	38.69	10	67	1.01	2.7441611	1.925 NA
21	38.69	10	67	1.01	2.7441611	1.925 NA
22	41.23	11	72	1.01	2.71049338	1.946 NA
23	456.24	125	788	1.011	2.65626753	2.032 NA
24	456.24	125	788	1.011	2.65626753	2.032 NA
25	456.24	125	788	1.011	2.65626753	2.032 NA
26	456.24	125	788	1.011	2.65626753	2.032 NA
27	456.24	125	788	1.011	2.65626753	2.032 NA
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37	456.24	125	788	1.011	2.65626753	2.032 NA
38	456.24	125	788	1.011	2.65626753	2.032 NA
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41	456.24	125	788	1.011	2.65626753	2.032 NA
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59	456.24	125	788	1.011	2.65626753	2.032 NA
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3	456.24	125	788	1.011	2.65626753	2.032 NA
4	790.66	253	1328	1.011	2.39204586	2.076 NA
5	790.66	253	1328	1.011	2.39204586	2.076 NA
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59	790.66	253	1328	1.011	2.39204586	2.076 NA
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31	790.66	253	1328	1.011	2.39204586	2.076	NA
32	790.66	253	1328	1.011	2.39204586	2.076	NA
33	790.66	253	1328	1.011	2.39204586	2.076	NA
34	804.54	258	1351	1.011	2.3885847	2.076	NA
35	42.45	14	70	1.007	2.32192809	1.802	0.07154974
36	42.45	14	70	1.007	2.32192809	1.802	0.07154974
37	42.45	14	70	1.007	2.32192809	1.802	0.07154974
38	42.45	14	70	1.007	2.32192809	1.802	0.07154974
39	42.45	14	70	1.007	2.32192809	1.802	0.07154974
40	42.45	14	70	1.007	2.32192809	1.802	0.07154974
41	42.45	14	70	1.007	2.32192809	1.802	0.07154974
42	42.45	14	70	1.007	2.32192809	1.802	0.07154974
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44	42.45	14	70	1.007	2.32192809	1.802	0.07154974
45	42.45	14	70	1.007	2.32192809	1.802	0.07154974
46	42.45	14	70	1.007	2.32192809	1.802	0.07154974
47	42.45	14	70	1.007	2.32192809	1.802	0.07154974
48	42.45	14	70	1.007	2.32192809	1.802	0.07154974
49	42.45	14	70	1.007	2.32192809	1.802	0.07154974
50	42.45	14	70	1.007	2.32192809	1.802	0.07154974
51	42.45	14	70	1.007	2.32192809	1.802	0.07154974
52	42.45	14	70	1.007	2.32192809	1.802	0.07154974
53	42.45	14	70	1.007	2.32192809	1.802	0.07154974
54	42.45	14	70	1.007	2.32192809	1.802	0.07154974
55	42.45	14	70	1.007	2.32192809	1.802	0.07154974
56	185.39	62	309	1.008	2.31726672	1.839	0.06584198
57	184.76	62	308	1.008	2.31259023	1.836	0.0663934
58	184.76	62	308	1.008	2.31259023	1.836	0.0663934
59	184.76	62	308	1.008	2.31259023	1.836	0.0663934
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3	184.76	62	308	1.008	2.31259023	1.836	0.0663934
4	184.76	62	308	1.008	2.31259023	1.836	0.0663934
5	184.76	62	308	1.008	2.31259023	1.836	0.0663934
6	184.76	62	308	1.008	2.31259023	1.836	0.0663934
7	184.76	62	308	1.008	2.31259023	1.836	0.0663934
8	184.76	62	308	1.008	2.31259023	1.836	0.0663934
9	184.76	62	308	1.008	2.31259023	1.836	0.0663934
10	50.47	17	84	1.008	2.30485458	1.886	0.05930402
11	50.47	17	84	1.008	2.30485458	1.886	0.05930402
12	50.47	17	84	1.008	2.30485458	1.886	0.05930402
13	50.47	17	84	1.008	2.30485458	1.886	0.05930402
14	50.47	17	84	1.008	2.30485458	1.886	0.05930402
15	50.47	17	84	1.008	2.30485458	1.886	0.05930402
16	636	220	1052	1.01	2.25755928	2.002	NA
17	636	220	1052	1.01	2.25755928	2.002	NA
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10	636	220	1052	1.01	2.25755928	2.002	NA
11	144.87	53	236	1.007	2.15472259	1.722	0.08505991
12	144.87	53	236	1.007	2.15472259	1.722	0.08505991
13	144.87	53	236	1.007	2.15472259	1.722	0.08505991
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15	144.87	53	236	1.007	2.15472259	1.722	0.08505991
16	144.87	53	236	1.007	2.15472259	1.722	0.08505991
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19	144.87	53	236	1.007	2.15472259	1.722	0.08505991
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23	144.87	53	236	1.007	2.15472259	1.722	0.08505991
24	144.87	53	236	1.007	2.15472259	1.722	0.08505991
25	144.87	53	236	1.007	2.15472259	1.722	0.08505991
26	144.87	53	236	1.007	2.15472259	1.722	0.08505991
27	144.87	53	236	1.007	2.15472259	1.722	0.08505991
28	144.87	53	236	1.007	2.15472259	1.722	0.08505991
29	144.87	53	236	1.007	2.15472259	1.722	0.08505991
30	144.87	53	236	1.007	2.15472259	1.722	0.08505991
31	144.87	53	236	1.007	2.15472259	1.722	0.08505991
32	144.87	53	236	1.007	2.15472259	1.722	0.08505991
33	144.87	53	236	1.007	2.15472259	1.722	0.08505991
34	144.87	53	236	1.007	2.15472259	1.722	0.08505991
35	144.87	53	236	1.007	2.15472259	1.722	0.08505991
36	144.87	53	236	1.007	2.15472259	1.722	0.08505991
37	144.87	53	236	1.007	2.15472259	1.722	0.08505991
38	144.87	53	236	1.007	2.15472259	1.722	0.08505991
39	144.87	53	236	1.007	2.15472259	1.722	0.08505991
40	144.87	53	236	1.007	2.15472259	1.722	0.08505991
41	144.87	53	236	1.007	2.15472259	1.722	0.08505991
42	144.87	53	236	1.007	2.15472259	1.722	0.08505991
43	144.87	53	236	1.007	2.15472259	1.722	0.08505991
44	144.87	53	236	1.007	2.15472259	1.722	0.08505991
45	144.87	53	236	1.007	2.15472259	1.722	0.08505991
46	144.87	53	236	1.007	2.15472259	1.722	0.08505991
47	144.87	53	236	1.007	2.15472259	1.722	0.08505991
48	144.87	53	236	1.007	2.15472259	1.722	0.08505991
49	144.87	53	236	1.007	2.15472259	1.722	0.08505991
50	144.87	53	236	1.007	2.15472259	1.722	0.08505991
51	144.87	53	236	1.007	2.15472259	1.722	0.08505991
52	144.87	53	236	1.007	2.15472259	1.722	0.08505991
53	144.87	53	236	1.007	2.15472259	1.722	0.08505991
54	144.87	53	236	1.007	2.15472259	1.722	0.08505991
55	144.87	53	236	1.007	2.15472259	1.722	0.08505991
56	144.87	53	236	1.007	2.15472259	1.722	0.08505991
57	144.87	53	236	1.007	2.15472259	1.722	0.08505991
58	144.87	53	236	1.007	2.15472259	1.722	0.08505991
59	144.87	53	236	1.007	2.15472259	1.722	0.08505991
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3	144.87	53	236	1.007	2.15472259	1.722	0.08505991
4	80.35	30	131	1.008	2.12653241	1.838	NA
5	80.35	30	131	1.008	2.12653241	1.838	NA
6	80.35	30	131	1.008	2.12653241	1.838	NA
7	80.35	30	131	1.008	2.12653241	1.838	NA
8	80.35	30	131	1.008	2.12653241	1.838	NA
9	80.35	30	131	1.008	2.12653241	1.838	NA
10	80.35	30	131	1.008	2.12653241	1.838	NA
11	80.35	30	131	1.008	2.12653241	1.838	NA
12	62.97	24	102	1.004	2.08746284	1.309	0.1906123
13	62.97	24	102	1.004	2.08746284	1.309	0.1906123
14	62.97	24	102	1.004	2.08746284	1.309	0.1906123
15	62.97	24	102	1.004	2.08746284	1.309	0.1906123
16	62.97	24	102	1.004	2.08746284	1.309	0.1906123
17	62.97	24	102	1.004	2.08746284	1.309	0.1906123
18	62.97	24	102	1.004	2.08746284	1.309	0.1906123
19	62.97	24	102	1.004	2.08746284	1.309	0.1906123
20	62.97	24	102	1.004	2.08746284	1.309	0.1906123
21	62.97	24	102	1.004	2.08746284	1.309	0.1906123
22	62.97	24	102	1.004	2.08746284	1.309	0.1906123
23	62.97	24	102	1.004	2.08746284	1.309	0.1906123
24	62.97	24	102	1.004	2.08746284	1.309	0.1906123
25	174.65	72	277	1.007	1.94381716	1.749	NA
26	174.65	72	277	1.007	1.94381716	1.749	NA
27	173.75	72	275	1.007	1.93336281	1.738	NA
28	173.75	72	275	1.007	1.93336281	1.738	NA
29	173.75	72	275	1.007	1.93336281	1.738	NA
30	173.75	72	275	1.007	1.93336281	1.738	NA
31	173.75	72	275	1.007	1.93336281	1.738	NA
32	173.75	72	275	1.007	1.93336281	1.738	NA
33	173.75	72	275	1.007	1.93336281	1.738	NA
34	173.75	72	275	1.007	1.93336281	1.738	NA
35	173.75	72	275	1.007	1.93336281	1.738	NA
36	173.75	72	275	1.007	1.93336281	1.738	NA
37	173.75	72	275	1.007	1.93336281	1.738	NA
38	173.75	72	275	1.007	1.93336281	1.738	NA
39	173.75	72	275	1.007	1.93336281	1.738	NA
40	173.75	72	275	1.007	1.93336281	1.738	NA
41	173.75	72	275	1.007	1.93336281	1.738	NA
42	173.75	72	275	1.007	1.93336281	1.738	NA
43	173.75	72	275	1.007	1.93336281	1.738	NA
44	173.75	72	275	1.007	1.93336281	1.738	NA
45	173.75	72	275	1.007	1.93336281	1.738	NA
46	173.75	72	275	1.007	1.93336281	1.738	NA
47	173.75	72	275	1.007	1.93336281	1.738	NA
48	173.75	72	275	1.007	1.93336281	1.738	NA
49	173.75	72	275	1.007	1.93336281	1.738	NA
50	173.75	72	275	1.007	1.93336281	1.738	NA
51	173.75	72	275	1.007	1.93336281	1.738	NA
52	173.75	72	275	1.007	1.93336281	1.738	NA
53	173.75	72	275	1.007	1.93336281	1.738	NA
54	173.75	72	275	1.007	1.93336281	1.738	NA
55	173.75	72	275	1.007	1.93336281	1.738	NA
56	173.75	72	275	1.007	1.93336281	1.738	NA
57	173.75	72	275	1.007	1.93336281	1.738	NA
58	173.75	72	275	1.007	1.93336281	1.738	NA
59	332.52	153	512	1.006	1.74261216	1.558	0.11912555
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3	322.17	152	492	1.007	1.69458699	1.734	0.08297435
4	322.17	152	492	1.007	1.69458699	1.734	0.08297435
5	322.17	152	492	1.007	1.69458699	1.734	0.08297435
6	322.17	152	492	1.007	1.69458699	1.734	0.08297435
7	322.17	152	492	1.007	1.69458699	1.734	0.08297435
8	322.17	152	492	1.007	1.69458699	1.734	0.08297435
9	322.17	152	492	1.007	1.69458699	1.734	0.08297435
10	322.17	152	492	1.007	1.69458699	1.734	0.08297435
11	322.17	152	492	1.007	1.69458699	1.734	0.08297435
12	322.17	152	492	1.007	1.69458699	1.734	0.08297435
13	322.17	152	492	1.007	1.69458699	1.734	0.08297435
14	322.17	152	492	1.007	1.69458699	1.734	0.08297435
15	322.17	152	492	1.007	1.69458699	1.734	0.08297435
16	322.17	152	492	1.007	1.69458699	1.734	0.08297435
17	322.17	152	492	1.007	1.69458699	1.734	0.08297435
18	322.17	152	492	1.007	1.69458699	1.734	0.08297435
19	322.17	152	492	1.007	1.69458699	1.734	0.08297435
20	322.17	152	492	1.007	1.69458699	1.734	0.08297435
21	322.17	152	492	1.007	1.69458699	1.734	0.08297435
22	322.17	152	492	1.007	1.69458699	1.734	0.08297435
23	322.17	152	492	1.007	1.69458699	1.734	0.08297435
24	322.17	152	492	1.007	1.69458699	1.734	0.08297435
25	322.17	152	492	1.007	1.69458699	1.734	0.08297435
26	322.17	152	492	1.007	1.69458699	1.734	0.08297435
27	322.17	152	492	1.007	1.69458699	1.734	0.08297435
28	322.17	152	492	1.007	1.69458699	1.734	0.08297435
29	322.17	152	492	1.007	1.69458699	1.734	0.08297435
30	322.17	152	492	1.007	1.69458699	1.734	0.08297435
31	322.17	152	492	1.007	1.69458699	1.734	0.08297435
32	322.17	152	492	1.007	1.69458699	1.734	0.08297435
33	322.17	152	492	1.007	1.69458699	1.734	0.08297435
34	322.17	152	492	1.007	1.69458699	1.734	0.08297435
35	322.17	152	492	1.007	1.69458699	1.734	0.08297435
36	322.17	152	492	1.007	1.69458699	1.734	0.08297435
37	322.17	152	492	1.007	1.69458699	1.734	0.08297435
38	322.17	152	492	1.007	1.69458699	1.734	0.08297435
39	268.79	130	408	1.003	1.65005753	1.052	NA
40	268.79	130	408	1.003	1.65005753	1.052	NA
41	268.79	130	408	1.003	1.65005753	1.052	NA
42	268.79	130	408	1.003	1.65005753	1.052	NA
43	268.79	130	408	1.003	1.65005753	1.052	NA
44	427.67	209	647	1.006	1.63026277	1.665	0.09598677
45	427.67	209	647	1.006	1.63026277	1.665	0.09598677
46	427.67	209	647	1.006	1.63026277	1.665	0.09598677
47	427.67	209	647	1.006	1.63026277	1.665	0.09598677
48	427.67	209	647	1.006	1.63026277	1.665	0.09598677
49	427.67	209	647	1.006	1.63026277	1.665	0.09598677
50	427.67	209	647	1.006	1.63026277	1.665	0.09598677
51	427.67	209	647	1.006	1.63026277	1.665	0.09598677
52	427.67	209	647	1.006	1.63026277	1.665	0.09598677
53	427.67	209	647	1.006	1.63026277	1.665	0.09598677
54	427.67	209	647	1.006	1.63026277	1.665	0.09598677
55	427.67	209	647	1.006	1.63026277	1.665	0.09598677
56	427.67	209	647	1.006	1.63026277	1.665	0.09598677
57	427.67	209	647	1.006	1.63026277	1.665	0.09598677
58	427.67	209	647	1.006	1.63026277	1.665	0.09598677
59	427.67	209	647	1.006	1.63026277	1.665	0.09598677
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3	427.67	209	647	1.006	1.63026277	1.665	0.09598677
4	427.67	209	647	1.006	1.63026277	1.665	0.09598677
5	427.67	209	647	1.006	1.63026277	1.665	0.09598677
6	427.67	209	647	1.006	1.63026277	1.665	0.09598677
7	427.67	209	647	1.006	1.63026277	1.665	0.09598677
8	427.67	209	647	1.006	1.63026277	1.665	0.09598677
9	427.67	209	647	1.006	1.63026277	1.665	0.09598677
10	427.67	209	647	1.006	1.63026277	1.665	0.09598677
11	427.67	209	647	1.006	1.63026277	1.665	0.09598677
12	427.67	209	647	1.006	1.63026277	1.665	0.09598677
13	427.67	209	647	1.006	1.63026277	1.665	0.09598677
14	427.67	209	647	1.006	1.63026277	1.665	0.09598677
15	427.67	209	647	1.006	1.63026277	1.665	0.09598677
16	427.67	209	647	1.006	1.63026277	1.665	0.09598677
17	427.67	209	647	1.006	1.63026277	1.665	0.09598677
18	427.67	209	647	1.006	1.63026277	1.665	0.09598677
19	427.67	209	647	1.006	1.63026277	1.665	0.09598677
20	427.67	209	647	1.006	1.63026277	1.665	0.09598677
21	427.67	209	647	1.006	1.63026277	1.665	0.09598677
22	427.67	209	647	1.006	1.63026277	1.665	0.09598677
23	427.67	209	647	1.006	1.63026277	1.665	0.09598677
24	427.67	209	647	1.006	1.63026277	1.665	0.09598677
25	427.67	209	647	1.006	1.63026277	1.665	0.09598677
26	427.67	209	647	1.006	1.63026277	1.665	0.09598677
27	427.67	209	647	1.006	1.63026277	1.665	0.09598677
28	427.67	209	647	1.006	1.63026277	1.665	0.09598677
29	427.67	209	647	1.006	1.63026277	1.665	0.09598677
30	427.67	209	647	1.006	1.63026277	1.665	0.09598677
31	427.67	209	647	1.006	1.63026277	1.665	0.09598677
32	427.67	209	647	1.006	1.63026277	1.665	0.09598677
33	427.67	209	647	1.006	1.63026277	1.665	0.09598677
34	429.78	210	649	1.006	1.62782915	1.66	0.0969
35	271.66	134	409	1.003	1.60986784	1.04	NA
36	271.66	134	409	1.003	1.60986784	1.04	NA
37							
38	239.51	122	357	1.003	1.54904293	0.982	NA
39	239.1	122	356	1.003	1.54499609	0.979	NA
40	239.1	122	356	1.003	1.54499609	0.979	NA
41	239.1	122	356	1.003	1.54499609	0.979	NA
42	239.1	122	356	1.003	1.54499609	0.979	NA
43	239.1	122	356	1.003	1.54499609	0.979	NA
44	239.1	122	356	1.003	1.54499609	0.979	NA
45	239.1	122	356	1.003	1.54499609	0.979	NA
46	239.1	122	356	1.003	1.54499609	0.979	NA
47	239.1	122	356	1.003	1.54499609	0.979	NA
48	239.1	122	356	1.003	1.54499609	0.979	NA
49	239.1	122	356	1.003	1.54499609	0.979	NA
50	239.1	122	356	1.003	1.54499609	0.979	NA
51	239.1	122	356	1.003	1.54499609	0.979	NA
52	239.1	122	356	1.003	1.54499609	0.979	NA
53	239.1	122	356	1.003	1.54499609	0.979	NA
54	239.1	122	356	1.003	1.54499609	0.979	NA
55	239.1	122	356	1.003	1.54499609	0.979	NA
56	239.1	122	356	1.003	1.54499609	0.979	NA
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58	239.1	122	356	1.003	1.54499609	0.979	NA
59	239.1	122	356	1.003	1.54499609	0.979	NA
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2							
3	239.1	122	356	1.003	1.54499609	0.979	NA
4	239.1	122	356	1.003	1.54499609	0.979	NA
5	239.1	122	356	1.003	1.54499609	0.979	NA
6	239.1	122	356	1.003	1.54499609	0.979	NA
7	239.1	122	356	1.003	1.54499609	0.979	NA
8	239.1	122	356	1.003	1.54499609	0.979	NA
9	239.1	122	356	1.003	1.54499609	0.979	NA
10	239.1	122	356	1.003	1.54499609	0.979	NA
11	239.1	122	356	1.003	1.54499609	0.979	NA
12	239.1	122	356	1.003	1.54499609	0.979	NA
13	239.1	122	356	1.003	1.54499609	0.979	NA
14	239.1	122	356	1.003	1.54499609	0.979	NA
15	239.1	122	356	1.003	1.54499609	0.979	NA
16	239.1	122	356	1.003	1.54499609	0.979	NA
17	239.1	122	356	1.003	1.54499609	0.979	NA
18	239.1	122	356	1.003	1.54499609	0.979	NA
19	239.1	122	356	1.003	1.54499609	0.979	NA
20	239.1	122	356	1.003	1.54499609	0.979	NA
21	239.1	122	356	1.003	1.54499609	0.979	NA
22	239.1	122	356	1.003	1.54499609	0.979	NA
23	239.1	122	356	1.003	1.54499609	0.979	NA
24	239.1	122	356	1.003	1.54499609	0.979	NA
25	239.1	122	356	1.003	1.54499609	0.979	NA
26	239.1	122	356	1.003	1.54499609	0.979	NA
27	239.1	122	356	1.003	1.54499609	0.979	NA
28	239.1	122	356	1.003	1.54499609	0.979	NA
29	239.1	122	356	1.003	1.54499609	0.979	NA
30	239.1	122	356	1.003	1.54499609	0.979	NA
31	239.1	122	356	1.003	1.54499609	0.979	NA
32	239.1	122	356	1.003	1.54499609	0.979	NA
33	239.1	122	356	1.003	1.54499609	0.979	NA
34	239.1	122	356	1.003	1.54499609	0.979	NA
35	239.1	122	356	1.003	1.54499609	0.979	NA
36	239.1	122	356	1.003	1.54499609	0.979	NA
37	239.1	122	356	1.003	1.54499609	0.979	NA
38	239.1	122	356	1.003	1.54499609	0.979	NA
39	239.1	122	356	1.003	1.54499609	0.979	NA
40	239.1	122	356	1.003	1.54499609	0.979	NA
41	239.1	122	356	1.003	1.54499609	0.979	NA
42	239.1	122	356	1.003	1.54499609	0.979	NA
43	239.1	122	356	1.003	1.54499609	0.979	NA
44	239.1	122	356	1.003	1.54499609	0.979	NA
45	239.1	122	356	1.003	1.54499609	0.979	NA
46	239.1	122	356	1.003	1.54499609	0.979	NA
47	239.1	122	356	1.003	1.54499609	0.979	NA
48	239.1	122	356	1.003	1.54499609	0.979	NA
49	239.1	122	356	1.003	1.54499609	0.979	NA
50	239.1	122	356	1.003	1.54499609	0.979	NA
51	239.1	122	356	1.003	1.54499609	0.979	NA
52	239.1	122	356	1.003	1.54499609	0.979	NA
53	239.1	122	356	1.003	1.54499609	0.979	NA
54	239.1	122	356	1.003	1.54499609	0.979	NA
55	239.1	122	356	1.003	1.54499609	0.979	NA
56	239.1	122	356	1.003	1.54499609	0.979	NA
57	239.78	123	357	1.003	1.53726576	0.975	NA
58	71.94	38	106	1.005	1.47999294	1.516	0.12940383
59							
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3	71.94	38	106	1.005	1.47999294	1.516	0.12940383
4	71.94	38	106	1.005	1.47999294	1.516	0.12940383
5	327.38	184	470	1.004	1.35295499	1.251	0.21108201
6	327.38	184	470	1.004	1.35295499	1.251	0.21108201
7	311.89	176	448	1.004	1.3479233	1.249	0.21180156
8	311.89	176	448	1.004	1.3479233	1.249	0.21180156
9	311.89	176	448	1.004	1.3479233	1.249	0.21180156
10	311.89	176	448	1.004	1.3479233	1.249	0.21180156
11	311.89	176	448	1.004	1.3479233	1.249	0.21180156
12	311.89	176	448	1.004	1.3479233	1.249	0.21180156
13	311.89	176	448	1.004	1.3479233	1.249	0.21180156
14	275.68	158	393	1.004	1.31460475	1.205	0.22830595
15	275.6	158	393	1.004	1.31460475	1.204	0.22849876
16	275.6	158	393	1.004	1.31460475	1.204	0.22849876
17	275.6	158	393	1.004	1.31460475	1.204	0.22849876
18	275.6	158	393	1.004	1.31460475	1.204	0.22849876
19	275.6	158	393	1.004	1.31460475	1.204	0.22849876
20	275.6	158	393	1.004	1.31460475	1.204	0.22849876
21	275.6	158	393	1.004	1.31460475	1.204	0.22849876
22	275.6	158	393	1.004	1.31460475	1.204	0.22849876
23	275.6	158	393	1.004	1.31460475	1.204	0.22849876
24	275.6	158	393	1.004	1.31460475	1.204	0.22849876
25	275.6	158	393	1.004	1.31460475	1.204	0.22849876
26	275.6	158	393	1.004	1.31460475	1.204	0.22849876
27	275.6	158	393	1.004	1.31460475	1.204	0.22849876
28	275.6	158	393	1.004	1.31460475	1.204	0.22849876
29	275.6	158	393	1.004	1.31460475	1.204	0.22849876
30	275.6	158	393	1.004	1.31460475	1.204	0.22849876
31	275.6	158	393	1.004	1.31460475	1.204	0.22849876
32	275.6	158	393	1.004	1.31460475	1.204	0.22849876
33	275.6	158	393	1.004	1.31460475	1.204	0.22849876
34	275.6	158	393	1.004	1.31460475	1.204	0.22849876
35	275.6	158	393	1.004	1.31460475	1.204	0.22849876
36	275.6	158	393	1.004	1.31460475	1.204	0.22849876
37	275.6	158	393	1.004	1.31460475	1.204	0.22849876
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40	275.6	158	393	1.004	1.31460475	1.204	0.22849876
41	275.6	158	393	1.004	1.31460475	1.204	0.22849876
42	275.6	158	393	1.004	1.31460475	1.204	0.22849876
43	260.91	151	371	1.004	1.29687064	1.192	0.23328097
44	260.91	151	371	1.004	1.29687064	1.192	0.23328097
45	260.91	151	371	1.004	1.29687064	1.192	0.23328097
46	260.91	151	371	1.004	1.29687064	1.192	0.23328097
47	260.91	151	371	1.004	1.29687064	1.192	0.23328097
48	260.91	151	371	1.004	1.29687064	1.192	0.23328097
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3	260.91	151	371	1.004	1.29687064	1.192	0.23328097
4	260.91	151	371	1.004	1.29687064	1.192	0.23328097
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27	260.91	151	371	1.004	1.29687064	1.192	0.23328097
28	81.33	48	115	1.003	1.26052755	1.05	0.29377339
29	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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41	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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43	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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59	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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3	81.33	48	115	1.003	1.26052755	1.05	0.29377339
4	81.33	48	115	1.003	1.26052755	1.05	0.29377339
5	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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8	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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13	81.33	48	115	1.003	1.26052755	1.05	0.29377339
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16	81.33	48	115	1.003	1.26052755	1.05	0.29377339
17	81.33	48	115	1.003	1.26052755	1.05	0.29377339
18	81.33	48	115	1.003	1.26052755	1.05	0.29377339
19	81.33	48	115	1.003	1.26052755	1.05	0.29377339
20	81.33	48	115	1.003	1.26052755	1.05	0.29377339
21	81.33	48	115	1.003	1.26052755	1.05	0.29377339
22	81.33	48	115	1.003	1.26052755	1.05	0.29377339
23	81.33	48	115	1.003	1.26052755	1.05	0.29377339
24	81.33	48	115	1.003	1.26052755	1.05	0.29377339
25	81.33	48	115	1.003	1.26052755	1.05	0.29377339
26	81.33	48	115	1.003	1.26052755	1.05	0.29377339
27	81.33	48	115	1.003	1.26052755	1.05	0.29377339
28	105.39	63	148	1.004	1.23217344	1.154	0.24859571
29	105.39	63	148	1.004	1.23217344	1.154	0.24859571
30	105.39	63	148	1.004	1.23217344	1.154	0.24859571
31	105.39	63	148	1.004	1.23217344	1.154	0.24859571
32	105.39	63	148	1.004	1.23217344	1.154	0.24859571
33	105.39	63	148	1.004	1.23217344	1.154	0.24859571
34	105.39	63	148	1.004	1.23217344	1.154	0.24859571
35	37.95	23	54	1.003	1.23132555	1.058	0.28985108
36	37.95	23	54	1.003	1.23132555	1.058	0.28985108
37	37.95	23	54	1.003	1.23132555	1.058	0.28985108
38	37.95	23	54	1.003	1.23132555	1.058	0.28985108
39	37.95	23	54	1.003	1.23132555	1.058	0.28985108
40	37.95	23	54	1.003	1.23132555	1.058	0.28985108
41	37.95	23	54	1.003	1.23132555	1.058	0.28985108
42	37.95	23	54	1.003	1.23132555	1.058	0.28985108
43	37.95	23	54	1.003	1.23132555	1.058	0.28985108
44	37.95	23	54	1.003	1.23132555	1.058	0.28985108
45	37.95	23	54	1.003	1.23132555	1.058	0.28985108
46	37.95	23	54	1.003	1.23132555	1.058	0.28985108
47	37.95	23	54	1.003	1.23132555	1.058	0.28985108
48	64.64	41	88	1.002	1.10187961	0.788	0.43061147
49	64.57	41	88	1.002	1.10187961	0.786	0.43163334
50	64.57	41	88	1.002	1.10187961	0.786	0.43163334
51	64.57	41	88	1.002	1.10187961	0.786	0.43163334
52	64.57	41	88	1.002	1.10187961	0.786	0.43163334
53	64.57	41	88	1.002	1.10187961	0.786	0.43163334
54	64.57	41	88	1.002	1.10187961	0.786	0.43163334
55	64.57	41	88	1.002	1.10187961	0.786	0.43163334
56	64.57	41	88	1.002	1.10187961	0.786	0.43163334
57	64.57	41	88	1.002	1.10187961	0.786	0.43163334
58	64.57	41	88	1.002	1.10187961	0.786	0.43163334
59	64.57	41	88	1.002	1.10187961	0.786	0.43163334
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3	522.29	336	709	1.003	1.07732439	1.064	0.28713039
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5	522.29	336	709	1.003	1.07732439	1.064	0.28713039
6	522.29	336	709	1.003	1.07732439	1.064	0.28713039
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19	522.29	336	709	1.003	1.07732439	1.064	0.28713039
20	522.29	336	709	1.003	1.07732439	1.064	0.28713039
21	522.29	336	709	1.003	1.07732439	1.064	0.28713039
22	524.96	338	712	1.003	1.07485399	1.063	0.28783915
23	524.96	338	712	1.003	1.07485399	1.063	0.28783915
24	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
25	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
26	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
27	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
28	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
29	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
30	3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
31	3596.89	2357	4837	1.004	1.03716078	1.106	0.26866729
32	3596.89	2357	4837	1.004	1.03716078	1.106	0.26866729
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43	3596.89	2357	4837	1.004	1.03716078	1.106	0.26866729
44	374.21	246	503	1.003	1.03190008	0.99	0.32194986
45	374.21	246	503	1.003	1.03190008	0.99	0.32194986
46	374.21	246	503	1.003	1.03190008	0.99	0.32194986
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17	374.21	246	503	1.003	1.03190008	0.99	0.32194986
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27	374.21	246	503	1.003	1.03190008	0.99	0.32194986
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30	374.21	246	503	1.003	1.03190008	0.99	0.32194986
31	374.21	246	503	1.003	1.03190008	0.99	0.32194986
32	5686.85	3748	7625	1.003	1.02461638	0.895	0.37066403
33	5686.85	3748	7625	1.003	1.02461638	0.895	0.37066403
34	5686.85	3748	7625	1.003	1.02461638	0.895	0.37066403
35	5686.85	3748	7625	1.003	1.02461638	0.895	0.37066403
36	5686.85	3748	7625	1.003	1.02461638	0.895	0.37066403
37	405.27	272	539	1.003	0.98667862	0.954	0.33999601
38	405.27	272	539	1.003	0.98667862	0.954	0.33999601
39	405.27	272	539	1.003	0.98667862	0.954	0.33999601
40	405.27	272	539	1.003	0.98667862	0.954	0.33999601
41	405.27	272	539	1.003	0.98667862	0.954	0.33999601
42	405.27	272	539	1.003	0.98667862	0.954	0.33999601
43	405.27	272	539	1.003	0.98667862	0.954	0.33999601
44	405.27	272	539	1.003	0.98667862	0.954	0.33999601
45	405.27	272	539	1.003	0.98667862	0.954	0.33999601
46	405.27	272	539	1.003	0.98667862	0.954	0.33999601
47	405.27	272	539	1.003	0.98667862	0.954	0.33999601
48	405.27	272	539	1.003	0.98667862	0.954	0.33999601
49	54.95	37	73	1.003	0.98037119	1.018	0.30886289
50	54.95	37	73	1.003	0.98037119	1.018	0.30886289
51	54.95	37	73	1.003	0.98037119	1.018	0.30886289
52	54.95	37	73	1.003	0.98037119	1.018	0.30886289
53	54.95	37	73	1.003	0.98037119	1.018	0.30886289
54	54.95	37	73	1.003	0.98037119	1.018	0.30886289
55	54.95	37	73	1.003	0.98037119	1.018	0.30886289
56	54.95	37	73	1.003	0.98037119	1.018	0.30886289
57	54.95	37	73	1.003	0.98037119	1.018	0.30886289
58	54.95	37	73	1.003	0.98037119	1.018	0.30886289
59	54.95	37	73	1.003	0.98037119	1.018	0.30886289
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3	58.39	40	76	1.003	0.92599942	0.899	0.36853809
4	58.39	40	76	1.003	0.92599942	0.899	0.36853809
5	58.39	40	76	1.003	0.92599942	0.899	0.36853809
6	58.39	40	76	1.003	0.92599942	0.899	0.36853809
7	58.39	40	76	1.003	0.92599942	0.899	0.36853809
8	58.39	40	76	1.003	0.92599942	0.899	0.36853809
9	58.39	40	76	1.003	0.92599942	0.899	0.36853809
10	58.39	40	76	1.003	0.92599942	0.899	0.36853809
11	58.39	40	76	1.003	0.92599942	0.899	0.36853809
12	58.39	40	76	1.003	0.92599942	0.899	0.36853809
13	58.39	40	76	1.003	0.92599942	0.899	0.36853809
14	58.39	40	76	1.003	0.92599942	0.899	0.36853809
15	58.39	40	76	1.003	0.92599942	0.899	0.36853809
16	58.39	40	76	1.003	0.92599942	0.899	0.36853809
17	58.39	40	76	1.003	0.92599942	0.899	0.36853809
18	58.39	40	76	1.003	0.92599942	0.899	0.36853809
19	58.39	40	76	1.003	0.92599942	0.899	0.36853809
20	58.39	40	76	1.003	0.92599942	0.899	0.36853809
21	58.39	40	76	1.003	0.92599942	0.899	0.36853809
22	58.39	40	76	1.003	0.92599942	0.899	0.36853809
23	59.89	42	78	1.003	0.8930848	0.873	0.38252063
24	608.24	427	790	1.004	0.88761658	1.036	0.30034281
25	608.24	427	790	1.004	0.88761658	1.036	0.30034281
26	608.24	427	790	1.004	0.88761658	1.036	0.30034281
27	608.24	427	790	1.004	0.88761658	1.036	0.30034281
28	608.24	427	790	1.004	0.88761658	1.036	0.30034281
29	608.24	427	790	1.004	0.88761658	1.036	0.30034281
30	608.24	427	790	1.004	0.88761658	1.036	0.30034281
31	606.25	426	786	1.004	0.88367588	1.032	0.30225578
32	606.25	426	786	1.004	0.88367588	1.032	0.30225578
33	606.25	426	786	1.004	0.88367588	1.032	0.30225578
34	606.25	426	786	1.004	0.88367588	1.032	0.30225578
35	606.25	426	786	1.004	0.88367588	1.032	0.30225578
36	606.25	426	786	1.004	0.88367588	1.032	0.30225578
37	606.25	426	786	1.004	0.88367588	1.032	0.30225578
38	606.25	426	786	1.004	0.88367588	1.032	0.30225578
39	606.25	426	786	1.004	0.88367588	1.032	0.30225578
40	606.25	426	786	1.004	0.88367588	1.032	0.30225578
41	606.25	426	786	1.004	0.88367588	1.032	0.30225578
42	606.25	426	786	1.004	0.88367588	1.032	0.30225578
43	606.25	426	786	1.004	0.88367588	1.032	0.30225578
44	606.25	426	786	1.004	0.88367588	1.032	0.30225578
45	606.25	426	786	1.004	0.88367588	1.032	0.30225578
46	606.25	426	786	1.004	0.88367588	1.032	0.30225578
47	606.25	426	786	1.004	0.88367588	1.032	0.30225578
48	606.25	426	786	1.004	0.88367588	1.032	0.30225578
49	606.25	426	786	1.004	0.88367588	1.032	0.30225578
50	606.25	426	786	1.004	0.88367588	1.032	0.30225578
51	606.25	426	786	1.004	0.88367588	1.032	0.30225578
52	606.25	426	786	1.004	0.88367588	1.032	0.30225578
53	606.25	426	786	1.004	0.88367588	1.032	0.30225578
54	606.25	426	786	1.004	0.88367588	1.032	0.30225578
55	606.25	426	786	1.004	0.88367588	1.032	0.30225578
56	606.25	426	786	1.004	0.88367588	1.032	0.30225578
57	606.25	426	786	1.004	0.88367588	1.032	0.30225578
58	606.25	426	786	1.004	0.88367588	1.032	0.30225578
59	606.25	426	786	1.004	0.88367588	1.032	0.30225578
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3	606.25	426	786	1.004	0.88367588	1.032	0.30225578
4	606.25	426	786	1.004	0.88367588	1.032	0.30225578
5	606.25	426	786	1.004	0.88367588	1.032	0.30225578
6	606.25	426	786	1.004	0.88367588	1.032	0.30225578
7	606.25	426	786	1.004	0.88367588	1.032	0.30225578
8	606.25	426	786	1.004	0.88367588	1.032	0.30225578
9	606.25	426	786	1.004	0.88367588	1.032	0.30225578
10	606.25	426	786	1.004	0.88367588	1.032	0.30225578
11	606.25	426	786	1.004	0.88367588	1.032	0.30225578
12	606.25	426	786	1.004	0.88367588	1.032	0.30225578
13	606.25	426	786	1.004	0.88367588	1.032	0.30225578
14	606.25	426	786	1.004	0.88367588	1.032	0.30225578
15	606.25	426	786	1.004	0.88367588	1.032	0.30225578
16	606.25	426	786	1.004	0.88367588	1.032	0.30225578
17	606.25	426	786	1.004	0.88367588	1.032	0.30225578
18	606.25	426	786	1.004	0.88367588	1.032	0.30225578
19	50.96	36	65	1.003	0.85244281	0.919	0.35816764
20	50.96	36	65	1.003	0.85244281	0.919	0.35816764
21	50.96	36	65	1.003	0.85244281	0.919	0.35816764
22	50.96	36	65	1.003	0.85244281	0.919	0.35816764
23	50.96	36	65	1.003	0.85244281	0.919	0.35816764
24	50.96	36	65	1.003	0.85244281	0.919	0.35816764
25	50.96	36	65	1.003	0.85244281	0.919	0.35816764
26	50.96	36	65	1.003	0.85244281	0.919	0.35816764
27	50.96	36	65	1.003	0.85244281	0.919	0.35816764
28	50.96	36	65	1.003	0.85244281	0.919	0.35816764
29	50.96	36	65	1.003	0.85244281	0.919	0.35816764
30	50.96	36	65	1.003	0.85244281	0.919	0.35816764
31	50.96	36	65	1.003	0.85244281	0.919	0.35816764
32	259.42	187	332	1.002	0.82814497	0.76	0.44711115
33	91.75	67	117	1.003	0.80427553	0.816	0.41436939
34	90.75	67	114	1.002	0.76680082	0.779	0.4360549
35	90.75	67	114	1.002	0.76680082	0.779	0.4360549
36	90.75	67	114	1.002	0.76680082	0.779	0.4360549
37	90.75	67	114	1.002	0.76680082	0.779	0.4360549
38	48.29	36	61	1.001	0.76081234	0.561	NA
39	48.29	36	61	1.001	0.76081234	0.561	NA
40	52.03	39	66	1.002	0.7589919	0.759	0.44794427
41	52.03	39	66	1.002	0.7589919	0.759	0.44794427
42	52.03	39	66	1.002	0.7589919	0.759	0.44794427
43	52.03	39	66	1.002	0.7589919	0.759	0.44794427
44	52.03	39	66	1.002	0.7589919	0.759	0.44794427
45	52.03	39	66	1.002	0.7589919	0.759	0.44794427
46	52.03	39	66	1.002	0.7589919	0.759	0.44794427
47	91.19	68	115	1.002	0.75802721	0.78	0.43556478
48	91.35	68	115	1.002	0.75802721	0.772	0.43997876
49	163.67	122	205	1.002	0.74874276	0.766	0.44342806
50	163.67	122	205	1.002	0.74874276	0.766	0.44342806
51	163.67	122	205	1.002	0.74874276	0.766	0.44342806
52	163.67	122	205	1.002	0.74874276	0.766	0.44342806
53	163.67	122	205	1.002	0.74874276	0.766	0.44342806
54	163.67	122	205	1.002	0.74874276	0.766	0.44342806
55	163.67	122	205	1.002	0.74874276	0.766	0.44342806
56	163.67	122	205	1.002	0.74874276	0.766	0.44342806
57	163.67	122	205	1.002	0.74874276	0.766	0.44342806
58	163.67	122	205	1.002	0.74874276	0.766	0.44342806
59	163.67	122	205	1.002	0.74874276	0.766	0.44342806
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3	163.67	122	205	1.002	0.74874276	0.766	0.44342806
4	163.67	122	205	1.002	0.74874276	0.766	0.44342806
5	163.67	122	205	1.002	0.74874276	0.766	0.44342806
6	163.67	122	205	1.002	0.74874276	0.766	0.44342806
7	163.67	122	205	1.002	0.74874276	0.766	0.44342806
8	163.67	122	205	1.002	0.74874276	0.766	0.44342806
9	163.67	122	205	1.002	0.74874276	0.766	0.44342806
10	163.67	122	205	1.002	0.74874276	0.766	0.44342806
11	163.67	122	205	1.002	0.74874276	0.766	0.44342806
12	163.67	122	205	1.002	0.74874276	0.766	0.44342806
13	163.67	122	205	1.002	0.74874276	0.766	0.44342806
14	163.67	122	205	1.002	0.74874276	0.766	0.44342806
15	163.67	122	205	1.002	0.74874276	0.766	0.44342806
16	163.67	122	205	1.002	0.74874276	0.766	0.44342806
17	163.67	122	205	1.002	0.74874276	0.766	0.44342806
18	163.67	122	205	1.002	0.74874276	0.766	0.44342806
19	163.67	122	205	1.002	0.74874276	0.766	0.44342806
20	163.67	122	205	1.002	0.74874276	0.766	0.44342806
21	163.67	122	205	1.002	0.74874276	0.766	0.44342806
22	163.67	122	205	1.002	0.74874276	0.766	0.44342806
23	163.67	122	205	1.002	0.74874276	0.766	0.44342806
24	163.67	122	205	1.002	0.74874276	0.766	0.44342806
25	163.67	122	205	1.002	0.74874276	0.766	0.44342806
26	163.67	122	205	1.002	0.74874276	0.766	0.44342806
27	163.67	122	205	1.002	0.74874276	0.766	0.44342806
28	163.67	122	205	1.002	0.74874276	0.766	0.44342806
29	163.67	122	205	1.002	0.74874276	0.766	0.44342806
30	163.67	122	205	1.002	0.74874276	0.766	0.44342806
31	163.67	122	205	1.002	0.74874276	0.766	0.44342806
32	163.67	122	205	1.002	0.74874276	0.766	0.44342806
33	163.67	122	205	1.002	0.74874276	0.766	0.44342806
34	163.67	122	205	1.002	0.74874276	0.766	0.44342806
35	163.67	122	205	1.002	0.74874276	0.766	0.44342806
36	89.27	67	112	1.002	0.74126573	0.763	0.44559638
37	89.27	67	112	1.002	0.74126573	0.763	0.44559638
38	89.27	67	112	1.002	0.74126573	0.763	0.44559638
39	89.27	67	112	1.002	0.74126573	0.763	0.44559638
40	89.27	67	112	1.002	0.74126573	0.763	0.44559638
41	89.27	67	112	1.002	0.74126573	0.763	0.44559638
42	89.27	67	112	1.002	0.74126573	0.763	0.44559638
43	89.27	67	112	1.002	0.74126573	0.763	0.44559638
44	89.27	67	112	1.002	0.74126573	0.763	0.44559638
45	89.27	67	112	1.002	0.74126573	0.763	0.44559638
46	89.27	67	112	1.002	0.74126573	0.763	0.44559638
47	89.27	67	112	1.002	0.74126573	0.763	0.44559638
48	89.27	67	112	1.002	0.74126573	0.763	0.44559638
49	89.27	67	112	1.002	0.74126573	0.763	0.44559638
50	89.27	67	112	1.002	0.74126573	0.763	0.44559638
51	89.27	67	112	1.002	0.74126573	0.763	0.44559638
52	89.27	67	112	1.002	0.74126573	0.763	0.44559638
53	89.27	67	112	1.002	0.74126573	0.763	0.44559638
54	89.27	67	112	1.002	0.74126573	0.763	0.44559638
55	288.94	218	360	1.003	0.72366877	0.867	0.38601358
56	288.94	218	360	1.003	0.72366877	0.867	0.38601358
57	288.94	218	360	1.003	0.72366877	0.867	0.38601358
58	288.94	218	360	1.003	0.72366877	0.867	0.38601358
59	288.94	218	360	1.003	0.72366877	0.867	0.38601358
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3	288.94	218	360	1.003	0.72366877	0.867	0.38601358
4	288.94	218	360	1.003	0.72366877	0.867	0.38601358
5	288.94	218	360	1.003	0.72366877	0.867	0.38601358
6	288.94	218	360	1.003	0.72366877	0.867	0.38601358
7	288.94	218	360	1.003	0.72366877	0.867	0.38601358
8	288.94	218	360	1.003	0.72366877	0.867	0.38601358
9	288.94	218	360	1.003	0.72366877	0.867	0.38601358
10	288.94	218	360	1.003	0.72366877	0.867	0.38601358
11	288.94	218	360	1.003	0.72366877	0.867	0.38601358
12	288.94	218	360	1.003	0.72366877	0.867	0.38601358
13	288.94	218	360	1.003	0.72366877	0.867	0.38601358
14	288.94	218	360	1.003	0.72366877	0.867	0.38601358
15	288.94	218	360	1.003	0.72366877	0.867	0.38601358
16	288.94	218	360	1.003	0.72366877	0.867	0.38601358
17	288.94	218	360	1.003	0.72366877	0.867	0.38601358
18	288.94	218	360	1.003	0.72366877	0.867	0.38601358
19	288.94	218	360	1.003	0.72366877	0.867	0.38601358
20	288.94	218	360	1.003	0.72366877	0.867	0.38601358
21	288.94	218	360	1.003	0.72366877	0.867	0.38601358
22	288.94	218	360	1.003	0.72366877	0.867	0.38601358
23	288.94	218	360	1.003	0.72366877	0.867	0.38601358
24	288.94	218	360	1.003	0.72366877	0.867	0.38601358
25	288.94	218	360	1.003	0.72366877	0.867	0.38601358
26	288.94	218	360	1.003	0.72366877	0.867	0.38601358
27	288.94	218	360	1.003	0.72366877	0.867	0.38601358
28	288.94	218	360	1.003	0.72366877	0.867	0.38601358
29	288.94	218	360	1.003	0.72366877	0.867	0.38601358
30	288.94	218	360	1.003	0.72366877	0.867	0.38601358
31	288.94	218	360	1.003	0.72366877	0.867	0.38601358
32	52.48	40	65	1.002	0.70043972	0.566	NA
33	52.19	40	64	1.002	0.67807191	0.738	0.46037501
34	52.19	40	64	1.002	0.67807191	0.738	0.46037501
35	76.76	59	94	1.003	0.6719458	0.778	0.43664989
36	76.76	59	94	1.003	0.6719458	0.778	0.43664989
37	76.76	59	94	1.003	0.6719458	0.778	0.43664989
38	76.76	59	94	1.003	0.6719458	0.778	0.43664989
39	76.76	59	94	1.003	0.6719458	0.778	0.43664989
40	76.76	59	94	1.003	0.6719458	0.778	0.43664989
41	76.76	59	94	1.003	0.6719458	0.778	0.43664989
42	76.76	59	94	1.003	0.6719458	0.778	0.43664989
43	76.76	59	94	1.003	0.6719458	0.778	0.43664989
44	76.76	59	94	1.003	0.6719458	0.778	0.43664989
45	76.76	59	94	1.003	0.6719458	0.778	0.43664989
46	76.76	59	94	1.003	0.6719458	0.778	0.43664989
47	76.76	59	94	1.003	0.6719458	0.778	0.43664989
48	76.76	59	94	1.003	0.6719458	0.778	0.43664989
49	76.76	59	94	1.003	0.6719458	0.778	0.43664989
50	76.76	59	94	1.003	0.6719458	0.778	0.43664989
51	76.76	59	94	1.003	0.6719458	0.778	0.43664989
52	76.76	59	94	1.003	0.6719458	0.778	0.43664989
53	76.76	59	94	1.003	0.6719458	0.778	0.43664989
54	76.76	59	94	1.003	0.6719458	0.778	0.43664989
55	76.76	59	94	1.003	0.6719458	0.778	0.43664989
56	76.76	59	94	1.003	0.6719458	0.778	0.43664989
57	76.76	59	94	1.003	0.6719458	0.778	0.43664989
58	76.76	59	94	1.003	0.6719458	0.778	0.43664989
59	76.76	59	94	1.003	0.6719458	0.778	0.43664989
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3	76.76	59	94	1.003	0.6719458	0.778	0.43664989
4	76.76	59	94	1.003	0.6719458	0.778	0.43664989
5	43.71	34	53	1.002	0.64045761	0.617	0.53710245
6	43.71	34	53	1.002	0.64045761	0.617	0.53710245
7	43.71	34	53	1.002	0.64045761	0.617	0.53710245
8	43.71	34	53	1.002	0.64045761	0.617	0.53710245
9	43.71	34	53	1.002	0.64045761	0.617	0.53710245
10	43.71	34	53	1.002	0.64045761	0.617	0.53710245
11	43.71	34	53	1.002	0.64045761	0.617	0.53710245
12	43.71	34	53	1.002	0.64045761	0.617	0.53710245
13	43.71	34	53	1.002	0.64045761	0.617	0.53710245
14	43.71	34	53	1.002	0.64045761	0.617	0.53710245
15	43.71	34	53	1.002	0.64045761	0.617	0.53710245
16	43.71	34	53	1.002	0.64045761	0.617	0.53710245
17	43.71	34	53	1.002	0.64045761	0.617	0.53710245
18	43.71	34	53	1.002	0.64045761	0.617	0.53710245
19	43.71	34	53	1.002	0.64045761	0.617	0.53710245
20	43.71	34	53	1.002	0.64045761	0.617	0.53710245
21	43.71	34	53	1.002	0.64045761	0.617	0.53710245
22	43.71	34	53	1.002	0.64045761	0.617	0.53710245
23	43.71	34	53	1.002	0.64045761	0.617	0.53710245
24	43.71	34	53	1.002	0.64045761	0.617	0.53710245
25	43.71	34	53	1.002	0.64045761	0.617	0.53710245
26	43.71	34	53	1.002	0.64045761	0.617	0.53710245
27	43.71	34	53	1.002	0.64045761	0.617	0.53710245
28	43.71	34	53	1.002	0.64045761	0.617	0.53710245
29	43.71	34	53	1.002	0.64045761	0.617	0.53710245
30	43.71	34	53	1.002	0.64045761	0.617	0.53710245
31	43.71	34	53	1.002	0.64045761	0.617	0.53710245
32	43.71	34	53	1.002	0.64045761	0.617	0.53710245
33	43.71	34	53	1.002	0.64045761	0.617	0.53710245
34	43.71	34	53	1.002	0.64045761	0.617	0.53710245
35	43.71	34	53	1.002	0.64045761	0.617	0.53710245
36	43.71	34	53	1.002	0.64045761	0.617	0.53710245
37	43.71	34	53	1.002	0.64045761	0.617	0.53710245
38	43.71	34	53	1.002	0.64045761	0.617	0.53710245
39	43.71	34	53	1.002	0.64045761	0.617	0.53710245
40	43.71	34	53	1.002	0.64045761	0.617	0.53710245
41	43.71	34	53	1.002	0.64045761	0.617	0.53710245
42	43.71	34	53	1.002	0.64045761	0.617	0.53710245
43	43.71	34	53	1.002	0.64045761	0.617	0.53710245
44	43.71	34	53	1.002	0.64045761	0.617	0.53710245
45	43.71	34	53	1.002	0.64045761	0.617	0.53710245
46	43.71	34	53	1.002	0.64045761	0.617	0.53710245
47	43.71	34	53	1.002	0.64045761	0.617	0.53710245
48	43.71	34	53	1.002	0.64045761	0.617	0.53710245
49	43.71	34	53	1.002	0.64045761	0.617	0.53710245
50	43.71	34	53	1.002	0.64045761	0.617	0.53710245
51	54.95	43	67	1.002	0.63982444	0.58	0.56203146
52	54.95	43	67	1.002	0.63982444	0.58	0.56203146
53	54.95	43	67	1.002	0.63982444	0.58	0.56203146
54	54.95	43	67	1.002	0.63982444	0.58	0.56203146
55	54.95	43	67	1.002	0.63982444	0.58	0.56203146
56	54.95	43	67	1.002	0.63982444	0.58	0.56203146
57	54.95	43	67	1.002	0.63982444	0.58	0.56203146
58	54.95	43	67	1.002	0.63982444	0.58	0.56203146
59	54.95	43	67	1.002	0.63982444	0.58	0.56203146
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4	54.95	43	67	1.002	0.63982444	0.58	0.56203146
5	54.95	43	67	1.002	0.63982444	0.58	0.56203146
6	54.95	43	67	1.002	0.63982444	0.58	0.56203146
7	54.95	43	67	1.002	0.63982444	0.58	0.56203146
8	54.95	43	67	1.002	0.63982444	0.58	0.56203146
9	54.95	43	67	1.002	0.63982444	0.58	0.56203146
10	54.95	43	67	1.002	0.63982444	0.58	0.56203146
11	54.95	43	67	1.002	0.63982444	0.58	0.56203146
12	54.95	43	67	1.002	0.63982444	0.58	0.56203146
13	54.95	43	67	1.002	0.63982444	0.58	0.56203146
14	54.95	43	67	1.002	0.63982444	0.58	0.56203146
15	54.95	43	67	1.002	0.63982444	0.58	0.56203146
16	54.95	43	67	1.002	0.63982444	0.58	0.56203146
17	54.95	43	67	1.002	0.63982444	0.58	0.56203146
18	54.95	43	67	1.002	0.63982444	0.58	0.56203146
19	54.95	43	67	1.002	0.63982444	0.58	0.56203146
20	54.95	43	67	1.002	0.63982444	0.58	0.56203146
21	54.95	43	67	1.002	0.63982444	0.58	0.56203146
22	54.95	43	67	1.002	0.63982444	0.58	0.56203146
23	54.95	43	67	1.002	0.63982444	0.58	0.56203146
24	54.95	43	67	1.002	0.63982444	0.58	0.56203146
25	54.95	43	67	1.002	0.63982444	0.58	0.56203146
26	54.95	43	67	1.002	0.63982444	0.58	0.56203146
27	54.95	43	67	1.002	0.63982444	0.58	0.56203146
28	493.51	387	600	1.003	0.63262893	0.768	0.44251288
29	69.58	55	84	1.002	0.61095771	0.64	0.52222472
30	69.58	55	84	1.002	0.61095771	0.64	0.52222472
31	69.58	55	84	1.002	0.61095771	0.64	0.52222472
32	69.58	55	84	1.002	0.61095771	0.64	0.52222472
33	69.58	55	84	1.002	0.61095771	0.64	0.52222472
34	69.58	55	84	1.002	0.61095771	0.64	0.52222472
35	69.58	55	84	1.002	0.61095771	0.64	0.52222472
36	69.58	55	84	1.002	0.61095771	0.64	0.52222472
37	69.58	55	84	1.002	0.61095771	0.64	0.52222472
38	69.58	55	84	1.002	0.61095771	0.64	0.52222472
39	69.58	55	84	1.002	0.61095771	0.64	0.52222472
40	69.58	55	84	1.002	0.61095771	0.64	0.52222472
41	69.58	55	84	1.002	0.61095771	0.64	0.52222472
42	69.58	55	84	1.002	0.61095771	0.64	0.52222472
43	69.58	55	84	1.002	0.61095771	0.64	0.52222472
44	69.58	55	84	1.002	0.61095771	0.64	0.52222472
45	69.58	55	84	1.002	0.61095771	0.64	0.52222472
46	69.58	55	84	1.002	0.61095771	0.64	0.52222472
47	69.58	55	84	1.002	0.61095771	0.64	0.52222472
48	69.58	55	84	1.002	0.61095771	0.64	0.52222472
49	69.58	55	84	1.002	0.61095771	0.64	0.52222472
50	69.58	55	84	1.002	0.61095771	0.64	0.52222472
51	69.58	55	84	1.002	0.61095771	0.64	0.52222472
52	69.58	55	84	1.002	0.61095771	0.64	0.52222472
53	72.4	57	87	1.002	0.61005348	0.691	0.48947759
54	72.4	57	87	1.002	0.61005348	0.691	0.48947759
55	72.4	57	87	1.002	0.61005348	0.691	0.48947759
56	72.4	57	87	1.002	0.61005348	0.691	0.48947759
57	72.4	57	87	1.002	0.61005348	0.691	0.48947759
58	72.4	57	87	1.002	0.61005348	0.691	0.48947759
59	72.4	57	87	1.002	0.61005348	0.691	0.48947759
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3	72.4	57	87	1.002	0.61005348	0.691	0.48947759
4	72.4	57	87	1.002	0.61005348	0.691	0.48947759
5	72.4	57	87	1.002	0.61005348	0.691	0.48947759
6	72.4	57	87	1.002	0.61005348	0.691	0.48947759
7	72.4	57	87	1.002	0.61005348	0.691	0.48947759
8	72.4	57	87	1.002	0.61005348	0.691	0.48947759
9	72.4	57	87	1.002	0.61005348	0.691	0.48947759
10	72.4	57	87	1.002	0.61005348	0.691	0.48947759
11	72.4	57	87	1.002	0.61005348	0.691	0.48947759
12	72.4	57	87	1.002	0.61005348	0.691	0.48947759
13	72.4	57	87	1.002	0.61005348	0.691	0.48947759
14	72.4	57	87	1.002	0.61005348	0.691	0.48947759
15	72.4	57	87	1.002	0.61005348	0.691	0.48947759
16	72.4	57	87	1.002	0.61005348	0.691	0.48947759
17	72.4	57	87	1.002	0.61005348	0.691	0.48947759
18	72.4	57	87	1.002	0.61005348	0.691	0.48947759
19	72.06	57	87	1.002	0.61005348	0.562	0.5739466
20	72.06	57	87	1.002	0.61005348	0.562	0.5739466
21	72.06	57	87	1.002	0.61005348	0.562	0.5739466
22	72.06	57	87	1.002	0.61005348	0.562	0.5739466
23	72.06	57	87	1.002	0.61005348	0.562	0.5739466
24	72.06	57	87	1.002	0.61005348	0.562	0.5739466
25	72.06	57	87	1.002	0.61005348	0.562	0.5739466
26	72.06	57	87	1.002	0.61005348	0.562	0.5739466
27	72.06	57	87	1.002	0.61005348	0.562	0.5739466
28	468.33	371	566	1.003	0.60938287	0.733	0.46350316
29	468.33	371	566	1.003	0.60938287	0.733	0.46350316
30	134.08	106	161	1.002	0.60299642	0.64	0.52193757
31	134.08	106	161	1.002	0.60299642	0.64	0.52193757
32	72.9	58	88	1.002	0.60145062	0.696	0.48653258
33	1028.87	819	1239	1.002	0.59724083	0.578	0.56345612
34	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
35	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
36	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
37	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
38	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
39	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
40	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
41	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
42	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
43	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
44	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
45	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
46	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
47	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
48	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
49	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
50	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
51	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
52	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
53	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
54	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
55	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
56	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
57	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
58	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
59	1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
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3	548.28	438	659	1.003	0.5893476	0.721	0.47064478
4	548.28	438	659	1.003	0.5893476	0.721	0.47064478
5	548.28	438	659	1.003	0.5893476	0.721	0.47064478
6	548.28	438	659	1.003	0.5893476	0.721	0.47064478
7	548.28	438	659	1.003	0.5893476	0.721	0.47064478
8	548.28	438	659	1.003	0.5893476	0.721	0.47064478
9	548.28	438	659	1.003	0.5893476	0.721	0.47064478
10	548.28	438	659	1.003	0.5893476	0.721	0.47064478
11	548.28	438	659	1.003	0.5893476	0.721	0.47064478
12	548.28	438	659	1.003	0.5893476	0.721	0.47064478
13	548.28	438	659	1.003	0.5893476	0.721	0.47064478
14	548.28	438	659	1.003	0.5893476	0.721	0.47064478
15	548.28	438	659	1.003	0.5893476	0.721	0.47064478
16	548.28	438	659	1.003	0.5893476	0.721	0.47064478
17	548.28	438	659	1.003	0.5893476	0.721	0.47064478
18	548.28	438	659	1.003	0.5893476	0.721	0.47064478
19	548.28	438	659	1.003	0.5893476	0.721	0.47064478
20	548.28	438	659	1.003	0.5893476	0.721	0.47064478
21	548.28	438	659	1.003	0.5893476	0.721	0.47064478
22	548.28	438	659	1.003	0.5893476	0.721	0.47064478
23	548.28	438	659	1.003	0.5893476	0.721	0.47064478
24	548.28	438	659	1.003	0.5893476	0.721	0.47064478
25	548.28	438	659	1.003	0.5893476	0.721	0.47064478
26	548.28	438	659	1.003	0.5893476	0.721	0.47064478
27	67.72	54	81	1.001	0.5849625	0.437	0.66180834
28	67.72	54	81	1.001	0.5849625	0.437	0.66180834
29	67.72	54	81	1.001	0.5849625	0.437	0.66180834
30	67.72	54	81	1.001	0.5849625	0.437	0.66180834
31	67.72	54	81	1.001	0.5849625	0.437	0.66180834
32	67.72	54	81	1.001	0.5849625	0.437	0.66180834
33	67.72	54	81	1.001	0.5849625	0.437	0.66180834
34	67.72	54	81	1.001	0.5849625	0.437	0.66180834
35	67.72	54	81	1.001	0.5849625	0.437	0.66180834
36	67.72	54	81	1.001	0.5849625	0.437	0.66180834
37	67.72	54	81	1.001	0.5849625	0.437	0.66180834
38	67.72	54	81	1.001	0.5849625	0.437	0.66180834
39	67.72	54	81	1.001	0.5849625	0.437	0.66180834
40	67.72	54	81	1.001	0.5849625	0.437	0.66180834
41	67.72	54	81	1.001	0.5849625	0.437	0.66180834
42	67.72	54	81	1.001	0.5849625	0.437	0.66180834
43	67.72	54	81	1.001	0.5849625	0.437	0.66180834
44	67.72	54	81	1.001	0.5849625	0.437	0.66180834
45	67.72	54	81	1.001	0.5849625	0.437	0.66180834
46	67.72	54	81	1.001	0.5849625	0.437	0.66180834
47	67.72	54	81	1.001	0.5849625	0.437	0.66180834
48	67.72	54	81	1.001	0.5849625	0.437	0.66180834
49	67.72	54	81	1.001	0.5849625	0.437	0.66180834
50	67.72	54	81	1.001	0.5849625	0.437	0.66180834
51	67.72	54	81	1.001	0.5849625	0.437	0.66180834
52	67.72	54	81	1.001	0.5849625	0.437	0.66180834
53	67.72	54	81	1.001	0.5849625	0.437	0.66180834
54	67.72	54	81	1.001	0.5849625	0.437	0.66180834
55	67.72	54	81	1.001	0.5849625	0.437	0.66180834
56	67.72	54	81	1.001	0.5849625	0.437	0.66180834
57	67.72	54	81	1.001	0.5849625	0.437	0.66180834
58	67.72	54	81	1.001	0.5849625	0.437	0.66180834
59	67.72	54	81	1.001	0.5849625	0.437	0.66180834
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3	67.72	54	81	1.001	0.5849625	0.437	0.66180834
4	67.72	54	81	1.001	0.5849625	0.437	0.66180834
5	67.72	54	81	1.001	0.5849625	0.437	0.66180834
6	68.75	55	82	1.001	0.57619229	0.433	0.6649149
7	125.01	101	149	1.002	0.56095704	0.61	0.5419706
8	125.01	101	149	1.002	0.56095704	0.61	0.5419706
9	125.01	101	149	1.002	0.56095704	0.61	0.5419706
10	125.01	101	149	1.002	0.56095704	0.61	0.5419706
11	125.01	101	149	1.002	0.56095704	0.61	0.5419706
12	125.01	101	149	1.002	0.56095704	0.61	0.5419706
13	125.01	101	149	1.002	0.56095704	0.61	0.5419706
14	125.01	101	149	1.002	0.56095704	0.61	0.5419706
15	125.01	101	149	1.002	0.56095704	0.61	0.5419706
16	125.01	101	149	1.002	0.56095704	0.61	0.5419706
17	125.01	101	149	1.002	0.56095704	0.61	0.5419706
18	125.01	101	149	1.002	0.56095704	0.61	0.5419706
19	125.01	101	149	1.002	0.56095704	0.61	0.5419706
20	125.01	101	149	1.002	0.56095704	0.61	0.5419706
21	125.01	101	149	1.002	0.56095704	0.61	0.5419706
22	125.01	101	149	1.002	0.56095704	0.61	0.5419706
23	125.01	101	149	1.002	0.56095704	0.61	0.5419706
24	125.01	101	149	1.002	0.56095704	0.61	0.5419706
25	125.01	101	149	1.002	0.56095704	0.61	0.5419706
26	125.01	101	149	1.002	0.56095704	0.61	0.5419706
27	125.01	101	149	1.002	0.56095704	0.61	0.5419706
28	125.01	101	149	1.002	0.56095704	0.61	0.5419706
29	125.01	101	149	1.002	0.56095704	0.61	0.5419706
30	125.01	101	149	1.002	0.56095704	0.61	0.5419706
31	125.01	101	149	1.002	0.56095704	0.61	0.5419706
32	125.01	101	149	1.002	0.56095704	0.61	0.5419706
33	125.01	101	149	1.002	0.56095704	0.61	0.5419706
34	54.47	45	64	1.002	0.5081469	0.545	0.58546446
35	54.47	45	64	1.002	0.5081469	0.545	0.58546446
36	54.47	45	64	1.002	0.5081469	0.545	0.58546446
37	54.47	45	64	1.002	0.5081469	0.545	0.58546446
38	54.47	45	64	1.002	0.5081469	0.545	0.58546446
39	54.47	45	64	1.002	0.5081469	0.545	0.58546446
40	54.47	45	64	1.002	0.5081469	0.545	0.58546446
41	54.47	45	64	1.002	0.5081469	0.545	0.58546446
42	54.47	45	64	1.002	0.5081469	0.545	0.58546446
43	54.47	45	64	1.002	0.5081469	0.545	0.58546446
44	54.47	45	64	1.002	0.5081469	0.545	0.58546446
45	54.47	45	64	1.002	0.5081469	0.545	0.58546446
46	54.47	45	64	1.002	0.5081469	0.545	0.58546446
47	54.47	45	64	1.002	0.5081469	0.545	0.58546446
48	54.47	45	64	1.002	0.5081469	0.545	0.58546446
49	54.47	45	64	1.002	0.5081469	0.545	0.58546446
50	54.47	45	64	1.002	0.5081469	0.545	0.58546446
51	54.47	45	64	1.002	0.5081469	0.545	0.58546446
52	54.47	45	64	1.002	0.5081469	0.545	0.58546446
53	54.47	45	64	1.002	0.5081469	0.545	0.58546446
54	54.47	45	64	1.002	0.5081469	0.545	0.58546446
55	54.47	45	64	1.002	0.5081469	0.545	0.58546446
56	506.22	424	588	1.002	0.47175189	0.61	0.54159641
57	506.22	424	588	1.002	0.47175189	0.61	0.54159641
58	506.22	424	588	1.002	0.47175189	0.61	0.54159641
59	506.22	424	588	1.002	0.47175189	0.61	0.54159641
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3	138.11	117	160	1.001	0.45156338	0.46	0.64521595
4	138.11	117	160	1.001	0.45156338	0.46	0.64521595
5	138.11	117	160	1.001	0.45156338	0.46	0.64521595
6	138.11	117	160	1.001	0.45156338	0.46	0.64521595
7	138.11	117	160	1.001	0.45156338	0.46	0.64521595
8	138.11	117	160	1.001	0.45156338	0.46	0.64521595
9	138.11	117	160	1.001	0.45156338	0.46	0.64521595
10	138.11	117	160	1.001	0.45156338	0.46	0.64521595
11	138.11	117	160	1.001	0.45156338	0.46	0.64521595
12	138.11	117	160	1.001	0.45156338	0.46	0.64521595
13	138.11	117	160	1.001	0.45156338	0.46	0.64521595
14	138.11	117	160	1.001	0.45156338	0.46	0.64521595
15	465.43	394	537	1.002	0.44672646	0.573	0.56640241
16	465.43	394	537	1.002	0.44672646	0.573	0.56640241
17	465.43	394	537	1.002	0.44672646	0.573	0.56640241
18	465.43	394	537	1.002	0.44672646	0.573	0.56640241
19	465.43	394	537	1.002	0.44672646	0.573	0.56640241
20	465.43	394	537	1.002	0.44672646	0.573	0.56640241
21	465.43	394	537	1.002	0.44672646	0.573	0.56640241
22	465.43	394	537	1.002	0.44672646	0.573	0.56640241
23	465.43	394	537	1.002	0.44672646	0.573	0.56640241
24	465.43	394	537	1.002	0.44672646	0.573	0.56640241
25	465.43	394	537	1.002	0.44672646	0.573	0.56640241
26	465.43	394	537	1.002	0.44672646	0.573	0.56640241
27	465.43	394	537	1.002	0.44672646	0.573	0.56640241
28	465.43	394	537	1.002	0.44672646	0.573	0.56640241
29	465.43	394	537	1.002	0.44672646	0.573	0.56640241
30	465.43	394	537	1.002	0.44672646	0.573	0.56640241
31	465.43	394	537	1.002	0.44672646	0.573	0.56640241
32	465.43	394	537	1.002	0.44672646	0.573	0.56640241
33	465.43	394	537	1.002	0.44672646	0.573	0.56640241
34	465.43	394	537	1.002	0.44672646	0.573	0.56640241
35	465.43	394	537	1.002	0.44672646	0.573	0.56640241
36	465.43	394	537	1.002	0.44672646	0.573	0.56640241
37	465.43	394	537	1.002	0.44672646	0.573	0.56640241
38	465.43	394	537	1.002	0.44672646	0.573	0.56640241
39	465.43	394	537	1.002	0.44672646	0.573	0.56640241
40	465.43	394	537	1.002	0.44672646	0.573	0.56640241
41	465.43	394	537	1.002	0.44672646	0.573	0.56640241
42	465.43	394	537	1.002	0.44672646	0.573	0.56640241
43	465.43	394	537	1.002	0.44672646	0.573	0.56640241
44	465.43	394	537	1.002	0.44672646	0.573	0.56640241
45	465.9	395	537	1.002	0.44306943	0.573	0.56661469
46	465.9	395	537	1.002	0.44306943	0.573	0.56661469
47	465.9	395	537	1.002	0.44306943	0.573	0.56661469
48	465.9	395	537	1.002	0.44306943	0.573	0.56661469
49	465.9	395	537	1.002	0.44306943	0.573	0.56661469
50	465.9	395	537	1.002	0.44306943	0.573	0.56661469
51	465.9	395	537	1.002	0.44306943	0.573	0.56661469
52	465.9	395	537	1.002	0.44306943	0.573	0.56661469
53	465.9	395	537	1.002	0.44306943	0.573	0.56661469
54	465.9	395	537	1.002	0.44306943	0.573	0.56661469
55	465.9	395	537	1.002	0.44306943	0.573	0.56661469
56	465.9	395	537	1.002	0.44306943	0.573	0.56661469
57	465.9	395	537	1.002	0.44306943	0.573	0.56661469
58	465.9	395	537	1.002	0.44306943	0.573	0.56661469
59	244.38	211	278	1.001	0.39784188	0.44	0.65978995
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3	244.38	211	278	1.001	0.39784188	0.44	0.65978995
4	99.49	86	113	1.001	0.39391421	0.436	0.66254595
5	91.19	79	103	1.001	0.38271978	0.401	0.68863385
6	91.19	79	103	1.001	0.38271978	0.401	0.68863385
7	91.19	79	103	1.001	0.38271978	0.401	0.68863385
8	91.19	79	103	1.001	0.38271978	0.401	0.68863385
9	91.19	79	103	1.001	0.38271978	0.401	0.68863385
10	91.19	79	103	1.001	0.38271978	0.401	0.68863385
11	91.19	79	103	1.001	0.38271978	0.401	0.68863385
12	91.19	79	103	1.001	0.38271978	0.401	0.68863385
13	91.19	79	103	1.001	0.38271978	0.401	0.68863385
14	91.19	79	103	1.001	0.38271978	0.401	0.68863385
15	91.19	79	103	1.001	0.38271978	0.401	0.68863385
16	91.19	79	103	1.001	0.38271978	0.401	0.68863385
17	91.19	79	103	1.001	0.38271978	0.401	0.68863385
18	91.19	79	103	1.001	0.38271978	0.401	0.68863385
19	91.19	79	103	1.001	0.38271978	0.401	0.68863385
20	91.19	79	103	1.001	0.38271978	0.401	0.68863385
21	91.19	79	103	1.001	0.38271978	0.401	0.68863385
22	91.19	79	103	1.001	0.38271978	0.401	0.68863385
23	91.19	79	103	1.001	0.38271978	0.401	0.68863385
24	91.19	79	103	1.001	0.38271978	0.401	0.68863385
25	91.19	79	103	1.001	0.38271978	0.401	0.68863385
26	91.19	79	103	1.001	0.38271978	0.401	0.68863385
27	91.19	79	103	1.001	0.38271978	0.401	0.68863385
28	91.19	79	103	1.001	0.38271978	0.401	0.68863385
29	91.19	79	103	1.001	0.38271978	0.401	0.68863385
30	91.19	79	103	1.001	0.38271978	0.401	0.68863385
31	5884.56	5123	6647	1.001	0.37571446	0.363	0.71665988
32	4385.39	3827	4944	1.001	0.36946484	0.331	0.74060492
33	148.91	132	166	1.001	0.33064531	0.378	0.70579331
34	148.91	132	166	1.001	0.33064531	0.378	0.70579331
35	148.91	132	166	1.001	0.33064531	0.378	0.70579331
36	148.91	132	166	1.001	0.33064531	0.378	0.70579331
37	148.91	132	166	1.001	0.33064531	0.378	0.70579331
38	148.91	132	166	1.001	0.33064531	0.378	0.70579331
39	148.91	132	166	1.001	0.33064531	0.378	0.70579331
40	148.91	132	166	1.001	0.33064531	0.378	0.70579331
41	148.91	132	166	1.001	0.33064531	0.378	0.70579331
42	128.74	115	143	1.001	0.31438129	0.356	0.72163001
43	128.74	115	143	1.001	0.31438129	0.356	0.72163001
44	128.74	115	143	1.001	0.31438129	0.356	0.72163001
45	128.74	115	143	1.001	0.31438129	0.356	0.72163001
46	128.74	115	143	1.001	0.31438129	0.356	0.72163001
47	128.74	115	143	1.001	0.31438129	0.356	0.72163001
48	128.74	115	143	1.001	0.31438129	0.356	0.72163001
49	128.74	115	143	1.001	0.31438129	0.356	0.72163001
50	128.74	115	143	1.001	0.31438129	0.356	0.72163001
51	128.74	115	143	1.001	0.31438129	0.356	0.72163001
52	128.74	115	143	1.001	0.31438129	0.356	0.72163001
53	128.74	115	143	1.001	0.31438129	0.356	0.72163001
54	128.74	115	143	1.001	0.31438129	0.356	0.72163001
55	128.74	115	143	1.001	0.31438129	0.356	0.72163001
56	128.74	115	143	1.001	0.31438129	0.356	0.72163001
57	128.74	115	143	1.001	0.31438129	0.356	0.72163001
58	128.74	115	143	1.001	0.31438129	0.356	0.72163001
59	128.74	115	143	1.001	0.31438129	0.356	0.72163001
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3	128.74	115	143	1.001	0.31438129	0.356	0.72163001
4	128.74	115	143	1.001	0.31438129	0.356	0.72163001
5	128.74	115	143	1.001	0.31438129	0.356	0.72163001
6	128.74	115	143	1.001	0.31438129	0.356	0.72163001
7	128.74	115	143	1.001	0.31438129	0.356	0.72163001
8	128.74	115	143	1.001	0.31438129	0.356	0.72163001
9	128.74	115	143	1.001	0.31438129	0.356	0.72163001
10	128.74	115	143	1.001	0.31438129	0.356	0.72163001
11	128.74	115	143	1.001	0.31438129	0.356	0.72163001
12	128.74	115	143	1.001	0.31438129	0.356	0.72163001
13	128.74	115	143	1.001	0.31438129	0.356	0.72163001
14	128.74	115	143	1.001	0.31438129	0.356	0.72163001
15	128.74	115	143	1.001	0.31438129	0.356	0.72163001
16	128.74	115	143	1.001	0.31438129	0.356	0.72163001
17	128.74	115	143	1.001	0.31438129	0.356	0.72163001
18	128.74	115	143	1.001	0.31438129	0.356	0.72163001
19	128.74	115	143	1.001	0.31438129	0.356	0.72163001
20	128.74	115	143	1.001	0.31438129	0.356	0.72163001
21	128.74	115	143	1.001	0.31438129	0.356	0.72163001
22	128.74	115	143	1.001	0.31438129	0.356	0.72163001
23	128.74	115	143	1.001	0.31438129	0.356	0.72163001
24	128.74	115	143	1.001	0.31438129	0.356	0.72163001
25	128.74	115	143	1.001	0.31438129	0.356	0.72163001
26	128.74	115	143	1.001	0.31438129	0.356	0.72163001
27	128.74	115	143	1.001	0.31438129	0.356	0.72163001
28	128.74	115	143	1.001	0.31438129	0.356	0.72163001
29	128.74	115	143	1.001	0.31438129	0.356	0.72163001
30	128.74	115	143	1.001	0.31438129	0.356	0.72163001
31	128.74	115	143	1.001	0.31438129	0.356	0.72163001
32	128.74	115	143	1.001	0.31438129	0.356	0.72163001
33	128.74	115	143	1.001	0.31438129	0.356	0.72163001
34	128.74	115	143	1.001	0.31438129	0.356	0.72163001
35	128.74	115	143	1.001	0.31438129	0.356	0.72163001
36	150.56	135	166	1.001	0.29822383	0.349	0.727184
37	59.5	53	65	1.001	0.29444736	0.267	0.78983058
38	59.5	53	65	1.001	0.29444736	0.267	0.78983058
39	202.49	182	223	1.001	0.29310526	0.371	0.7103846
40	202.49	182	223	1.001	0.29310526	0.371	0.7103846
41	380.36	343	417	1.001	0.28183881	0.343	0.73148779
42	380.36	343	417	1.001	0.28183881	0.343	0.73148779
43	380.01	343	417	1.001	0.28183881	0.343	0.73122458
44	380.01	343	417	1.001	0.28183881	0.343	0.73122458
45	380.01	343	417	1.001	0.28183881	0.343	0.73122458
46	380.01	343	417	1.001	0.28183881	0.343	0.73122458
47	380.01	343	417	1.001	0.28183881	0.343	0.73122458
48	380.01	343	417	1.001	0.28183881	0.343	0.73122458
49	380.01	343	417	1.001	0.28183881	0.343	0.73122458
50	380.01	343	417	1.001	0.28183881	0.343	0.73122458
51	380.01	343	417	1.001	0.28183881	0.343	0.73122458
52	380.01	343	417	1.001	0.28183881	0.343	0.73122458
53	380.01	343	417	1.001	0.28183881	0.343	0.73122458
54	380.01	343	417	1.001	0.28183881	0.343	0.73122458
55	380.01	343	417	1.001	0.28183881	0.343	0.73122458
56	380.01	343	417	1.001	0.28183881	0.343	0.73122458
57	380.01	343	417	1.001	0.28183881	0.343	0.73122458
58	380.01	343	417	1.001	0.28183881	0.343	0.73122458
59	380.01	343	417	1.001	0.28183881	0.343	0.73122458
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3	380.01	343	417	1.001	0.28183881	0.343	0.73122458
4	380.01	343	417	1.001	0.28183881	0.343	0.73122458
5	380.01	343	417	1.001	0.28183881	0.343	0.73122458
6	380.01	343	417	1.001	0.28183881	0.343	0.73122458
7	380.01	343	417	1.001	0.28183881	0.343	0.73122458
8	380.01	343	417	1.001	0.28183881	0.343	0.73122458
9	380.01	343	417	1.001	0.28183881	0.343	0.73122458
10	380.01	343	417	1.001	0.28183881	0.343	0.73122458
11	380.01	343	417	1.001	0.28183881	0.343	0.73122458
12	380.01	343	417	1.001	0.28183881	0.343	0.73122458
13	380.01	343	417	1.001	0.28183881	0.343	0.73122458
14	380.01	343	417	1.001	0.28183881	0.343	0.73122458
15	380.01	343	417	1.001	0.28183881	0.343	0.73122458
16	380.01	343	417	1.001	0.28183881	0.343	0.73122458
17	380.01	343	417	1.001	0.28183881	0.343	0.73122458
18	380.01	343	417	1.001	0.28183881	0.343	0.73122458
19	380.01	343	417	1.001	0.28183881	0.343	0.73122458
20	380.01	343	417	1.001	0.28183881	0.343	0.73122458
21	380.01	343	417	1.001	0.28183881	0.343	0.73122458
22	145.09	131	159	1.001	0.27945995	0.206	0.83686919
23	148.47	135	161	1	0.25410128	0.19	0.84922835
24	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
25	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
26	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
27	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
28	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
29	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
30	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
31	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
32	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
33	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
34	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
35	3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
36	279.49	257	302	1.001	0.23278019	0.25	0.80277995
37	279.49	257	302	1.001	0.23278019	0.25	0.80277995
38	279.49	257	302	1.001	0.23278019	0.25	0.80277995
39	279.49	257	302	1.001	0.23278019	0.25	0.80277995
40	279.49	257	302	1.001	0.23278019	0.25	0.80277995
41	279.49	257	302	1.001	0.23278019	0.25	0.80277995
42	279.49	257	302	1.001	0.23278019	0.25	0.80277995
43	279.49	257	302	1.001	0.23278019	0.25	0.80277995
44	279.49	257	302	1.001	0.23278019	0.25	0.80277995
45	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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51	279.49	257	302	1.001	0.23278019	0.25	0.80277995
52	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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57	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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59	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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3	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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5	279.49	257	302	1.001	0.23278019	0.25	0.80277995
6	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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9	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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20	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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22	279.49	257	302	1.001	0.23278019	0.25	0.80277995
23	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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33	279.49	257	302	1.001	0.23278019	0.25	0.80277995
34	279.49	257	302	1.001	0.23278019	0.25	0.80277995
35	279.49	257	302	1.001	0.23278019	0.25	0.80277995
36	279.49	257	302	1.001	0.23278019	0.25	0.80277995
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38	279.49	257	302	1.001	0.23278019	0.25	0.80277995
39	279.49	257	302	1.001	0.23278019	0.25	0.80277995
40	291.05	268	314	1.001	0.22853156	0.246	0.80573394
41	171.6	158	185	1	0.22760071	0.164	0.86972278
42	171.6	158	185	1	0.22760071	0.164	0.86972278
43	171.6	158	185	1	0.22760071	0.164	0.86972278
44	171.6	158	185	1	0.22760071	0.164	0.86972278
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46	171.6	158	185	1	0.22760071	0.164	0.86972278
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59	171.6	158	185	1	0.22760071	0.164	0.86972278
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3	171.6	158	185	1	0.22760071	0.164	0.86972278
4	171.6	158	185	1	0.22760071	0.164	0.86972278
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12	171.6	158	185	1	0.22760071	0.164	0.86972278
13	171.6	158	185	1	0.22760071	0.164	0.86972278
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20	171.6	158	185	1	0.22760071	0.164	0.86972278
21	171.6	158	185	1	0.22760071	0.164	0.86972278
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23	171.6	158	185	1	0.22760071	0.164	0.86972278
24	171.6	158	185	1	0.22760071	0.164	0.86972278
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26	171.6	158	185	1	0.22760071	0.164	0.86972278
27	171.6	158	185	1	0.22760071	0.164	0.86972278
28	171.6	158	185	1	0.22760071	0.164	0.86972278
29	171.6	158	185	1	0.22760071	0.164	0.86972278
30	172.25	159	186	1	0.22627586	0.167	0.86753177
31	197.57	183	212	1.001	0.21222062	0.264	0.7918615
32	197.57	183	212	1.001	0.21222062	0.264	0.7918615
33	186.85	173	200	1.001	0.20922796	0.26	0.79454113
34	186.85	173	200	1.001	0.20922796	0.26	0.79454113
35	186.85	173	200	1.001	0.20922796	0.26	0.79454113
36	186.85	173	200	1.001	0.20922796	0.26	0.79454113
37	186.85	173	200	1.001	0.20922796	0.26	0.79454113
38	186.85	173	200	1.001	0.20922796	0.26	0.79454113
39	186.85	173	200	1.001	0.20922796	0.26	0.79454113
40	186.85	173	200	1.001	0.20922796	0.26	0.79454113
41	186.85	173	200	1.001	0.20922796	0.26	0.79454113
42	186.85	173	200	1.001	0.20922796	0.26	0.79454113
43	186.85	173	200	1.001	0.20922796	0.26	0.79454113
44	327.25	304	350	1	0.2032836	0.163	0.87045425
45	318.09	296	340	1	0.19993757	0.164	0.86992485
46	533.46	497	570	1.001	0.19771607	0.223	0.82382762
47	533.46	497	570	1.001	0.19771607	0.223	0.82382762
48	305.55	285	326	1	0.19391005	0.153	0.8785945
49	305.55	285	326	1	0.19391005	0.153	0.8785945
50	305.55	285	326	1	0.19391005	0.153	0.8785945
51	305.1	285	325	1	0.1894778	0.15	0.8811123
52	305.1	285	325	1	0.1894778	0.15	0.8811123
53	305.1	285	325	1	0.1894778	0.15	0.8811123
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59	305.1	285	325	1	0.1894778	0.15	0.8811123
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3	305.1	285	325	1	0.1894778	0.15	0.8811123
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21	305.1	285	325	1	0.1894778	0.15	0.8811123
22	305.1	285	325	1	0.1894778	0.15	0.8811123
23	305.1	285	325	1	0.1894778	0.15	0.8811123
24	305.1	285	325	1	0.1894778	0.15	0.8811123
25	305.1	285	325	1	0.1894778	0.15	0.8811123
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27	305.1	285	325	1	0.1894778	0.15	0.8811123
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31	305.1	285	325	1	0.1894778	0.15	0.8811123
32	305.1	285	325	1	0.1894778	0.15	0.8811123
33	305.1	285	325	1	0.1894778	0.15	0.8811123
34	305.1	285	325	1	0.1894778	0.15	0.8811123
35	305.1	285	325	1	0.1894778	0.15	0.8811123
36	305.1	285	325	1	0.1894778	0.15	0.8811123
37	305.1	285	325	1	0.1894778	0.15	0.8811123
38	305.1	285	325	1	0.1894778	0.15	0.8811123
39	115.29	108	122	1.001	0.17584984	0.168	0.86626012
40	115.29	108	122	1.001	0.17584984	0.168	0.86626012
41	207.54	196	219	1.001	0.16007722	0.2	0.84177747
42	207.54	196	219	1.001	0.16007722	0.2	0.84177747
43	207.54	196	219	1.001	0.16007722	0.2	0.84177747
44	207.54	196	219	1.001	0.16007722	0.2	0.84177747
45	207.54	196	219	1.001	0.16007722	0.2	0.84177747
46	207.54	196	219	1.001	0.16007722	0.2	0.84177747
47	207.54	196	219	1.001	0.16007722	0.2	0.84177747
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49	207.54	196	219	1.001	0.16007722	0.2	0.84177747
50	207.54	196	219	1.001	0.16007722	0.2	0.84177747
51	183.24	174	193	1	0.14951354	0.115	0.90880066
52	183.24	174	193	1	0.14951354	0.115	0.90880066
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59	183.24	174	193	1	0.14951354	0.115	0.90880066
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3	183.24	174	193	1	0.14951354	0.115	0.90880066
4	178.82	170	188	1.001	0.14519792	0.155	0.87666722
5	178.82	170	188	1.001	0.14519792	0.155	0.87666722
6	178.82	170	188	1.001	0.14519792	0.155	0.87666722
7	178.82	170	188	1.001	0.14519792	0.155	0.87666722
8	178.82	170	188	1.001	0.14519792	0.155	0.87666722
9	178.82	170	188	1.001	0.14519792	0.155	0.87666722
10	178.82	170	188	1.001	0.14519792	0.155	0.87666722
11	178.82	170	188	1.001	0.14519792	0.155	0.87666722
12	178.82	170	188	1.001	0.14519792	0.155	0.87666722
13	178.82	170	188	1.001	0.14519792	0.155	0.87666722
14	178.82	170	188	1.001	0.14519792	0.155	0.87666722
15	95.41	91	100	1	0.13606155	0.123	0.9020904
16	95.41	91	100	1	0.13606155	0.123	0.9020904
17	95.41	91	100	1	0.13606155	0.123	0.9020904
18	95.41	91	100	1	0.13606155	0.123	0.9020904
19	95.41	91	100	1	0.13606155	0.123	0.9020904
20	95.41	91	100	1	0.13606155	0.123	0.9020904
21	95.41	91	100	1	0.13606155	0.123	0.9020904
22	97.48	93	102	1.001	0.13326653	0.153	0.87801743
23	97.48	93	102	1.001	0.13326653	0.153	0.87801743
24	100.35	96	105	1	0.12928302	0.139	0.88976693
25	68.66	66	72	1	0.12553088	0.149	0.88183704
26	68.66	66	72	1	0.12553088	0.149	0.88183704
27	68.66	66	72	1	0.12553088	0.149	0.88183704
28	68.66	66	72	1	0.12553088	0.149	0.88183704
29	68.66	66	72	1	0.12553088	0.149	0.88183704
30	68.66	66	72	1	0.12553088	0.149	0.88183704
31	68.66	66	72	1	0.12553088	0.149	0.88183704
32	68.66	66	72	1	0.12553088	0.149	0.88183704
33	68.66	66	72	1	0.12553088	0.149	0.88183704
34	68.66	66	72	1	0.12553088	0.149	0.88183704
35	68.66	66	72	1	0.12553088	0.149	0.88183704
36	68.66	66	72	1	0.12553088	0.149	0.88183704
37	68.66	66	72	1	0.12553088	0.149	0.88183704
38	68.66	66	72	1	0.12553088	0.149	0.88183704
39	187.03	179	195	1	0.12351454	0.09	0.92816155
40	187.03	179	195	1	0.12351454	0.09	0.92816155
41	187.03	179	195	1	0.12351454	0.09	0.92816155
42	187.03	179	195	1	0.12351454	0.09	0.92816155
43	187.03	179	195	1	0.12351454	0.09	0.92816155
44	187.03	179	195	1	0.12351454	0.09	0.92816155
45	187.03	179	195	1	0.12351454	0.09	0.92816155
46	187.03	179	195	1	0.12351454	0.09	0.92816155
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52	187.03	179	195	1	0.12351454	0.09	0.92816155
53	187.03	179	195	1	0.12351454	0.09	0.92816155
54	187.03	179	195	1	0.12351454	0.09	0.92816155
55	187.03	179	195	1	0.12351454	0.09	0.92816155
56	90.86	88	94	1	0.09515723	0.079	0.93668218
57	106.51	103	110	1	0.09485919	0.097	0.92234618
58	106.51	103	110	1	0.09485919	0.097	0.92234618
59	106.51	103	110	1	0.09485919	0.097	0.92234618
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3	119.17	116	123	1	0.08453351	0.101	0.91988506
4	119.17	116	123	1	0.08453351	0.101	0.91988506
5	119.17	116	123	1	0.08453351	0.101	0.91988506
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8	119.17	116	123	1	0.08453351	0.101	0.91988506
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16	119.17	116	123	1	0.08453351	0.101	0.91988506
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19	119.17	116	123	1	0.08453351	0.101	0.91988506
20	119.17	116	123	1	0.08453351	0.101	0.91988506
21	119.17	116	123	1	0.08453351	0.101	0.91988506
22	119.17	116	123	1	0.08453351	0.101	0.91988506
23	119.17	116	123	1	0.08453351	0.101	0.91988506
24	119.17	116	123	1	0.08453351	0.101	0.91988506
25	119.17	116	123	1	0.08453351	0.101	0.91988506
26	119.17	116	123	1	0.08453351	0.101	0.91988506
27	119.17	116	123	1	0.08453351	0.101	0.91988506
28	119.17	116	123	1	0.08453351	0.101	0.91988506
29	119.17	116	123	1	0.08453351	0.101	0.91988506
30	119.17	116	123	1	0.08453351	0.101	0.91988506
31	121.76	118	125	1	0.08314124	0.103	0.91798369
32	110.33	107	113	1	0.07871198	0.095	0.92413182
33	110.33	107	113	1	0.07871198	0.095	0.92413182
34	110.33	107	113	1	0.07871198	0.095	0.92413182
35	256.62	250	264	1	0.07860983	0.082	0.93443419
36	291.88	285	299	1	0.06918357	0.092	0.92658997
37	56.08	55	57	1	0.0515303	0.046	0.96318627
38	461.71	454	470	1	0.04996846	0.062	0.95081656
39	461.71	454	470	1	0.04996846	0.062	0.95081656
40	461.71	454	470	1	0.04996846	0.062	0.95081656
41	461.71	454	470	1	0.04996846	0.062	0.95081656
42	461.71	454	470	1	0.04996846	0.062	0.95081656
43	461.71	454	470	1	0.04996846	0.062	0.95081656
44	63.99	63	65	1	0.04508789	0.025	0.97972935
45	63.99	63	65	1	0.04508789	0.025	0.97972935
46	63.99	63	65	1	0.04508789	0.025	0.97972935
47	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
48	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
49	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
50	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
51	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
52	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
53	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
54	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
55	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
56	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
57	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
58	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
59	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
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3	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
4	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
5	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
6	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
7	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
8	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
9	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
10	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
11	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
12	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
13	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
14	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
15	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
16	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
17	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
18	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
19	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
20	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
21	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
22	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
23	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
24	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
25	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
26	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
27	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
28	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
29	1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
30	19474.19	19244	19705	1	0.03415304	0.038	0.96979777
31	55.75	55	56	1	0.02599521	0.045	0.96400203
32	55.75	55	56	1	0.02599521	0.045	0.96400203
33	55.75	55	56	1	0.02599521	0.045	0.96400203
34	55.75	55	56	1	0.02599521	0.045	0.96400203
35	55.75	55	56	1	0.02599521	0.045	0.96400203
36	55.75	55	56	1	0.02599521	0.045	0.96400203
37	55.75	55	56	1	0.02599521	0.045	0.96400203
38	55.75	55	56	1	0.02599521	0.045	0.96400203
39	55.75	55	56	1	0.02599521	0.045	0.96400203
40	55.75	55	56	1	0.02599521	0.045	0.96400203
41							
42	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
43	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
44	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
45	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
46	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
47	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
48	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
49	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
50	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
51	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
52	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
53	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
54	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
55	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
56	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
57	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
58	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
59	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
60							



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3	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
4	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
5	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
6	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
7	37566.59	37315	37818	1	0.01931738	0.02	0.98421645
8							
9	6460.62	6419	6502	1	0.018535	0.021	0.98285815
10	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
11	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
12	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
13	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
14	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
15	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
16	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
17	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
18	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
19	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
20	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
21	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
22	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
23	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
24	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
25	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
26	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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31	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
32	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
33	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
34	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
35	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
36	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
37	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
38	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
39	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
40	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
41	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
42	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
43	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
44	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
45	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
46	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
47	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
48	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
49	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
50	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
51	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
52	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
53	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
54	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
55	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
56	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
57	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
58	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
59	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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3	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
4	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
5	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
7	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
8	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
9	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
10	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
11	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
12	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
13	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
14	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
15	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
16	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
17	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
18	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
19	6433.82	6394	6473	1	0.01771576	0.021	0.98357156
20	6442.49	6403	6482	1	0.01769101	0.021	0.98339667
21	6442.49	6403	6482	1	0.01769101	0.021	0.98339667
22	6442.49	6403	6482	1	0.01769101	0.021	0.98339667
23	6442.49	6403	6482	1	0.01769101	0.021	0.98339667
24	37699.49	37477	37922	1	0.01702958	0.017	0.98611562
25	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
26	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
27	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
28	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
29	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
30	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
31	43484.42	43461	43508	1	0.00155933	0.002	0.99873247
32	363.7	364	364	1	0	-0.003	0.9972818
33	363.7	364	364	1	0	-0.003	0.9972818
34	363.7	364	364	1	0	-0.003	0.9972818
35	363.7	364	364	1	0	-0.003	0.9972818
36	363.7	364	364	1	0	-0.003	0.9972818
37	363.7	364	364	1	0	-0.003	0.9972818
38	363.7	364	364	1	0	-0.003	0.9972818
39	363.7	364	364	1	0	-0.003	0.9972818
40	363.7	364	364	1	0	-0.003	0.9972818
41	363.7	364	364	1	0	-0.003	0.9972818
42	363.7	364	364	1	0	-0.003	0.9972818
43	363.7	364	364	1	0	-0.003	0.9972818
44	363.7	364	364	1	0	-0.003	0.9972818
45	363.7	364	364	1	0	-0.003	0.9972818
46	363.7	364	364	1	0	-0.003	0.9972818
47	363.7	364	364	1	0	-0.003	0.9972818
48	363.7	364	364	1	0	-0.003	0.9972818
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53	363.7	364	364	1	0	-0.003	0.9972818
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55	363.7	364	364	1	0	-0.003	0.9972818
56	363.7	364	364	1	0	-0.003	0.9972818
57	363.7	364	364	1	0	-0.003	0.9972818
58	363.7	364	364	1	0	-0.003	0.9972818
59	363.7	364	364	1	0	-0.003	0.9972818
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3	363.7	364	364	1	0	-0.003	0.9972818
4	363.7	364	364	1	0	-0.003	0.9972818
5	363.7	364	364	1	0	-0.003	0.9972818
6	363.7	364	364	1	0	-0.003	0.9972818
7	363.7	364	364	1	0	-0.003	0.9972818
8							
9	335.09	335	335	1	0	0	0.9996958
10	335.09	335	335	1	0	0	0.9996958
11	335.09	335	335	1	0	0	0.9996958
12	335.09	335	335	1	0	0	0.9996958
13	335.09	335	335	1	0	0	0.9996958
14	335.09	335	335	1	0	0	0.9996958
15	335.09	335	335	1	0	0	0.9996958
16	335.09	335	335	1	0	0	0.9996958
17	335.09	335	335	1	0	0	0.9996958
18	335.09	335	335	1	0	0	0.9996958
19	335.09	335	335	1	0	0	0.9996958
20	335.09	335	335	1	0	0	0.9996958
21	335.09	335	335	1	0	0	0.9996958
22	335.09	335	335	1	0	0	0.9996958
23	335.09	335	335	1	0	0	0.9996958
24	335.09	335	335	1	0	0	0.9996958
25	335.09	335	335	1	0	0	0.9996958
26	335.09	335	335	1	0	0	0.9996958
27	335.09	335	335	1	0	0	0.9996958
28	335.09	335	335	1	0	0	0.9996958
29	335.09	335	335	1	0	0	0.9996958
30	335.09	335	335	1	0	0	0.9996958
31	335.09	335	335	1	0	0	0.9996958
32	335.09	335	335	1	0	0	0.9996958
33	335.09	335	335	1	0	0	0.9996958
34	335.09	335	335	1	0	0	0.9996958
35	335.09	335	335	1	0	0	0.9996958
36	335.09	335	335	1	0	0	0.9996958
37	335.09	335	335	1	0	0	0.9996958
38	335.09	335	335	1	0	0	0.9996958
39	335.09	335	335	1	0	0	0.9996958
40	335.09	335	335	1	0	0	0.9996958
41	335.09	335	335	1	0	0	0.9996958
42	335.09	335	335	1	0	0	0.9996958
43	335.09	335	335	1	0	0	0.9996958
44	335.09	335	335	1	0	0	0.9996958
45							
46	247.64	249	247	1	-0.0116347	-0.012	0.99038722
47	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
48	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
49	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
50	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
51	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
52	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
53	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
54	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
55	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
56	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
57	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
58	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
59	23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
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3	5299.88	5384	5216	1	-0.0457345	-0.05	0.96011256
4	11348.02	11600	11096	1	-0.0640851	-0.079	0.93736682
5	11348.02	11600	11096	1	-0.0640851	-0.079	0.93736682
6	516.35	530	502	1	-0.078305	-0.088	0.93002306
7	516.35	530	502	1	-0.078305	-0.088	0.93002306
8	516.35	530	502	1	-0.078305	-0.088	0.93002306
9	516.35	530	502	1	-0.078305	-0.088	0.93002306
10	516.35	530	502	1	-0.078305	-0.088	0.93002306
11	516.35	530	502	1	-0.078305	-0.088	0.93002306
12	516.35	530	502	1	-0.078305	-0.088	0.93002306
13	516.35	530	502	1	-0.078305	-0.088	0.93002306
14	516.35	530	502	1	-0.078305	-0.088	0.93002306
15	516.35	530	502	1	-0.078305	-0.088	0.93002306
16	388.68	400	378	1	-0.0816138	-0.094	0.92502052
17	388.68	400	378	1	-0.0816138	-0.094	0.92502052
18	388.68	400	378	1	-0.0816138	-0.094	0.92502052
19	388.68	400	378	1	-0.0816138	-0.094	0.92502052
20	388.68	400	378	1	-0.0816138	-0.094	0.92502052
21	388.68	400	378	1	-0.0816138	-0.094	0.92502052
22	388.68	400	378	1	-0.0816138	-0.094	0.92502052
23	388.68	400	378	1	-0.0816138	-0.094	0.92502052
24	388.68	400	378	1	-0.0816138	-0.094	0.92502052
25	388.68	400	378	1	-0.0816138	-0.094	0.92502052
26	388.68	400	378	1	-0.0816138	-0.094	0.92502052
27	388.68	400	378	1	-0.0816138	-0.094	0.92502052
28	388.68	400	378	1	-0.0816138	-0.094	0.92502052
29	388.68	400	378	1	-0.0816138	-0.094	0.92502052
30	388.68	400	378	1	-0.0816138	-0.094	0.92502052
31	388.68	400	378	1	-0.0816138	-0.094	0.92502052
32	388.68	400	378	1	-0.0816138	-0.094	0.92502052
33	388.68	400	378	1	-0.0816138	-0.094	0.92502052
34	388.68	400	378	1	-0.0816138	-0.094	0.92502052
35	388.68	400	378	1	-0.0816138	-0.094	0.92502052
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37	388.68	400	378	1	-0.0816138	-0.094	0.92502052
38	388.68	400	378	1	-0.0816138	-0.094	0.92502052
39	388.68	400	378	1	-0.0816138	-0.094	0.92502052
40	388.68	400	378	1	-0.0816138	-0.094	0.92502052
41	388.68	400	378	1	-0.0816138	-0.094	0.92502052
42	388.68	400	378	1	-0.0816138	-0.094	0.92502052
43	388.68	400	378	1	-0.0816138	-0.094	0.92502052
44	388.68	400	378	1	-0.0816138	-0.094	0.92502052
45	388.68	400	378	1	-0.0816138	-0.094	0.92502052
46	388.68	400	378	1	-0.0816138	-0.094	0.92502052
47	388.68	400	378	1	-0.0816138	-0.094	0.92502052
48	388.68	400	378	1	-0.0816138	-0.094	0.92502052
49	66.12	68	64	1	-0.0874628	-0.066	0.94756194
50	65.25	67	63	1	-0.0888093	-0.094	0.92513432
51	65.25	67	63	1	-0.0888093	-0.094	0.92513432
52	65.25	67	63	1	-0.0888093	-0.094	0.92513432
53	65.25	67	63	1	-0.0888093	-0.094	0.92513432
54	65.25	67	63	1	-0.0888093	-0.094	0.92513432
55	65.25	67	63	1	-0.0888093	-0.094	0.92513432
56	65.25	67	63	1	-0.0888093	-0.094	0.92513432
57	65.25	67	63	1	-0.0888093	-0.094	0.92513432
58	65.25	67	63	1	-0.0888093	-0.094	0.92513432
59	65.25	67	63	1	-0.0888093	-0.094	0.92513432
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3	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
4	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
5	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
6	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
7	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
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9	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
10	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
11	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
12	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
13	65.25	67	63	1	-0.0888093	-0.094	0.92513432	
14	385.05	397	373	1	-0.0899634	-0.081	0.935329	
15	385.05	397	373	1	-0.0899634	-0.081	0.935329	
16	385.05	397	373	1	-0.0899634	-0.081	0.935329	
17	385.05	397	373	1	-0.0899634	-0.081	0.935329	
18	385.05	397	373	1	-0.0899634	-0.081	0.935329	
19	385.05	397	373	1	-0.0899634	-0.081	0.935329	
20	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
21	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
22	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
23	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
24	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
25	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
26	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
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29	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
30	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
31	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
32	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
33	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
34	176.23	183	170	1	-0.1063089	-0.126	0.89950882	
35	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
36	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
37	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
38	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
39	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
40	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
41	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
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48	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
49	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
50	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
51	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
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57	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
58	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
59	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354	
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3	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
4	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
5	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
6	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
7	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
8	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
9	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
10	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
11	154653.38	160722	148585	1	-0.1132789	-0.099	0.92105354
12	16649.39	17335	15964	1	-0.1188657	-0.101	0.91935059
13	16649.39	17335	15964	1	-0.1188657	-0.101	0.91935059
14	16649.39	17335	15964	1	-0.1188657	-0.101	0.91935059
15	16649.39	17335	15964	1	-0.1188657	-0.101	0.91935059
16	325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
17	325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
18	325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
19	325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
20	367.54	384	351	0.999	-0.1296353	-0.147	0.88282692
21	2350.02	2457	2243	1	-0.1314682	-0.13	0.89684263
22	2350.02	2457	2243	1	-0.1314682	-0.13	0.89684263
23	2379.37	2489	2269	1	-0.1335096	-0.132	0.89478386
24	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
25	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
26	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
27	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
28	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
29	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
30	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
31	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
32	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
33	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
34	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
35	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
36	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
37	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
38	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
39	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
40	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
41	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
42	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
43	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
44	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
45	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
46	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
47	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
48	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
49	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
50	322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
51	705.37	743	668	0.999	-0.1535141	-0.192	0.84795306
52	705.37	743	668	0.999	-0.1535141	-0.192	0.84795306
53	826.88	871	783	0.999	-0.1536604	-0.168	0.86627939
54	826.88	871	783	0.999	-0.1536604	-0.168	0.86627939
55	826.88	871	783	0.999	-0.1536604	-0.168	0.86627939
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59	826.88	871	783	0.999	-0.1536604	-0.168	0.86627939
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3	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
4	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
5	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
6	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
7	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
8	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
9	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
10	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
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12	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
13	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
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15	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
16	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
17	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
18	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
19	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
20	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
21	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
22	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
23	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
24	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
25	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
26	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
27	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
28	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
29	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
30	687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
31	40876.58	43295	38458	1	-0.1709167	-0.16	0.87261571
32	40876.58	43295	38458	1	-0.1709167	-0.16	0.87261571
33							
34	40423.86	42817	38031	1	-0.1710078	-0.16	0.87313129
35	159.75	169	150	1	-0.1720607	-0.164	0.86979297
36	159.75	169	150	1	-0.1720607	-0.164	0.86979297
37	159.75	169	150	1	-0.1720607	-0.164	0.86979297
38	159.75	169	150	1	-0.1720607	-0.164	0.86979297
39	159.75	169	150	1	-0.1720607	-0.164	0.86979297
40	159.75	169	150	1	-0.1720607	-0.164	0.86979297
41	159.75	169	150	1	-0.1720607	-0.164	0.86979297
42	159.75	169	150	1	-0.1720607	-0.164	0.86979297
43	159.75	169	150	1	-0.1720607	-0.164	0.86979297
44	159.75	169	150	1	-0.1720607	-0.164	0.86979297
45	159.75	169	150	1	-0.1720607	-0.164	0.86979297
46	159.75	169	150	1	-0.1720607	-0.164	0.86979297
47	159.75	169	150	1	-0.1720607	-0.164	0.86979297
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49	159.75	169	150	1	-0.1720607	-0.164	0.86979297
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54	159.75	169	150	1	-0.1720607	-0.164	0.86979297
55	159.75	169	150	1	-0.1720607	-0.164	0.86979297
56	159.75	169	150	1	-0.1720607	-0.164	0.86979297
57	159.75	169	150	1	-0.1720607	-0.164	0.86979297
58	159.75	169	150	1	-0.1720607	-0.164	0.86979297
59	159.75	169	150	1	-0.1720607	-0.164	0.86979297
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3	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
4	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
5	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
6	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
7	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
8	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
9	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
10	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
11	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
12	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
13	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
14	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
15	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
16	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
17	93.97	100	88	1	-0.1844246	-0.174	0.86208683	
18	92.94	99	86	0.999	-0.2030919	-0.23	0.81805809	
19	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
20	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
21	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
22	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
23	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
24	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
25	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
26	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
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32	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
33	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
34	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
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37	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
38	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
39	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
40	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
41	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
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46	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
47	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
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49	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
50	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
51	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
52	7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211	
53	7406.14	7945	6867	0.999	-0.2103673	-0.284	0.7763552	
54	7406.14	7945	6867	0.999	-0.2103673	-0.284	0.7763552	
55	7406.14	7945	6867	0.999	-0.2103673	-0.284	0.7763552	
56	7548.95	8113	6985	0.999	-0.2159754	-0.291	0.77092824	
57	7548.95	8113	6985	0.999	-0.2159754	-0.291	0.77092824	
58	7548.95	8113	6985	0.999	-0.2159754	-0.291	0.77092824	
59	7548.95	8113	6985	0.999	-0.2159754	-0.291	0.77092824	
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3	7548.95	8113	6985	0.999	-0.2159754	-0.291	0.77092824
4	45.44	49	42	0.999	-0.2223924	-0.202	0.8397141
5	70.76	76	65	1	-0.2255597	-0.058	NA
6	70.76	76	65	1	-0.2255597	-0.058	NA
7	70.76	76	65	1	-0.2255597	-0.058	NA
8	70.76	76	65	1	-0.2255597	-0.058	NA
9	70.76	76	65	1	-0.2255597	-0.058	NA
10	70.76	76	65	1	-0.2255597	-0.058	NA
11	70.76	76	65	1	-0.2255597	-0.058	NA
12	70.76	76	65	1	-0.2255597	-0.058	NA
13	70.76	76	65	1	-0.2255597	-0.058	NA
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19	70.76	76	65	1	-0.2255597	-0.058	NA
20	70.76	76	65	1	-0.2255597	-0.058	NA
21	70.76	76	65	1	-0.2255597	-0.058	NA
22	70.76	76	65	1	-0.2255597	-0.058	NA
23	70.76	76	65	1	-0.2255597	-0.058	NA
24	70.76	76	65	1	-0.2255597	-0.058	NA
25	70.76	76	65	1	-0.2255597	-0.058	NA
26	70.76	76	65	1	-0.2255597	-0.058	NA
27	70.76	76	65	1	-0.2255597	-0.058	NA
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29	70.76	76	65	1	-0.2255597	-0.058	NA
30	70.76	76	65	1	-0.2255597	-0.058	NA
31	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
32	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
33	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
34	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
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38	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
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59	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
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3	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
4	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
5	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
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19	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
20	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
21	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
22	4502.45	4868	4137	0.999	-0.2347442	-0.238	0.81163701
23	3947.77	4270	3625	0.999	-0.2362551	-0.216	0.82914349
24	3947.77	4270	3625	0.999	-0.2362551	-0.216	0.82914349
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26	3816	4149	3483	0.999	-0.2524332	-0.238	0.81214347
27	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
28	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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36	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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38	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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43	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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50	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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59	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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3	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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17	10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
18	3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
19	3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
20	3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
21	3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
22	3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
23	3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
24	88	96	80	0.999	-0.2630344	-0.296	0.76754171
25	88	96	80	0.999	-0.2630344	-0.296	0.76754171
26	88	96	80	0.999	-0.2630344	-0.296	0.76754171
27	959.94	1050	869	0.999	-0.2729612	-0.348	0.72787069
28	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
29	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
30	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
31	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
32	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
33	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
34	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
35	57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
36	20998.43	23080	18916	0.999	-0.2870362	-0.276	0.78260435
37	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
38	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
39	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
40	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
41	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
42	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
43	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
44	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
45	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
46	20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
47	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
48	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
49	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
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3	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
4	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
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19	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
20	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
21	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
22	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
23	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
24	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
25	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
26	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
27	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
28	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
29	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
30	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
31	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
32	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
33	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
34	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
35	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
36	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
37	20636.53	22694	18579	0.999	-0.2886381	-0.277	0.78173469
38	20647.31	22708	18586	0.999	-0.2889843	-0.277	0.78149503
39	3701.86	4072	3332	0.999	-0.2893492	-0.263	0.79265493
40	20737.94	22813	18663	0.999	-0.2896753	-0.278	0.78100729
41	20737.94	22813	18663	0.999	-0.2896753	-0.278	0.78100729
42	20737.94	22813	18663	0.999	-0.2896753	-0.278	0.78100729
43	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
44	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
45	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
46	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
47	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
48	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
49	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
50	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
51	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
52	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
53	3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
54	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
55	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
56	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
57	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
58	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
59	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
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3	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
4	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
5	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
6	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
7	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
8	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
9	20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
10	338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
11	338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
12	338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
13	338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
14	1090.26	1203	978	0.999	-0.2987303	-0.381	0.70345402
15	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
16	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
17	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
18	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
19	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
20	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
21	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
22	169.68	187	152	0.999	-0.2989669	-0.352	0.7251722
23	3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
24	3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
25	3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
26	3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
27	3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
28	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
29	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
30	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
31	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
32	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
33	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
34	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
35	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
36	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
37	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
38	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
39	171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
40	5152.37	5710	4595	0.999	-0.3134259	-0.373	0.70920272
41	5152.37	5710	4595	0.999	-0.3134259	-0.373	0.70920272
42	5152.37	5710	4595	0.999	-0.3134259	-0.373	0.70920272
43	105.37	117	94	0.998	-0.3157759	-0.406	0.6848422
44	144.39	160	128	0.999	-0.3219281	-0.34	0.73378703
45	12048.53	13437	10660	0.999	-0.3340036	-0.357	0.72120175
46	12048.53	13437	10660	0.999	-0.3340036	-0.357	0.72120175
47	12048.53	13437	10660	0.999	-0.3340036	-0.357	0.72120175
48	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
49	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
50	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
51	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
52	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
53	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
54	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
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56	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
57	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
58	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
59	13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
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3	12257.71	13722	10793	0.999	-0.3463948	-0.413	0.67983967
4	12257.71	13722	10793	0.999	-0.3463948	-0.413	0.67983967
5	12271.67	13740	10804	0.999	-0.3468165	-0.413	0.67943045
6	12271.67	13740	10804	0.999	-0.3468165	-0.413	0.67943045
7	12271.67	13740	10804	0.999	-0.3468165	-0.413	0.67943045
8	12271.67	13740	10804	0.999	-0.3468165	-0.413	0.67943045
9	12988.06	14551	11425	0.998	-0.3489241	-0.456	0.64857196
10	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
11	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
12	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
13	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
14	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
15	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
16	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
17	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
18	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
19	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
20	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
21	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
22	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
23	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
24	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
25	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
26	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
27	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
28	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
29	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
30	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
31	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
32	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
33	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
34	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
35	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
36	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
37	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
38	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
39	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
40	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
41	55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
42	140.2	158	122	0.999	-0.3730434	-0.362	0.71728644
43	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
44	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
45	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
46	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
47	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
48	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
49	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
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51	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
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53	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
54	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
55	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
56	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
57	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
58	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
59	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
60	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977

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3	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
4	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
5	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
6	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
7	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
8	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
9	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
10	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
11	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
12	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
13	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
14	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
15	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
16	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
17	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
18	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
19	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
20	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
21	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
22	70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
23	286.36	324	249	0.999	-0.3798481	-0.424	0.67151471
24	286.36	324	249	0.999	-0.3798481	-0.424	0.67151471
25	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
26	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
27	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
28	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
29	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
30	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
31	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
32	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
33	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
34	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
35	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
36	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
37	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
38	273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
39	222.36	252	192	0.999	-0.3923174	-0.367	0.71389273
40	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
41	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
42	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
43	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
44	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
45	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
46	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
47	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
48	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
49	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
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53	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
54	289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
55	1157.14	1317	998	0.998	-0.4001436	-0.469	0.63925448
56	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
57	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
58	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
59	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
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3	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
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11	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
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13	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
14	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
15	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
16	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
17	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
18	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
19	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
20	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
21	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
22	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
23	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
24	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
25	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
26	216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
27	1301.41	1486	1117	0.998	-0.4118049	-0.468	0.63987864
28	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
29	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
30	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
31	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
32	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
33	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
34	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
35	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
36	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
37	1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
38	291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
39	291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
40	291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
41	291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
42	291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
43	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
45	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
46	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
47	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
48	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
49	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
50	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
51	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
52	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
53	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
54	44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
55	71.58	82	61	0.999	-0.4268147	-0.333	0.73912638
56	73.48	85	63	0.999	-0.432111	-0.424	0.67140481
57	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
58	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
59	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
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3	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
4	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
5	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
6	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
7	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
8	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
9	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
11	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
12	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
13	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
14	10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
15	3700.6	4285	3116	0.998	-0.4596	-0.502	0.61583562
16	3700.6	4285	3116	0.998	-0.4596	-0.502	0.61583562
17	1617.32	1873	1362	0.998	-0.4596242	-0.567	0.57042232
18	405.15	472	338	0.998	-0.4817636	-0.486	0.62687205
19	83.92	98	70	0.998	-0.4854268	-0.542	0.58771849
20	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
21	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
22	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
23	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
24	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
25	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
26	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
27	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
28	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
29	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
30	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
31	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
32	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
33	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
34	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
35	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
36	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
37	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
38	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
39	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
40	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
41	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
42	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
43	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
44	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
45	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
46	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
47	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
48	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
49	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
50	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
51	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
52	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
53	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
54	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
55	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
56	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
57	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
58	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
59	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
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3	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
4	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
5	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
6	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
7	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
8	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
9	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
10	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
11	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
12	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
13	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
14	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
15	59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
16	181.54	212	151	0.998	-0.4895157	-0.553	0.57998893
17	181.31	212	151	0.998	-0.4895157	-0.552	0.58089997
18	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
19	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
20	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
21	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
22	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
23	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
24	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
25	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
26	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
27	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
28	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
29	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
30	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
31	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
32	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
33	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
34	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
35	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
36	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
37	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
38	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
39	180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
40	60.49	71	50	0.998	-0.5058909	-0.507	0.61247395
41	60.49	71	50	0.998	-0.5058909	-0.507	0.61247395
42	60.49	71	50	0.998	-0.5058909	-0.507	0.61247395
43	9637.02	11376	7899	0.998	-0.5262514	-0.541	0.58840402
44	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
45	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
46	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
47	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
48	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
49	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
50	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
51	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
52	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
53	9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
54	295.68	349	242	0.997	-0.52822	-0.69	0.49031927
55	295.68	349	242	0.997	-0.52822	-0.69	0.49031927
56	295.68	349	242	0.997	-0.52822	-0.69	0.49031927
57	295.68	349	242	0.997	-0.52822	-0.69	0.49031927
58	295.68	349	242	0.997	-0.52822	-0.69	0.49031927
59	295.68	349	242	0.997	-0.52822	-0.69	0.49031927
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3	429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
4	429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
5	429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
6	429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
7	429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
8	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
9	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
10	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
11	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
12	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
13	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
14	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
15	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
16	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
17	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
18	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
19	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
20	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
21	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
22	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
23	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
24	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
25	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
26	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
27	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
28	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
29	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
30	121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
31	52566.48	63130	42003	0.998	-0.5878334	-0.7	0.48368857
32	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
33	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
34	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
35	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
36	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
37	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
38	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
39	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
40	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
41	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
42	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
43	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
44	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
45	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
46	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
47	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
48	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
49	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
50	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
51	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
52	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
53	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
54	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
55	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
56	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
57	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
58	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
59	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
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3	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
4	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
5	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
6	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
7	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
8	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
9	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
10	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
11	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
12	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
13	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
14	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
15	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
16	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
17	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
18	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
19	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
20	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
21	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
22	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
23	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
24	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
25	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
26	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
27	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
28	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
29	50865.29	61209	40521	0.997	-0.595074	-0.706	0.48017854
30	50881.71	61230	40533	0.997	-0.5951417	-0.706	0.48015451
31	50881.71	61230	40533	0.997	-0.5951417	-0.706	0.48015451
32	50881.71	61230	40533	0.997	-0.5951417	-0.706	0.48015451
33	50881.71	61230	40533	0.997	-0.5951417	-0.706	0.48015451
34	50881.71	61230	40533	0.997	-0.5951417	-0.706	0.48015451
35	50881.71	61230	40533	0.997	-0.5951417	-0.706	0.48015451
36	51080.12	61513	40647	0.997	-0.5977425	-0.709	0.47855111
37	51080.12	61513	40647	0.997	-0.5977425	-0.709	0.47855111
38	51080.12	61513	40647	0.997	-0.5977425	-0.709	0.47855111
39	51080.12	61513	40647	0.997	-0.5977425	-0.709	0.47855111
40	74050.66	90004	58097	0.998	-0.6315255	-0.648	0.51692531
41	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
42	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
43	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
44	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
45	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
46	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
47	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
48	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
49	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
50	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
51	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
52	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
53	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
54	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
55	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
56	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
57	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
58	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
59	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
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3	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
4	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
5	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
6	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
7	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
8	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
9	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
10	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
11	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
12	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
13	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
14	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
15	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
16	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
17	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
18	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
19	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
20	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
21	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
22	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
23	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
24	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
25	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
26	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
27	73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
28	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
29	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
30	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
31	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
32	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
33	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
35	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
36	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
37	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
38	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
39	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
40	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
41	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
42	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
43	34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
44	11945.94	14613	9279	0.998	-0.6552111	-0.598	0.55017117
45	11945.94	14613	9279	0.998	-0.6552111	-0.598	0.55017117
46	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
47	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
48	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
49	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
50	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
51	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
52	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
53	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
54	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
55	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
56	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
57	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
58	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
59	1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
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3	402.47	498	307	0.997	-0.6979071	-0.802	0.42252068
4	59.11	73	45	0.998	-0.6979715	-0.744	0.45708247
5	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
6	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
7	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
8	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
10	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
11	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
12	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
13	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
14	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
15	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
16	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
17	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
18	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
19	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
20	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
21	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
22	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
23	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
24	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
25	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
26	9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
27	92.56	115	70	0.997	-0.716207	-0.808	0.41890161
28	14160.18	17640	10681	0.997	-0.7238038	-0.863	0.38813449
29	14160.18	17640	10681	0.997	-0.7238038	-0.863	0.38813449
30	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
31	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
32	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
33	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
34	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
35	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
36	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
37	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
38	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
39	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
40	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
41	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
42	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
43	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
44	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
45	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
46	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
47	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
48	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
49	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
50	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
51	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
52	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
53	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
54	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
55	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
56	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
57	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
58	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
59	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
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3	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
4	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
5	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
6	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
7	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
8	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
9	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
10	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
11	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
12	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
13	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
14	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
15	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
16	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
17	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
18	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
19	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
20	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
21	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
22	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
23	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
24	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
25	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
26	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
27	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
28	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
29	650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
30	651.18	815	487	0.997	-0.7428783	-0.867	0.38611964
31	75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
32	75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
33	75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
34	75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
35	75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
36	131.91	167	97	0.998	-0.7837915	-0.753	0.45150374
37	8917.48	11316	6518	0.997	-0.7958628	-0.948	0.34324251
38	8917.48	11316	6518	0.997	-0.7958628	-0.948	0.34324251
39	8917.48	11316	6518	0.997	-0.7958628	-0.948	0.34324251
40	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
41	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
42	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
43	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
44	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
45	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
46	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
47	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
48	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
49	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
50	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
51	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
52	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
53	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
54	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
55	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
56	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
57	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
58	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
59	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
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3	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
4	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
5	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
6	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
7	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
9	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
10	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
11	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
12	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
13	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
14	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
15	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
16	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
17	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
18	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
19	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
20	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
21	8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
22	116.13	148	85	0.998	-0.8000624	-0.622	NA
23	116.13	148	85	0.998	-0.8000624	-0.622	NA
24	129.88	165	94	0.998	-0.8117334	-0.772	0.43997844
25	1905.75	2429	1383	0.998	-0.8125613	-0.787	0.43113665
26	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
27	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
28	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
29	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
30	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
31	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
32	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
33	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
34	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
35	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
36	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
37	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
38	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
39	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
40	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
41	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
42	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
43	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
44	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
45	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
46	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
47	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
48	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
49	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
50	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
51	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
52	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
53	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
54	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
55	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
56	10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
57	610.96	781	441	0.997	-0.8245439	-0.878	0.38004258
58	567.3	727	408	0.996	-0.8333862	-0.981	0.32673794
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3	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
4	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
5	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
6	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
7	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
8	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
9	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
10	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
11	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
12	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
13	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
14	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
15	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
16	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
17	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
18	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
19	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
20	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
21	348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
22	14920.99	19181	10661	0.996	-0.8473352	-1.001	0.31680124
23	50.52	65	36	0.997	-0.8524428	-0.867	0.38608549
24	2607.45	3361	1854	0.996	-0.8582493	-1.026	0.30488752
25	2518.33	3258	1779	0.996	-0.8729201	-1.037	0.2999259
26	2518.33	3258	1779	0.996	-0.8729201	-1.037	0.2999259
27	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
28	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
29	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
30	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
31	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
32	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
33	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
34	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
35	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
36	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
37	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
38	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
39	2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
40	76.6	100	54	0.997	-0.8889687	-1.001	0.31673814
41	76.6	100	54	0.997	-0.8889687	-1.001	0.31673814
42	76.6	100	54	0.997	-0.8889687	-1.001	0.31673814
43	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
44	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
45	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
46	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
47	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
48	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
49	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
50	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
51	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
52	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
53	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
54	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
55	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
56	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
57	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
58	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
59	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
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3	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
4	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
5	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
6	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
7	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
8	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
9	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
10	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
11	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
12	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
13	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
14	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
15	436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
16	523.23	681	366	0.996	-0.8958111	-1.051	0.29343267
17	2465.19	3209	1721	0.996	-0.8988767	-1.088	0.27662661
18	404.24	527	281	0.996	-0.9072328	-1.055	0.29121466
19	403.74	527	280	0.996	-0.9123761	-1.058	0.28988532
20	403.74	527	280	0.996	-0.9123761	-1.058	0.28988532
21	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
22	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
23	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
24	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
25	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
26	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
27	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
28	68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
29	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
30	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
31	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
32	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
33	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
34	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
35	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
36	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
37	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
38	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
39	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
40	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
41	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
42	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
43	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
44	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
45	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
46	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
47	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
48	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
49	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
50	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
51	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
52	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
53	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
54	6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
55	3396.98	4459	2335	0.997	-0.9332976	-1.014	0.31065541
56	3396.98	4459	2335	0.997	-0.9332976	-1.014	0.31065541
57	11221.4	14731	7712	0.996	-0.9336784	-1.083	0.27870223
58	3400.45	4464	2337	0.997	-0.9336793	-1.014	0.31054327
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3	3400.45	4464	2337	0.997	-0.9336793	-1.014	0.31054327
4	5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
5	5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
6	5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
7	5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
8	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
9	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
10	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
11	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
12	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
13	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
14	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
15	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
16	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
17	5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
18	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
19	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
20	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
21	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
22	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
23	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
24	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
25	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
26	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
27	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
28	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
29	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
30	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
31	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
32	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
33	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
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37	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
38	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
39	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
40	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
41	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
42	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
43	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
44	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
45	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
46	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
47	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
48	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
49	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
50	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
51	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
52	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
53	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
54	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
55	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
56	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
57	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
58	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
59	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
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3	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
4	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
5	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
6	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
7	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
8	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
9	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
10	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
11	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
12	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
13	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
14	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
15	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
16	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
17	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
18	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
19	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
20	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
21	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
22	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
23	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
24	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
25	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
26	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
27	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
28	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
29	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
30	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
31	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
32	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
33	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
34	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
35	11060.49	14543	7578	0.996	-0.9404359	-1.087	0.27690788
36	11095.07	14590	7599	0.996	-0.9410984	-1.088	0.27659444
37							
38	729.95	960	500	0.997	-0.9411063	-1.021	0.30744734
39	729.95	960	500	0.997	-0.9411063	-1.021	0.30744734
40	729.95	960	500	0.997	-0.9411063	-1.021	0.30744734
41							
42	731.98	963	501	0.997	-0.9427252	-1.022	0.30683827
43	6287.05	8288	4286	0.996	-0.9513922	-1.089	0.27611283
44	6287.05	8288	4286	0.996	-0.9513922	-1.089	0.27611283
45							
46	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
47	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
48	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
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51	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
52	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
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54	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
55	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
56	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
57							
58	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
59	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
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7	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
8	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
9	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
10	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
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15	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
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17	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
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37	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
38	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
39	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
40	6243.96	8246	4242	0.996	-0.9589498	-1.095	0.2735755
41	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
42	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
43	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
44	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
45	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
46	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
47	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
48	445.57	590	302	0.998	-0.9661664	-0.79	0.42980971
49	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
50	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
51	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
52	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
53	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
54	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
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56	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
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59	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
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4	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
5	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
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8	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
9	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
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12	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
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22	2022.28	2683	1362	0.996	-0.9781204	-1.181	0.23775145
23	109.18	146	72	0.998	-1.0198996	-0.795	NA
24	396.88	540	254	0.998	-1.0881309	-0.783	NA
25	52.74	74	32	0.998	-1.2094534	-0.898	0.3693508
26	366.47	520	213	0.998	-1.2876582	-0.905	NA
27	266.39	378	154	0.997	-1.2954559	-1.081	0.27972876
28	266.39	378	154	0.997	-1.2954559	-1.081	0.27972876
29	266.39	378	154	0.997	-1.2954559	-1.081	0.27972876
30	266.39	378	154	0.997	-1.2954559	-1.081	0.27972876
31	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
32	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
33	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
34	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
35	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
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37	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
38	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
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40	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
41	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
42	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
43	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
44	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
45	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
46	1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
47	1566.79	2234	900	0.997	-1.3116323	-1.143	0.25303822
48	404.88	609	201	0.998	-1.5992467	-0.858	NA
49	404.88	609	201	0.998	-1.5992467	-0.858	NA
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55	404.88	609	201	0.998	-1.5992467	-0.858	NA
56	215.73	372	60	0.991	-2.6322682	-1.854	0.06379377
57	100.29	178	23	0.996	-2.9521715	-0.79	NA
58	100.29	178	23	0.996	-2.9521715	-0.79	NA
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3	100.29	178	23	0.996	-2.9521715	-0.79 NA
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17	100.29	178	23	0.996	-2.9521715	-0.79 NA
18	102.05	181	23	0.996	-2.9762839	-0.795 NA
19	102.05	181	23	0.996	-2.9762839	-0.795 NA
20	102.05	181	23	0.996	-2.9762839	-0.795 NA
21	102.05	181	23	0.996	-2.9762839	-0.795 NA
22	79.35	156	3	0.873	-5.7004397	-2.812 NA
23	79.35	156	3	0.873	-5.7004397	-2.812 NA
24	79.35	156	3	0.873	-5.7004397	-2.812 NA
25	79.35	156	3	0.873	-5.7004397	-2.812 NA
26	79.35	156	3	0.873	-5.7004397	-2.812 NA
27	79.35	156	3	0.873	-5.7004397	-2.812 NA
28	79.35	156	3	0.873	-5.7004397	-2.812 NA
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30	79.35	156	3	0.873	-5.7004397	-2.812 NA
31	79.35	156	3	0.873	-5.7004397	-2.812 NA
32	79.35	156	3	0.873	-5.7004397	-2.812 NA
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36	79.35	156	3	0.873	-5.7004397	-2.812 NA
37	79.35	156	3	0.873	-5.7004397	-2.812 NA
38	79.35	156	3	0.873	-5.7004397	-2.812 NA
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40	79.35	156	3	0.873	-5.7004397	-2.812 NA
41	79.35	156	3	0.873	-5.7004397	-2.812 NA
42	79.35	156	3	0.873	-5.7004397	-2.812 NA
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44	79.35	156	3	0.873	-5.7004397	-2.812 NA
45	79.35	156	3	0.873	-5.7004397	-2.812 NA
46	79.35	156	3	0.873	-5.7004397	-2.812 NA
47	79.35	156	3	0.873	-5.7004397	-2.812 NA
48	79.35	156	3	0.873	-5.7004397	-2.812 NA
49	79.35	156	3	0.873	-5.7004397	-2.812 NA
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59	79.35	156	3	0.873	-5.7004397	-2.812 NA
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13	79.35	156	3	0.873	-5.7004397	-2.812 NA
14	79.35	156	3	0.873	-5.7004397	-2.812 NA
15	79.35	156	3	0.873	-5.7004397	-2.812 NA
16	79.35	156	3	0.873	-5.7004397	-2.812 NA
17	79.35	156	3	0.873	-5.7004397	-2.812 NA
18	79.35	156	3	0.873	-5.7004397	-2.812 NA
19	79.35	156	3	0.873	-5.7004397	-2.812 NA
20	79.35	156	3	0.873	-5.7004397	-2.812 NA
21	79.35	156	3	0.873	-5.7004397	-2.812 NA
22	79.35	156	3	0.873	-5.7004397	-2.812 NA
23	79.35	156	3	0.873	-5.7004397	-2.812 NA
24	79.35	156	3	0.873	-5.7004397	-2.812 NA
25	79.35	156	3	0.873	-5.7004397	-2.812 NA
26	149.72	298	1	0.945	-8.2191685	-2.105 NA
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3	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
4	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
5	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
6	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
7	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
8	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
9	0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
10	0.99848065	0.3698	0.9254	0.6273	0.6273	TRUE	0.135
11	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
12	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
13	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
14	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
15	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
16	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
17	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
18	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
19	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
20	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
21	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
22	0.99848065	1.4366	0.902	1.1906	1.1906	TRUE	3.4109
23	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
24	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
25	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
26	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
27	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
28	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
29	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
30	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
31	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
32	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
33	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
34	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
35	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
36	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
37	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
38	0.99848065	1.8349	0.912	1.3772	1.3772	TRUE	0.8975
39	NA	10	0.9131	3.778	10	TRUE	38.4286
40	NA	10	0.9153	3.7555	10	TRUE	38.4242
41	NA	10	0.9547	3.5328	10	TRUE	38.1432
42	NA	10	0.9691	3.9333	10	TRUE	38.054
43	NA	10	0.9796	3.908	10	TRUE	37.8974
44	NA	10	0.9801	3.907	10	TRUE	37.889
45	NA	10	1.0014	3.4243	10	TRUE	37.6283
46	NA	10	1.0217	3.844	10	TRUE	37.3926
47	NA	10	1.2632	3.8574	10	TRUE	34.3386
48	NA	10	1.266	3.8576	10	TRUE	34.3033
49	NA	10	1.3274	3.3816	3.3816	TRUE	38.6105
50	NA	10	1.3672	3.3995	3.3995	TRUE	38.1316
51	NA	10	0.9016	4.0394	10	TRUE	38.4149
52	NA	10	0.8954	4.428	10	TRUE	38.3422
53	NA	10	0.8918	4.7954	10	TRUE	38.2585
54	NA	10	0.9095	3.9194	10	TRUE	38.4327
55							
56							
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3	NA	10	0.9185	3.8272	10	TRUE	38.4125
4	NA	10	0.929	3.7519	10	TRUE	38.3528
5	NA	10	0.9998	3.6394	10	TRUE	37.6422
6	NA	2.6879	0.9662	1.8089	1.8089	TRUE	34.9219
7	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
8	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
9	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
10	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
11	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
12	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
13	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
14	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
15	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
16	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
17	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
18	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
19	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
20	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
21	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
22	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
23	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
24	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
25	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
26	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
27	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
28	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
29	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
30	NA	3.25	1.2234	2.0631	2.0631	TRUE	30.087
31	NA	2.0885	1.1116	1.6022	1.6022	TRUE	30.9412
32	NA	2.075	1.1727	1.6265	1.6265	TRUE	29.8463
33	NA	2.812	0.9715	1.8717	1.8717	TRUE	33.7721
34	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
35	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
36	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
37	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
38	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
39	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
40	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
41	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
42	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
43	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
44	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
45	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
46	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
47	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
48	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
49	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
50	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
51	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
52	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
53	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
54	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
55	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
56	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
57	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
58	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
59	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
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3	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
4	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
5	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
6	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
7	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
8	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
9	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
10	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
11	NA	2.8116	0.9715	1.8716	1.8716	TRUE	33.77
12	NA	2.8246	0.9711	1.8778	1.8778	TRUE	33.7829
13	NA	2.1309	0.9632	1.5483	1.5483	TRUE	33.549
14	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
15	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
16	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
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19	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
20	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
21	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
22	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
23	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
24	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
25	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
26	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
27	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
28	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
29	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
30	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
31	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
32	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
33	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
34	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
35	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
36	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
37	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
38	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
39	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
40	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
41	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
42	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
43	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
44	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
45	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
46	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
47	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
48	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
49	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
50	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
51	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
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53	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
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55	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
56	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
57	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
58	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
59	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
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3	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
4	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
5	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
6	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
7	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
8	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
9	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
10	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
11	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
12	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
13	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
14	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
15	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
16	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
17	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
18	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
19	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
20	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
21	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
22	NA	2.1306	0.9632	1.5482	1.5482	TRUE	33.5469
23	NA	2.1613	1.1674	1.6593	1.6593	TRUE	27.2604
24	NA	2.1613	1.1674	1.6593	1.6593	TRUE	27.2604
25	NA	2.1613	1.1674	1.6593	1.6593	TRUE	27.2604
26	NA	2.1613	1.1674	1.6593	1.6593	TRUE	27.2604
27	NA	2.1613	1.1674	1.6593	1.6593	TRUE	27.2604
28	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
29	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
30	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
31	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
32	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
33	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
34	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
35	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
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38	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
39	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
40	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
41	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
42	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
43	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
44	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
45	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
46	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
47	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
48	NA	2.0897	1.2904	1.686	1.686	TRUE	25.687
49	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
50	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
51	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
52	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
53	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
54	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
55	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
56	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
57	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
58	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
59	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
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2							
3	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
4	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
5	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
6	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
7	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
8	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
9	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
10	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
11	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
12	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
13	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
14	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
15	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
16	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
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18	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
19	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
20	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
21	NA	1.5663	1.1896	1.384	1.384	TRUE	26.1921
22	NA	1.6213	1.1709	1.4027	1.4027	TRUE	26.8095
23	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
24	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
25	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
26	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
27	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
28	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
29	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
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32	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
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40	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
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44	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
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46	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
47	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
48	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
49	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
50	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
51	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
52	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
53	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
54	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
55	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
56	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
57	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
58	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
59	NA	1.5392	0.912	1.229	1.229	TRUE	28.6108
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2							
3	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
4	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
5	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
6	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
7	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
8	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
9	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
10	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
11	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
12	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
13	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
14	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
15	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
16	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
17	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
18	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
19	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
20	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
21	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
22	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
23	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
24	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
25	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
26	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
27	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
28	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
29	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
30	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
31	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
32	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
33	NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
34	NA	1.0067	0.9009	0.951	0.951	TRUE	24.865
35	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
36	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
37	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
38	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
39	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
40	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
41	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
42	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
43	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
44	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
45	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
46	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
47	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
48	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
49	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
50	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
51	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
52	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
53	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
54	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
55	0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
56	0.99848065	1.2907	0.9496	1.1325	1.1325	TRUE	7.36
57	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
58	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
59	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
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3	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
4	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
5	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
6	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
7	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
8	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
9	0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
10	0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
11	0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
12	0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
13	0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
14	0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
15	0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
16	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
17	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
18	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
19	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
20	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
21	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
22	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
23	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
24	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
25	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
26	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
27	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
28	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
29	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
30	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
31	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
32	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
33	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
34	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
35	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
36	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
37	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
38	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
39	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
40	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
41	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
42	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
43	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
44	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
45	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
46	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
47	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
48	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
49	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
50	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
51	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
52	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
53	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
54	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
55	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
56	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
57	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
58	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
59	NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869
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2							
3	0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
4	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
5	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
6	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
7	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
8	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
9	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
10	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
11	NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
12	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
13	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
14	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
15	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
16	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
17	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
18	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
19	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
20	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
21	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
22	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
23	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
24	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
25	0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
26	NA	0.8102	0.9535	0.8783	0.8783	TRUE	20.3384
27	NA	0.8102	0.9535	0.8783	0.8783	TRUE	20.3384
28	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
29	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
30	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
31	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
32	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
33	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
34	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
35	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
36	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
37	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
38	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
39	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
40	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
41	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
42	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
43	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
44	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
45	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
46	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
47	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
48	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
49	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
50	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
51	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
52	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
53	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
54	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
55	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
56	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
57	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
58	NA	0.8134	0.9538	0.8802	0.8802	TRUE	20.4049
59	0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
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2							
3	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
4	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
5	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
6	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
7	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
8	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
9	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
10	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
11	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
12	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
13	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
14	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
15	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
16	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
17	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
18	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
19	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
20	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
21	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
22	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
23	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
24	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
25	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
26	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
27	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
28	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
29	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
30	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
31	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
32	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
33	0.99848065	0.4939	0.9137	0.6898	0.6898	TRUE	12.6189
34	0.99848065	0.4932	0.9136	0.6894	0.6894	TRUE	11.9383
35	NA	2.5286	0.9295	1.7188	1.7188	TRUE	21.0823
36	NA	2.5286	0.9295	1.7188	1.7188	TRUE	21.0823
37	NA	2.6557	0.9353	1.7794	1.7794	TRUE	23.6516
38	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
39	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
40	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
41	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
42	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
43	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
44	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
45	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
46	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
47	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
48	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
49	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
50	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
51	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
52	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
53	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
54	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
55	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
56	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
57	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
58	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
59	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
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2							
3	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
4	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
5	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
6	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
7	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
8	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
9	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
10	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
11	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
12	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
13	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
14	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
15	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
16	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
17	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
18	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
19	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
20	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
21	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
22	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
23	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
24	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
25	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
26	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
27	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
28	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
29	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
30	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
31	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
32	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
33	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
34	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
35	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
36	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
37	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
38	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
39	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
40	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
41	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
42	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
43	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
44	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
45	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
46	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
47	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
48	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
49	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
50	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
51	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
52	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
53	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
54	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
55	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
56	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
57	NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
58	NA	2.6668	0.9352	1.7851	1.7851	TRUE	23.7809
59	0.99848065	0.3573	1.0494	0.6766	0.6766	TRUE	7.4465
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2							
3	0.99848065	0.3573	1.0494	0.6766	0.6766	TRUE	7.4465
4	0.99848065	0.3573	1.0494	0.6766	0.6766	TRUE	7.4465
5	0.99848065	0.748	0.9221	0.8317	0.8317	TRUE	2.4767
6	0.99848065	0.748	0.9221	0.8317	0.8317	TRUE	2.4767
7	0.99848065	0.7516	0.9239	0.8345	0.8345	TRUE	2.2837
8	0.99848065	0.7516	0.9239	0.8345	0.8345	TRUE	2.2837
9	0.99848065	0.7516	0.9239	0.8345	0.8345	TRUE	2.2837
10	0.99848065	0.7516	0.9239	0.8345	0.8345	TRUE	2.2837
11	0.99848065	0.7516	0.9239	0.8345	0.8345	TRUE	2.2837
12	0.99848065	0.7516	0.9239	0.8345	0.8345	TRUE	2.2837
13	0.99848065	0.7754	0.9289	0.8495	0.8495	TRUE	1.8077
14	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
15	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
16	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
17	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
18	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
19	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
20	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
21	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
22	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
23	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
24	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
25	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
26	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
27	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
28	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
29	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
30	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
31	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
32	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
33	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
34	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
35	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
36	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
37	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
38	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
39	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
40	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
41	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
42	0.99848065	0.7753	0.9289	0.8495	0.8495	TRUE	1.8067
43	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
44	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
45	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
46	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
47	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
48	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
49	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
50	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
51	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
52	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
53	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
54	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
55	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
56	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
57	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
58	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
59	0.99848065	0.787	0.9313	0.8567	0.8567	TRUE	1.6487
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2							
3	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
4	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
5	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
6	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
7	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
8	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
9	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
10	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
11	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
12	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
13	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
14	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
15	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
16	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
17	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
18	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
19	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
20	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
21	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
22	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
23	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
24	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
25	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
26	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
27	0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
28	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
29	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
30	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
31	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
32	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
33	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
34	0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
35	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
36	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
37	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
38	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
39	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
40	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
41	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
42	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
43	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
44	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
45	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
46	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
47	0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
48	0.99848065	1.6677	1.0678	1.363	1.363	TRUE	1.2491
49	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
50	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
51	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
52	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
53	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
54	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
55	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
56	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
57	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
58	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
59	0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
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2							
3	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
4	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
5	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
6	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
7	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
8	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
9	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
10	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
11	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
12	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
13	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
14	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
15	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
16	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
17	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
18	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
19	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
20	0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
21	0.99848065	0.5787	0.9087	0.7345	0.7345	TRUE	1.2044
22	0.99848065	0.5787	0.9087	0.7345	0.7345	TRUE	1.2044
23	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
24	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
25	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
26	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
27	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
28	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
29	0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
30	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
31	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
32	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
33	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
34	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
35	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
36	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
37	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
38	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
39	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
40	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
41	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
42	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
43	0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
44	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
45	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
46	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
47	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
48	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
49	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
50	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
51	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
52	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
53	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
54	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
55	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
56	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
57	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
58	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
59	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
60							

1							
2							
3	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
4	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
5	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
6	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
7	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
8	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
9	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
10	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
11	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
12	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
13	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
14	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
15	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
16	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
17	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
18	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
19	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
20	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
21	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
22	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
23	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
24	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
25	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
26	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
27	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
28	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
29	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
30	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
31	0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
32	0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
33	0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
34	0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
35	0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
36	0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
37	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
38	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
39	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
40	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
41	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
42	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
43	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
44	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
45	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
46	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
47	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
48	0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
49	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
50	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
51	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
52	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
53	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
54	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
55	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
56	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
57	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
58	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
59	0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
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2							
3	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
4	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
5	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
6	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
7	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
8	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
9	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
10	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
11	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
12	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
13	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
14	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
15	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
16	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
17	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
18	0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
19	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
20	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
21	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
22	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
23	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
24	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
25	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
26	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
27	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
28	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
29	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
30	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
31	0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
32	0.99848065	0.7787	0.9315	0.8514	0.8514	TRUE	0.4832
33	0.99848065	0.3817	1.0142	0.6778	0.6778	TRUE	5.3986
34	0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
35	0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
36	0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
37	0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
38	0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
39	NA	1.6013	1.1293	1.3727	1.3727	TRUE	22.8793
40	NA	1.6013	1.1293	1.3727	1.3727	TRUE	22.8793
41	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
42	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
43	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
44	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
45	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
46	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
47	0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
48	0.99848065	0.3783	1.015	0.6759	0.6759	TRUE	7.2141
49	0.99848065	0.3895	1.0147	0.6823	0.6823	TRUE	5.4956
50	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
51	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
52	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
53	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
54	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
55	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
56	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
57	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
58	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
59	0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
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2							
3	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
4	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
5	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
6	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
7	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
8	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
9	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
10	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
11	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
12	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
13	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
14	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
15	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
16	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
17	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
18	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
19	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
20	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
21	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
22	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
23	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
24	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
25	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
26	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
27	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
28	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
29	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
30	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
31	0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
32	NA	1.2555	1.1099	1.1857	1.1857	TRUE	20.02
33							
34	0.99848065	0.1579	1.1111	0.5903	0.5903	TRUE	2.1772
35	0.99848065	0.1579	1.1111	0.5903	0.5903	TRUE	2.1772
36	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
37	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
38	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
39	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
40	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
41	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
42	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
43	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
44	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
45	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
46	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
47	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
48	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
49	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
50	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
51	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
52	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
53	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
54	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
55	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
56	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
57	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
58	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
59	0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
60							





1							
2							
3	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
4	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
5	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
6	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
7	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
8	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
9	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
10	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
11	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
12	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
13	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
14	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
15	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
16	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
17	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
18	0.99848065	0.1099	1.0484	0.5297	0.5297	TRUE	1.4828
19	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
20	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
21	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
22	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
23	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
24	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
25	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
26	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
27	0.99848065	0.5449	1.0491	0.7845	0.7845	TRUE	2.2755
28	0.99848065	0.151	0.9114	0.4916	0.4916	TRUE	1.7065
29	0.99848065	0.151	0.9114	0.4916	0.4916	TRUE	1.7065
30	0.99848065	0.3373	0.9738	0.6332	0.6332	TRUE	0.5599
31	0.99848065	0.3373	0.9738	0.6332	0.6332	TRUE	0.5599
32	0.99848065	0.1105	1.0473	0.5294	0.5294	TRUE	1.443
33	0.99848065	0.6522	0.8977	0.7685	0.7685	TRUE	0.3985
34	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
35	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
36	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
37	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
38	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
39	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
40	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
41	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
42	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
43	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
44	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
45	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
46	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
47	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
48	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
49	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
50	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
51	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
52	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
53	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
54	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
55	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
56	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
57	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
58	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
59	0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
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3	0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
4	0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
5	0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
6	0.99848065	1.4311	1.057	1.2486	1.2486	TRUE	5.0296
7	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
8	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
9	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
10	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
11	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
12	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
13	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
14	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
15	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
16	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
17	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
18	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
19	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
20	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
21	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
22	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
23	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
24	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
25	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
26	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
27	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
28	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
29	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
30	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
31	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
32	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
33	0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
34	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
35	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
36	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
37	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
38	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
39	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
40	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
41	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
42	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
43	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
44	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
45	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
46	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
47	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
48	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
49	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
50	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
51	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
52	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
53	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
54	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
55	0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
56	0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274
57	0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274
58	0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274
59	0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274
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3	0.99848065	0.2934	0.9343	0.5826	0.5826	TRUE	3.5417
4	0.99848065	0.3142	1.0042	0.6308	0.6308	TRUE	4.182
5	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
6	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
7	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
8	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
9	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
10	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
11	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
12	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
13	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
14	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
15	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
16	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
17	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
18	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
19	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
20	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
21	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
22	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
23	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
24	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
25	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
26	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
27	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
28	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
29	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
30	0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
31	0.99848065	0.6941	0.8883	0.7717	0.7717	TRUE	1.0172
32	0.99848065	0.9043	0.889	0.8974	0.8974	TRUE	0.5704
33	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
34	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
35	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
36	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
37	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
38	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
39	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
40	0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
41	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
42	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
43	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
44	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
45	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
46	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
47	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
48	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
49	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
50	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
51	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
52	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
53	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
54	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
55	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
56	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
57	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
58	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
59	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
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3	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
4	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
5	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
6	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
7	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
8	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
9	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
10	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
11	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
12	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
13	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
14	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
15	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
16	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
17	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
18	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
19	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
20	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
21	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
22	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
23	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
24	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
25	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
26	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
27	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
28	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
29	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
30	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
31	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
32	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
33	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
34	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
35	0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
36	0.99848065	0.1783	0.9642	0.5363	0.5363	TRUE	0.7762
37	0.99848065	0.5592	1.0835	0.8027	0.8027	TRUE	5.2847
38	0.99848065	0.5592	1.0835	0.8027	0.8027	TRUE	5.2847
39	0.99848065	0.0755	0.9442	0.4607	0.4607	TRUE	0.299
40	0.99848065	0.0755	0.9442	0.4607	0.4607	TRUE	0.299
41	0.99848065	0.1305	0.9171	0.4815	0.4815	TRUE	1.1233
42	0.99848065	0.1305	0.9171	0.4815	0.4815	TRUE	1.1233
43	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
44	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
45	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
46	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
47	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
48	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
49	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
50	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
51	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
52	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
53	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
54	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
55	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
56	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
57	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
58	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
59	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
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2							
3	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
4	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
5	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
6	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
7	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
8	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
9	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
10	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
11	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
12	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
13	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
14	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
15	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
16	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
17	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
18	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
19	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
20	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
21	0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
22	0.99848065	1.6087	0.9672	1.2919	1.2919	TRUE	3.7481
23	0.99848065	1.5678	0.9653	1.2711	1.2711	TRUE	5.9406
24	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
25	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
26	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
27	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
28	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
29	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
30	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
31	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
32	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
33	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
34	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
35	0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
36	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
37	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
38	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
39	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
40	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
41	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
42	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
43	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
44	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
45	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
46	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
47	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
48	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
49	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
50	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
51	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
52	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
53	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
54	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
55	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
56	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
57	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
58	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
59	0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
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3	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
4	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
5	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
6	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
7	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
8	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
9	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
10	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
11	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
12	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
13	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
14	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
15	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
16	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
17	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
18	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
19	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
20	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
21	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
22	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
23	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
24	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
25	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
26	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
27	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
28	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
29	0.99848065	1.7065	0.9547	1.3331	1.3331	TRUE	1.1716
30	0.99848065	1.7106	0.9544	1.335	1.335	TRUE	1.1853
31	0.99848065	0.0633	0.9457	0.4545	0.4545	TRUE	1.2571
32	0.99848065	0.0633	0.9457	0.4545	0.4545	TRUE	1.2571
33	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
34	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
35	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
36	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
37	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
38	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
39	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
40	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
41	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
42	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
43	0.99848065	0.0694	0.9491	0.4603	0.4603	TRUE	1.3204
44	0.99848065	1.2568	0.9222	1.093	1.093	TRUE	0.3286
45	0.99848065	1.2821	0.9232	1.1061	1.1061	TRUE	0.3134
46	0.99848065	0.2652	0.9083	0.5569	0.5569	TRUE	1.9845
47	0.99848065	0.2652	0.9083	0.5569	0.5569	TRUE	1.9845
48	0.99848065	0.2652	0.9083	0.5569	0.5569	TRUE	1.9845
49	0.99848065	1.2599	0.9247	1.0957	1.0957	TRUE	0.3569
50	0.99848065	1.2599	0.9247	1.0957	1.0957	TRUE	0.3569
51	0.99848065	1.2599	0.9247	1.0957	1.0957	TRUE	0.3569
52	0.99848065	1.2599	0.9247	1.0957	1.0957	TRUE	0.3569
53	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
54	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
55	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
56	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
57	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
58	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
59	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
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3	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
4	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
5	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
6	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
7	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
8	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
9	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
10	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
11	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
12	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
13	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
14	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
15	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
16	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
17	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
18	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
19	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
20	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
21	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
22	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
23	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
24	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
25	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
26	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
27	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
28	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
29	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
30	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
31	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
32	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
33	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
34	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
35	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
36	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
37	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
38	0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
39	0.99848065	0.5081	0.9881	0.7317	0.7317	TRUE	3.3237
40	0.99848065	0.5081	0.9881	0.7317	0.7317	TRUE	3.3237
41	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
42	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
43	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
44	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
45	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
46	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
47	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
48	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
49	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
50	0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
51	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
52	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
53	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
54	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
55	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
56	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
57	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
58	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
59	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
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3	0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
4	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
5	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
6	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
7	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
8	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
9	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
10	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
11	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
12	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
13	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
14	0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
15	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
16	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
17	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
18	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
19	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
20	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
21	0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
22	0.99848065	0.1091	1.0067	0.5141	0.5141	TRUE	0.23
23	0.99848065	0.1091	1.0067	0.5141	0.5141	TRUE	0.23
24	0.99848065	0.1036	1.0032	0.5088	0.5088	TRUE	0.237
25	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
26	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
27	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
28	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
29	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
30	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
31	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
32	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
33	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
34	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
35	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
36	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
37	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
38	0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
39	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
40	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
41	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
42	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
43	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
44	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
45	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
46	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
47	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
48	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
49	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
50	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
51	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
52	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
53	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
54	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
55	0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
56	0.99848065	0.792	1.0154	0.8978	0.8978	TRUE	0.3103
57	0.99848065	0.1605	0.9965	0.5385	0.5385	TRUE	0.2503
58	0.99848065	0.1605	0.9965	0.5385	0.5385	TRUE	0.2503
59	0.99848065	0.1605	0.9965	0.5385	0.5385	TRUE	0.2503
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3	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
4	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
5	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
6	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
7	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
8	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
9	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
10	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
11	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
12	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
13	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
14	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
15	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
16	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
17	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
18	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
19	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
20	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
21	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
22	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
23	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
24	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
25	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
26	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
27	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
28	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
29	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
30	0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
31	0.99848065	0.1459	0.9827	0.5237	0.5237	TRUE	0.4203
32	0.99848065	0.1594	0.9926	0.536	0.536	TRUE	0.2103
33	0.99848065	0.1594	0.9926	0.536	0.536	TRUE	0.2103
34	0.99848065	0.1594	0.9926	0.536	0.536	TRUE	0.2103
35	0.99848065	0.3389	0.932	0.6116	0.6116	TRUE	0.3884
36	0.99848065	0.0147	0.9265	0.41	0.41	TRUE	0.2902
37	0.99848065	0.3436	1.0955	0.6931	0.6931	TRUE	0.8144
38	0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
39	0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
40	0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
41	0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
42	0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
43	0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
44	0.99848065	0.8108	1.0697	0.9368	0.9368	TRUE	1.3683
45	0.99848065	0.8108	1.0697	0.9368	0.9368	TRUE	1.3683
46	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
47	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
48	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
49	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
50	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
51	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
52	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
53	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
54	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
55	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
56	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
57	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
58	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
59	0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
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3	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
4	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
5	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
6	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
7	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
8	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
9	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
10	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
11	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
12	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
13	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
14	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
15	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
16	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
17	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
18	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
19	0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
20	0.99848065	0.2086	0.8881	0.5232	0.5232	TRUE	5.7287
21	0.99848065	0.2086	0.8881	0.5232	0.5232	TRUE	5.7287
22	0.99848065	0.2086	0.8881	0.5232	0.5232	TRUE	5.7287
23	0.99848065	0.2086	0.8881	0.5232	0.5232	TRUE	5.7287
24	0.99848065	0.5149	0.8866	0.6889	0.6889	TRUE	0.4773
25	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
26	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
27	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
28	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
29	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
30	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
31	0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
32	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
33	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
34	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
35	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
36	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
37	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
38	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
39	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
40	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
41	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
42	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
43	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
44	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
45	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
46	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
47	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
48	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
49	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
50	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
51	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
52	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
53	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
54	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
55	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
56	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
57	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
58	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
59	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
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3	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
4	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
5	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
6	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
7	0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
8	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
9	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
10	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
11	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
12	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
13	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
14	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
15	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
16	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
17	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
18	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
19	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
20	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
21	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
22	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
23	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
24	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
25	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
26	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
27	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
28	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
29	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
30	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
31	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
32	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
33	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
34	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
35	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
36	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
37	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
38	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
39	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
40	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
41	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
42	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
43	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
44	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
45	0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
46	0.99848065	0.2221	0.9337	0.5449	0.5449	TRUE	0.2481
47	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
48	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
49	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
50	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
51	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
52	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
53	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
54	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
55	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
56	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
57	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
58	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
59	0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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3	0.99848065	0.3593	0.8885	0.6035	0.6035	TRUE	0.2656
4	0.99848065	0.1494	0.8873	0.4786	0.4786	TRUE	2.258
5	0.99848065	0.1494	0.8873	0.4786	0.4786	TRUE	2.258
6	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
7	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
8	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
9	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
10	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
11	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
12	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
13	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
14	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
15	0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
16	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
17	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
18	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
19	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
20	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
21	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
22	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
23	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
24	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
25	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
26	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
27	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
28	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
29	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
30	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
31	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
32	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
33	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
34	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
35	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
36	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
37	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
38	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
39	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
40	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
41	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
42	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
43	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
44	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
45	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
46	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
47	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
48	0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
49	0.99848065	0.8624	1.0637	0.9577	0.9577	TRUE	1.3669
50	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
51	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
52	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
53	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
54	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
55	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
56	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
57	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
58	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
59	0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
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2							
3	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
4	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
5	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
6	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
7	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
8	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
9	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
10	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
11	0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
12	0.99848065	1.0949	0.887	0.9941	0.9941	TRUE	0.4982
13	0.99848065	1.0949	0.887	0.9941	0.9941	TRUE	0.4982
14	0.99848065	1.0949	0.887	0.9941	0.9941	TRUE	0.4982
15	0.99848065	0.2376	0.9224	0.5483	0.5483	TRUE	0.4362
16	0.99848065	0.2376	0.9224	0.5483	0.5483	TRUE	0.4362
17	0.99848065	0.2376	0.9224	0.5483	0.5483	TRUE	0.4362
18	0.99848065	0.2233	0.9182	0.538	0.538	TRUE	0.3609
19	0.99848065	0.6111	0.8913	0.7432	0.7432	TRUE	0.3525
20	0.99848065	0.6111	0.8913	0.7432	0.7432	TRUE	0.3525
21	0.99848065	0.5965	0.8912	0.7353	0.7353	TRUE	0.342
22	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
23	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
24	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
25	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
26	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
27	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
28	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
29	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
30	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
31	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
32	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
33	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
34	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
35	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
36	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
37	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
38	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
39	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
40	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
41	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
42	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
43	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
44	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
45	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
46	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
47	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
48	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
49	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
50	0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
51	0.99848065	0.0977	0.9029	0.4535	0.4535	TRUE	0.6743
52	0.99848065	0.0977	0.9029	0.4535	0.4535	TRUE	0.6743
53	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
54	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
55	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
56	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
57	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
58	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
59	0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
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3	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
4	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
5	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
6	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
7	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
8	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
9	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
10	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
11	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
12	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
13	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
14	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
15	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
16	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
17	0.99848065	0.7116	1.0112	0.8528	0.8528	TRUE	0.6114
18	0.99848065	0.197	1.0126	0.567	0.567	TRUE	2.0055
19	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
20	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
21	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
22	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
23	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
24	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
25	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
26	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
27	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
28	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
29	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
30	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
31	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
32	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
33	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
34	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
35	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
36	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
37	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
38	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
39	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
40	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
41	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
42	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
43	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
44	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
45	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
46	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
47	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
48	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
49	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
50	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
51	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
52	0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
53	0.99848065	0.0232	0.8879	0.3955	0.3955	TRUE	0.4118
54	0.99848065	0.0232	0.8879	0.3955	0.3955	TRUE	0.4118
55	0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
56	0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
57	0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
58	0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
59	0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
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3	0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
4	0.99848065	0.6705	1.1445	0.8923	0.8923	TRUE	1.1361
5	0.99848065	0.6705	1.1445	0.8923	0.8923	TRUE	1.1361
6	NA	10	1.0521	3.9213	10	TRUE	34.5483
7	NA	10	1.0521	3.9213	10	TRUE	34.5483
8	NA	10	1.0521	3.9213	10	TRUE	34.5483
9	NA	10	1.0521	3.9213	10	TRUE	34.5483
10	NA	10	1.0521	3.9213	10	TRUE	34.5483
11	NA	10	1.0521	3.9213	10	TRUE	34.5483
12	NA	10	1.0521	3.9213	10	TRUE	34.5483
13	NA	10	1.0521	3.9213	10	TRUE	34.5483
14	NA	10	1.0521	3.9213	10	TRUE	34.5483
15	NA	10	1.0521	3.9213	10	TRUE	34.5483
16	NA	10	1.0521	3.9213	10	TRUE	34.5483
17	NA	10	1.0521	3.9213	10	TRUE	34.5483
18	NA	10	1.0521	3.9213	10	TRUE	34.5483
19	NA	10	1.0521	3.9213	10	TRUE	34.5483
20	NA	10	1.0521	3.9213	10	TRUE	34.5483
21	NA	10	1.0521	3.9213	10	TRUE	34.5483
22	NA	10	1.0521	3.9213	10	TRUE	34.5483
23	NA	10	1.0521	3.9213	10	TRUE	34.5483
24	NA	10	1.0521	3.9213	10	TRUE	34.5483
25	NA	10	1.0521	3.9213	10	TRUE	34.5483
26	NA	10	1.0521	3.9213	10	TRUE	34.5483
27	NA	10	1.0521	3.9213	10	TRUE	34.5483
28	NA	10	1.0521	3.9213	10	TRUE	34.5483
29	NA	10	1.0521	3.9213	10	TRUE	34.5483
30	NA	10	1.0521	3.9213	10	TRUE	34.5483
31	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
32	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
33	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
34	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
35	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
36	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
37	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
38	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
39	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
40	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
41	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
42	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
43	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
44	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
45	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
46	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
47	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
48	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
49	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
50	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
51	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
52	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
53	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
54	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
55	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
56	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
57	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
58	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
59	0.99848065	0.5447	0.8889	0.6992	0.6992	TRUE	9.2955
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3	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
4	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
5	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
6	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
7	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
8	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
9	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
10	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
11	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
12	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
13	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
14	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
15	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
16	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
17	0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
18	0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
19	0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
20	0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
21	0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
22	0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
23	0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
24	0.99848065	0.1947	1.0196	0.5692	0.5692	TRUE	2.0003
25	0.99848065	0.1947	1.0196	0.5692	0.5692	TRUE	2.0003
26	0.99848065	0.1947	1.0196	0.5692	0.5692	TRUE	2.0003
27	0.99848065	0.0874	0.8985	0.4443	0.4443	TRUE	0.5052
28	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
29	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
30	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
31	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
32	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
33	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
34	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
35	0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
36	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3573
37	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
38	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
39	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
40	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
41	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
42	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
43	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
44	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
45	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
46	0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3574
47	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
48	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
49	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
50	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
51	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
52	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
53	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
54	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
55	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
56	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
57	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
58	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
59	0.99848065	0.6875	0.8869	0.7821	0.7821	TRUE	0.3605
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2							
3	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
4	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
5	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
6	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
7	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
8	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
9	0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
10	0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
11	0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
12	0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
13	0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
14	0.99848065	0.0828	0.8971	0.4406	0.4406	TRUE	0.283
15	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
16	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
17	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
18	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
19	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
20	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
21	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
22	0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
23	0.99848065	0.8752	0.8893	0.8814	0.8814	TRUE	0.5692
24	0.99848065	0.8752	0.8893	0.8814	0.8814	TRUE	0.5692
25	0.99848065	0.8752	0.8893	0.8814	0.8814	TRUE	0.5692
26	0.99848065	0.8752	0.8893	0.8814	0.8814	TRUE	0.5692
27	0.99848065	0.8752	0.8893	0.8814	0.8814	TRUE	0.5692
28	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
29	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
30	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
31	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
32	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
33	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
34	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
35	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
36	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
37	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
38	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
39	0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
40	0.99848065	0.1776	0.8886	0.5085	0.5085	TRUE	0.1556
41	0.99848065	0.1776	0.8886	0.5085	0.5085	TRUE	0.1556
42	0.99848065	0.1776	0.8886	0.5085	0.5085	TRUE	0.1556
43	0.99848065	0.0109	0.9976	0.4432	0.4432	TRUE	0.2926
44	0.99848065	0.3774	0.9676	0.6502	0.6502	TRUE	9.0847
45	0.99848065	0.3655	0.8873	0.6313	0.6313	TRUE	0.6019
46	0.99848065	0.3655	0.8873	0.6313	0.6313	TRUE	0.6019
47	0.99848065	0.3655	0.8873	0.6313	0.6313	TRUE	0.6019
48	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
49	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
50	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
51	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
52	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
53	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
54	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
55	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
56	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
57	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
58	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
59	0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
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3	0.99848065	0.1729	0.8873	0.5077	0.5077	TRUE	0.2551
4	0.99848065	0.1729	0.8873	0.5077	0.5077	TRUE	0.2551
5	0.99848065	0.1729	0.8873	0.5077	0.5077	TRUE	0.2551
6	0.99848065	0.1728	0.8873	0.5075	0.5075	TRUE	0.2563
7	0.99848065	0.1728	0.8873	0.5075	0.5075	TRUE	0.2563
8	0.99848065	0.0627	0.8872	0.4222	0.4222	TRUE	0.8517
9	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
10	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
11	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
12	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
13	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
14	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
15	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
16	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
17	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
18	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
19	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
20	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
21	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
22	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
23	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
24	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
25	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
26	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
27	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
28	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
29	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
30	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
31	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
32	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
33	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
34	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
35	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
36	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
37	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
38	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
39	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
40	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
41	0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
42	0.99848065	0.4707	0.97	0.7029	0.7029	TRUE	0.8753
43	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
44	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
45	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
46	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
47	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
48	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
49	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
50	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
51	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
52	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
53	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
54	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
55	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
56	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
57	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
58	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
59	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
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3	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
4	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
5	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
6	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
7	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
8	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
9	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
10	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
11	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
12	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
13	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
14	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
15	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
16	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
17	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
18	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
19	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
20	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
21	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
22	0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
23	0.99848065	0.2943	0.9273	0.5838	0.5838	TRUE	0.8903
24	0.99848065	0.2943	0.9273	0.5838	0.5838	TRUE	0.8903
25	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
26	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
27	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
28	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
29	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
30	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
31	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
32	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
33	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
34	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
35	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
36	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
37	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
38	0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
39	0.99848065	0.6933	0.9391	0.8195	0.8195	TRUE	1.0902
40	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
41	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
42	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
43	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
44	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
45	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
46	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
47	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
48	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
49	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
50	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
51	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
52	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
53	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
54	0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
55	0.99848065	0.2203	0.8964	0.5261	0.5261	TRUE	1.181
56	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
57	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
58	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
59	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
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3	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
4	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
5	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
6	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
7	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
8	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
9	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
10	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
11	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
12	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
13	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
14	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
15	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
16	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
17	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
18	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
19	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
20	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
21	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
22	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
23	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
24	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
25	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
26	0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
27	0.99848065	0.2909	0.8953	0.5586	0.5586	TRUE	5.1055
28	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
29	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
30	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
31	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
32	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
33	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
34	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
35	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
36	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
37	0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
38	0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
39	0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
40	0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
41	0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
42	0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
43	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
44	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
45	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
46	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
47	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
48	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
49	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
50	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
51	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
52	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
53	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
54	0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
55	0.99848065	1.1796	1.0502	1.1171	1.1171	TRUE	6.9224
56	0.99848065	0.5311	1.046	0.771	0.771	TRUE	0.4632
57	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
58	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
59	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
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3	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
4	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
5	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
6	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
7	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
8	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
9	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
10	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
11	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
12	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
13	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
14	0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
15	0.99848065	0.4067	0.8895	0.6039	0.6039	TRUE	3.4941
16	0.99848065	0.4067	0.8895	0.6039	0.6039	TRUE	3.4941
17	0.99848065	0.1377	0.8936	0.4743	0.4743	TRUE	2.3521
18	0.99848065	0.5386	0.9153	0.7151	0.7151	TRUE	0.7391
19	0.99848065	0.1594	1.0261	0.5525	0.5525	TRUE	0.1968
20	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
21	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
22	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
23	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
24	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
25	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
26	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
27	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
28	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
29	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
30	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
31	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
32	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
33	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
34	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
35	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
36	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
37	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
38	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
39	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
40	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
41	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
42	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
43	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
44	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
45	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
46	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
47	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
48	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
49	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
50	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
51	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
52	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
53	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
54	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
55	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
56	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
57	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
58	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
59	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
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3	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
4	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
5	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
6	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
7	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
8	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
9	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
10	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
11	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
12	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
13	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
14	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
15	0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
16	0.99848065	0.2604	0.9509	0.5746	0.5746	TRUE	0.6009
17	0.99848065	0.263	0.951	0.5761	0.5761	TRUE	0.6047
18	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
19	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
20	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
21	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
22	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
23	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
24	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
25	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
26	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
27	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
28	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
29	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
30	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
31	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
32	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
33	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
34	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
35	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
36	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
37	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
38	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
39	0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
40	0.99848065	0.346	1.0803	0.683	0.683	TRUE	1.847
41	0.99848065	0.346	1.0803	0.683	0.683	TRUE	1.847
42	0.99848065	0.5005	0.8875	0.6815	0.6815	TRUE	0.1437
43	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
44	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
45	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
46	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
47	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
48	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
49	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
50	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
51	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
52	0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
53	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
54	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
55	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
56	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
57	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
58	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
59	0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
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3	0.99848065	0.2421	0.9155	0.5477	0.5477	TRUE	0.3769
4	0.99848065	0.2431	1.0848	0.6267	0.6267	TRUE	0.2227
5	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
6	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
7	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
8	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
9	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
10	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
11	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
12	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
13	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
14	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
15	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
16	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
17	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
18	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
19	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
20	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
21	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
22	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
23	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
24	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
25	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
26	0.99848065	1.1971	0.8875	1.0466	1.0466	TRUE	0.4986
27	0.99848065	0.1383	1.0131	0.5302	0.5302	TRUE	2.9615
28	0.99848065	0.1809	0.8871	0.5069	0.5069	TRUE	0.7899
29	0.99848065	0.1809	0.8871	0.5069	0.5069	TRUE	0.7899
30	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
31	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
32	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
33	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
34	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
35	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
36	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
37	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
38	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
39	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
40	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
41	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
42	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
43	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
44	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
45	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
46	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
47	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
48	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
49	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
50	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
51	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
52	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
53	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
54	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
55	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
56	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
57	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
58	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
59	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
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3	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
4	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
5	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
6	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
7	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
8	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
9	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
10	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
11	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
12	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
13	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
14	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
15	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
16	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
17	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
18	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
19	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
20	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
21	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
22	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
23	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
24	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
25	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
26	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
27	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
28	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
29	0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
30	0.99848065	0.2206	0.9043	0.5279	0.5279	TRUE	0.3113
31	0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
32	0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
33	0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
34	0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
35	0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
36	0.99848065	0.5817	0.9753	0.766	0.766	TRUE	5.8724
37	0.99848065	0.1759	0.8876	0.508	0.508	TRUE	0.1534
38	0.99848065	0.1759	0.8876	0.508	0.508	TRUE	0.1534
39	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
40	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
41	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
42	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
43	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
44	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
45	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
46	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
47	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
48	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
49	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
50	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
51	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
52	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
53	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
54	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
55	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
56	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
57	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
58	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
59	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
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2							
3	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
4	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
5	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
6	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
7	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
8	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
9	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
10	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
11	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
12	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
13	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
14	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
15	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
16	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
17	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
18	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
19	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
20	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
21	0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
22	NA	1.3338	0.9873	1.1659	1.1659	TRUE	19.7433
23	NA	1.3338	0.9873	1.1659	1.1659	TRUE	19.7433
24	0.99848065	0.5797	0.9766	0.7656	0.7656	TRUE	6.8216
25	0.99848065	0.6576	0.8925	0.7687	0.7687	TRUE	0.9719
26	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
27	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
28	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
29	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
30	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
31	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
32	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
33	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
34	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
35	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
36	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
37	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
38	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
39	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
40	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
41	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
42	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
43	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
44	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
45	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
46	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
47	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
48	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
49	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
50	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
51	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
52	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
53	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
54	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
55	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
56	0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
57	0.99848065	0.4035	0.9055	0.6362	0.6362	TRUE	5.1643
58	0.99848065	0.201	0.907	0.5221	0.5221	TRUE	0.2014
59	0.99848065	0.201	0.907	0.5221	0.5221	TRUE	0.2014
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3	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
4	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
5	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
6	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
7	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
8	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
9	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
10	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
11	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
12	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
13	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
14	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
15	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
16	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
17	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
18	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
19	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
20	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
21	0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
22	0.99848065	0.2307	0.8871	0.5163	0.5163	TRUE	3.7539
23	0.99848065	0.3279	1.1185	0.6909	0.6909	TRUE	0.1222
24	0.99848065	0.1886	0.8908	0.5043	0.5043	TRUE	0.4283
25	0.99848065	0.199	0.891	0.5107	0.5107	TRUE	0.314
26	0.99848065	0.199	0.891	0.5107	0.5107	TRUE	0.314
27	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
28	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
29	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
30	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
31	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
32	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
33	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
34	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
35	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
36	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
37	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
38	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
39	0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
40	0.99848065	0.187	1.0395	0.5773	0.5773	TRUE	0.2223
41	0.99848065	0.187	1.0395	0.5773	0.5773	TRUE	0.2223
42	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
43	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
44	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
45	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
46	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
47	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
48	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
49	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
50	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
51	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
52	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
53	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
54	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
55	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
56	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
57	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
58	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
59	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
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3	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
4	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
5	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
6	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
7	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
8	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
9	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
10	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
11	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
12	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
13	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
14	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
15	0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
16	0.99848065	0.2055	0.9087	0.523	0.523	TRUE	0.9043
17	0.99848065	0.1794	0.8911	0.4919	0.4919	TRUE	0.2225
18	0.99848065	0.2111	0.9153	0.5293	0.5293	TRUE	0.1463
19	0.99848065	0.2105	0.9154	0.5289	0.5289	TRUE	0.1455
20	0.99848065	0.2105	0.9154	0.5289	0.5289	TRUE	0.1455
21	0.99848065	0.2105	0.9154	0.5289	0.5289	TRUE	0.1455
22	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
23	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
24	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
25	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
26	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
27	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
28	0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
29	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
30	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
31	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
32	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
33	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
34	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
35	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
36	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
37	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
38	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
39	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
40	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
41	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
42	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
43	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
44	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
45	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
46	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
47	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
48	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
49	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
50	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
51	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
52	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
53	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
54	0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
55	0.99848065	0.3703	0.8898	0.6103	0.6103	TRUE	9.5306
56	0.99848065	0.3703	0.8898	0.6103	0.6103	TRUE	9.5306
57	0.99848065	0.2728	0.8873	0.5354	0.5354	TRUE	2.5672
58	0.99848065	0.3706	0.8898	0.6104	0.6104	TRUE	9.536
59	0.99848065	0.3706	0.8898	0.6104	0.6104	TRUE	9.536
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3	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
4	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
5	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
6	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
7	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
8	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
9	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
10	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
11	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
12	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
13	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
14	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
15	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
16	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
17	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
18	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
19	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
20	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
21	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
22	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
23	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
24	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
25	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
26	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
27	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
28	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
29	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
30	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
31	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
32	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
33	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
34	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
35	0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
36	0.99848065	0.2808	0.8874	0.539	0.539	TRUE	2.8694
37	0.99848065	0.3633	0.9024	0.6122	0.6122	TRUE	3.1789
38	0.99848065	0.3633	0.9024	0.6122	0.6122	TRUE	3.1789
39	0.99848065	0.3633	0.9024	0.6122	0.6122	TRUE	3.1789
40	0.99848065	0.3633	0.9024	0.6122	0.6122	TRUE	3.1789
41	0.99848065	0.3628	0.9023	0.6119	0.6119	TRUE	2.9924
42	0.99848065	0.25	0.8882	0.5496	0.5496	TRUE	0.2022
43	0.99848065	0.25	0.8882	0.5496	0.5496	TRUE	0.2022
44	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
45	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
46	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
47	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
48	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
49	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
50	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
51	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
52	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
53	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
54	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
55	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
56	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
57	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
58	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
59	0.99848065	0.2539	0.8882	0.5526	0.5526	TRUE	0.2003
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2							
3	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
4	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
5	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
6	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
7	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
8	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
9	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
10	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
11	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
12	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
13	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
14	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
15	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
16	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
17	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
18	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
19	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
20	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
21	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
22	0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
23	NA	1.3182	0.9938	1.1611	1.1611	TRUE	19.3212
24	NA	1.8446	0.9159	1.3852	1.3852	TRUE	27.308
25	0.99848065	1.4413	1.1088	1.2777	1.2777	TRUE	3.8058
26	NA	1.9927	0.9183	1.4593	1.4593	TRUE	28.4691
27	0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
28	0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
29	0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
30	0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
31	0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
32	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
33	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
34	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
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37	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
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39	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
40	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
41	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
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43	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
44	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
45	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
46	0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
47	0.99848065	1.0296	0.8938	0.9479	0.9479	TRUE	16.4382
48	NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
49	NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
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55	NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
56	0.99848065	1.9474	0.9407	1.4455	1.4455	TRUE	0.3724
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16	NA	10	1.0033	4.5623	10	TRUE	32.3951
17	NA	10	1.0033	4.5623	10	TRUE	32.3951
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19	NA	10	1.0013	4.5666	10	TRUE	32.4775
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41	NA	6.8182	1.0342	2.8523	2.8523	TRUE	29.6685
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26	NA	10	0.9647	3.0817	10	TRUE	33.2758
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10 128.333333 0 0  
11 128.333333 0 0  
12 128.333333 0 0  
13 128.333333 0 0  
14 128.333333 0 0  
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25 128.333333 0 0  
26 128.333333 0 0  
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58 128.333333 0 0  
59 128.333333 0 0  
60

Do not distribute



1			
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4	128.333333	0	0
5	128.333333	0	0
6	128.333333	0	0
7	128.333333	0	0
8	128.333333	0	0
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25	128.333333	0	0
26	128.333333	0	0
27	128.333333	0	0
28	165	0	0
29	165	0	0
30	165	0	0
31	165	0	0
32	165	0	0
33	165	0	0
34	165	0	0
35	55.3333333	0	0
36	55.3333333	0	0
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38	55.3333333	0	0
39	55.3333333	0	0
40	55.3333333	0	0
41	55.3333333	0	0
42	55.3333333	0	0
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44	55.3333333	0	0
45	55.3333333	0	0
46	55.3333333	0	0
47	55.3333333	0	0
48	102.166667	0	0
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53	102	0	0
54	102	0	0
55	102	0	0
56	102	0	0
57	102	0	0
58	102	0	0
59	102	0	0
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1			
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9	102	0	0
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57	715.5	0	0
58	715.5	0	0
59	715.5	0	0
60			

1			
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7	715.5	0	0
8	715.5	0	0
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21	715.5	0	0
22	718.16667	0	0
23	718.16667	0	0
24	5297.16667	0	0
25	5297.16667	0	0
26	5297.16667	0	0
27	5297.16667	0	0
28	5297.16667	0	0
29	5297.16667	0	0
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57	469	0	0
58	469	0	0
59	469	0	0
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1			
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55	75.3333333	0	0
56	75.3333333	0	0
57	75.3333333	0	0
58	75.3333333	0	0
59	75.3333333	0	0
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1			
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3	85.6666667	0	0
4	85.6666667	0	0
5	85.6666667	0	0
6	85.6666667	0	0
7	85.6666667	0	0
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24	826	0	0
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28	826	0	0
29	826	0	0
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32	822.5	0	0
33	822.5	0	0
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55	822.5	0	0
56	822.5	0	0
57	822.5	0	0
58	822.5	0	0
59	822.5	0	0
60			

1			
2			
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6	822.5	0	0
7	822.5	0	0
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33	107.166667	0	0
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38	105.166667	0	0
39	76.666667	0	0
40	76.666667	0	0
41	73	0	0
42	73	0	0
43	73	0	0
44	73	0	0
45	73	0	0
46	73	0	0
47	73	0	0
48	106	0	0
49	105.666667	0	0
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55	234.666667	0	0
56	234.666667	0	0
57	234.666667	0	0
58	234.666667	0	0
59	234.666667	0	0
60			



1			
2			
3	234.666667	0	0
4	234.666667	0	0
5	234.666667	0	0
6	234.666667	0	0
7	234.666667	0	0
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34	234.666667	0	0
35	234.666667	0	0
36	103.166667	0	0
37	103.166667	0	0
38	103.166667	0	0
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43	103.166667	0	0
44	103.166667	0	0
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46	103.166667	0	0
47	103.166667	0	0
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49	103.166667	0	0
50	103.166667	0	0
51	103.166667	0	0
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54	103.166667	0	0
55	333	0	0
56	333	0	0
57	333	0	0
58	333	0	0
59	333	0	0
60			

1			
2			
3	333	0	0
4	333	0	0
5	333	0	0
6	333	0	0
7	333	0	0
8	333	0	0
9	333	0	0
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26	333	0	0
27	333	0	0
28	333	0	0
29	333	0	0
30	333	0	0
31	333	0	0
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33			
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35	64.8333333	0	0
36	91	0	0
37	91	0	0
38	91	0	0
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53	91	0	0
54	91	0	0
55	91	0	0
56	91	0	0
57	91	0	0
58	91	0	0
59	91	0	0
60			

1			
2			
3	91	0	0
4	91	0	0
5	91	0	0
6	63	0	0
7	63	0	0
8	63	0	0
9	63	0	0
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57	62.3333333	0	0
58	62.3333333	0	0
59	62.3333333	0	0
60			

Do not distribute

1			
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3	62.3333333	0	0
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5	62.3333333	0	0
6	62.3333333	0	0
7	62.3333333	0	0
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27	62.3333333	0	0
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29			
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53			
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55	89.5	0	0
56	89.5	0	0
57	89.5	0	0
58	89.5	0	0
59	89.5	0	0
60			

1			
2			
3	89.5	0	0
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5	89.5	0	0
6	89.5	0	0
7	89.5	0	0
8	89.5	0	0
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25	79.666667	0	0
26	79.666667	0	0
27	79.666667	0	0
28	522	0	0
29	522	0	0
30	522	0	0
31	161.166667	0	0
32	161.166667	0	0
33	161.166667	0	0
34	90	0	0
35	1241.16667	0	0
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37	1240.5	0	0
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57	1240.5	0	0
58	1240.5	0	0
59	1240.5	0	0
60			

1			
2			
3	1240.5	0	0
4	1240.5	0	0
5	1240.5	0	0
6	1240.5	0	0
7	1240.5	0	0
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53	501.833333	0	0
54	501.833333	0	0
55	501.833333	0	0
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miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start
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aggcaagaugcuggcauagcugu	Phvul.007G103100.1	2	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.3	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.2	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G198200.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.3	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.2	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G198200.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G214600.7	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G150800.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G261000.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G214600.7	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G150800.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G261000.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G022900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G128900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.4	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.3	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G174100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G040500.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G018100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G290000.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G040800.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.3	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G022900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G128900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.4	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.3	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G174100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G040500.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G018100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G290000.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G040800.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.3	3.5	-1	1



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4	aggcaagaugcuggcauagcugu	Phvul.010G000700.2	3.5	-1	1
5	aggcaagaugcuggcauagcugu	Phvul.009G032100.1	4	-1	1
6	aggcaagaugcuggcauagcugu	Phvul.009G243500.2	4	-1	1
7	aggcaagaugcuggcauagcugu	Phvul.002G061200.1	4	-1	1
8	aggcaagaugcuggcauagcugu	Phvul.008G061900.3	4	-1	1
9	aggcaagaugcuggcauagcugu	Phvul.008G061900.2	4	-1	1
10	aggcaagaugcuggcauagcugu	Phvul.008G061900.1	4	-1	1
11	aggcaagaugcuggcauagcugu	Phvul.009G226500.1	4	-1	1
12	aggcaagaugcuggcauagcugu	Phvul.009G226500.2	4	-1	1
13	aggcaagaugcuggcauagcugu	Phvul.009G242900.3	4	-1	1
14	aggcaagaugcuggcauagcugu	Phvul.009G242900.4	4	-1	1
15	aggcaagaugcuggcauagcugu	Phvul.009G242900.2	4	-1	1
16	aggcaagaugcuggcauagcugu	Phvul.009G242900.1	4	-1	1
17	aggcaagaugcuggcauagcugu	Phvul.002G133900.2	4	-1	1
18	aggcaagaugcuggcauagcugu	Phvul.009G106900.1	4	-1	1
19	aggcaagaugcuggcauagcugu	Phvul.009G036300.1	4	-1	1
20	aggcaagaugcuggcauagcugu	Phvul.009G192300.1	4	-1	1
21	aggcaagaugcuggcauagcugu	Phvul.003G112400.1	4	-1	1
22	aggcaagaugcuggcauagcugu	Phvul.009G032100.1	4	-1	1
23	aggcaagaugcuggcauagcugu	Phvul.009G243500.2	4	-1	1
24	aggcaagaugcuggcauagcugu	Phvul.002G061200.1	4	-1	1
25	aggcaagaugcuggcauagcugu	Phvul.008G061900.3	4	-1	1
26	aggcaagaugcuggcauagcugu	Phvul.008G061900.2	4	-1	1
27	aggcaagaugcuggcauagcugu	Phvul.008G061900.1	4	-1	1
28	aggcaagaugcuggcauagcugu	Phvul.009G226500.1	4	-1	1
29	aggcaagaugcuggcauagcugu	Phvul.009G226500.2	4	-1	1
30	aggcaagaugcuggcauagcugu	Phvul.009G242900.3	4	-1	1
31	aggcaagaugcuggcauagcugu	Phvul.009G242900.4	4	-1	1
32	aggcaagaugcuggcauagcugu	Phvul.009G242900.2	4	-1	1
33	aggcaagaugcuggcauagcugu	Phvul.009G242900.1	4	-1	1
34	aggcaagaugcuggcauagcugu	Phvul.002G133900.2	4	-1	1
35	aggcaagaugcuggcauagcugu	Phvul.009G106900.1	4	-1	1
36	aggcaagaugcuggcauagcugu	Phvul.009G036300.1	4	-1	1
37	aggcaagaugcuggcauagcugu	Phvul.009G192300.1	4	-1	1
38	aggcaagaugcuggcauagcugu	Phvul.003G112400.1	4	-1	1
39	aggcaagaugcuggcauagcugu	Phvul.009G032100.1	4	-1	1
40	aggcaagaugcuggcauagcugu	Phvul.009G243500.2	4	-1	1
41	aggcaagaugcuggcauagcugu	Phvul.002G061200.1	4	-1	1
42	aggcaagaugcuggcauagcugu	Phvul.008G061900.3	4	-1	1
43	aggcaagaugcuggcauagcugu	Phvul.008G061900.2	4	-1	1
44	aggcaagaugcuggcauagcugu	Phvul.008G061900.1	4	-1	1
45	aggcaagaugcuggcauagcugu	Phvul.009G226500.1	4	-1	1
46	aggcaagaugcuggcauagcugu	Phvul.009G226500.2	4	-1	1
47	aggcaagaugcuggcauagcugu	Phvul.009G242900.3	4	-1	1
48	aggcaagaugcuggcauagcugu	Phvul.009G242900.4	4	-1	1
49	aggcaagaugcuggcauagcugu	Phvul.009G242900.2	4	-1	1
50	aggcaagaugcuggcauagcugu	Phvul.009G242900.1	4	-1	1
51	aggcaagaugcuggcauagcugu	Phvul.002G133900.2	4	-1	1
52	aggcaagaugcuggcauagcugu	Phvul.009G106900.1	4	-1	1
53	aggcaagaugcuggcauagcugu	Phvul.009G036300.1	4	-1	1
54	aggcaagaugcuggcauagcugu	Phvul.009G192300.1	4	-1	1
55	aggcaagaugcuggcauagcugu	Phvul.003G112400.1	4	-1	1
56	aggcaagaugcuggcauagcugu	Phvul.006G151200.1	4.5	-1	1
57	aggcaagaugcuggcauagcugu	Phvul.006G104300.2	4.5	-1	1
58	aggcaagaugcuggcauagcugu	Phvul.006G104300.1	4.5	-1	1
59	aggcaagaugcuggcauagcugu	Phvul.011G033500.1	4.5	-1	1
60	aggcaagaugcuggcauagcugu	Phvul.008G038200.1	4.5	-1	1
	aggcaagaugcuggcauagcugu	Phvul.002G022400.1	4.5	-1	1
	aggcaagaugcuggcauagcugu	Phvul.L001644.1	4.5	-1	1

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3	aggcaagaugcuggcauagcugu	Phvul.001G264132.1	4.5	-1	1
4	aggcaagaugcuggcauagcugu	Phvul.009G019100.1	4.5	-1	1
5	aggcaagaugcuggcauagcugu	Phvul.009G073900.1	4.5	-1	1
6	aggcaagaugcuggcauagcugu	Phvul.003G159700.1	4.5	-1	1
7	aggcaagaugcuggcauagcugu	Phvul.006G151200.1	4.5	-1	1
8	aggcaagaugcuggcauagcugu	Phvul.006G104300.2	4.5	-1	1
9	aggcaagaugcuggcauagcugu	Phvul.006G104300.1	4.5	-1	1
10	aggcaagaugcuggcauagcugu	Phvul.011G033500.1	4.5	-1	1
11	aggcaagaugcuggcauagcugu	Phvul.008G038200.1	4.5	-1	1
12	aggcaagaugcuggcauagcugu	Phvul.002G022400.1	4.5	-1	1
13	aggcaagaugcuggcauagcugu	Phvul.L001644.1	4.5	-1	1
14	aggcaagaugcuggcauagcugu	Phvul.001G264132.1	4.5	-1	1
15	aggcaagaugcuggcauagcugu	Phvul.009G019100.1	4.5	-1	1
16	aggcaagaugcuggcauagcugu	Phvul.009G073900.1	4.5	-1	1
17	aggcaagaugcuggcauagcugu	Phvul.003G159700.1	4.5	-1	1
18	aggcaagaugcuggcauagcugu	Phvul.001G214600.7	5	-1	1
19	aggcaagaugcuggcauagcugu	Phvul.009G228600.1	5	-1	1
20	aggcaagaugcuggcauagcugu	Phvul.009G035800.1	5	-1	1
21	aggcaagaugcuggcauagcugu	Phvul.011G134100.1	5	-1	1
22	aggcaagaugcuggcauagcugu	Phvul.011G134000.1	5	-1	1
23	aggcaagaugcuggcauagcugu	Phvul.011G130800.1	5	-1	1
24	aggcaagaugcuggcauagcugu	Phvul.011G081100.1	5	-1	1
25	aggcaagaugcuggcauagcugu	Phvul.011G133300.1	5	-1	1
26	aggcaagaugcuggcauagcugu	Phvul.007G247800.1	5	-1	1
27	aggcaagaugcuggcauagcugu	Phvul.004G172000.1	5	-1	1
28	aggcaagaugcuggcauagcugu	Phvul.010G031700.2	5	-1	1
29	aggcaagaugcuggcauagcugu	Phvul.010G031700.3	5	-1	1
30	aggcaagaugcuggcauagcugu	Phvul.005G105800.1	5	-1	1
31	aggcaagaugcuggcauagcugu	Phvul.009G021200.1	5	-1	1
32	aggcaagaugcuggcauagcugu	Phvul.009G226800.1	5	-1	1
33	aggcaagaugcuggcauagcugu	Phvul.006G162000.1	5	-1	1
34	aggcaagaugcuggcauagcugu	Phvul.002G038300.1	5	-1	1
35	aggcaagaugcuggcauagcugu	Phvul.007G188300.1	5	-1	1
36	aggcaagaugcuggcauagcugu	Phvul.004G084688.1	5	-1	1
37	aggcaagaugcuggcauagcugu	Phvul.L001859.1	5	-1	1
38	aggcaagaugcuggcauagcugu	Phvul.002G027900.1	5	-1	1
39	aggcaagaugcuggcauagcugu	Phvul.005G180700.1	5	-1	1
40	aggcaagaugcuggcauagcugu	Phvul.004G153700.1	5	-1	1
41	aggcaagaugcuggcauagcugu	Phvul.001G214600.7	5	-1	1
42	aggcaagaugcuggcauagcugu	Phvul.009G228600.1	5	-1	1
43	aggcaagaugcuggcauagcugu	Phvul.009G035800.1	5	-1	1
44	aggcaagaugcuggcauagcugu	Phvul.011G134100.1	5	-1	1
45	aggcaagaugcuggcauagcugu	Phvul.011G134000.1	5	-1	1
46	aggcaagaugcuggcauagcugu	Phvul.011G130800.1	5	-1	1
47	aggcaagaugcuggcauagcugu	Phvul.011G081100.1	5	-1	1
48	aggcaagaugcuggcauagcugu	Phvul.011G133300.1	5	-1	1
49	aggcaagaugcuggcauagcugu	Phvul.007G247800.1	5	-1	1
50	aggcaagaugcuggcauagcugu	Phvul.004G172000.1	5	-1	1
51	aggcaagaugcuggcauagcugu	Phvul.010G031700.2	5	-1	1
52	aggcaagaugcuggcauagcugu	Phvul.010G031700.3	5	-1	1
53	aggcaagaugcuggcauagcugu	Phvul.005G105800.1	5	-1	1
54	aggcaagaugcuggcauagcugu	Phvul.009G021200.1	5	-1	1
55	aggcaagaugcuggcauagcugu	Phvul.009G226800.1	5	-1	1
56	aggcaagaugcuggcauagcugu	Phvul.006G162000.1	5	-1	1
57	aggcaagaugcuggcauagcugu	Phvul.002G038300.1	5	-1	1
58	aggcaagaugcuggcauagcugu	Phvul.007G188300.1	5	-1	1
59	aggcaagaugcuggcauagcugu	Phvul.004G084688.1	5	-1	1
60	aggcaagaugcuggcauagcugu	Phvul.L001859.1	5	-1	1

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3	aggcaagaugcuggcauagcugu	Phvul.011G130800.1	5	-1	1
4	aggcaagaugcuggcauagcugu	Phvul.011G081100.1	5	-1	1
5	aggcaagaugcuggcauagcugu	Phvul.011G133300.1	5	-1	1
6	aggcaagaugcuggcauagcugu	Phvul.007G247800.1	5	-1	1
7	aggcaagaugcuggcauagcugu	Phvul.004G172000.1	5	-1	1
8	aggcaagaugcuggcauagcugu	Phvul.010G031700.2	5	-1	1
9	aggcaagaugcuggcauagcugu	Phvul.010G031700.3	5	-1	1
10	aggcaagaugcuggcauagcugu	Phvul.005G105800.1	5	-1	1
11	aggcaagaugcuggcauagcugu	Phvul.009G021200.1	5	-1	1
12	aggcaagaugcuggcauagcugu	Phvul.009G226800.1	5	-1	1
13	aggcaagaugcuggcauagcugu	Phvul.006G162000.1	5	-1	1
14	aggcaagaugcuggcauagcugu	Phvul.002G038300.1	5	-1	1
15	aggcaagaugcuggcauagcugu	Phvul.007G188300.1	5	-1	1
16	aggcaagaugcuggcauagcugu	Phvul.004G084688.1	5	-1	1
17	aggcaagaugcuggcauagcugu	Phvul.L001859.1	5	-1	1
18	aggcaagaugcuggcauagcugu	Phvul.002G027900.1	5	-1	1
19	aggcaagaugcuggcauagcugu	Phvul.005G180700.1	5	-1	1
20	aggcaagaugcuggcauagcugu	Phvul.004G153700.1	5	-1	1
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miRNA_end	Target_start	Target_end	miRNA_alignment	Target_alignment	Inhibition
23	1845	1867	AGGCAAGAU(	UGGAUUAUG	Cleavage
23	1845	1867	AGGCAAGAU(	UGGAUUAUG	Cleavage
23	1031	1053	AGGCAAGAU(	CAAGCUAUG(	Cleavage
23	1656	1678	AGGCAAGAU(	CAAGCUAUG(	Cleavage
23	1656	1678	AGGCAAGAU(	CAAGCUAUG(	Cleavage
23	775	797	AGGCAAGAU(	AAACUUAUG(	Cleavage
23	1031	1053	AGGCAAGAU(	CAAGCUAUG(	Cleavage
23	1656	1678	AGGCAAGAU(	CAAGCUAUG(	Cleavage
23	1656	1678	AGGCAAGAU(	CAAGCUAUG(	Cleavage
23	775	797	AGGCAAGAU(	AAACUUAUG(	Cleavage
23	1055	1077	AGGCAAGAU(	UCAUCUAUG(	Cleavage
23	1403	1425	AGGCAAGAU(	AGAACUCUG(	Cleavage
23	1694	1716	AGGCAAGAU(	UCUCCUUUG(	Cleavage
23	1055	1077	AGGCAAGAU(	UCAUCUAUG(	Cleavage
23	1403	1425	AGGCAAGAU(	AGAACUCUG(	Cleavage
23	1694	1716	AGGCAAGAU(	UCUCCUUUG(	Cleavage
23	94	116	AGGCAAGAU(	ACAACUGUG(	Cleavage
23	798	820	AGGCAAGAU(	CCAACUGUG(	Cleavage
23	573	595	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	573	595	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	1468	1490	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	1468	1490	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	2981	3002	AGGCAAGAU(	GCACCUAU-C(	Cleavage
23	1638	1660	AGGCAAGAU(	GAAACUAUG(	Cleavage
23	1884	1906	AGGCAAGAU(	AGCAUUAUG(	Cleavage
23	1140	1162	AGGCAAGAU(	ACUUCAGUG(	Cleavage
23	1074	1096	AGGCAAGAU(	UAACCUCUG(	Cleavage
23	1003	1025	AGGCAAGAU(	CAUUCUAUG(	Cleavage
23	1003	1025	AGGCAAGAU(	CAUUCUAUG(	Cleavage
23	1003	1025	AGGCAAGAU(	CAUUCUAUG(	Cleavage
23	94	116	AGGCAAGAU(	ACAACUGUG(	Cleavage
23	798	820	AGGCAAGAU(	CCAACUGUG(	Cleavage
23	573	595	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	573	595	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	1468	1490	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	1468	1490	AGGCAAGAU(	GCUGAUUAU(	Cleavage
23	2981	3002	AGGCAAGAU(	GCACCUAU-C(	Cleavage
23	1638	1660	AGGCAAGAU(	GAAACUAUG(	Cleavage
23	1884	1906	AGGCAAGAU(	AGCAUUAUG(	Cleavage
23	1140	1162	AGGCAAGAU(	ACUUCAGUG(	Cleavage
23	1074	1096	AGGCAAGAU(	UAACCUCUG(	Cleavage
23	1003	1025	AGGCAAGAU(	CAUUCUAUG(	Cleavage





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4	23	1000	1022 AGGCAAGAU(:..... :..... :AUAGCUAUG) Cleavage
5	23	1064	1086 AGGCAAGAU(:... :..... :AUAGCAAUG) Cleavage
6	23	1000	1022 AGGCAAGAU(:..... :..... :AUAGCUAUG) Cleavage
7	23	1232	1255 AGGCAAGAU( :..... :..... :CAAGCUAUG) Translation
8	23	1770	1792 AGGCAAGAU( :... :..... :...UCAGUUUUG) Cleavage
9	23	2276	2298 AGGCAAGAU(:... :..... :GCAGUUUCG) Cleavage
10	23	2353	2375 AGGCAAGAU(:... :..... :GCAGUUUCG) Cleavage
11	23	2353	2375 AGGCAAGAU(:... :..... :GCAGUUUCG) Cleavage
12	23	1513	1535 AGGCAAGAU(:... :..... :...AUAGCACUG) Cleavage
13	23	733	755 AGGCAAGAU( :... :..... :UUAGUAAUG) Translation
14	23	733	755 AGGCAAGAU( :... :..... :UUAGUAAUG) Translation
15	23	809	831 AGGCAAGAU(: :... :..... :ACUGCUAAG) Cleavage
16	23	809	831 AGGCAAGAU(: :... :..... :ACUGCUAAG) Cleavage
17	23	1197	1220 AGGCA-AGAU :..... :..... :GGUGCUAUG) Cleavage
18	23	1385	1407 AGGCAAGAU(: :..... :..... :AUUGCUAUG) Cleavage
19	23	277	299 AGGCAAGAU(: :..... :..... :ACACCCGUG) Cleavage
20	23	2137	2159 AGGCAAGAU( :..... :..... :UUGGUUGUG) Cleavage
21	23	2137	2159 AGGCAAGAU( :..... :..... :UUGGUUGUG) Cleavage
22	23	693	716 AGGCAAGAU( : :..... :..... :UUAUCUGUG) Translation
23	23	34	56 AGGCAAGAU(: :... :..... :AAAGCUUUG) Translation
24	23	1702	1724 AGGCAAGAU(:... : :..... :AUUGAUUUG) Cleavage
25	23	1702	1724 AGGCAAGAU(:... : :..... :AUUGAUUUG) Cleavage
26	23	606	628 AGGCAAGAU( : :..... :...UGAGCAAUG) Cleavage
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	Target_Desc.	Multiplicity	Target_Acc.	locusName	Pfam	
1						
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5	pacid=371666	1	Phvul.007G103100	Phvul.007G103100	PF02127	
6	pacid=371666	1	Phvul.007G103100	Phvul.007G103100	PF02127	
7	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
8	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
9	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
10	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
11	pacid=371750	1	Phvul.002G198200	Phvul.002G198200	PF12847	
12	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
13	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
14	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
15	pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650	
16	pacid=371750	1	Phvul.002G198200	Phvul.002G198200	PF12847	
17	pacid=371692	2	Phvul.001G214600	Phvul.001G214600		0
18	pacid=371516	1	Phvul.009G150800	Phvul.009G150800	PF03151	
19	pacid=371743	1	Phvul.002G261000	Phvul.002G261000	PF12070	
20	pacid=371692	2	Phvul.001G214600	Phvul.001G214600		0
21	pacid=371516	1	Phvul.009G150800	Phvul.009G150800	PF03151	
22	pacid=371743	1	Phvul.002G261000	Phvul.002G261000	PF12070	
23	pacid=371685	1	Phvul.001G022900	Phvul.001G022900	PF00447	
24	pacid=371580	1	Phvul.008G128900	Phvul.008G128900	PF00097	
25	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
26	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
27	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
28	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
29	pacid=371478	1	Phvul.003G174100	Phvul.003G174100	PF03144,PF00	
30	pacid=371593	1	Phvul.008G040500	Phvul.008G040500	PF00854	
31	pacid=371633	1	Phvul.004G018100	Phvul.004G018100	PF02705	
32	pacid=371602	1	Phvul.008G290000	Phvul.008G290000	PF00627,PF00	
33	pacid=371525	1	Phvul.005G040800	Phvul.005G040800	PF04652	
34	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	
35	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	
36	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	
37	pacid=371685	1	Phvul.001G022900	Phvul.001G022900	PF00447	
38	pacid=371580	1	Phvul.008G128900	Phvul.008G128900	PF00097	
39	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
40	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
41	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
42	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
43	pacid=371478	1	Phvul.003G174100	Phvul.003G174100	PF03144,PF00	
44	pacid=371593	1	Phvul.008G040500	Phvul.008G040500	PF00854	
45	pacid=371633	1	Phvul.004G018100	Phvul.004G018100	PF02705	
46	pacid=371602	1	Phvul.008G290000	Phvul.008G290000	PF00627,PF00	
47	pacid=371525	1	Phvul.005G040800	Phvul.005G040800	PF04652	
48	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	
49	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	
50	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	
51	pacid=371685	1	Phvul.001G022900	Phvul.001G022900	PF00447	
52	pacid=371580	1	Phvul.008G128900	Phvul.008G128900	PF00097	
53	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
54	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
55	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
56	pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483	
57	pacid=371478	1	Phvul.003G174100	Phvul.003G174100	PF03144,PF00	
58	pacid=371593	1	Phvul.008G040500	Phvul.008G040500	PF00854	
59	pacid=371633	1	Phvul.004G018100	Phvul.004G018100	PF02705	
60	pacid=371602	1	Phvul.008G290000	Phvul.008G290000	PF00627,PF00	
61	pacid=371525	1	Phvul.005G040800	Phvul.005G040800	PF04652	
62	pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11	

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4	pacid=371440	1 Phvul.010G000700	Phvul.010G000700	PF12295,PF11
5	pacid=371440	1 Phvul.010G000700	Phvul.010G000700	PF12295,PF11
6	pacid=371489	1 Phvul.009G032100	Phvul.009G032100	PF04674
7	pacid=371515	1 Phvul.009G243500	Phvul.009G243500	PF00856
8	pacid=371751	1 Phvul.002G061200	Phvul.002G061200	PF08244,PF11
9	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
10	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
11	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
12	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
13	pacid=371514	1 Phvul.009G226500	Phvul.009G226500	PF16124,PF00
14	pacid=371514	1 Phvul.009G226500	Phvul.009G226500	PF16124,PF00
15	pacid=371506	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
16	pacid=371506	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
17	pacid=371506	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
18	pacid=371505	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
19	pacid=371505	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
20	pacid=371774	1 Phvul.002G133900	Phvul.002G133900	0
21	pacid=371497	1 Phvul.009G106900	Phvul.009G106900	PF10255
22	pacid=371504	1 Phvul.009G036300	Phvul.009G036300	PF00249
23	pacid=371489	1 Phvul.009G192300	Phvul.009G192300	PF13414
24	pacid=371446	1 Phvul.003G112400	Phvul.003G112400	PF04802
25	pacid=371489	1 Phvul.009G032100	Phvul.009G032100	PF04674
26	pacid=371515	1 Phvul.009G243500	Phvul.009G243500	PF00856
27	pacid=371751	1 Phvul.002G061200	Phvul.002G061200	PF08244,PF11
28	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
29	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
30	pacid=371613	1 Phvul.008G061900	Phvul.008G061900	PF07690
31	pacid=371514	1 Phvul.009G226500	Phvul.009G226500	PF16124,PF00
32	pacid=371514	1 Phvul.009G226500	Phvul.009G226500	PF16124,PF00
33	pacid=371506	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
34	pacid=371506	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
35	pacid=371506	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
36	pacid=371505	1 Phvul.009G242900	Phvul.009G242900	PF07687,PF01
37	pacid=371774	1 Phvul.002G133900	Phvul.002G133900	0
38	pacid=371497	1 Phvul.009G106900	Phvul.009G106900	PF10255
39	pacid=371504	1 Phvul.009G036300	Phvul.009G036300	PF00249
40	pacid=371489	1 Phvul.009G192300	Phvul.009G192300	PF13414
41	pacid=371446	1 Phvul.003G112400	Phvul.003G112400	PF04802
42	pacid=371734	1 Phvul.006G151200	Phvul.006G151200	PF00849
43	pacid=371721	1 Phvul.006G104300	Phvul.006G104300	PF06101
44	pacid=371721	1 Phvul.006G104300	Phvul.006G104300	PF06101
45	pacid=371563	1 Phvul.011G033500	Phvul.011G033500	PF01535,PF13
46	pacid=371588	1 Phvul.008G038200	Phvul.008G038200	PF00249
47	pacid=371787	1 Phvul.002G022400	Phvul.002G022400	PF01535,PF13
48	pacid=371742	1 Phvul.L001644	Phvul.L001644	PF14432,PF01
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4	pacid=371686	1 Phvul.001G264132	Phvul.001G264132	PF00270
5	pacid=371502	1 Phvul.009G019100	Phvul.009G019100	PF01399,PF08
6	pacid=371514	1 Phvul.009G073900	Phvul.009G073900	0
7	pacid=371469	1 Phvul.003G159700	Phvul.003G159700	PF08263,PF13
8	pacid=371734	1 Phvul.006G151200	Phvul.006G151200	PF00849
9	pacid=371721	1 Phvul.006G104300	Phvul.006G104300	PF06101
10	pacid=371721	1 Phvul.006G104300	Phvul.006G104300	PF06101
11	pacid=371563	1 Phvul.011G033500	Phvul.011G033500	PF01535,PF13
12	pacid=371588	1 Phvul.008G038200	Phvul.008G038200	PF00249
13	pacid=371787	1 Phvul.002G022400	Phvul.002G022400	PF01535,PF13
14	pacid=371742	1 Phvul.L001644	Phvul.L001644	PF14432,PF01
15	pacid=371686	1 Phvul.001G264132	Phvul.001G264132	PF00270
16	pacid=371502	1 Phvul.009G019100	Phvul.009G019100	PF01399,PF08
17	pacid=371514	1 Phvul.009G073900	Phvul.009G073900	0
18	pacid=371469	1 Phvul.003G159700	Phvul.003G159700	PF08263,PF13
19	pacid=371692	2 Phvul.001G214600	Phvul.001G214600	0
20	pacid=371486	1 Phvul.009G228600	Phvul.009G228600	PF06596
21	pacid=371491	1 Phvul.009G035800	Phvul.009G035800	PF07714,PF14
22	pacid=371564	1 Phvul.011G134100	Phvul.011G134100	PF08246,PF00
23	pacid=371557	1 Phvul.011G134000	Phvul.011G134000	PF08246,PF00
24	pacid=371547	1 Phvul.011G130800	Phvul.011G130800	PF08246,PF00
25	pacid=371568	1 Phvul.011G081100	Phvul.011G081100	PF08246,PF00
26	pacid=371571	1 Phvul.011G133300	Phvul.011G133300	PF08246,PF00
27	pacid=371674	1 Phvul.007G247800	Phvul.007G247800	PF12922,PF12
28	pacid=371622	1 Phvul.004G172000	Phvul.004G172000	0
29	pacid=371435	1 Phvul.010G031700	Phvul.010G031700	PF04130
30	pacid=371435	1 Phvul.010G031700	Phvul.010G031700	PF04130
31	pacid=371533	1 Phvul.005G105800	Phvul.005G105800	PF05623
32	pacid=371519	1 Phvul.009G021200	Phvul.009G021200	0
33	pacid=371493	1 Phvul.009G226800	Phvul.009G226800	PF04525
34	pacid=371719	1 Phvul.006G162000	Phvul.006G162000	PF00097,PF05
35	pacid=371757	1 Phvul.002G038300	Phvul.002G038300	PF06101
36	pacid=371658	1 Phvul.007G188300	Phvul.007G188300	PF11721,PF07
37	pacid=371636	1 Phvul.004G084688	Phvul.004G084688	PF08263,PF00
38	pacid=371521	1 Phvul.L001859	Phvul.L001859	0
39	pacid=371753	1 Phvul.002G027900	Phvul.002G027900	PF00190
40	pacid=371530	1 Phvul.005G180700	Phvul.005G180700	PF00690,PF00
41	pacid=371631	1 Phvul.004G153700	Phvul.004G153700	PF13041,PF01
42	pacid=371692	2 Phvul.001G214600	Phvul.001G214600	0
43	pacid=371486	1 Phvul.009G228600	Phvul.009G228600	PF06596
44	pacid=371491	1 Phvul.009G035800	Phvul.009G035800	PF07714,PF14
45	pacid=371564	1 Phvul.011G134100	Phvul.011G134100	PF08246,PF00
46	pacid=371557	1 Phvul.011G134000	Phvul.011G134000	PF08246,PF00
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3	pacid=371547	1 Phvul.011G130800	Phvul.011G130800	PF08246,PF00
4	pacid=371568	1 Phvul.011G081100	Phvul.011G081100	PF08246,PF00
5	pacid=371571	1 Phvul.011G133300	Phvul.011G133300	PF08246,PF00
6	pacid=371674	1 Phvul.007G247800	Phvul.007G247800	PF12922,PF12
7	pacid=371622	1 Phvul.004G172000	Phvul.004G172000	0
8	pacid=371435	1 Phvul.010G031700	Phvul.010G031700	PF04130
9	pacid=371435	1 Phvul.010G031700	Phvul.010G031700	PF04130
10	pacid=371533	1 Phvul.005G105800	Phvul.005G105800	PF05623
11	pacid=371519	1 Phvul.009G021200	Phvul.009G021200	0
12	pacid=371493	1 Phvul.009G226800	Phvul.009G226800	PF04525
13	pacid=371719	1 Phvul.006G162000	Phvul.006G162000	PF00097,PF05
14	pacid=371757	1 Phvul.002G038300	Phvul.002G038300	PF06101
15	pacid=371658	1 Phvul.007G188300	Phvul.007G188300	PF11721,PF07
16	pacid=371636	1 Phvul.004G084688	Phvul.004G084688	PF08263,PF00
17	pacid=371521	1 Phvul.L001859	Phvul.L001859	0
18	pacid=371753	1 Phvul.002G027900	Phvul.002G027900	PF00190
19	pacid=371530	1 Phvul.005G180700	Phvul.005G180700	PF00690,PF00
20	pacid=371631	1 Phvul.004G153700	Phvul.004G153700	PF13041,PF01
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Panther	KOG	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol
PTHR28570,P		0 3.4.11.21	K01267	GO:0008270,(	AT5G04710.1 0
PTHR28570,P		0 3.4.11.21	K01267	GO:0008270,(	AT5G04710.1 0
PTHR23324,P		0	0	0	0 AT4G39170.1 0
PTHR23324,P		0	0	0	0 AT4G39170.1 0
PTHR23324,P		0	0	0	0 AT4G39170.1 0
PTHR21404	KOG1045		0	0 GO:0008173,(	AT4G20910.1 CRM2,HEN1
PTHR23324,P		0	0	0	0 AT4G39170.1 0
PTHR23324,P		0	0	0	0 AT4G39170.1 0
PTHR23324,P		0	0	0	0 AT4G39170.1 0
PTHR21404	KOG1045		0	0 GO:0008173,(	AT4G20910.1 CRM2,HEN1
PTHR34210,P		0	0	0	0 AT3G62330.1 0
PTHR11132,P	KOG1444		0 K15356		0 AT2G13650.1 GONST1
PTHR21243,P		0	0	0 GO:0006351,(	AT4G40050.1 0
PTHR34210,P		0	0	0	0 AT3G62330.1 0
PTHR11132,P	KOG1444		0 K15356		0 AT2G13650.1 GONST1
PTHR21243,P		0	0	0 GO:0006351,(	AT4G40050.1 0
PTHR10015,P		0	0 K09419	GO:0043565,(	AT1G46264.1 AT-HSFB4,HSF
PTHR10825,P		0 6.3.2.19	K10695	GO:0046872	AT5G44280.1 ATRING1A,RIM
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR23115,P		0 3.6.5.3	K12852	GO:0005525	AT1G06220.1 CLO,GFA1,ME
PTHR11654,P		0	0	0 GO:0016020,(	AT1G32450.1 NRT1.5
PTHR30540,P		0	0 K03549	GO:0071805,(	AT5G14880.1 0
PTHR13779,P		0 3.6.1.3	K07478	GO:0005524	AT1G24290.1 0
PTHR12741,P		0 2.4.1.34	K11000	GO:0003843	AT2G31960.2 ATGSL03,ATG
PTHR15245,P	KOG1895		0	0	0 AT5G01400.1 ESP4
PTHR15245,P	KOG1895		0	0	0 AT5G01400.1 ESP4
PTHR15245,P	KOG1895		0	0	0 AT5G01400.1 ESP4
PTHR10015,P		0	0 K09419	GO:0043565,(	AT1G46264.1 AT-HSFB4,HSF
PTHR10825,P		0 6.3.2.19	K10695	GO:0046872	AT5G44280.1 ATRING1A,RIM
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR22572,P	KOG1322	2.7.7.27		0 GO:0016779,(	AT1G27680.1 APL2
PTHR23115,P		0 3.6.5.3	K12852	GO:0005525	AT1G06220.1 CLO,GFA1,ME
PTHR11654,P		0	0	0 GO:0016020,(	AT1G32450.1 NRT1.5
PTHR30540,P		0	0 K03549	GO:0071805,(	AT5G14880.1 0
PTHR13779,P		0 3.6.1.3	K07478	GO:0005524	AT1G24290.1 0
PTHR12741,P		0 2.4.1.34	K11000	GO:0003843	AT2G31960.2 ATGSL03,ATG
PTHR15245,P	KOG1895		0	0	0 AT5G01400.1 ESP4

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3	PTHR15245,P <sup>-</sup>	KOG1895	0	0	0	AT5G01400.1	ESP4		
4	PTHR15245,P <sup>-</sup>	KOG1895	0	0	0	AT5G01400.1	ESP4		
5	PTHR15245,P <sup>-</sup>	KOG1895	0	0	0	AT5G01400.1	ESP4		
6	PTHR31279,P <sup>-</sup>		0	0	0	AT4G08950.1	EXO		
7	PTHR13271,P <sup>-</sup>		0	2.1.1.127	0	GO:0005515	AT4G20130.1	PTAC14	
8	PTHR31953,P <sup>-</sup>		0	3.2.1.26	K01193	GO:0004575,(	AT1G12240.1	ATBETAFRUCT	
9	PTHR31953,P <sup>-</sup>		0	3.2.1.26	K01193	GO:0004575,(	AT1G12240.1	ATBETAFRUCT	
10	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
11	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
12	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
13	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
14	PTHR13710,P <sup>-</sup>	KOG0352	3.6.4.12	K10901	0	GO:0005524,(	AT4G35740.1	ATRECCQ3,Recl	
15	PTHR13710,P <sup>-</sup>	KOG0352	3.6.4.12	K10901	0	GO:0005524,(	AT4G35740.1	ATRECCQ3,Recl	
16	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
17	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
18	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
19	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
20	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
21	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
22	0	0	0	0	0	0	0	0	0
23	PTHR13242	KOG3677	0	K15029	0	GO:0005852,(	AT5G25754.1		0
24	PTHR21717,P <sup>-</sup>		0	0	0	0	AT1G09710.2		0
25	PTHR21717,P <sup>-</sup>		0	0	0	0	AT1G09710.2		0
26	PTHR16193	KOG1128	0	0	0	0	AT5G17270.1		0
27	PTHR23318,P <sup>-</sup>	KOG2175	0	K17491	0	0	AT3G06670.1		0
28	PTHR23318,P <sup>-</sup>	KOG2175	0	K17491	0	0	AT3G06670.1		0
29	PTHR31279,P <sup>-</sup>		0	0	0	0	AT4G08950.1	EXO	
30	PTHR13271,P <sup>-</sup>		0	2.1.1.127	0	GO:0005515	AT4G20130.1	PTAC14	
31	PTHR31953,P <sup>-</sup>		0	3.2.1.26	K01193	GO:0004575,(	AT1G12240.1	ATBETAFRUCT	
32	PTHR31953,P <sup>-</sup>		0	3.2.1.26	K01193	GO:0004575,(	AT1G12240.1	ATBETAFRUCT	
33	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
34	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
35	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
36	PTHR11662,P <sup>-</sup>	KOG2532	0		0	GO:0055085,(	AT4G00370.1	ANTR2,PHT4;4	
37	PTHR13710,P <sup>-</sup>	KOG0352	3.6.4.12	K10901	0	GO:0005524,(	AT4G35740.1	ATRECCQ3,Recl	
38	PTHR13710,P <sup>-</sup>	KOG0352	3.6.4.12	K10901	0	GO:0005524,(	AT4G35740.1	ATRECCQ3,Recl	
39	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
40	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
41	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
42	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
43	PTHR32494,P <sup>-</sup>		0	3.5.3.9	0	GO:0016787,(	AT4G20070.1	AAH,ATAAH	
44	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0
46	PTHR13242	KOG3677	0	K15029	0	GO:0005852,(	AT5G25754.1		0
47	PTHR21717,P <sup>-</sup>		0	0	0	0	AT1G09710.2		0
48	PTHR21717,P <sup>-</sup>		0	0	0	0	AT1G09710.2		0
49	PTHR16193	KOG1128	0	0	0	0	AT5G17270.1		0
50	PTHR23318,P <sup>-</sup>	KOG2175	0	K17491	0	0	AT3G06670.1		0
51	PTHR11079,P <sup>-</sup>	KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1		0
52	PTHR17204,P <sup>-</sup>		0	0	0	0	AT3G04350.1		0
53	PTHR17204,P <sup>-</sup>		0	0	0	0	AT3G04350.1		0
54	PTHR17204,P <sup>-</sup>		0	0	0	0	AT3G04350.1		0
55	PTHR24015,P <sup>-</sup>		0	0	0	0	AT2G21090.1		0
56	PTHR10641,P <sup>-</sup>		0	0	0	0	AT1G66370.1	AtMYB113,M	
57	PTHR24015,P <sup>-</sup>		0	0	0	0	AT3G50420.1		0
58	PTHR24015,P <sup>-</sup>		0	0	0	0	AT3G50420.1		0
59	PTHR24015,P <sup>-</sup>		0	0	0	0	AT1G25360.1		0
60	PTHR24015,P <sup>-</sup>		0	0	0	0	AT1G25360.1		0



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3	PTHR18934,P <sup>-</sup>	0 3.6.4.13		0 GO:0005524,(AT3G26560.1	0
4	PTHR10758,P <sup>-</sup>	0	0 K03033	GO:0005515,(AT1G20200.1 EMB2719,HA	
5	PTHR37613	0	0	0 0 0	0
6					
7	PTHR27008,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0005515,(AT2G26730.1	0
8					
9	PTHR11079,P <sup>-</sup> KOG1919	5.4.99.24		0 GO:0009982,(AT4G21770.1	0
10	PTHR17204,P <sup>-</sup>	0	0	0 0 AT3G04350.1	0
11	PTHR17204,P <sup>-</sup>	0	0	0 0 AT3G04350.1	0
12	PTHR24015,P <sup>-</sup>	0	0	0 0 AT2G21090.1	0
13					
14	PTHR10641,P <sup>-</sup>	0	0	0 0 AT1G66370.1 AtMYB113,M	
15	PTHR24015,P <sup>-</sup>	0	0	0 0 AT3G50420.1	0
16	PTHR24015,P <sup>-</sup>	0	0	0 0 AT1G25360.1	0
17					
18	PTHR18934,P <sup>-</sup>	0 3.6.4.13		0 GO:0005524,(AT3G26560.1	0
19	PTHR10758,P <sup>-</sup>	0	0 K03033	GO:0005515,(AT1G20200.1 EMB2719,HA	
20	PTHR37613	0	0	0 0 0	0
21					
22	PTHR27008,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0005515,(AT2G26730.1	0
23	PTHR34210,P <sup>-</sup>	0	0	0 0 AT3G62330.1	0
24	PTHR34455,P <sup>-</sup>	0	0	0 GO:0016020,(AT2G06520.1 PSBX	
25					
26	PTHR23257,P <sup>-</sup> KOG0192	2.7.11.1		0 GO:0006468,(AT4G24480.1	0
27	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
28	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
29	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
30	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
31	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
32	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
33					
34	PTHR14222,P <sup>-</sup>	0	0 K06677	GO:0007076 AT3G57060.2	0
35	PTHR35505,P <sup>-</sup>	0	0	0 0 AT5G11780.1	0
36	PTHR19302,P <sup>-</sup>	0	0 K16569	GO:0005815,(AT5G17410.2	0
37	PTHR19302,P <sup>-</sup>	0	0 K16569	GO:0005815,(AT5G17410.2	0
38	PTHR31343,P <sup>-</sup>	0	0	0 0 AT4G03420.1	0
39	PTHR34936,P <sup>-</sup>	0	0	0 0 AT1G20460.1	0
40	PTHR31087,P <sup>-</sup>	0	0	0 0 AT2G05910.1	0
41					
42	PTHR21319,P <sup>-</sup> KOG1940	6.3.2.19	K10144	GO:0046872,(AT5G18650.1	0
43	PTHR17204,P <sup>-</sup>	0	0	0 0 AT5G43950.1	0
44	PTHR27003,P <sup>-</sup> KOG1187	2.7.11.1		0 GO:0006468,(AT5G28680.1 ANX2	
45	PTHR27000,P <sup>-</sup> KOG1187	2.7.10.1		0 GO:0005515,(AT1G34420.1	0
46					
47	0	0	0	0 0 0	0
48					
49	PTHR31189,P <sup>-</sup>	0	0	0 GO:0045735 AT2G18540.1	0
50	PTHR24093,P <sup>-</sup>	0 3.6.3.6	K01535	GO:0046872,(AT1G80660.1 AHA9,HA9	
51	PTHR24015,P <sup>-</sup>	0	0	0 0 AT5G66520.1	0
52	PTHR34210,P <sup>-</sup>	0	0	0 0 AT3G62330.1	0
53	PTHR34455,P <sup>-</sup>	0	0	0 GO:0016020,(AT2G06520.1 PSBX	
54					
55	PTHR23257,P <sup>-</sup> KOG0192	2.7.11.1		0 GO:0006468,(AT4G24480.1	0
56	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
57	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0 GO:0008234,(AT5G45890.1 SAG12	
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3	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0	GO:0008234,(AT5G45890.1 SAG12	
4	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0	GO:0008234,(AT5G45890.1 SAG12	
5	PTHR12411,P <sup>-</sup> KOG1543	3.4.22.33		0	GO:0008234,(AT5G45890.1 SAG12	
6	PTHR14222,P <sup>-</sup>	0	0 K06677	0	GO:0007076 AT3G57060.2	0
7	PTHR35505,P <sup>-</sup>	0	0	0	0 AT5G11780.1	0
8	PTHR19302,P <sup>-</sup>	0	0 K16569	0	GO:0005815,(AT5G17410.2	0
9	PTHR19302,P <sup>-</sup>	0	0 K16569	0	GO:0005815,(AT5G17410.2	0
10	PTHR31343,P <sup>-</sup>	0	0	0	0 AT4G03420.1	0
11	PTHR34936,P <sup>-</sup>	0	0	0	0 AT1G20460.1	0
12	PTHR31087,P <sup>-</sup>	0	0	0	0 AT2G05910.1	0
13	PTHR21319,P <sup>-</sup> KOG1940	6.3.2.19	K10144	0	GO:0046872,(AT5G18650.1	0
14	PTHR17204,P <sup>-</sup>	0	0	0	0 AT5G43950.1	0
15	PTHR27003,P <sup>-</sup> KOG1187	2.7.11.1		0	GO:0006468,(AT5G28680.1 ANX2	
16	PTHR27000,P <sup>-</sup> KOG1187	2.7.10.1		0	GO:0005515,(AT1G34420.1	0
17	0	0	0	0	0 0 0	0
18	PTHR31189,P <sup>-</sup>	0	0	0	GO:0045735 AT2G18540.1	0
19	PTHR24093,P <sup>-</sup>	0 3.6.3.6	K01535	0	GO:0046872,(AT1G80660.1 AHA9,HA9	
20	PTHR24015,P <sup>-</sup>	0	0	0	0 AT5G66520.1	0
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arabi-defline	ID	Annot_defline	IDENTIFIER
Zn-dependent exopeptidases superfamily prot	Phvul.007G10PTHR28570:	SI	Phvul.007G10
Zn-dependent exopeptidases superfamily prot	Phvul.007G10PTHR28570:	SI	Phvul.007G10
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00PTHR23324:	SI	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00PTHR23324:	SI	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00PTHR23324:	SI	Phvul.009G00
double-stranded RNA binding protein-related ,	Phvul.002G19PTHR21404 - I		Phvul.002G19
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00PTHR23324:	SI	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00PTHR23324:	SI	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00PTHR23324:	SI	Phvul.009G00
double-stranded RNA binding protein-related ,	Phvul.002G19PTHR21404 - I		Phvul.002G19
Zinc knuckle (CCHC-type) family protein	0	0	Phvul.001G21
golgi nucleotide sugar transporter 1	Phvul.009G15K15356 - GDP		Phvul.009G15
Protein of unknown function (DUF3550/UPF0€	Phvul.002G26PF12070 - Pro		Phvul.002G26
Zinc knuckle (CCHC-type) family protein	0	0	Phvul.001G21
golgi nucleotide sugar transporter 1	Phvul.009G15K15356 - GDP		Phvul.009G15
Protein of unknown function (DUF3550/UPF0€	Phvul.002G26PF12070 - Pro		Phvul.002G26
heat shock transcription factor B4	Phvul.001G02PTHR10015:	SI	Phvul.001G02
RING 1A	Phvul.008G12PTHR10825:	SI	Phvul.008G12
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
Ribosomal protein S5/Elongation factor G/III/v	Phvul.003G17K12852 - 116		Phvul.003G17
nitrate transporter 1.5	Phvul.008G04PTHR11654:	SI	Phvul.008G04
Potassium transporter family protein	Phvul.004G01PTHR30540:	SI	Phvul.004G01
AAA-type ATPase family protein	Phvul.008G29K07478 - puta		Phvul.008G29
glucan synthase-like 3	Phvul.005G04PTHR12741:	SI	Phvul.005G04
HEAT repeat-containing protein	Phvul.010G00PTHR15245//I		Phvul.010G00
HEAT repeat-containing protein	Phvul.010G00PTHR15245//I		Phvul.010G00
HEAT repeat-containing protein	Phvul.010G00PTHR15245//I		Phvul.010G00
heat shock transcription factor B4	Phvul.001G02PTHR10015:	SI	Phvul.001G02
RING 1A	Phvul.008G12PTHR10825:	SI	Phvul.008G12
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21PTHR22572//I		Phvul.001G21
Ribosomal protein S5/Elongation factor G/III/v	Phvul.003G17K12852 - 116		Phvul.003G17
nitrate transporter 1.5	Phvul.008G04PTHR11654:	SI	Phvul.008G04
Potassium transporter family protein	Phvul.004G01PTHR30540:	SI	Phvul.004G01
AAA-type ATPase family protein	Phvul.008G29K07478 - puta		Phvul.008G29
glucan synthase-like 3	Phvul.005G04PTHR12741:	SI	Phvul.005G04
HEAT repeat-containing protein	Phvul.010G00PTHR15245//I		Phvul.010G00

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3	HEAT repeat-containing protein	Phvul.010G00PTHR15245//IPhvul.010G00	
4	HEAT repeat-containing protein	Phvul.010G00PTHR15245//IPhvul.010G00	
5	Phosphate-responsive 1 family protein	Phvul.009G03PTHR31279:SI	Phvul.009G03
6	plastid transcriptionally active 14	Phvul.009G24PTHR13271:SI	Phvul.009G24
7	plastid transcriptionally active 14	Phvul.009G24PTHR13271:SI	Phvul.009G24
8	Glycosyl hydrolases family 32 protein	Phvul.002G06PTHR31953:SI	Phvul.002G06
9	Glycosyl hydrolases family 32 protein	Phvul.002G06PTHR31953:SI	Phvul.002G06
10	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
11	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
12	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
13	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
14	DEAD/DEAH box RNA helicase family protein	Phvul.009G22PTHR13710:SI	Phvul.009G22
15	DEAD/DEAH box RNA helicase family protein	Phvul.009G22PTHR13710:SI	Phvul.009G22
16	DEAD/DEAH box RNA helicase family protein	Phvul.009G22PTHR13710:SI	Phvul.009G22
17	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
18	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
19	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
20	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
21	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
22		0	0
23	RNA polymerase I-associated factor PAF67	Phvul.009G10K15029 - tran:	Phvul.009G10
24	Homeodomain-like superfamily protein	Phvul.009G03PTHR21717:SI	Phvul.009G03
25	Homeodomain-like superfamily protein	Phvul.009G03PTHR21717:SI	Phvul.009G03
26	Protein prenyltransferase superfamily protei	Phvul.009G19KOG1128 - Un	Phvul.009G19
27	binding	Phvul.003G11K17491 - prot:	Phvul.003G11
28	Phosphate-responsive 1 family protein	Phvul.009G03PTHR31279:SI	Phvul.009G03
29	Phosphate-responsive 1 family protein	Phvul.009G03PTHR31279:SI	Phvul.009G03
30	plastid transcriptionally active 14	Phvul.009G24PTHR13271:SI	Phvul.009G24
31	plastid transcriptionally active 14	Phvul.009G24PTHR13271:SI	Phvul.009G24
32	Glycosyl hydrolases family 32 protein	Phvul.002G06PTHR31953:SI	Phvul.002G06
33	Glycosyl hydrolases family 32 protein	Phvul.002G06PTHR31953:SI	Phvul.002G06
34	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
35	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
36	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
37	Major facilitator superfamily protein	Phvul.008G06PTHR11662:SI	Phvul.008G06
38	DEAD/DEAH box RNA helicase family protein	Phvul.009G22PTHR13710:SI	Phvul.009G22
39	DEAD/DEAH box RNA helicase family protein	Phvul.009G22PTHR13710:SI	Phvul.009G22
40	DEAD/DEAH box RNA helicase family protein	Phvul.009G22PTHR13710:SI	Phvul.009G22
41	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
42	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
43	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
44	allantoate amidohydrolase	Phvul.009G24K02083 - allan	Phvul.009G24
45		0	0
46	RNA polymerase I-associated factor PAF67	Phvul.009G10K15029 - tran:	Phvul.009G10
47	Homeodomain-like superfamily protein	Phvul.009G03PTHR21717:SI	Phvul.009G03
48	Homeodomain-like superfamily protein	Phvul.009G03PTHR21717:SI	Phvul.009G03
49	Protein prenyltransferase superfamily protei	Phvul.009G19KOG1128 - Un	Phvul.009G19
50	binding	Phvul.003G11K17491 - prot:	Phvul.003G11
51	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SI	Phvul.006G15
52	Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SI	Phvul.006G15
53	Plant protein of unknown function (DUF946)	Phvul.006G10PTHR17204//IPhvul.006G10	
54	Plant protein of unknown function (DUF946)	Phvul.006G10PTHR17204//IPhvul.006G10	
55	Pentatricopeptide repeat (PPR-like) superfamil	Phvul.011G03PF01535//PF1	Phvul.011G03
56	myb domain protein 113	Phvul.008G03PTHR10641:SI	Phvul.008G03
57	myb domain protein 113	Phvul.008G03PTHR10641:SI	Phvul.008G03
58	Pentatricopeptide repeat (PPR) superfamily pr	Phvul.002G02PF01535//PF1	Phvul.002G02
59	Pentatricopeptide repeat (PPR) superfamily pr	Phvul.L00164PF01535//PF1	Phvul.L00164
60	Pentatricopeptide repeat (PPR) superfamily pr	Phvul.L00164PF01535//PF1	Phvul.L00164

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ATP-dependent RNA helicase, putative	Phvul.001G26PTHR18934//IPhvu	l.001G26
PAM domain (PCI/PINT associated module) prc	Phvul.009G01K03033 - 26S	lPhvul.009G01
	0	0 Phvul.009G07
Leucine-rich repeat protein kinase family prote	Phvul.003G15PF00069//PFC	Phvul.003G15
Pseudouridine synthase family protein	Phvul.006G15PTHR11079:SI	Phvul.006G15
Plant protein of unknown function (DUF946)	Phvul.006G10PTHR17204//IPhvu	l.006G10
Plant protein of unknown function (DUF946)	Phvul.006G10PTHR17204//IPhvu	l.006G10
Pentatricopeptide repeat (PPR-like) superfamil	Phvul.011G03PF01535//PF1	Phvul.011G03
myb domain protein 113	Phvul.008G03PTHR10641:SI	Phvul.008G03
Pentatricopeptide repeat (PPR) superfamily pr	Phvul.002G02PF01535//PF1	Phvul.002G02
Pentatricopeptide repeat (PPR) superfamily pr	Phvul.L00164PF01535//PF1	Phvul.L00164
ATP-dependent RNA helicase, putative	Phvul.001G26PTHR18934//IPhvu	l.001G26
PAM domain (PCI/PINT associated module) prc	Phvul.009G01K03033 - 26S	lPhvul.009G01
	0	0 Phvul.009G07
Leucine-rich repeat protein kinase family prote	Phvul.003G15PF00069//PFC	Phvul.003G15
Zinc knuckle (CCHC-type) family protein	0	0 Phvul.001G21
photosystem II subunit X	Phvul.009G22PTHR34455:SI	Phvul.009G22
Protein kinase superfamily protein	Phvul.009G03PTHR23257:SI	Phvul.009G03
senescence-associated gene 12	Phvul.011G13PTHR12411:SI	Phvul.011G13
senescence-associated gene 12	Phvul.011G13PTHR12411:SI	Phvul.011G13
senescence-associated gene 12	Phvul.011G13PTHR12411:SI	Phvul.011G13
senescence-associated gene 12	Phvul.011G08PTHR12411//IPhvu	l.011G08
senescence-associated gene 12	Phvul.011G13PTHR12411:SI	Phvul.011G13
binding	Phvul.007G24K06677 - conc	Phvul.007G24
	0	0 Phvul.004G17
Spc97 / Spc98 family of spindle pole body (SBP	Phvul.010G03K16569 - gam	Phvul.010G03
Spc97 / Spc98 family of spindle pole body (SBP	Phvul.010G03K16569 - gam	Phvul.010G03
Protein of unknown function (DUF789)	Phvul.005G10PTHR31343:SI	Phvul.005G10
	0	0 Phvul.009G02
Protein of unknown function (DUF567)	Phvul.009G22PTHR31087:SI	Phvul.009G22
CHY-type/CTCHY-type/RING-type Zinc finger p	Phvul.006G16PTHR21319//IPhvu	l.006G16
Plant protein of unknown function (DUF946)	Phvul.002G03PTHR17204//IPhvu	l.002G03
Malectin/receptor-like protein kinase family pi	Phvul.007G18PTHR27003:SI	Phvul.007G18
leucine-rich repeat transmembrane protein kir	Phvul.004G08PTHR27000:SI	Phvul.004G08
	0	0 Phvul.L00185
RmlC-like cupins superfamily protein	Phvul.002G02PTHR31189:SI	Phvul.002G02
H(+)-ATPase 9	Phvul.005G18PTHR24093:SI	Phvul.005G18
Tetratricopeptide repeat (TPR)-like superfamil	Phvul.004G15PF01535//PF1	Phvul.004G15
Zinc knuckle (CCHC-type) family protein	0	0 Phvul.001G21
photosystem II subunit X	Phvul.009G22PTHR34455:SI	Phvul.009G22
Protein kinase superfamily protein	Phvul.009G03PTHR23257:SI	Phvul.009G03
senescence-associated gene 12	Phvul.011G13PTHR12411:SI	Phvul.011G13
senescence-associated gene 12	Phvul.011G13PTHR12411:SI	Phvul.011G13

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 3 senescence-associated gene 12 Phvul.011G13PTHR12411:SI Phvul.011G13  
 4 senescence-associated gene 12 Phvul.011G08PTHR12411://IPhvul.011G08  
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 6 binding Phvul.007G24K06677 - conc Phvul.007G24  
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 8 0 0 0 Phvul.004G17  
 9  
 10 Spc97 / Spc98 family of spindle pole body (SBP Phvul.010G03K16569 - gam Phvul.010G03  
 11 Spc97 / Spc98 family of spindle pole body (SBP Phvul.010G03K16569 - gam Phvul.010G03  
 12 Protein of unknown function (DUF789) Phvul.005G10PTHR31343:SI Phvul.005G10  
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 14 0 0 0 Phvul.009G02  
 15 Protein of unknown function (DUF567) Phvul.009G22PTHR31087:SI Phvul.009G22  
 16 CHY-type/CTCHY-type/RING-type Zinc finger p Phvul.006G16PTHR21319://IPhvul.006G16  
 17 Plant protein of unknown function (DUF946) Phvul.002G03PTHR17204://IPhvul.002G03  
 18 Malectin/receptor-like protein kinase family p Phvul.007G18PTHR27003:SI Phvul.007G18  
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 21 0 0 0 Phvul.L00185  
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 24 H(+)-ATPase 9 Phvul.005G18PTHR24093:SI Phvul.005G18  
 25 Tetratricopeptide repeat (TPR)-like superfamily Phvul.004G15PF01535://PF1 Phvul.004G15  
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NAME	DESCRIPTION
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Protein home	M18-class aspartyl aminopeptidase (DAP) (original description: pacid=37166631 tran
Protein home	M18-class aspartyl aminopeptidase (DAP) (original description: pacid=37166631 tran
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RNA processir	miRNA/siRNA methyltransferase (HEN1) (original description: pacid=37175057 transi
not assigned.ε	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C
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Solute transp	nucleotide sugar transporter (GONST1 2 3 4) (original description: pacid=37151677
not assigned.r	no hits & (original description: pacid=37174363 transcript=Phvul.002G261000.1 locu
not assigned.r	no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
Solute transp	nucleotide sugar transporter (GONST1 2 3 4) (original description: pacid=37151677
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RNA biosynth	transcription factor (HSF) (original description: pacid=37168548 transcript=Phvul.001
Chromatin orę	modification writer component RING1 of modification writer protein components (o
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
RNA processir	protein factor SNU114/U5-116kDa of U5 small nuclear ribonucleoprotein particle (sn
Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37159373 transcript=Phvu
Solute transp	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37163324 tr
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RNA processir	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA processir	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA processir	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA biosynth	transcription factor (HSF) (original description: pacid=37168548 transcript=Phvul.001
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Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
RNA processir	protein factor SNU114/U5-116kDa of U5 small nuclear ribonucleoprotein particle (sn
Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37159373 transcript=Phvu
Solute transp	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37163324 tr
not assigned.r	no hits & (original description: pacid=37160223 transcript=Phvul.008G290000.1 locu
not assigned.ε	(original description: pacid=37152506 transcript=Phvul.005G040800.1 locus=Phvul.C
RNA processir	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF



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3 RNA processir component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF  
4 RNA processir component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF  
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7 Carbohydrate acid beta-fructofuranosidase (VIN) (original description: pacid=37175113 transcript=  
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22 Protein home protease (Papain) (original description: pacid=37155727 transcript=Phvul.011G1340C  
23 Protein home protease (Papain) (original description: pacid=37154718 transcript=Phvul.011G1308C  
24 Protein home protease (Papain) (original description: pacid=37156814 transcript=Phvul.011G0811C  
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45 Protein home protease (Papain) (original description: pacid=37155727 transcript=Phvul.011G1340C  
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 vvl.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &  
 vvl.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &  
 vvl.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &  
 rRNP) (original description: pacid=37147800 transcript=Phvul.003G174100.1 locus=Phvul.003G1741  
 jl.008G040500.1 locus=Phvul.008G040500 ID=Phvul.008G040500.1.v2.1 annot-version=v2.1) &  
 ranscript=Phvul.004G018100.1 locus=Phvul.004G018100 ID=Phvul.004G018100.1.v2.1 annot-versio  
 js=Phvul.008G290000 ID=Phvul.008G290000.1.v2.1 annot-version=v2.1)  
 J05G040800 ID=Phvul.005G040800.1.v2.1 annot-version=v2.1) & Callose synthase 2 OS=Arabidopsi  
 ) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G



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3 J01G264132 ID=Phvul.001G264132.1.v2.1 annot-version=v2.1) & Probable pre-mRNA-splicing facto  
4 J2 transcript=Phvul.009G019100.1 locus=Phvul.009G019100 ID=Phvul.009G019100.1.v2.1 annot-ve  
5 js=Phvul.009G073900 ID=Phvul.009G073900.1.v2.1 annot-version=v2.1)  
6 159700.1 locus=Phvul.003G159700 ID=Phvul.003G159700.1.v2.1 annot-version=v2.1) &  
7 J06G151200 ID=Phvul.006G151200.1.v2.1 annot-version=v2.1) & RNA pseudouridine synthase 6, cf  
8 js=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)  
9 js=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)  
10 J11G033500 ID=Phvul.011G033500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain  
11 J8G038200.1 locus=Phvul.008G038200 ID=Phvul.008G038200.1.v2.1 annot-version=v2.1) &  
12 J02G022400 ID=Phvul.002G022400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain  
13 644 ID=Phvul.L001644.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein A  
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15 J2 transcript=Phvul.009G019100.1 locus=Phvul.009G019100 ID=Phvul.009G019100.1.v2.1 annot-ve  
16 js=Phvul.009G073900 ID=Phvul.009G073900.1.v2.1 annot-version=v2.1)  
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18 js=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)  
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20 009G035800.1 locus=Phvul.009G035800 ID=Phvul.009G035800.1.v2.1 annot-version=v2.1) &  
21 00.1 locus=Phvul.011G134100 ID=Phvul.011G134100.1.v2.1 annot-version=v2.1) &  
22 00.1 locus=Phvul.011G134000 ID=Phvul.011G134000.1.v2.1 annot-version=v2.1) &  
23 00.1 locus=Phvul.011G130800 ID=Phvul.011G130800.1.v2.1 annot-version=v2.1) &  
24 00.1 locus=Phvul.011G081100 ID=Phvul.011G081100.1.v2.1 annot-version=v2.1) &  
25 00.1 locus=Phvul.011G133300 ID=Phvul.011G133300.1.v2.1 annot-version=v2.1) &  
26 ranscript=Phvul.007G247800.1 locus=Phvul.007G247800 ID=Phvul.007G247800.1.v2.1 annot-versic  
27 js=Phvul.004G172000 ID=Phvul.004G172000.1.v2.1 annot-version=v2.1)  
28 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170  
29 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170  
30 js=Phvul.005G105800 ID=Phvul.005G105800.1.v2.1 annot-version=v2.1)  
31 js=Phvul.009G021200 ID=Phvul.009G021200.1.v2.1 annot-version=v2.1)  
32 J09G226800 ID=Phvul.009G226800.1.v2.1 annot-version=v2.1) & Protein LURP-one-related 6 OS=A  
33 J06G162000 ID=Phvul.006G162000.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase MIEL1  
34 js=Phvul.002G038300 ID=Phvul.002G038300.1.v2.1 annot-version=v2.1)  
35 G188300.1 locus=Phvul.007G188300 ID=Phvul.007G188300.1.v2.1 annot-version=v2.1) &  
36 i084688.1 locus=Phvul.004G084688 ID=Phvul.004G084688.1.v2.1 annot-version=v2.1) &  
37 hvul.L001859 ID=Phvul.L001859.1.v2.1 annot-version=v2.1)  
38 J02G027900 ID=Phvul.002G027900.2.v2.1 annot-version=v2.1) & Vicilin-like seed storage protein A  
39 ranscript=Phvul.005G180700.1 locus=Phvul.005G180700 ID=Phvul.005G180700.1.v2.1 annot-versic  
40 J04G153700 ID=Phvul.004G153700.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain  
41 js=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)  
42 hvul.009G228600.1 locus=Phvul.009G228600 ID=Phvul.009G228600.1.v2.1 annot-version=v2.1) &  
43 009G035800.1 locus=Phvul.009G035800 ID=Phvul.009G035800.1.v2.1 annot-version=v2.1) &  
44 00.1 locus=Phvul.011G134100 ID=Phvul.011G134100.1.v2.1 annot-version=v2.1) &  
45 00.1 locus=Phvul.011G134000 ID=Phvul.011G134000.1.v2.1 annot-version=v2.1) &  
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3 00.1 locus=Phvul.011G130800 ID=Phvul.011G130800.1.v2.1 annot-version=v2.1) &  
4 00.1 locus=Phvul.011G081100 ID=Phvul.011G081100.1.v2.1 annot-version=v2.1) &  
5 00.1 locus=Phvul.011G133300 ID=Phvul.011G133300.1.v2.1 annot-version=v2.1) &  
6 :ranscript=Phvul.007G247800.1 locus=Phvul.007G247800 ID=Phvul.007G247800.1.v2.1 annot-versic  
7  
8 us=Phvul.004G172000 ID=Phvul.004G172000.1.v2.1 annot-version=v2.1)  
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10 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170  
11 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170  
12 us=Phvul.005G105800 ID=Phvul.005G105800.1.v2.1 annot-version=v2.1)  
13 us=Phvul.009G021200 ID=Phvul.009G021200.1.v2.1 annot-version=v2.1)  
14 009G226800 ID=Phvul.009G226800.1.v2.1 annot-version=v2.1) & Protein LURP-one-related 6 OS=A  
15 006G162000 ID=Phvul.006G162000.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase MIEL1  
16 us=Phvul.002G038300 ID=Phvul.002G038300.1.v2.1 annot-version=v2.1)  
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18 0188300.1 locus=Phvul.007G188300 ID=Phvul.007G188300.1.v2.1 annot-version=v2.1) &  
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20 i084688.1 locus=Phvul.004G084688 ID=Phvul.004G084688.1.v2.1 annot-version=v2.1) &  
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22 hvul.L001859 ID=Phvul.L001859.1.v2.1 annot-version=v2.1)  
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24 002G027900 ID=Phvul.002G027900.2.v2.1 annot-version=v2.1) & Vicilin-like seed storage protein A  
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26 004G153700 ID=Phvul.004G153700.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain  
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3 ;000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &  
4 ;000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &  
5 sis thaliana (sp|q9zpe7|exo\_arath : 404.0)  
6 1 annot-version=v2.1) &  
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14 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3\_arath : 811.0)  
15 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3\_arath : 811.0)  
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23 nnot-version=v2.1) &  
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27 .1 annot-version=v2.1) &  
28 sis thaliana (sp|q9zpe7|exo\_arath : 404.0)  
29 1 annot-version=v2.1) &  
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36 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3\_arath : 811.0)  
37 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3\_arath : 811.0)  
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45 nnot-version=v2.1) &  
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50 .1 annot-version=v2.1) &  
51 nloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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55 ing protein At2g21090 OS=Arabidopsis thaliana (sp|q9skq4|pp167\_arath : 607.0)  
56  
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58 ing protein At3g50420 OS=Arabidopsis thaliana (sp|q9sct2|pp277\_arath : 413.0)  
59 t1g25360 OS=Arabidopsis thaliana (sp|q9fri5|ppr57\_arath : 1008.0)  
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2  
3 or ATP-dependent RNA helicase DEAH5 OS=Arabidopsis thaliana (sp|q38953|deah5\_arath : 438.0)  
4 version=v2.1) &

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7  
8 chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6\_arath : 622.0)  
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10  
11  
12 binding protein At2g21090 OS=Arabidopsis thaliana (sp|q9skq4|pp167\_arath : 607.0)  
13

14  
15 binding protein At3g50420 OS=Arabidopsis thaliana (sp|q9sct2|pp277\_arath : 413.0)

16 At1g25360 OS=Arabidopsis thaliana (sp|q9fri5|ppr57\_arath : 1008.0)

17  
18 or ATP-dependent RNA helicase DEAH5 OS=Arabidopsis thaliana (sp|q38953|deah5\_arath : 438.0)  
19 version=v2.1) &

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34 on=v2.1) &

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36 )0.5.v2.1 annot-version=v2.1) &

37 )0.5.v2.1 annot-version=v2.1) &

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41 Arabidopsis thaliana (sp|q9zuf7|lor6\_arath : 232.0)

42 OS=Arabidopsis thaliana (sp|q8vzk0|miel1\_arath : 409.0)  
43  
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49 At2g18540 OS=Arabidopsis thaliana (sp|f4iqk5|vcl21\_arath : 226.0)

50 on=v2.1) &

51 binding protein At5g66520 OS=Arabidopsis thaliana (sp|q9fjy7|pp449\_arath : 417.0)  
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7 on=v2.1) &  
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10 )0.5.v2.1 annot-version=v2.1) &

11 )0.5.v2.1 annot-version=v2.1) &  
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15 rabidopsis thaliana (sp|q9zuf7|lor6\_arath : 232.0)

16 OS=Arabidopsis thaliana (sp|q8vzk0|miel1\_arath : 409.0)  
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24 on=v2.1) &  
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26 ing protein At5g66520 OS=Arabidopsis thaliana (sp|q9fjy7|pp449\_arath : 417.0)  
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	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
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3	aaaccguuacca	Phvul.004G064100.1	3	-1	1	22
4	aaaccguuacca	Phvul.009G096000.1	3	-1	1	22
5	aaaccguuacca	Phvul.008G049000.1	3	-1	1	22
6	aaaccguuacca	Phvul.004G064100.1	3	-1	1	23
7	aaaccguuacca	Phvul.009G096000.1	3	-1	1	23
8	aaaccguuacca	Phvul.004G064100.1	3	-1	1	23
9	aaaccguuacca	Phvul.009G096000.1	3	-1	1	23
10	aaaccguuacca	Phvul.004G064100.1	3	-1	1	23
11	aaaccguuacca	Phvul.009G096000.1	3	-1	1	23
12	aaaccguuacca	Phvul.009G196100.1	3.5	-1	1	22
13	aaaccguuacca	Phvul.008G199900.1	3.5	-1	1	22
14	aaaccguuacca	Phvul.007G157000.1	3.5	-1	1	22
15	aaaccguuacca	Phvul.009G104850.1	3.5	-1	1	22
16	aaaccguuacca	Phvul.004G038100.1	3.5	-1	1	22
17	aaaccguuacca	Phvul.011G073600.2	3.5	-1	1	22
18	aaaccguuacca	Phvul.011G073600.1	3.5	-1	1	22
19	aaaccguuacca	Phvul.L001604.3	3.5	-1	1	22
20	aaaccguuacca	Phvul.L001604.2	3.5	-1	1	22
21	aaaccguuacca	Phvul.L001604.1	3.5	-1	1	22
22	aaaccguuacca	Phvul.004G160700.1	3.5	-1	1	22
23	aaaccguuacca	Phvul.011G152300.3	3.5	-1	1	22
24	aaaccguuacca	Phvul.011G152300.2	3.5	-1	1	22
25	aaaccguuacca	Phvul.011G152300.1	3.5	-1	1	22
26	aaaccguuacca	Phvul.003G229300.1	3.5	-1	1	22
27	aaaccguuacca	Phvul.003G229300.2	3.5	-1	1	22
28	aaaccguuacca	Phvul.003G178200.1	3.5	-1	1	22
29	aaaccguuacca	Phvul.009G196100.1	3.5	-1	1	23
30	aaaccguuacca	Phvul.008G199900.1	3.5	-1	1	23
31	aaaccguuacca	Phvul.007G157000.1	3.5	-1	1	23
32	aaaccguuacca	Phvul.004G160700.1	3.5	-1	1	23
33	aaaccguuacca	Phvul.009G104850.1	3.5	-1	1	23
34	aaaccguuacca	Phvul.L001604.3	3.5	-1	1	23
35	aaaccguuacca	Phvul.L001604.2	3.5	-1	1	23
36	aaaccguuacca	Phvul.L001604.1	3.5	-1	1	23
37	aaaccguuacca	Phvul.004G038100.1	3.5	-1	1	23
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39	aaaccguuacca	Phvul.011G073600.1	3.5	-1	1	23
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46	aaaccguuacca	Phvul.L001604.2	3.5	-1	1	23
47	aaaccguuacca	Phvul.L001604.1	3.5	-1	1	23
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50	aaaccguuacca	Phvul.011G073600.1	3.5	-1	1	23
51	aaaccguuacca	Phvul.009G196100.1	3.5	-1	1	23
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53	aaaccguuacca	Phvul.007G157000.1	3.5	-1	1	23
54	aaaccguuacca	Phvul.004G160700.1	3.5	-1	1	23
55	aaaccguuacca	Phvul.009G104850.1	3.5	-1	1	23
56	aaaccguuacca	Phvul.L001604.3	3.5	-1	1	23
57	aaaccguuacca	Phvul.L001604.2	3.5	-1	1	23
58	aaaccguuacca	Phvul.L001604.1	3.5	-1	1	23
59	aaaccguuacca	Phvul.004G038100.1	3.5	-1	1	23
60	aaaccguuacca	Phvul.011G073600.2	3.5	-1	1	23

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2	aaaccguuacca Phvul.011G073600.1	3.5	-1	1	23
3	aaaccguuacca Phvul.002G289600.3	4	-1	1	22
4	aaaccguuacca Phvul.002G289600.1	4	-1	1	22
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6	aaaccguuacca Phvul.002G041900.1	4	-1	1	22
7	aaaccguuacca Phvul.010G108300.1	4	-1	1	22
8	aaaccguuacca Phvul.006G148800.1	4	-1	1	22
9	aaaccguuacca Phvul.006G214700.4	4	-1	1	22
10	aaaccguuacca Phvul.006G214700.3	4	-1	1	22
11	aaaccguuacca Phvul.006G214700.2	4	-1	1	22
12	aaaccguuacca Phvul.006G214700.1	4	-1	1	22
13	aaaccguuacca Phvul.002G231800.1	4	-1	1	22
14	aaaccguuacca Phvul.005G137000.3	4	-1	1	22
15	aaaccguuacca Phvul.005G137000.1	4	-1	1	22
16	aaaccguuacca Phvul.005G137000.4	4	-1	1	22
17	aaaccguuacca Phvul.005G137000.6	4	-1	1	22
18	aaaccguuacca Phvul.002G226900.1	4	-1	1	22
19	aaaccguuacca Phvul.005G137000.5	4	-1	1	22
20	aaaccguuacca Phvul.005G137000.2	4	-1	1	22
21	aaaccguuacca Phvul.007G222000.1	4	-1	1	22
22	aaaccguuacca Phvul.007G029200.1	4	-1	1	22
23	aaaccguuacca Phvul.003G058400.1	4	-1	1	22
24	aaaccguuacca Phvul.002G250000.1	4	-1	1	22
25	aaaccguuacca Phvul.004G028100.1	4	-1	1	22
26	aaaccguuacca Phvul.008G216700.1	4	-1	1	22
27	aaaccguuacca Phvul.008G216700.1	4	-1	1	22
28	aaaccguuacca Phvul.002G190100.1	4	-1	1	22
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30	aaaccguuacca Phvul.001G036500.1	4	-1	1	22
31	aaaccguuacca Phvul.005G102100.2	4	-1	1	22
32	aaaccguuacca Phvul.005G102100.1	4	-1	1	22
33	aaaccguuacca Phvul.002G289600.3	4	-1	1	23
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35	aaaccguuacca Phvul.002G289600.2	4	-1	1	23
36	aaaccguuacca Phvul.002G041900.1	4	-1	1	23
37	aaaccguuacca Phvul.006G148800.1	4	-1	1	23
38	aaaccguuacca Phvul.010G108300.1	4	-1	1	23
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57	aaaccguuacca Phvul.004G019300.1	5	-1	1	23
58	aaaccguuacca Phvul.004G019300.1	5	-1	1	23
59	aaaccguuacca Phvul.011G069000.1	5	-1	1	23
60	aaaccguuacca Phvul.002G231800.1	5	-1	1	23
	aaaccguuacca Phvul.L001687.1	5	-1	1	23

1					
2	aaaccguuacca Phvul.011G102400.1	5	-1	1	23
3	aaaccguuacca Phvul.006G037000.1	5	-1	1	23
4	aaaccguuacca Phvul.009G104850.1	5	-1	1	23
5	aaaccguuacca Phvul.009G104850.1	5	-1	1	23
6	aaaccguuacca Phvul.009G104850.1	5	-1	1	23
7	aaaccguuacca Phvul.009G104850.1	5	-1	1	23
8	aaaccguuacca Phvul.003G158800.1	5	-1	1	23
9	aaaccguuacca Phvul.001G057200.1	5	-1	1	23
10	aaaccguuacca Phvul.001G057200.1	5	-1	1	23
11	aaaccguuacca Phvul.004G057900.1	5	-1	1	23
12	aaaccguuacca Phvul.007G027000.1	5	-1	1	23
13	aaaccguuacca Phvul.007G027000.1	5	-1	1	23
14	aaaccguuacca Phvul.009G063500.1	5	-1	1	23
15	aaaccguuacca Phvul.009G063500.1	5	-1	1	23
16	aaaccguuacca Phvul.008G060700.1	5	-1	1	23
17	aaaccguuacca Phvul.011G110000.1	5	-1	1	23
18	aaaccguuacca Phvul.010G003800.1	5	-1	1	23
19	aaaccguuacca Phvul.009G063500.2	5	-1	1	23
20	aaaccguuacca Phvul.006G206800.1	5	-1	1	23
21	aaaccguuacca Phvul.006G206800.1	5	-1	1	23
22	aaaccguuacca Phvul.005G054600.1	5	-1	1	23
23	aaaccguuacca Phvul.005G054600.1	5	-1	1	23
24	aaaccguuacca Phvul.001G024200.1	5	-1	1	23
25	aaaccguuacca Phvul.006G098000.1	5	-1	1	23
26	aaaccguuacca Phvul.006G098000.1	5	-1	1	23
27	aaaccguuacca Phvul.008G033500.1	5	-1	1	23
28	aaaccguuacca Phvul.011G028900.1	5	-1	1	23
29	aaaccguuacca Phvul.011G028900.1	5	-1	1	23
30	aaaccguuacca Phvul.008G036100.2	5	-1	1	23
31	aaaccguuacca Phvul.008G036100.1	5	-1	1	23
32	aaaccguuacca Phvul.008G036100.1	5	-1	1	23
33	aaaccguuacca Phvul.004G061900.1	5	-1	1	23
34	aaaccguuacca Phvul.006G048000.1	5	-1	1	23
35	aaaccguuacca Phvul.007G156900.1	5	-1	1	23
36					
37					
38					
39					
40					
41					
42					
43					
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	Target_start	Target_end	miRNA_align	alignment	Target_align	Inhibition	Target_Desc.
1							
2							
3		119	140	AAACCGUUAC	:: :: :::::GCCUUUGUC	/Cleavage	pacid=371619
4		646	667	AAACCGUUAC	:: ::::: :AUAUUAUA	/Cleavage	pacid=371509
5							
6		1051	1072	AAACCGUUAC	:: :::::UCGUGAAUA	/Cleavage	pacid=371614
7		118	140	AAACCGUUAC	:: :: :::::GGCCUUUGU	/Cleavage	pacid=371619
8							
9		645	667	AAACCGUUAC	:: ::::: :UAUAUUAU	/Cleavage	pacid=371509
10		118	140	AAACCGUUAC	:: :: :::::GGCCUUUGU	/Cleavage	pacid=371619
11		645	667	AAACCGUUAC	:: ::::: :UAUAUUAU	/Cleavage	pacid=371509
12		138	159	AAACCGUUAC	:: ::::: AAUUCAGUA	(Translation	pacid=371489
13							
14		645	666	AAACCGUUAC	:: :::::GGCUCAGUA	/Translation	pacid=371593
15		1217	1238	AAACCGUUAC	:: :::::ACCACAGUAA	Cleavage	pacid=371664
16		193	214	AAACCGUUAC	:: :::::GUUUUGGUG	Cleavage	pacid=371513
17							
18		1819	1840	AAACCGUUAC	:: :::::UUCUCAGAA	/Translation	pacid=371635
19		2711	2732	AAACCGUUAC	:: :::::AUAUUGGUG	/Cleavage	pacid=371550
20		2714	2735	AAACCGUUAC	:: :::::AUAUUGGUG	/Cleavage	pacid=371550
21							
22		321	342	AAACCGUUAC	:: :::::GUUUCAGAA	(Cleavage	pacid=371574
23		298	319	AAACCGUUAC	:: :::::GUUUCAGAA	(Cleavage	pacid=371574
24		316	337	AAACCGUUAC	:: :::::GUUUCAGAA	(Cleavage	pacid=371574
25							
26		28	49	AAACCGUUAC	:: :::::GAGACAGCA	/Cleavage	pacid=371620
27		1182	1203	AAACCGUUAC	:: :::::AUAUCAGAG	/Cleavage	pacid=371556
28		1264	1285	AAACCGUUAC	:: :::::AUAUCAGAG	/Cleavage	pacid=371556
29							
30		1264	1285	AAACCGUUAC	:: :::::AUAUCAGAG	/Cleavage	pacid=371556
31		43	64	AAACCGUUAC	:: :::::GUAUUGAUG	Cleavage	pacid=371470
32		43	64	AAACCGUUAC	:: :::::GUAUUGAUG	Cleavage	pacid=371470
33							
34		121	142	AAACCGUUAC	:: :::::CCAUCAGCAA	Cleavage	pacid=371453
35		137	159	AAACCGUUAC	:: :::::CAAUUCAGU	/Translation	pacid=371489
36		644	666	AAACCGUUAC	:: :::::GGGCUCAGU	/Translation	pacid=371593
37							
38		1216	1238	AAACCGUUAC	:: :::::AACCACAGUA	Cleavage	pacid=371664
39		27	49	AAACCGUUAC	:: :::::AGAGACAGCA	/Cleavage	pacid=371620
40		192	214	AAACCGUUAC	:: :::::GGUUUUGGU	Cleavage	pacid=371513
41		320	342	AAACCGUUAC	:: :::::AGUUUCAGA	/Cleavage	pacid=371574
42							
43		297	319	AAACCGUUAC	:: :::::AGUUUCAGA	/Cleavage	pacid=371574
44		315	337	AAACCGUUAC	:: :::::AGUUUCAGA	/Cleavage	pacid=371574
45							
46		1818	1840	AAACCGUUAC	:: :::::GUUCUCAGA	/Translation	pacid=371635
47		2710	2732	AAACCGUUAC	:: :::::AAUAAUGGU	(Cleavage	pacid=371550
48		2713	2735	AAACCGUUAC	:: :::::AAUAAUGGU	(Cleavage	pacid=371550
49							
50		137	159	AAACCGUUAC	:: :::::CAAUUCAGU	/Translation	pacid=371489
51		644	666	AAACCGUUAC	:: :::::GGGCUCAGU	/Translation	pacid=371593
52		1216	1238	AAACCGUUAC	:: :::::AACCACAGUA	Cleavage	pacid=371664
53							
54		27	49	AAACCGUUAC	:: :::::AGAGACAGCA	/Cleavage	pacid=371620
55		192	214	AAACCGUUAC	:: :::::GGUUUUGGU	Cleavage	pacid=371513
56		320	342	AAACCGUUAC	:: :::::AGUUUCAGA	/Cleavage	pacid=371574
57							
58		297	319	AAACCGUUAC	:: :::::AGUUUCAGA	/Cleavage	pacid=371574
59		315	337	AAACCGUUAC	:: :::::AGUUUCAGA	/Cleavage	pacid=371574
60							
		1818	1840	AAACCGUUAC	:: :::::GUUCUCAGA	/Translation	pacid=371635
		2710	2732	AAACCGUUAC	:: :::::AAUAAUGGU	(Cleavage	pacid=371550

1				
2	2713	2735 AAACCGUUAC	.....: AAUAAUGGU/Cleavage	pacid=371550
3	1940	1961 AAACCGUUAC::	.....: AAAUUAGUA/Cleavage	pacid=371781
4	1944	1965 AAACCGUUAC::	.....: AAAUUAGUA/Cleavage	pacid=371781
5				
6	1972	1993 AAACCGUUAC::	.....: AAAUUAGUA/Cleavage	pacid=371781
7	156	177 AAACCGUUAC	.....: GUUUGAGUA Cleavage	pacid=371748
8	1163	1184 AAACCGUUAC::	.....: AUCUCGGUC/Cleavage	pacid=371440
9				
10	1130	1151 AAACCGUUAC::	.....: GACAAGGUC/Cleavage	pacid=371723
11	968	989 AAACCGUUAC::	.....: AUCAUAGUG/Translation	pacid=371726
12	968	989 AAACCGUUAC::	.....: AUCAUAGUG/Translation	pacid=371726
13	968	989 AAACCGUUAC::	.....: AUCAUAGUG/Translation	pacid=371726
14	968	989 AAACCGUUAC::	.....: AUCAUAGUG/Translation	pacid=371726
15	968	989 AAACCGUUAC::	.....: AUCAUAGUG/Translation	pacid=371726
16	711	732 AAACCGUUAC	.....: AUGCAAGUA/Cleavage	pacid=371777
17				
18	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
19	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
20	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
21	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
22	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
23	3174	3195 AAACCGUUAC	.....: UCUUUGGUA Cleavage	pacid=371783
24	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
25	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
26	2616	2637 AAACCGUUAC	.....: GUGGCAGUA/Cleavage	pacid=371537
27	724	745 AAACCGUUAC	.....: CAGGUGGUG/Cleavage	pacid=371648
28	702	723 AAACCGUUAC	.....: CCGUCAGUG/Cleavage	pacid=371659
29				
30	1489	1510 AAACCGUUAC	.....: CAUUAACUA/Cleavage	pacid=371463
31	1252	1273 AAACCGUUAC	.....: UUAACAGUG/Translation	pacid=371746
32	503	524 AAACCGUUAC	.....: GUAGUAGUA/Translation	pacid=371631
33	240	261 AAACCGUUAC	.....: GUUUCCUG/Cleavage	pacid=371598
34	342	363 AAACCGUUAC	.....: GUUUCCUG/Cleavage	pacid=371598
35	990	1011 AAACCGUUAC::	.....: GAAUUAGCA/Cleavage	pacid=371773
36	1310	1331 AAACCGUUAC.....	.....: GGUUCAACA/Cleavage	pacid=371619
37	381	402 AAACCGUUAC::	.....: GAAUCAGAA/Translation	pacid=371707
38	1572	1593 AAACCGUUAC	.....: CUUUGAGUA/Cleavage	pacid=371530
39	1575	1596 AAACCGUUAC	.....: CUUUGAGUA/Cleavage	pacid=371530
40	1939	1961 AAACCGUUAC::	.....: AAAUUAGU/Cleavage	pacid=371781
41	1943	1965 AAACCGUUAC::	.....: AAAUUAGU/Cleavage	pacid=371781
42	1971	1993 AAACCGUUAC::	.....: AAAUUAGU/Cleavage	pacid=371781
43	155	177 AAACCGUUAC::	.....: AGUUUGAGU Cleavage	pacid=371748
44	1129	1151 AAACCGUUAC::	.....: GGACAAGGU/Cleavage	pacid=371723
45	1162	1184 AAACCGUUAC::	.....: CAUCUCGGUC/Cleavage	pacid=371440
46	967	989 AAACCGUUAC::	.....: CAUCAUAGU(Translation	pacid=371726
47	967	989 AAACCGUUAC::	.....: CAUCAUAGU(Translation	pacid=371726
48	967	989 AAACCGUUAC::	.....: CAUCAUAGU(Translation	pacid=371726
49	967	989 AAACCGUUAC::	.....: CAUCAUAGU(Translation	pacid=371726
50	239	261 AAACCGUUAC	.....: GGUUCCCU/Cleavage	pacid=371598
51	341	363 AAACCGUUAC	.....: GGUUCCCU/Cleavage	pacid=371598
52	380	402 AAACCGUUAC::	.....: GGAAUCAGA/Translation	pacid=371707
53	1939	1961 AAACCGUUAC::	.....: AAAUUAGU/Cleavage	pacid=371781
54	1943	1965 AAACCGUUAC::	.....: AAAUUAGU/Cleavage	pacid=371781
55				
56				
57				
58				
59				
60				







1			
2	442	463 AAACCGUUAC	UGCUCGGUU Cleavage pacid=371668
3	1173	1194 AAACCGUUAC	:GUGUUGGUG Cleavage pacid=371668
4	41	62 AAACCGUUAC::	AAAAUGGUG Cleavage pacid=371540
5	113	134 AAACCGUUAC::	AAAUUAGUU Translation pacid=371600
6	291	312 AAACCGUUAC::	GAAUUUCCUG Cleavage pacid=371598
7	278	299 AAACCGUUAC::	GAAUUAGUA Translation pacid=371432
8	278	299 AAACCGUUAC::	GAAUUAGUA Translation pacid=371432
9	1831	1852 AAACCGUUAC::	AAGUUAAUG Cleavage pacid=371641
10	1059	1080 AAACCGUUAC	:ACAGCAGUAC Cleavage pacid=371626
11	2504	2525 AAACCGUUAC::	AAAUCAGAA Translation pacid=371527
12	187	209 AAACCGUUAC::	AAAUUUAGU Cleavage pacid=371425
13	549	571 AAACCGUUAC::	AAAUUUAGU Cleavage pacid=371425
14	519	541 AAACCGUUAC	:UACACAGU Cleavage pacid=371712
15	1108	1130 AAACCGUUAC::	GAACUUCAU Cleavage pacid=371611
16	1346	1370 AAACCGUUAC	:CGACUGACAC Cleavage pacid=371501
17	1393	1417 AAACCGUUAC	:CGACUGACAC Cleavage pacid=371501
18	1474	1498 AAACCGUUAC	:CGACUGACAC Cleavage pacid=371501
19	1479	1503 AAACCGUUAC	:CGACUGACAC Cleavage pacid=371501
20	592	614 AAACCGUUAC	:CAAUACAGU Cleavage pacid=371679
21	223	245 AAACCGUUAC	:UGAUUCAGU Cleavage pacid=371431
22	664	686 AAACCGUUAC	:GGUGGUGGU Cleavage pacid=371548
23	1237	1259 AAACCGUUAC::	GGACAAGGU Cleavage pacid=371723
24	1030	1052 AAACCGUUAC::	GGGCAAGGU Cleavage pacid=371723
25	277	299 AAACCGUUAC::	AGAAUUAGU Translation pacid=371432
26	277	299 AAACCGUUAC::	AGAAUUAGU Translation pacid=371432
27	1058	1080 AAACCGUUAC	:AACAGCAGU Cleavage pacid=371626
28	790	812 AAACCGUUAC::	GAGUUCAUU Translation pacid=371763
29	987	1009 AAACCGUUAC::	GGACACAUU Cleavage pacid=371655
30	1396	1418 AAACCGUUAC	:UUACUCAGC Cleavage pacid=371726
31	675	697 AAACCGUUAC	:UAUGACAGU Cleavage pacid=371501
32	788	810 AAACCGUUAC	:ACUUUUAGU Cleavage pacid=371645
33	819	841 AAACCGUUAC	:UUUACUAGA Cleavage pacid=371457
34	31	53 AAACCGUUAC::	GAAAAUGGU Cleavage pacid=371540
35	36	58 AAACCGUUAC::	GAAAAUGGU Cleavage pacid=371540
36	5	27 AAACCGUUAC	:CAAUAUUGU Cleavage pacid=371690
37	867	889 AAACCGUUAC	:AGUAGUAGU Cleavage pacid=371654
38	867	889 AAACCGUUAC	:AGUAGUAGU Cleavage pacid=371654
39	494	516 AAACCGUUAC	:GCAAUCGGU Cleavage pacid=371552
40	40	62 AAACCGUUAC::	GAAAAUGGU Cleavage pacid=371540
41	112	134 AAACCGUUAC::	GAAUUUAGU Translation pacid=371600
42	343	365 AAACCGUUAC::	AACUUCAGU Cleavage pacid=371523
43	583	605 AAACCGUUAC	:UAUAAUGGU Cleavage pacid=371741
44	3047	3069 AAACCGUUAC::	AUGUUCAGU Translation pacid=371717
45	290	312 AAACCGUUAC::	GGAUUUCCU Cleavage pacid=371598
46	323	345 AAACCGUUAC::	AAGGACAGU Cleavage pacid=371570
47	1385	1407 AAACCGUUAC	:ACUAUCAGU Cleavage pacid=371423

1			
2	159	181 AAACCGUUAC :: ::::: GCACUAUGU/Cleavage	pacid=371773
3	1830	1852 AAACCGUUAC:: :: :: GAAGUUAUU/Cleavage	pacid=371641
4	447	469 AAACCGUUAC ::::: GAUGUCAGU/Cleavage	pacid=371702
5	187	209 AAACCGUUAC::: : : : AAAUUUAGU/Cleavage	pacid=371425
6	549	571 AAACCGUUAC::: : : : AAAUUUAGU/Cleavage	pacid=371425
7	519	541 AAACCGUUAC :: ::::: UAACACAGU/Cleavage	pacid=371712
8			
9	1108	1130 AAACCGUUAC::: . : : : GAACUUCAU/Cleavage	pacid=371611
10	1346	1370 AAACCGUUAC :: ::::: CGACUGACAC/Cleavage	pacid=371501
11	1393	1417 AAACCGUUAC :: ::::: CGACUGACAC/Cleavage	pacid=371501
12	1474	1498 AAACCGUUAC :: ::::: CGACUGACAC/Cleavage	pacid=371501
13	1479	1503 AAACCGUUAC :: ::::: CGACUGACAC/Cleavage	pacid=371501
14	592	614 AAACCGUUAC :: ::::: CAUACAGU/Cleavage	pacid=371679
15	223	245 AAACCGUUAC : : : : UGAUUCAGU/Cleavage	pacid=371431
16	664	686 AAACCGUUAC . : : : : GGUGGUGGU/Cleavage	pacid=371548
17	1237	1259 AAACCGUUAC::: : : : GGACAAGGU/Cleavage	pacid=371723
18	1030	1052 AAACCGUUAC::: : : : GGGCAAGGU/Cleavage	pacid=371723
19	277	299 AAACCGUUAC::: : : : AGAAUUAGU/Translation	pacid=371432
20	277	299 AAACCGUUAC::: : : : AGAAUUAGU/Translation	pacid=371432
21	1058	1080 AAACCGUUAC ::::: AACAGCAGU/Cleavage	pacid=371626
22	790	812 AAACCGUUAC::: : : : GAGUUCAUU/Translation	pacid=371763
23	987	1009 AAACCGUUAC::: : : : GGACACAUU/Cleavage	pacid=371655
24	1396	1418 AAACCGUUAC ::::: UUACUCAGC/Cleavage	pacid=371726
25	675	697 AAACCGUUAC ::::: UAUGACAGU/Cleavage	pacid=371501
26	788	810 AAACCGUUAC : : : : ACUUUAGU/Cleavage	pacid=371645
27	819	841 AAACCGUUAC . : : : : UUUACUAGA/Cleavage	pacid=371457
28	31	53 AAACCGUUAC::: : : : GAAAUGGU/Cleavage	pacid=371540
29	36	58 AAACCGUUAC::: : : : GAAAUGGU/Cleavage	pacid=371540
30	5	27 AAACCGUUAC :: . : : : : CAUAUUGU/Cleavage	pacid=371690
31	867	889 AAACCGUUAC : : : : : AGUAGUAGU/Cleavage	pacid=371654
32	867	889 AAACCGUUAC : : : : : AGUAGUAGU/Cleavage	pacid=371654
33	494	516 AAACCGUUAC : : : : : GCAAUCGGU/Cleavage	pacid=371552
34	40	62 AAACCGUUAC::: : : : GAAAUGGU/Cleavage	pacid=371540
35	112	134 AAACCGUUAC::: : : : GAAUUAGU/Translation	pacid=371600
36	343	365 AAACCGUUAC::: : : : AACUUCAGU/Cleavage	pacid=371523
37	583	605 AAACCGUUAC . : : : : UAUAUGGU/Cleavage	pacid=371741
38	3047	3069 AAACCGUUAC: : : : : AUGUUCAGU/Translation	pacid=371717
39	290	312 AAACCGUUAC::: . : : : : GGAUUCCU/Cleavage	pacid=371598
40	323	345 AAACCGUUAC::: : : : AAGGACAGU/Cleavage	pacid=371570
41	1385	1407 AAACCGUUAC ::::: ACUAUCAGU/Cleavage	pacid=371423
42	159	181 AAACCGUUAC :: ::::: GCACUAUGU/Cleavage	pacid=371773
43	1830	1852 AAACCGUUAC:: :: :: GAAGUUAUU/Cleavage	pacid=371641
44	447	469 AAACCGUUAC ::::: GAUGUCAGU/Cleavage	pacid=371702
45	500	522 AAACCGUUAC ::::: GAUGUCAGU/Cleavage	pacid=371702
46	1264	1285 AAACCGUUAC::: : : : GAUUCGGU/Cleavage	pacid=371548
47	514	535 AAACCGUUAC: . : : : : GAAUUGGCA/Cleavage	pacid=371548
48	838	859 AAACCGUUAC: . : : : : GAAUUGGCA/Cleavage	pacid=371548

1			
2	904	925 AAACCGUUAC:: :...:: :GAAUUGGCA/ Cleavage	pacid=371548
3	1102	1123 AAACCGUUAC:: :...:: :GAAUUGGCA/ Cleavage	pacid=371548
4	1054	1075 AAACCGUUAC : :...:: :GUUUAGGUG Cleavage	pacid=371548
5	1535	1556 AAACCGUUAC:: :...:: :AACACAGUAA Cleavage	pacid=371621
6	1540	1561 AAACCGUUAC:: :...:: :AACACAGUAA Cleavage	pacid=371621
7			
8	625	646 AAACCGUUAC :...:: :GAGCAGGUG( Cleavage	pacid=371513
9	715	736 AAACCGUUAC :...:: :GAGCAGGUG( Cleavage	pacid=371513
10	859	880 AAACCGUUAC :...:: :GAGCAGGUG( Cleavage	pacid=371513
11	958	979 AAACCGUUAC:: :...:: :GACCCGUAA Cleavage	pacid=371460
12	509	530 AAACCGUUAC:: :...:: :AGCGUGGUG Cleavage	pacid=371718
13	522	543 AAACCGUUAC:: :...:: :AACUCACAAA Cleavage	pacid=371779
14	311	332 AAACCGUUAC:: :...:: :GAUUUGGUG Cleavage	pacid=371548
15	328	349 AAACCGUUAC:: :...:: :AAUGCAGUG/ Cleavage	pacid=371642
16	132	153 AAACCGUUAC:: :...:: :AACACAGCAA Cleavage	pacid=371533
17	1460	1481 AAACCGUUAC :...:: :GUCAUGGUU Cleavage	pacid=371723
18	1020	1041 AAACCGUUAC:: :...:: :GGCUUGGUG Translation	pacid=371550
19	608	629 AAACCGUUAC :...:: :AUUAUGGUU Cleavage	pacid=371741
20	3142	3163 AAACCGUUAC :...:: :UAUUCAGCAC Cleavage	pacid=371544
21	2698	2719 AAACCGUUAC:: :...:: :AAUUCACUAC Cleavage	pacid=371680
22	1224	1245 AAACCGUUAC :...:: :UAUUCAGUG/ Translation	pacid=371578
23	155	176 AAACCGUUAC :...:: :UUCUUGGUC Cleavage	pacid=371617
24	210	231 AAACCGUUAC :...:: :GUUUCAGUG/ Cleavage	pacid=371708
25	797	818 AAACCGUUAC :...:: :GUUUUGGUA Translation	pacid=371501
26	361	382 AAACCGUUAC :...:: :GUGGCGGUA Cleavage	pacid=371573
27	788	809 AAACCGUUAC :...:: :GGAGUGGUA Cleavage	pacid=371583
28	682	703 AAACCGUUAC :...:: :GGAGUGGUA Cleavage	pacid=371731
29	350	371 AAACCGUUAC:: :...:: :GACUCCUGC Cleavage	pacid=371712
30	550	571 AAACCGUUAC:: :...:: :GGUUUGGUG Cleavage	pacid=371609
31	2	23 AAACCGUUAC:: :...:: :AACACAUAGA Cleavage	pacid=371609
32	1144	1165 AAACCGUUAC:: :...:: :AUCUUAGUG/ Cleavage	pacid=371512
33	2	23 AAACCGUUAC:: :...:: :AACACAUAGA Cleavage	pacid=371609
34	419	440 AAACCGUUAC:: :...:: :GACUCCUGC Cleavage	pacid=371741
35	712	733 AAACCGUUAC :...:: :CAAUAGUG( Cleavage	pacid=371699
36	1245	1266 AAACCGUUAC :...:: :GUCUUAGUG/ Cleavage	pacid=371562
37	265	286 AAACCGUUAC:: :...:: :AGUUCAGAA/ Cleavage	pacid=371626
38	445	466 AAACCGUUAC:: :...:: :AGUUAGGUG Cleavage	pacid=371737
39	1970	1991 AAACCGUUAC :...:: :UGUUUACUA Cleavage	pacid=371509
40	1324	1345 AAACCGUUAC :...:: :GCUAUGGUA/ Cleavage	pacid=371526
41	1263	1285 AAACCGUUAC:: :...:: :GGAUUCGGU/ Cleavage	pacid=371548
42	513	535 AAACCGUUAC:: :...:: :GGAAUUGGC/ Cleavage	pacid=371548
43	837	859 AAACCGUUAC:: :...:: :GGAAUUGGC/ Cleavage	pacid=371548
44	903	925 AAACCGUUAC:: :...:: :GGAAUUGGC/ Cleavage	pacid=371548
45	1101	1123 AAACCGUUAC:: :...:: :GGAAUUGGC/ Cleavage	pacid=371548
46	1053	1075 AAACCGUUAC :...:: :GGUUUAGGU Cleavage	pacid=371548
47	508	530 AAACCGUUAC:: :...:: :AAGCGUGGU( Cleavage	pacid=371718
48	521	543 AAACCGUUAC:: :...:: :AACUCACAA Cleavage	pacid=371779
49			
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2	131	153 AAACCGUUAC:::: :: ::::: :AAACACAGCA Cleavage	pacid=371533
3	1534	1556 AAACCGUUAC:::: ::::: : GAACACAGUA Cleavage	pacid=371621
4	1539	1561 AAACCGUUAC:::: ::::: : GAACACAGUA Cleavage	pacid=371621
5			
6	1019	1041 AAACCGUUAC:::: ::::: : : :::::AGGCUUGGU Translation	pacid=371550
7	709	732 AAACCGUUAC:::: :: ::::: : : :::::AAAUGCAAGL Cleavage	pacid=371777
8	349	371 AAACCGUUAC:::: ::::: : : ::::: :AGACUCCCUC Cleavage	pacid=371712
9			
10	310	332 AAACCGUUAC:::: ::::: : : ::::: :GGAUUUGGU Cleavage	pacid=371548
11	418	440 AAACCGUUAC:::: ::::: : : ::::: :AGACUCCCUC Cleavage	pacid=371741
12			
13	714	736 AAACCGUUAC ::::: : : ::::: :GGAGCAGGU Cleavage	pacid=371513
14	858	880 AAACCGUUAC ::::: : : ::::: :GGAGCAGGU Cleavage	pacid=371513
15	624	646 AAACCGUUAC ::::: : : ::::: :GGAGCAGGU Cleavage	pacid=371513
16	957	979 AAACCGUUAC ::::: : : ::::: :UGACCCGGU Cleavage	pacid=371460
17			
18	209	231 AAACCGUUAC: ::::: : : ::::: :AGUUUCAGU Cleavage	pacid=371708
19	2329	2350 AAACCGUUAC:::: ::::: : : ::::: :AGAUUCAGU Cleavage	pacid=371623
20	327	349 AAACCGUUAC ::::: : : ::::: : :CAAUGCAGU Cleavage	pacid=371642
21			
22	818	840 AAACCGUUAC: ::::: : : ::::: : :AACCUCAUUC Cleavage	pacid=371492
23	1223	1245 AAACCGUUAC: ::::: : : ::::: : :AUAUUCAGU Translation	pacid=371578
24	736	758 AAACCGUUAC:::: ::::: : : ::::: :AGGCUCACCA Cleavage	pacid=371570
25			
26	331	353 AAACCGUUAC: ::::: : : ::::: : :AGAAUCAGU Cleavage	pacid=371433
27	740	762 AAACCGUUAC: ::::: : : ::::: : :AACCUCAUUC Cleavage	pacid=371492
28	607	629 AAACCGUUAC: ::::: : : ::::: : :GAUUAUGGU Cleavage	pacid=371741
29			
30	3141	3163 AAACCGUUAC ::::: : : ::::: : :GUAUUCAGC Cleavage	pacid=371544
31	2697	2719 AAACCGUUAC ::::: : : ::::: : :UAAUUCACU Cleavage	pacid=371680
32	154	176 AAACCGUUAC: ::::: : : ::::: : :AAGAUUAGU Translation	pacid=371718
33	295	317 AAACCGUUAC ::::: : : ::::: : :UCAGUCUGU Cleavage	pacid=371718
34			
35	549	571 AAACCGUUAC:::: ::::: : : ::::: :GGGUUUGGU Cleavage	pacid=371609
36	1176	1198 AAACCGUUAC: ::::: : : ::::: : :AAGUACACU Cleavage	pacid=371552
37			
38	1	23 AAACCGUUAC:::: ::::: : : ::::: : :GAACACAUAC Cleavage	pacid=371609
39	1	23 AAACCGUUAC:::: ::::: : : ::::: : :GAACACAUAC Cleavage	pacid=371609
40	264	286 AAACCGUUAC:::: ::::: : : ::::: : :GAGUUCAGA Cleavage	pacid=371626
41	444	466 AAACCGUUAC: ::::: : : ::::: : :GAGUUAGGU Cleavage	pacid=371737
42			
43	1325	1347 AAACCGUUAC: ::::: : : ::::: : :AACCACAGUA Cleavage	pacid=371640
44	1263	1285 AAACCGUUAC:::: ::::: : : ::::: :GGAUUCGGU Cleavage	pacid=371548
45	513	535 AAACCGUUAC: ::::: : : ::::: : :GGAAUUGGC Cleavage	pacid=371548
46			
47	837	859 AAACCGUUAC: ::::: : : ::::: : :GGAAUUGGC Cleavage	pacid=371548
48	903	925 AAACCGUUAC: ::::: : : ::::: : :GGAAUUGGC Cleavage	pacid=371548
49	1101	1123 AAACCGUUAC: ::::: : : ::::: : :GGAAUUGGC Cleavage	pacid=371548
50			
51	1053	1075 AAACCGUUAC ::::: : : ::::: : :GGUUUAGGU Cleavage	pacid=371548
52	508	530 AAACCGUUAC: ::::: : : ::::: : :AAGCGUGGU Cleavage	pacid=371718
53	521	543 AAACCGUUAC:::: ::::: : : ::::: : :AAACUCACAA Cleavage	pacid=371779
54			
55	131	153 AAACCGUUAC:::: ::::: : : ::::: : :AAACACAGCA Cleavage	pacid=371533
56	1534	1556 AAACCGUUAC:::: ::::: : : ::::: : :GAACACAGUA Cleavage	pacid=371621
57	1539	1561 AAACCGUUAC:::: ::::: : : ::::: : :GAACACAGUA Cleavage	pacid=371621
58			
59	1019	1041 AAACCGUUAC:::: ::::: : : ::::: : :AGGCUUGGU Translation	pacid=371550
60	709	732 AAACCGUUAC:::: :: ::::: : : ::::: :AAAUGCAAGL Cleavage	pacid=371777
	349	371 AAACCGUUAC:::: ::::: : : ::::: : :AGACUCCCUC Cleavage	pacid=371712

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2	310	332 AAACCGUUAC.....: GGAAUUUGGU Cleavage	pacid=371548
3	418	440 AAACCGUUAC:..... :AGACUCCCUC Cleavage	pacid=371741
4	714	736 AAACCGUUAC :.....: GGAGCAGGU Cleavage	pacid=371513
5	858	880 AAACCGUUAC :.....: GGAGCAGGU Cleavage	pacid=371513
6	624	646 AAACCGUUAC :.....: GGAGCAGGU Cleavage	pacid=371513
7	957	979 AAACCGUUAC : : : : :UGACCCGGU Cleavage	pacid=371460
8	209	231 AAACCGUUAC: : : : :AGUUUCAGU Cleavage	pacid=371708
9	2329	2350 AAACCGUUAC: : : : :AGAUUCAGU Cleavage	pacid=371623
10	327	349 AAACCGUUAC : : : : :CAAUGCAGU Cleavage	pacid=371642
11	818	840 AAACCGUUAC: : : : :AACCUCAUUC Cleavage	pacid=371492
12	1223	1245 AAACCGUUAC: : : : :AUAUUCAGU Translation	pacid=371578
13	736	758 AAACCGUUAC: : : : :AGGCUCACCA Cleavage	pacid=371570
14	331	353 AAACCGUUAC: : : : :AGAAUCAGU Cleavage	pacid=371433
15	740	762 AAACCGUUAC: : : : :AACCUCAUUC Cleavage	pacid=371492
16	607	629 AAACCGUUAC: : : : :GAUUAUGGU Cleavage	pacid=371741
17	3141	3163 AAACCGUUAC : : : : :GUAUUCAGC Cleavage	pacid=371544
18	2697	2719 AAACCGUUAC : : : : :UAAUUCACU Cleavage	pacid=371680
19	154	176 AAACCGUUAC: : : : :AAGAUUAGU Translation	pacid=371718
20	295	317 AAACCGUUAC : : : : :UCAGUCUGU Cleavage	pacid=371718
21	549	571 AAACCGUUAC.....: GGGUUUGGU Cleavage	pacid=371609
22	1176	1198 AAACCGUUAC: : : : :AAGUACACU Cleavage	pacid=371552
23	1	23 AAACCGUUAC: : : : :GAACACAUAC Cleavage	pacid=371609
24	1	23 AAACCGUUAC: : : : :GAACACAUAC Cleavage	pacid=371609
25	264	286 AAACCGUUAC: : : : :GAGUUCAGA Cleavage	pacid=371626
26	444	466 AAACCGUUAC: : : : :GAGUUAGGU Cleavage	pacid=371737
27	1325	1347 AAACCGUUAC: : : : :AACCACAGUA Cleavage	pacid=371640
28			
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	Multiplicity	peptideName	locusName	Pfam	Panther	KOG
1						
2						
3	1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
4	1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
5	1	Phvul.008G049000	Phvul.008G049000	PF00793	PTHR21057,P	0
6	1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
7	1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
8	1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
9	1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
10	1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
11	1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
12	1	Phvul.009G196100	Phvul.009G196100		0 PTHR33494,P	0
13	1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
14	1	Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
15	4	Phvul.009G104850	Phvul.009G104850		0	0
16	1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
17	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
18	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
19	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
20	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
21	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
22	1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15PTHR13622,P		KOG4313
23	1	Phvul.011G152300	Phvul.011G152300	PF08276,PF00PTHR27002,P		KOG1187
24	1	Phvul.011G152300	Phvul.011G152300	PF08276,PF00PTHR27002,P		KOG1187
25	1	Phvul.011G152300	Phvul.011G152300	PF08276,PF00PTHR27002,P		KOG1187
26	1	Phvul.003G229300	Phvul.003G229300	PF10260	PTHR13527,P	KOG3249
27	1	Phvul.003G229300	Phvul.003G229300	PF10260	PTHR13527,P	KOG3249
28	1	Phvul.003G178200	Phvul.003G178200	PF02153	PTHR11811,P	0
29	1	Phvul.009G196100	Phvul.009G196100		0 PTHR33494,P	0
30	1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
31	1	Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
32	1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15PTHR13622,P		KOG4313
33	4	Phvul.009G104850	Phvul.009G104850		0	0
34	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
35	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
36	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
37	1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
38	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
39	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
40	1	Phvul.009G196100	Phvul.009G196100		0 PTHR33494,P	0
41	1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
42	1	Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
43	1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15PTHR13622,P		KOG4313
44	4	Phvul.009G104850	Phvul.009G104850		0	0
45	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
46	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
47	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
48	1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
49	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
50	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
51	1	Phvul.009G196100	Phvul.009G196100		0 PTHR33494,P	0
52	1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
53	1	Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
54	1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15PTHR13622,P		KOG4313
55	4	Phvul.009G104850	Phvul.009G104850		0	0
56	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
57	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
58	1	Phvul.L001604	Phvul.L001604		0 PTHR36390	0
59	1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
60	1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0

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2	1 Phvul.011G073600	Phvul.011G073600	PF02309,PF02PTHR31384,P		0
3	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
4	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
5	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
6	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
7	1 Phvul.002G041900	Phvul.002G041900	0 PTHR35105,P		0
8	1 Phvul.010G108300	Phvul.010G108300	PF01176 PTHR21668,P	KOG3403	
9					
10	4 Phvul.006G148800	Phvul.006G148800	0 0		0
11	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
12	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
13	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
14	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
15	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
16	1 Phvul.002G231800	Phvul.002G231800	PF00011 PTHR11527,P	KOG0710	
17	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
18	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
19	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
20	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
21	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
22	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
23	1 Phvul.002G226900	Phvul.002G226900	PF03031,PF00PTHR23081,P	KOG0323	
24	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
25	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
26	1 Phvul.005G137000	Phvul.005G137000	PF02037,PF02PTHR10782,P	KOG2169	
27	1 Phvul.007G222000	Phvul.007G222000	0 0		0
28	1 Phvul.007G029200	Phvul.007G029200	PF07797 PTHR33130,P		0
29	1 Phvul.003G058400	Phvul.003G058400	PF14416,PF13PTHR32285,P		0
30	1 Phvul.002G250000	Phvul.002G250000	PF02493,PF01PTHR23086,P		0
31	1 Phvul.004G028100	Phvul.004G028100	PF00271,PF12PTHR12131,P		0
32	3 Phvul.008G216700	Phvul.008G216700	0 0		0
33	3 Phvul.008G216700	Phvul.008G216700	0 0		0
34	3 Phvul.008G216700	Phvul.008G216700	0 0		0
35	1 Phvul.002G190100	Phvul.002G190100	PF00467,PF01PTHR10497	KOG3418	
36	1 Phvul.004G087000	Phvul.004G087000	PF07731,PF07PTHR11709,P	KOG1263	
37	1 Phvul.001G036500	Phvul.001G036500	0 PTHR10593,P		0
38	1 Phvul.005G102100	Phvul.005G102100	PF13639 PTHR22763,P		0
39	1 Phvul.005G102100	Phvul.005G102100	PF13639 PTHR22763,P		0
40	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
41	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
42	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
43	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
44	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
45	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
46	1 Phvul.002G041900	Phvul.002G041900	0 PTHR35105,P		0
47	3 Phvul.006G148800	Phvul.006G148800	0 0		0
48	1 Phvul.010G108300	Phvul.010G108300	PF01176 PTHR21668,P	KOG3403	
49	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
50	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
51	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
52	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P	KOG0229	
53	3 Phvul.008G216700	Phvul.008G216700	0 0		0
54	3 Phvul.008G216700	Phvul.008G216700	0 0		0
55	1 Phvul.001G036500	Phvul.001G036500	0 PTHR10593,P		0
56	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0
57	1 Phvul.002G289600	Phvul.002G289600	PF00153 PTHR24089,P		0



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2	1 Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P <sup>-</sup>	0
3	1 Phvul.002G041900	Phvul.002G041900		0 PTHR35105,P <sup>-</sup>	0
4	3 Phvul.006G148800	Phvul.006G148800	0	0	0
5					
6	1 Phvul.010G108300	Phvul.010G108300	PF01176	PTHR21668,P <sup>-</sup>	KOG3403
7	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P <sup>-</sup>		KOG0229
8	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P <sup>-</sup>		KOG0229
9					
10	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P <sup>-</sup>		KOG0229
11	1 Phvul.006G214700	Phvul.006G214700	PF02493,PF01PTHR23086,P <sup>-</sup>		KOG0229
12	3 Phvul.008G216700	Phvul.008G216700	0	0	0
13					
14	3 Phvul.008G216700	Phvul.008G216700	0	0	0
15	1 Phvul.001G036500	Phvul.001G036500	0	PTHR10593,P <sup>-</sup>	0
16	1 Phvul.001G052300	Phvul.001G052300	0	PTHR35697,P <sup>-</sup>	0
17					
18	1 Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
19	1 Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
20	<b>1 Phvul.009G100000</b>	<b>Phvul.009G100000</b>	<b>PF00240,PF13PTHR24006</b>	<b>KOG1863</b>	
21					
22	1 Phvul.009G100000	Phvul.009G100000	PF00240,PF13PTHR24006		KOG1863
23	1 Phvul.009G100000	Phvul.009G100000	PF00240,PF13PTHR24006		KOG1863
24	1 Phvul.009G100000	Phvul.009G100000	PF00240,PF13PTHR24006		KOG1863
25					
26	1 Phvul.001G073300	Phvul.001G073300		0 PTHR35697,P <sup>-</sup>	0
27	1 Phvul.008G279750	Phvul.008G279750	PF03552	PTHR13301,P <sup>-</sup>	0
28	1 Phvul.010G152600	Phvul.010G152600	PF11145	PTHR33389,P <sup>-</sup>	0
29					
30	1 Phvul.006G021500	Phvul.006G021500	PF14577,PF14PTHR33232,P <sup>-</sup>		0
31	1 Phvul.009G177300	Phvul.009G177300	PF00787,PF13PTHR12326,P <sup>-</sup>		0
32	1 Phvul.007G147400	Phvul.007G147400	PF00005,PF00PTHR24221,P <sup>-</sup>		0
33					
34	1 Phvul.003G178100	Phvul.003G178100	PF00226,PF01PTHR24078,P <sup>-</sup>		KOG0714
35	2 Phvul.011G102400	Phvul.011G102400	0	0	0
36	1 Phvul.001G106800	Phvul.001G106800	PF00249	PTHR10641,P <sup>-</sup>	KOG0048
37	1 Phvul.007G261100	Phvul.007G261100	PF08327,PF09PTHR13009,P <sup>-</sup>		KOG2936
38	1 Phvul.007G261100	Phvul.007G261100	PF08327,PF09PTHR13009,P <sup>-</sup>		KOG2936
39	1 Phvul.011G187600	Phvul.011G187600	PF11605,PF04PTHR13128,P <sup>-</sup>		KOG2760
40					
41	4 Phvul.006G148800	Phvul.006G148800	0	0	0
42					
43	4 Phvul.006G148800	Phvul.006G148800	0	0	0
44	1 Phvul.002G044500	Phvul.002G044500	PF14432,PF13PTHR24015,P <sup>-</sup>		0
45	1 Phvul.007G113300	Phvul.007G113300	PF08031,PF01PTHR32448,P <sup>-</sup>		0
46					
47	2 Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P <sup>-</sup>	0
48	1 Phvul.010G144900	Phvul.010G144900	PF00349,PF03PTHR19443,P <sup>-</sup>		0
49	1 Phvul.002G083800	Phvul.002G083800	PF00249	PTHR10641,P <sup>-</sup>	0
50					
51	1 Phvul.001G067500	Phvul.001G067500		0 PTHR34194,P <sup>-</sup>	0
52	1 Phvul.001G067500	Phvul.001G067500		0 PTHR34194,P <sup>-</sup>	0
53	1 Phvul.001G067500	Phvul.001G067500		0 PTHR34194,P <sup>-</sup>	0
54					
55	1 Phvul.006G045600	Phvul.006G045600	PF00439	PTHR22881,P <sup>-</sup>	0
56	1 Phvul.010G156000	Phvul.010G156000	PF04525	PTHR31087,P <sup>-</sup>	0
57	2 Phvul.007G055500	Phvul.007G055500	PF07690	PTHR23500,P <sup>-</sup>	KOG0254
58	2 Phvul.007G055500	Phvul.007G055500	PF07690	PTHR23500,P <sup>-</sup>	KOG0254
59	1 Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P <sup>-</sup>	0
60	1 Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P <sup>-</sup>	0

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2	2	Phvul.007G055200	Phvul.007G055200	PF07690	PTHR23500,P	KOG0254		
3	2	Phvul.007G055200	Phvul.007G055200	PF07690	PTHR23500,P	KOG0254		
4	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P		0	
5	1	Phvul.008G273100	Phvul.008G273100	PF00149	PTHR11668,P		0	
6	3	Phvul.008G216700	Phvul.008G216700		0	0	0	
7	1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338		
8	1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338		
9	1	Phvul.007G270500	Phvul.007G270500	PF00400,PF08	PTHR22840		0	
10	1	Phvul.004G125900	Phvul.004G125900	PF00999	PTHR16254,P	KOG1650		
11	1	Phvul.005G027200	Phvul.005G027200	PF00931	PTHR23155,P	KOG4658		
12	1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105		0	
13	1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105		0	
14	1	Phvul.001G052300	Phvul.001G052300		0 PTHR35697,P		0	
15	1	Phvul.008G279750	Phvul.008G279750	PF03552	PTHR13301,P		0	
16	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
17	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
18	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
19	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
20	1	Phvul.001G073300	Phvul.001G073300		0 PTHR35697,P		0	
21	1	Phvul.010G152600	Phvul.010G152600	PF11145	PTHR33389,P		0	
22	2	Phvul.011G102400	Phvul.011G102400		0	0	0	
23	3	Phvul.006G148800	Phvul.006G148800		0	0	0	
24	3	Phvul.006G148800	Phvul.006G148800		0	0	0	
25	1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338		
26	1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338		
27	1	Phvul.004G125900	Phvul.004G125900	PF00999	PTHR16254,P	KOG1650		
28	1	Phvul.002G044500	Phvul.002G044500	PF14432,PF13	PTHR24015,P		0	
29	1	Phvul.007G113300	Phvul.007G113300	PF08031,PF01	PTHR32448,P		0	
30	1	Phvul.006G021500	Phvul.006G021500	PF14577,PF14	PTHR33232,P		0	
31	1	Phvul.009G177300	Phvul.009G177300	PF00787,PF13	PTHR12326,P		0	
32	1	Phvul.007G147400	Phvul.007G147400	PF00005,PF00	PTHR24221,P		0	
33	1	Phvul.003G178100	Phvul.003G178100	PF00226,PF01	PTHR24078,P	KOG0714		
34	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P		0	
35	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P		0	
36	1	Phvul.001G106800	Phvul.001G106800	PF00249	PTHR10641,P	KOG0048		
37	1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936		
38	1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936		
39	1	Phvul.011G187600	Phvul.011G187600	PF11605,PF04	PTHR13128,P	KOG2760		
40	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P		0	
41	1	Phvul.008G273100	Phvul.008G273100	PF00149	PTHR11668,P		0	
42	1	Phvul.005G065300	Phvul.005G065300	PF11145	PTHR33389,P		0	
43	2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P		0	
44	1	Phvul.006G045600	Phvul.006G045600	PF00439	PTHR22881,P		0	
45	3	Phvul.008G216700	Phvul.008G216700		0	0	0	
46	1	Phvul.011G111800	Phvul.011G111800		0	0	0	
47	1	Phvul.010G144900	Phvul.010G144900	PF00349,PF03	PTHR19443,P		0	

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2	1	Phvul.002G083800	Phvul.002G083800	PF00249	PTHR10641,P <sup>-</sup>			0
3	1	Phvul.007G270500	Phvul.007G270500	PF00400,PF08	PTHR22840			0
4	1	Phvul.001G067500	Phvul.001G067500		0 PTHR34194,P <sup>-</sup>			0
5	1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105			0
6	1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105			0
7	1	Phvul.001G052300	Phvul.001G052300		0 PTHR35697,P <sup>-</sup>			0
8	1	Phvul.008G279750	Phvul.008G279750	PF03552	PTHR13301,P <sup>-</sup>			0
9	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
10	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
11	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
12	1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863		
13	1	Phvul.001G073300	Phvul.001G073300		0 PTHR35697,P <sup>-</sup>			0
14	1	Phvul.010G152600	Phvul.010G152600	PF11145	PTHR33389,P <sup>-</sup>			0
15	2	Phvul.011G102400	Phvul.011G102400		0	0		0
16	3	Phvul.006G148800	Phvul.006G148800		0	0		0
17	3	Phvul.006G148800	Phvul.006G148800		0	0		0
18	1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P <sup>-</sup>	KOG2338		
19	1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P <sup>-</sup>	KOG2338		
20	1	Phvul.004G125900	Phvul.004G125900	PF00999	PTHR16254,P <sup>-</sup>	KOG1650		
21	1	Phvul.002G044500	Phvul.002G044500	PF14432,PF13	PTHR24015,P <sup>-</sup>			0
22	1	Phvul.007G113300	Phvul.007G113300	PF08031,PF01	PTHR32448,P <sup>-</sup>			0
23	1	Phvul.006G021500	Phvul.006G021500	PF14577,PF14	PTHR33232,P <sup>-</sup>			0
24	1	Phvul.009G177300	Phvul.009G177300	PF00787,PF13	PTHR12326,P <sup>-</sup>			0
25	1	Phvul.007G147400	Phvul.007G147400	PF00005,PF00	PTHR24221,P <sup>-</sup>			0
26	1	Phvul.003G178100	Phvul.003G178100	PF00226,PF01	PTHR24078,P <sup>-</sup>	KOG0714		
27	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P <sup>-</sup>			0
28	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P <sup>-</sup>			0
29	1	Phvul.001G106800	Phvul.001G106800	PF00249	PTHR10641,P <sup>-</sup>	KOG0048		
30	1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P <sup>-</sup>	KOG2936		
31	1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P <sup>-</sup>	KOG2936		
32	1	Phvul.011G187600	Phvul.011G187600	PF11605,PF04	PTHR13128,P <sup>-</sup>	KOG2760		
33	1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P <sup>-</sup>			0
34	1	Phvul.008G273100	Phvul.008G273100	PF00149	PTHR11668,P <sup>-</sup>			0
35	1	Phvul.005G065300	Phvul.005G065300	PF11145	PTHR33389,P <sup>-</sup>			0
36	2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P <sup>-</sup>			0
37	1	Phvul.006G045600	Phvul.006G045600	PF00439	PTHR22881,P <sup>-</sup>			0
38	3	Phvul.008G216700	Phvul.008G216700		0	0		0
39	1	Phvul.011G111800	Phvul.011G111800		0	0		0
40	1	Phvul.010G144900	Phvul.010G144900	PF00349,PF03	PTHR19443,P <sup>-</sup>			0
41	1	Phvul.002G083800	Phvul.002G083800	PF00249	PTHR10641,P <sup>-</sup>			0
42	1	Phvul.007G270500	Phvul.007G270500	PF00400,PF08	PTHR22840			0
43	1	Phvul.001G067500	Phvul.001G067500		0 PTHR34194,P <sup>-</sup>			0
44	1	Phvul.001G067500	Phvul.001G067500		0 PTHR34194,P <sup>-</sup>			0
45	6	Phvul.011G133575	Phvul.011G133575		0	0		0
46	6	Phvul.011G133575	Phvul.011G133575		0	0		0
47	6	Phvul.011G133575	Phvul.011G133575		0	0		0

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2	6	Phvul.011G133575	Phvul.011G133575	0	0
3	6	Phvul.011G133575	Phvul.011G133575	0	0
4	6	Phvul.011G133575	Phvul.011G133575	0	0
5					
6	1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13PTHR32285,P <sup>-</sup>	0
7	1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13PTHR32285,P <sup>-</sup>	0
8	4	Phvul.009G104850	Phvul.009G104850	0	0
9					
10	4	Phvul.009G104850	Phvul.009G104850	0	0
11	4	Phvul.009G104850	Phvul.009G104850	0	0
12	1	Phvul.003G158800	Phvul.003G158800	PF00704	PTHR11177,P <sup>-</sup> KOG2806
13	1	Phvul.006G173500	Phvul.006G173500	PF00847	PTHR31194,P <sup>-</sup>
14					0
15	1	Phvul.002G183700	Phvul.002G183700	0	0
16					
17	2	Phvul.011G102400	Phvul.011G102400	0	0
18	1	Phvul.007G027000	Phvul.007G027000	PF00847	PTHR31194,P <sup>-</sup>
19	1	Phvul.005G043000	Phvul.005G043000	PF06101	PTHR17204,P <sup>-</sup>
20					0
21	4	Phvul.006G148800	Phvul.006G148800	0	0
22	1	Phvul.011G069000	Phvul.011G069000	PF01535,PF13PTHR24015,P <sup>-</sup>	0
23	2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P <sup>-</sup>
24	1	Phvul.005G054600	Phvul.005G054600	PF01926,PF11PTHR23115,P <sup>-</sup>	0
25					
26	1	Phvul.001G024200	Phvul.001G024200	PF00225	PTHR24115,P <sup>-</sup>
27	1	Phvul.008G060700	Phvul.008G060700	PF01554	PTHR11206,P <sup>-</sup> KOG1347
28	1	Phvul.004G147900	Phvul.004G147900	PF14531	PTHR24361,P <sup>-</sup> KOG0581
29	1	Phvul.001G057200	Phvul.001G057200	PF01269	PTHR10335
30					KOG1596
31	1	Phvul.009G046200	Phvul.009G046200	PF07145,PF14PTHR24012	KOG0131
32	1	Phvul.011G133400	Phvul.011G133400	0	PTHR35420
33					0
34	1	Phvul.008G111100	Phvul.008G111100	PF13639	PTHR14155,P <sup>-</sup>
35	1	Phvul.006G070000	Phvul.006G070000	PF13639	PTHR14155,P <sup>-</sup> KOG4172
36	1	Phvul.L001687	Phvul.L001687	PF02458	PTHR31642,P <sup>-</sup>
37					0
38	1	Phvul.008G033500	Phvul.008G033500	PF00076	PTHR24012
39					0
40	1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P <sup>-</sup>
41	1	Phvul.009G198900	Phvul.009G198900	PF05185	PTHR11006,P <sup>-</sup> KOG1499
42	1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P <sup>-</sup>
43					0
44	1	Phvul.006G037000	Phvul.006G037000	PF02458	PTHR31642,P <sup>-</sup>
45					0
46	1	Phvul.001G205600	Phvul.001G205600	PF13414,PF11PTHR17130,P <sup>-</sup>	0
47	1	Phvul.011G159400	Phvul.011G159400	PF14259,PF00PTHR24012,P <sup>-</sup>	KOG4205
48	1	Phvul.004G061900	Phvul.004G061900	PF07690	PTHR23500,P <sup>-</sup> KOG0254
49	1	Phvul.006G048000	Phvul.006G048000	PF00026	PTHR13683,P <sup>-</sup> KOG1339
50	1	Phvul.009G007900	Phvul.009G007900	0	0
51					0
52	1	Phvul.005G067950	Phvul.005G067950	PF03634	PTHR31072,P <sup>-</sup>
53					0
54	6	Phvul.011G133575	Phvul.011G133575	0	0
55	6	Phvul.011G133575	Phvul.011G133575	0	0
56	6	Phvul.011G133575	Phvul.011G133575	0	0
57	6	Phvul.011G133575	Phvul.011G133575	0	0
58	6	Phvul.011G133575	Phvul.011G133575	0	0
59	6	Phvul.011G133575	Phvul.011G133575	0	0
60	1	Phvul.006G173500	Phvul.006G173500	PF00847	PTHR31194,P <sup>-</sup>
	1	Phvul.002G183700	Phvul.002G183700	0	0

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2	1 Phvul.005G043000	Phvul.005G043000	PF06101	PTHR17204,P		0
3	1 Phvul.004G019300	Phvul.004G019300	PF14416,PF13PTHR32285,P			0
4	1 Phvul.004G019300	Phvul.004G019300	PF14416,PF13PTHR32285,P			0
5	1 Phvul.011G069000	Phvul.011G069000	PF01535,PF13PTHR24015,P			0
6	1 Phvul.002G231800	Phvul.002G231800	PF00011	PTHR11527,P	KOG0710	
7	1 Phvul.L001687	Phvul.L001687	PF02458	PTHR31642,P		0
8						
9	2 Phvul.011G102400	Phvul.011G102400		0	0	0
10						
11	1 Phvul.006G037000	Phvul.006G037000	PF02458	PTHR31642,P		0
12	4 Phvul.009G104850	Phvul.009G104850		0	0	0
13						
14	4 Phvul.009G104850	Phvul.009G104850		0	0	0
15	4 Phvul.009G104850	Phvul.009G104850		0	0	0
16	1 Phvul.003G158800	Phvul.003G158800	PF00704	PTHR11177,P	KOG2806	
17	1 Phvul.001G057200	Phvul.001G057200	PF01269	PTHR10335	KOG1596	
18						
19	1 Phvul.004G057900	Phvul.004G057900	PF01535,PF13PTHR24015,P			0
20	1 Phvul.007G027000	Phvul.007G027000	PF00847	PTHR31194,P		0
21						
22	1 Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513	
23	1 Phvul.008G060700	Phvul.008G060700	PF01554	PTHR11206,P	KOG1347	
24	1 Phvul.011G110000	Phvul.011G110000	PF02984,PF00PTHR10177,P		KOG0656	
25						
26	1 Phvul.010G003800	Phvul.010G003800	PF00854	PTHR11654,P	KOG1237	
27	1 Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513	
28	2 Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P		0
29						
30	1 Phvul.005G054600	Phvul.005G054600	PF01926,PF11PTHR23115,P			0
31	1 Phvul.001G024200	Phvul.001G024200	PF00225	PTHR24115,P		0
32	2 Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P		0
33						
34	2 Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P		0
35	1 Phvul.008G033500	Phvul.008G033500	PF00076	PTHR24012		0
36	1 Phvul.011G028900	Phvul.011G028900	PF01966	PTHR33594,P		0
37						
38	1 Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P		0
39	1 Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P		0
40	1 Phvul.004G061900	Phvul.004G061900	PF07690	PTHR23500,P	KOG0254	
41	1 Phvul.006G048000	Phvul.006G048000	PF00026	PTHR13683,P	KOG1339	
42						
43	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P		0
44	6 Phvul.011G133575	Phvul.011G133575		0	0	0
45	6 Phvul.011G133575	Phvul.011G133575		0	0	0
46	6 Phvul.011G133575	Phvul.011G133575		0	0	0
47	6 Phvul.011G133575	Phvul.011G133575		0	0	0
48	6 Phvul.011G133575	Phvul.011G133575		0	0	0
49	6 Phvul.011G133575	Phvul.011G133575		0	0	0
50	6 Phvul.011G133575	Phvul.011G133575		0	0	0
51	6 Phvul.011G133575	Phvul.011G133575		0	0	0
52	1 Phvul.006G173500	Phvul.006G173500	PF00847	PTHR31194,P		0
53	1 Phvul.002G183700	Phvul.002G183700		0	0	0
54						
55	1 Phvul.005G043000	Phvul.005G043000	PF06101	PTHR17204,P		0
56	1 Phvul.004G019300	Phvul.004G019300	PF14416,PF13PTHR32285,P			0
57	1 Phvul.004G019300	Phvul.004G019300	PF14416,PF13PTHR32285,P			0
58	1 Phvul.011G069000	Phvul.011G069000	PF01535,PF13PTHR24015,P			0
59	1 Phvul.002G231800	Phvul.002G231800	PF00011	PTHR11527,P	KOG0710	
60	1 Phvul.L001687	Phvul.L001687	PF02458	PTHR31642,P		0

1						
2	2	Phvul.011G102400	Phvul.011G102400	0	0	0
3	1	Phvul.006G037000	Phvul.006G037000	PF02458	PTHR31642,P <sup>-</sup>	0
4	4	Phvul.009G104850	Phvul.009G104850	0	0	0
5	4	Phvul.009G104850	Phvul.009G104850	0	0	0
6	4	Phvul.009G104850	Phvul.009G104850	0	0	0
7	1	Phvul.003G158800	Phvul.003G158800	PF00704	PTHR11177,P <sup>-</sup>	KOG2806
8	1	Phvul.001G057200	Phvul.001G057200	PF01269	PTHR10335	KOG1596
9	1	Phvul.004G057900	Phvul.004G057900	PF01535,PF13	PTHR24015,P <sup>-</sup>	0
10	1	Phvul.007G027000	Phvul.007G027000	PF00847	PTHR31194,P <sup>-</sup>	0
11	1	Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513
12	1	Phvul.008G060700	Phvul.008G060700	PF01554	PTHR11206,P <sup>-</sup>	KOG1347
13	1	Phvul.011G110000	Phvul.011G110000	PF02984,PF00	PTHR10177,P <sup>-</sup>	KOG0656
14	1	Phvul.010G003800	Phvul.010G003800	PF00854	PTHR11654,P <sup>-</sup>	KOG1237
15	1	Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513
16	2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P <sup>-</sup>	0
17	1	Phvul.005G054600	Phvul.005G054600	PF01926,PF11	PTHR23115,P <sup>-</sup>	0
18	1	Phvul.001G024200	Phvul.001G024200	PF00225	PTHR24115,P <sup>-</sup>	0
19	2	Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P <sup>-</sup>	0
20	2	Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P <sup>-</sup>	0
21	1	Phvul.008G033500	Phvul.008G033500	PF00076	PTHR24012	0
22	1	Phvul.011G028900	Phvul.011G028900	PF01966	PTHR33594,P <sup>-</sup>	0
23	1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P <sup>-</sup>	0
24	1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P <sup>-</sup>	0
25	1	Phvul.004G061900	Phvul.004G061900	PF07690	PTHR23500,P <sup>-</sup>	KOG0254
26	1	Phvul.006G048000	Phvul.006G048000	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
27	1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P <sup>-</sup>	0
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1	KEGG	KOG	GO	Best-hit-arabi-arabi-symbol	
2	3.1.27.1	K01166	GO:0033897,(	AT1G14220.1	0
3		0	0	0 AT2G18660.1 PNP-A	
4	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4 AtkdsA1	
5	3.1.27.1	K01166	GO:0033897,(	AT1G14220.1	0
6		0	0	0 AT2G18660.1 PNP-A	
7	3.1.27.1	K01166	GO:0033897,(	AT1G14220.1	0
8		0	0	0 AT2G18660.1 PNP-A	
9	3.1.27.1	K01166	GO:0033897,(	AT1G14220.1	0
10		0	0	0 AT2G18660.1 PNP-A	
11		0	0	0 AT2G24100.1	0
12		0	0	GO:0016021,(	AT1G34470.1
13		0	0	0 AT2G37570.1 SLT1	
14		0	0	0 0	0
15		0	0	0 AT4G17430.1	0
16		0	0	GO:0006355,(	AT5G60450.1 ARF4
17		0	0	GO:0006355,(	AT5G60450.1 ARF4
18		0	0	0 AT5G07890.1	0
19		0	0	0 AT5G07890.1	0
20		0	0	0 AT5G07890.1	0
21	2.7.6.2		0	GO:0016787 AT5G19460.1 atnudt20,NUC	
22	2.7.11.1		0	GO:0048544,(	AT4G27290.1
23	2.7.11.1		0	GO:0048544,(	AT4G27290.1
24	2.7.11.1		0	GO:0048544,(	AT4G27290.1
25		0	0	0 AT2G35360.1	0
26		0	0	0 AT2G35360.1	0
27	1.3.1.78	K15227	GO:0055114,(	AT5G34930.1	0
28		0	0	0 AT2G24100.1	0
29		0	0	GO:0016021,(	AT1G34470.1
30		0	0	0 AT2G37570.1 SLT1	
31	2.7.6.2		0	GO:0016787 AT5G19460.1 atnudt20,NUC	
32		0	0	0 0	0
33		0	0	0 AT5G07890.1	0
34		0	0	0 AT5G07890.1	0
35		0	0	0 AT5G07890.1	0
36		0	0	0 AT5G07890.1	0
37		0	0	0 AT4G17430.1	0
38		0	0	GO:0006355,(	AT5G60450.1 ARF4
39		0	0	GO:0006355,(	AT5G60450.1 ARF4
40		0	0	0 AT2G24100.1	0
41		0	0	GO:0016021,(	AT1G34470.1
42		0	0	0 AT2G37570.1 SLT1	
43	2.7.6.2		0	GO:0016787 AT5G19460.1 atnudt20,NUC	
44		0	0	0 0	0
45		0	0	0 AT5G07890.1	0
46		0	0	0 AT5G07890.1	0
47		0	0	0 AT5G07890.1	0
48		0	0	0 AT5G07890.1	0
49		0	0	0 AT4G17430.1	0
50		0	0	GO:0006355,(	AT5G60450.1 ARF4
51		0	0	GO:0006355,(	AT5G60450.1 ARF4
52		0	0	0 AT2G24100.1	0
53		0	0	GO:0016021,(	AT1G34470.1
54		0	0	0 AT2G37570.1 SLT1	
55	2.7.6.2		0	GO:0016787 AT5G19460.1 atnudt20,NUC	
56		0	0	0 0	0
57		0	0	0 AT5G07890.1	0
58		0	0	0 AT5G07890.1	0
59		0	0	0 AT5G07890.1	0
60		0	0	0 AT4G17430.1	0
		0	0	GO:0006355,(	AT5G60450.1 ARF4



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2		0	0	GO:0006355,(CAT5G60450.1 ARF4	
3		0	0	0 AT4G11440.1	0
4		0	0	0 AT4G11440.1	0
5		0	0	0 AT4G11440.1	0
6		0	0	0 AT4G11440.1	0
7		0	0	0 AT1G64980.1	0
8		0	0	0 AT1G64980.1	0
9		0 K03236	GO:0006413,(CAT2G04520.1		0
10		0	0	0	0
11	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
12	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
13	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
14	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
15	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
16		0 K13993	0	AT1G07400.1	0
17		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
18		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
19		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
20		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
21		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
22		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
23	3.1.3.16	K18998	0	AT4G21670.1 ATCPL1,CPL1,I	
24		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
25		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
26		0	0	GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1	
27		0	0	0	0
28		0	0	0 AT1G25370.1	0
29		0	0	0 AT2G34070.1 TBL37	
30		0	0	0 AT2G34070.1 TBL37	
31	2.7.1.68	K00889	GO:0046488,(CAT1G10900.1		0
32	3.6.4.13	K17675	GO:0016817 AT5G39840.1		0
33		0	0	0	0
34		0	0	0	0
35		0	0	0	0
36		0 K02901	GO:0006412,(CAT4G15000.1		0
37	1.10.3.2	K05909	GO:0055114,(CAT5G48100.1 ATLAC15,LAC1		
38		0	0	0 AT3G50700.1 AtIDD2,IDD2	
39		0	0	0 AT3G50700.1 AtIDD2,IDD2	
40		0	0	GO:0008270,(CAT4G28370.1	0
41		0	0	GO:0008270,(CAT4G28370.1	0
42		0	0	GO:0008270,(CAT4G28370.1	0
43		0	0	0 AT4G11440.1	0
44		0	0	0 AT4G11440.1	0
45		0	0	0 AT4G11440.1	0
46		0	0	0 AT4G11440.1	0
47		0	0	0 AT1G64980.1	0
48		0	0	0	0
49		0 K03236	GO:0006413,(CAT2G04520.1		0
50		0	0	0	0
51	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
52	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
53	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
54	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
55	2.7.1.68		0	GO:0046488,(CAT1G10900.1	0
56		0	0	0	0
57		0	0	0	0
58		0	0	0	0
59		0	0	0 AT3G50700.1 AtIDD2,IDD2	
60		0	0	0 AT4G11440.1	0
		0	0	0 AT4G11440.1	0

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2		0	0	0 AT4G11440.1	0
3		0	0	0 AT1G64980.1	0
4		0	0	0 0	0
5					
6		0 K03236		GO:0006413,(AT2G04520.1	0
7	2.7.1.68			0 GO:0046488,(AT1G10900.1	0
8	2.7.1.68			0 GO:0046488,(AT1G10900.1	0
9	2.7.1.68			0 GO:0046488,(AT1G10900.1	0
10	2.7.1.68			0 GO:0046488,(AT1G10900.1	0
11	2.7.1.68			0 GO:0046488,(AT1G10900.1	0
12		0	0	0 0	0
13		0	0	0 0	0
14		0	0	0 AT3G50700.1 AtIDD2,IDD2	
15		0	0	0 AT5G48920.1 TED7	
16		0	0	0 AT1G30240.2	0
17		0	0	0 AT1G30240.2	0
18		0	0	0 AT1G30240.2	0
19		0	0	0 AT1G30240.2	0
20	3.4.19.12	K11858		GO:0005515 AT3G49600.1 ATUBP26,SUP	
21	3.4.19.12	K11858		GO:0005515 AT3G49600.1 ATUBP26,SUP	
22	3.4.19.12	K11858		GO:0005515 AT3G49600.1 ATUBP26,SUP	
23	3.4.19.12	K11858		GO:0005515 AT3G49600.1 ATUBP26,SUP	
24	3.4.19.12	K11858		GO:0005515 AT3G49600.1 ATUBP26,SUP	
25		0	0	0 AT1G43790.1 TED6	
26	2.4.1.12			0 GO:0030244,(AT1G55850.1 ATCSLE1,CSLE	
27		0	0	0 AT1G52780.1	0
28		0	0	0 AT3G01680.1	0
29		0	0	0 GO:0035091 AT3G48195.1	0
30		0	0	0 GO:0035091 AT3G48195.1	0
31	3.6.3.44	K05658		GO:0016887,(AT2G36910.1 ABCB1,ATPGP	
32		0 K09510		0 AT2G20560.1	0
33		0	0	0 0 0	0
34		0 K09422		0 AT5G17800.1 AtMYB56,MYE	
35		0	0	0 GO:0006950,(AT3G12050.1	0
36		0	0	0 GO:0006950,(AT3G12050.1	0
37		0 K12190		GO:0043130,(AT5G04920.1	0
38		0	0	0 0 0	0
39		0	0	0 0 0	0
40		0	0	0 AT4G14820.1	0
41		0	0	0 GO:0055114,(AT5G44390.1	0
42		0	0	0 GO:0003723 AT1G78160.1 APUM7,PUM7	
43	2.7.1.1	K00844		GO:0016773,(AT2G19860.1 ATHXK2,HXK2	
44		0 K09422		0 AT1G69560.1 ATMYB105,LC	
45		0	0	0 AT4G01170.1	0
46		0	0	0 AT4G01170.1	0
47		0	0	0 AT4G01170.1	0
48		0 K11723		GO:0005515 AT5G55040.1	0
49		0	0	0 AT3G15810.1	0
50		0	0	0 GO:0055085,(AT5G26340.1 ATSTP13,MSS	
51		0	0	0 GO:0055085,(AT5G26340.1 ATSTP13,MSS	
52		0	0	0 AT2G43465.1	0
53		0	0	0 AT2G43465.1	0
54		0	0	0 AT2G43465.1	0
55		0	0	0 AT2G43465.1	0
56		0	0	0 AT2G43465.1	0
57		0	0	0 AT2G43465.1	0
58		0	0	0 AT2G43465.1	0
59		0	0	0 AT2G43465.1	0
60		0	0	0 AT2G43465.1	0

1				
2		0	0 GO:0055085,(CAT5G26340.1 ATSTP13,MSS	
3		0	0 GO:0055085,(CAT5G26340.1 ATSTP13,MSS	
4		0	0	0 AT2G43465.1
5		0	0	0 AT2G43465.1
6	3.1.3.16	K15423	GO:0016787	AT5G55260.1 PPX-2,PPX2
7		0	0	0 0 0
8		0	0	0 AT5G54130.2
9		0	0	0 AT5G54130.2
10		0	0	0 AT5G54130.2
11		0 K10599	GO:0005515	AT2G33340.1 MAC3B
12		0	0 GO:0055085,(CAT5G51710.2 ATKEA5,KEA5	
13		0	0 GO:0043531	AT3G14470.1
14		0	0	0 AT1G30240.2
15		0	0	0 AT1G30240.2
16		0	0	0 AT1G30240.2
17		0	0	0 AT5G48920.1 TED7
18		0	0	0 AT5G48920.1 TED7
19	2.4.1.12		0 GO:0030244,(CAT1G55850.1 ATCSLE1,CSLE	
20	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP
21	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP
22	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP
23	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP
24	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP
25		0	0	0 AT1G43790.1 TED6
26		0	0	0 AT1G52780.1
27		0	0	0 AT1G52780.1
28		0	0	0 0 0
29		0	0	0 0 0
30		0	0	0 0 0
31		0	0	0 0 0
32		0	0	0 AT5G54130.2
33		0	0	0 AT5G54130.2
34		0	0	0 AT5G54130.2
35		0	0 GO:0055085,(CAT5G51710.2 ATKEA5,KEA5	
36		0	0	0 AT4G14820.1
37		0	0 GO:0055114,(CAT5G44390.1	
38		0	0	0 AT3G01680.1
39		0	0	0 AT3G01680.1
40		0	0 GO:0035091	AT3G48195.1
41	3.6.3.44	K05658	GO:0016887,(CAT2G36910.1 ABCB1,ATPGP	
42		0 K09510	0	0 AT2G20560.1
43		0	0	0 AT2G20560.1
44		0	0	0 AT2G43465.1
45		0	0	0 AT2G43465.1
46		0	0	0 AT2G43465.1
47		0 K09422	0	0 AT5G17800.1 AtMYB56,MYE
48		0	0 GO:0006950,(CAT3G12050.1	
49		0	0 GO:0006950,(CAT3G12050.1	
50		0 K12190	GO:0043130,(CAT5G04920.1	
51		0	0	0 AT2G43465.1
52		0	0	0 AT2G43465.1
53	3.1.3.16	K15423	GO:0016787	AT5G55260.1 PPX-2,PPX2
54		0	0	0 AT4G21700.1
55		0	0 GO:0003723	AT1G78160.1 APUM7,PUM7
56		0	0	0 AT1G78160.1 APUM7,PUM7
57		0 K11723	GO:0005515	AT5G55040.1
58		0	0	0 0 0
59		0	0	0 0 0
60		0	0	0 AT4G28210.1 emb1923
	2.7.1.1	K00844	GO:0016773,(CAT2G19860.1 ATHXK2,HXK2	

1					
2		0 K09422		0 AT1G69560.1 ATMYB105,LC	
3		0 K10599	GO:0005515	AT2G33340.1 MAC3B	
4		0	0	0 AT4G01170.1	0
5		0	0	0 AT1G30240.2	0
6		0	0	0 AT1G30240.2	0
7		0	0	0 AT5G48920.1 TED7	
8		0	0	0 AT5G48920.1 TED7	
9					
10	2.4.1.12		0 GO:0030244,(	AT1G55850.1 ATCSLE1,CSLE	
11	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP	
12	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP	
13	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP	
14	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP	
15	3.4.19.12	K11858	GO:0005515	AT3G49600.1 ATUBP26,SUP	
16		0	0	0 AT1G43790.1 TED6	
17		0	0	0 AT1G52780.1	0
18		0	0	0	0
19		0	0	0	0
20		0	0	0	0
21		0	0	0	0
22		0	0	0	0
23		0	0	0 AT5G54130.2	0
24		0	0	0 AT5G54130.2	0
25		0	0	0 GO:0055085,(	AT5G51710.2 ATKEA5,KEA5
26		0	0	0 AT4G14820.1	0
27		0	0	0 AT4G14820.1	0
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32	3.6.3.44	K05658	GO:0016887,(	AT2G36910.1 ABCB1,ATPGP	
33		0 K09510		0 AT2G20560.1	0
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44	3.1.3.16	K15423	GO:0016787	AT5G55260.1 PPX-2,PPX2	
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52	2.7.1.1	K00844	GO:0016773,(	AT2G19860.1 ATHXK2,HXK2	
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6		0	0	0 AT3G28150.1 TBL22	
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12		0 K01183	GO:0005975,(AT4G19810.1		0
13		0	0 GO:0006355,(AT5G19790.1 RAP2.11		
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18		0	0 GO:0006355,(AT3G25890.1		0
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22		0	0	0 AT1G02420.1	0
23		0	0 GO:0003723 AT1G78160.1 APUM7,PUM7		
24	3.6.5.3	K02519	GO:0005525 AT1G17220.1 FUG1		
25	3.6.4.4	K10395	GO:0008017,(AT5G47820.1 FRA1		
26		0 K03327	GO:0055085,(AT4G00350.1		0
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28	2.7.12.2		0	0 AT1G73500.1 ATMKK9,MKK	
29	3.6.4.13	K14563	GO:0008168,(AT5G52470.1 ATFBR1,ATFIB		
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34		0	0 GO:0008270,(AT5G58580.1 ATL63,TL63		
35		0	0	0	0
36	2.3.1.133		0 GO:0016747 AT2G19070.1 SHT		
37		0 K12741	GO:0003676 AT5G61030.1 GR-RBP3		
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39	2.7.11.1		0	0 AT3G29270.2	0
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44		0	0	0 AT1G02910.1 LPA1	
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3		0	0	0 AT3G28150.1 TBL22	
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16		0 K01183		GO:0005975,(AT4G19810.1	0
17	3.6.4.13	K14563		GO:0008168,(AT5G52470.1 ATFBR1,ATFIB	
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19		0	0	GO:0006355,(AT3G25890.1	0
20		0	0	GO:0006629 AT2G26560.1 PLA IIA,PLA2A	
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22		0 K03327		GO:0055085,(AT4G00350.1	0
23		0 K18812		GO:0005634,(AT4G03270.1 CYCD6;1	
24		0	0	GO:0016020,(AT3G53960.1	0
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26		0	0	GO:0003723 AT1G78160.1 APUM7,PUM7	
27		0	0	GO:0003723 AT1G78160.1 APUM7,PUM7	
28	3.6.5.3	K02519		GO:0005525 AT1G17220.1 FUG1	
29	3.6.4.4	K10395		GO:0008017,(AT5G47820.1 FRA1	
30	2.3.1.1		0	GO:0008080 AT3G22560.1	0
31	2.3.1.1		0	GO:0008080 AT3G22560.1	0
32		0 K12741		GO:0003676 AT5G61030.1 GR-RBP3	
33		0 K06950		0 AT1G17330.1	0
34	2.7.11.1		0	0 AT3G29270.2	0
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36		0	0	GO:0055085,(AT5G16150.3 GLT1,PGLCT	
37	3.4.23.12		0	GO:0006508,(AT5G10770.1	0
38		0	0	0 AT2G37570.1 SLT1	
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51		0	0	0	0
52		0	0	GO:0006355,(AT5G19790.1 RAP2.11	
53		0	0	0	0
54		0	0	0 AT2G44260.2	0
55		0	0	0 AT3G28150.1 TBL22	
56		0	0	0 AT3G28150.1 TBL22	
57		0	0	0 AT1G02420.1	0
58		0	0	0 AT1G07400.1	0
59		0 K13993		0 AT1G07400.1	0
60	2.3.1.133		0	GO:0016747 AT2G19070.1 SHT	

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2		0	0	0	0
3	2.3.1.133	K13065	GO:0016747	AT2G19070.1	SHT
4		0	0	0	0
5		0	0	0	0
6		0	0	0	0
7		0	0	0	0
8		0	K01183	GO:0005975,(	AT4G19810.1
9	3.6.4.13	K14563	GO:0008168,(	AT5G52470.1	ATFBR1,ATFIB
10		0	0	0	AT1G79490.1
11		0	0	GO:0006355,(	AT3G25890.1
12		0	0	GO:0006629	AT2G26560.1
13		0	0	GO:0006629	AT2G26560.1
14		0	K03327	GO:0055085,(	AT4G00350.1
15		0	K18812	GO:0005634,(	AT4G03270.1
16		0	0	GO:0016020,(	AT3G53960.1
17		0	0	GO:0006629	AT2G26560.1
18		0	0	GO:0003723	AT1G78160.1
19	3.6.5.3	K02519	GO:0005525	AT1G17220.1	FUG1
20	3.6.4.4	K10395	GO:0008017,(	AT5G47820.1	FRA1
21	2.3.1.1		0	GO:0008080	AT3G22560.1
22	2.3.1.1		0	GO:0008080	AT3G22560.1
23		0	K12741	GO:0003676	AT5G61030.1
24		0	K06950	0	AT1G17330.1
25	2.7.11.1		0	0	AT3G29270.2
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27		0	0	GO:0055085,(	AT5G16150.3
28	3.4.23.12		0	GO:0006508,(	AT5G10770.1
29		0	0	0	AT2G37570.1
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1	arabi-defline	ID	Annot_defline	IDENTIFIER
2	Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:Si	Phvul.004G06
3	plant natriuretic peptide A	Phvul.009G09	PTHR22595://I	Phvul.009G09
4	Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de	Phvul.008G04
5	Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:Si	Phvul.004G06
6	plant natriuretic peptide A	Phvul.009G09	PTHR22595://I	Phvul.009G09
7	Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:Si	Phvul.004G06
8	plant natriuretic peptide A	Phvul.009G09	PTHR22595://I	Phvul.009G09
9	Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:Si	Phvul.004G06
10	plant natriuretic peptide A	Phvul.009G09	PTHR22595://I	Phvul.009G09
11		0	0	0 Phvul.009G19
12	Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
13	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:Si	Phvul.007G15
14		0	0	0 Phvul.009G10
15	O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
16	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
17	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
18	myosin heavy chain-related		0	0 Phvul.L00160
19	myosin heavy chain-related		0	0 Phvul.L00160
20	myosin heavy chain-related		0	0 Phvul.L00160
21	nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
22	S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:Si	Phvul.011G15
23	S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:Si	Phvul.011G15
24	S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:Si	Phvul.011G15
25	ubiquitin family protein	Phvul.003G22	PTHR13527:Si	Phvul.003G22
26	ubiquitin family protein	Phvul.003G22	PTHR13527:Si	Phvul.003G22
27	arogenate dehydrogenase	Phvul.003G17	1.3.1.78 - Aro	Phvul.003G17
28		0	0	0 Phvul.009G19
29	Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
30	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:Si	Phvul.007G15
31	nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
32		0	0	0 Phvul.009G10
33	myosin heavy chain-related		0	0 Phvul.L00160
34	myosin heavy chain-related		0	0 Phvul.L00160
35	myosin heavy chain-related		0	0 Phvul.L00160
36	O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
37	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
38	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
39		0	0	0 Phvul.009G19
40	Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
41	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:Si	Phvul.007G15
42	nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
43		0	0	0 Phvul.009G10
44	myosin heavy chain-related		0	0 Phvul.L00160
45	myosin heavy chain-related		0	0 Phvul.L00160
46	myosin heavy chain-related		0	0 Phvul.L00160
47	O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
48	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
49	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
50		0	0	0 Phvul.009G19
51	Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
52	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:Si	Phvul.007G15
53	nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
54		0	0	0 Phvul.009G10
55	myosin heavy chain-related		0	0 Phvul.L00160
56	myosin heavy chain-related		0	0 Phvul.L00160
57	myosin heavy chain-related		0	0 Phvul.L00160
58	O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
59	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07

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2	auxin response factor 4	Phvul.011G07	PTHR31384:Si	Phvul.011G07
3	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
4	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
5	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
6	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
7	Nucleotide-diphospho-sugar transferases superf	0	0	Phvul.002G04
8	Nucleic acid-binding, OB-fold-like protein	Phvul.010G10	K03236 - tran:	Phvul.010G10
9		0	0	0 Phvul.006G14
10		0	0	0 Phvul.006G14
11	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
12	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
13	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
14	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
15	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
16	HSP20-like chaperones superfamily protein	Phvul.002G23	PTHR11527:Si	Phvul.002G23
17	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
18	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
19	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
20	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
21	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
22	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
23	C-terminal domain phosphatase-like 1	Phvul.002G22	PTHR23081:Si	Phvul.002G22
24	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
25	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
26	DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:Si	Phvul.005G13
27		0	0	0 Phvul.007G22
28	Protein of unknown function (DUF1639)	Phvul.007G02	PF07797 - Pro	Phvul.007G02
29	TRICHOME BIREFRINGENCE-LIKE 37	Phvul.003G05	PTHR32285:Si	Phvul.003G05
30	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.002G25	PTHR23086:Si	Phvul.002G25
31	ATP-dependent RNA helicase, mitochondrial, pu	Phvul.004G02	PTHR12131:Si	Phvul.004G02
32		0	0	0 Phvul.008G21
33		0	0	0 Phvul.008G21
34		0	0	0 Phvul.008G21
35		0	0	0 Phvul.008G21
36	Ribosomal L27e protein family	Phvul.002G19	K02901 - large	Phvul.002G19
37	Laccase/Diphenol oxidase family protein	Phvul.004G08	PTHR11709:Si	Phvul.004G08
38	indeterminate(ID)-domain 2	Phvul.001G03	PTHR10593:Si	Phvul.001G03
39	RING/U-box superfamily protein	Phvul.005G10	PTHR22763:Si	Phvul.005G10
40	RING/U-box superfamily protein	Phvul.005G10	PTHR22763:Si	Phvul.005G10
41	RING/U-box superfamily protein	Phvul.005G10	PTHR22763:Si	Phvul.005G10
42	RING/U-box superfamily protein	Phvul.005G10	PTHR22763:Si	Phvul.005G10
43	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
44	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
45	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
46	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
47	Nucleotide-diphospho-sugar transferases superf	0	0	Phvul.002G04
48		0	0	0 Phvul.006G14
49	Nucleic acid-binding, OB-fold-like protein	Phvul.010G10	K03236 - tran:	Phvul.010G10
50	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
51	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
52	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
53	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
54	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
55	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
56		0	0	0 Phvul.008G21
57		0	0	0 Phvul.008G21
58		0	0	0 Phvul.008G21
59	indeterminate(ID)-domain 2	Phvul.001G03	PTHR10593:Si	Phvul.001G03
60	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28

1				
2	Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:Si	Phvul.002G28
3	Nucleotide-diphospho-sugar transferases superf	0	0	Phvul.002G04
4		0	0	Phvul.006G14
5				
6	Nucleic acid-binding, OB-fold-like protein	Phvul.010G10	K03236 - tran:	Phvul.010G10
7	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
8	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
9				
10	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
11	Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:Si	Phvul.006G21
12		0	0	Phvul.008G21
13		0	0	Phvul.008G21
14				
15	indeterminate(ID)-domain 2	Phvul.001G03	PTHR10593:Si	Phvul.001G03
16	tracheary element differentiation-related 7	0	0	Phvul.001G05
17				
18		0	Phvul.010G11	PF08167 - rRN
19		0	Phvul.010G11	PF08167 - rRN
20	<b>ubiquitin-specific protease 26</b>	<b>Phvul.009G10</b>	<b>K11858 - ubiq</b>	<b>Phvul.009G10</b>
21	ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
22	ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
23	ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
24	ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
25	tracheary element differentiation-related 6	0	0	Phvul.001G07
26	cellulose synthase like E1	Phvul.008G27	PTHR13301//I	Phvul.008G27
27	Protein of unknown function (DUF2921)	Phvul.010G15	PF11145 - Pro	Phvul.010G15
28		0	Phvul.006G02	PF14577 - Sie
29				
30				
31	Phox (PX) domain-containing protein	Phvul.009G17	PTHR12326 - I	Phvul.009G17
32	ATP binding cassette subfamily B1	Phvul.007G14	PTHR24221:Si	Phvul.007G14
33	DNAJ heat shock family protein	Phvul.003G17	PTHR24078:Si	Phvul.003G17
34		0	0	Phvul.011G10
35	myb domain protein 56	Phvul.001G10	PTHR10641:Si	Phvul.001G10
36	Aha1 domain-containing protein	Phvul.007G26	PTHR13009 - I	Phvul.007G26
37	Aha1 domain-containing protein	Phvul.007G26	PTHR13009 - I	Phvul.007G26
38	EAP30/Vps36 family protein	Phvul.011G18	K12190 - ESCF	Phvul.011G18
39		0	0	Phvul.006G14
40		0	0	Phvul.006G14
41				
42	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.002G04	PF01535//PF1	Phvul.002G04
43	FAD-binding Berberine family protein	Phvul.007G11	PF01565//PF	Phvul.007G11
44	pumilio 7	Phvul.006G20	PTHR12537:Si	Phvul.006G20
45	hexokinase 2	Phvul.010G14	PTHR19443//I	Phvul.010G14
46	myb domain protein 105	Phvul.002G08	PTHR10641:Si	Phvul.002G08
47		0	Phvul.001G06	PTHR34194:Si
48		0	Phvul.001G06	PTHR34194:Si
49		0	Phvul.001G06	PTHR34194:Si
50				
51	DNA-binding bromodomain-containing protein	Phvul.006G04	PTHR22881:Si	Phvul.006G04
52	Protein of unknown function (DUF567)	Phvul.010G15	PTHR31087:Si	Phvul.010G15
53	Major facilitator superfamily protein	Phvul.007G05	PTHR23500:Si	Phvul.007G05
54	Major facilitator superfamily protein	Phvul.007G05	PTHR23500:Si	Phvul.007G05
55	RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:Si	Phvul.005G15
56	RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:Si	Phvul.005G15

1	Major facilitator superfamily protein	Phvul.007G05 PTHR23500:SiPhvul.007G05
2	Major facilitator superfamily protein	Phvul.007G05 PTHR23500:SiPhvul.007G05
3	Major facilitator superfamily protein	Phvul.007G05 PTHR23500:SiPhvul.007G05
4	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
5	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
6	protein phosphatase X 2	Phvul.008G27K15423 - serirPhvul.008G27
7		0 0 0 Phvul.008G21
8	Calcium-binding endonuclease/exonuclease/phc	Phvul.010G12 PTHR12121//IPhvul.010G12
9	Calcium-binding endonuclease/exonuclease/phc	Phvul.010G12 PTHR12121//IPhvul.010G12
10	Calcium-binding endonuclease/exonuclease/phc	Phvul.010G12 PTHR12121//IPhvul.010G12
11	MOS4-associated complex 3B	Phvul.007G27K10599 - pre-iPhvul.007G27
12	K <sup>+</sup> efflux antiporter 5	Phvul.004G12 PTHR16254:SiPhvul.004G12
13	K <sup>+</sup> efflux antiporter 5	Phvul.004G12 PTHR16254:SiPhvul.004G12
14	NB-ARC domain-containing disease resistance p	Phvul.005G02 PTHR23155//IPhvul.005G02
15		0 Phvul.010G11 PF08167 - rRNPhvul.010G11
16		0 Phvul.010G11 PF08167 - rRNPhvul.010G11
17		0 Phvul.010G11 PF08167 - rRNPhvul.010G11
18	tracheary element differentiation-related 7	0 0 Phvul.001G05
19	cellulose synthase like E1	Phvul.008G27 PTHR13301//IPhvul.008G27
20	ubiquitin-specific protease 26	Phvul.009G10K11858 - ubiq Phvul.009G10
21	ubiquitin-specific protease 26	Phvul.009G10K11858 - ubiq Phvul.009G10
22	ubiquitin-specific protease 26	Phvul.009G10K11858 - ubiq Phvul.009G10
23	ubiquitin-specific protease 26	Phvul.009G10K11858 - ubiq Phvul.009G10
24	ubiquitin-specific protease 26	Phvul.009G10K11858 - ubiq Phvul.009G10
25	ubiquitin-specific protease 26	Phvul.009G10K11858 - ubiq Phvul.009G10
26	tracheary element differentiation-related 6	0 0 Phvul.001G07
27	Protein of unknown function (DUF2921)	Phvul.010G15 PF11145 - ProPhvul.010G15
28		0 0 0 Phvul.011G10
29		0 0 0 Phvul.011G10
30		0 0 0 Phvul.006G14
31		0 0 0 Phvul.006G14
32	Calcium-binding endonuclease/exonuclease/phc	Phvul.010G12 PTHR12121//IPhvul.010G12
33	Calcium-binding endonuclease/exonuclease/phc	Phvul.010G12 PTHR12121//IPhvul.010G12
34	Calcium-binding endonuclease/exonuclease/phc	Phvul.010G12 PTHR12121//IPhvul.010G12
35	K <sup>+</sup> efflux antiporter 5	Phvul.004G12 PTHR16254:SiPhvul.004G12
36	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.002G04 PF01535//PF1Phvul.002G04
37	FAD-binding Berberine family protein	Phvul.007G11 PF01565//PFCPhvul.007G11
38	FAD-binding Berberine family protein	Phvul.007G11 PF01565//PFCPhvul.007G11
39		0 Phvul.006G02 PF14577 - SiePhvul.006G02
40	Phox (PX) domain-containing protein	Phvul.009G17 PTHR12326 - IPhvul.009G17
41	ATP binding cassette subfamily B1	Phvul.007G14 PTHR24221:SiPhvul.007G14
42	ATP binding cassette subfamily B1	Phvul.007G14 PTHR24221:SiPhvul.007G14
43	DNAJ heat shock family protein	Phvul.003G17 PTHR24078:SiPhvul.003G17
44	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
45	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
46	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
47	myb domain protein 56	Phvul.001G10 PTHR10641:SiPhvul.001G10
48	Aha1 domain-containing protein	Phvul.007G26 PTHR13009 - IPhvul.007G26
49	Aha1 domain-containing protein	Phvul.007G26 PTHR13009 - IPhvul.007G26
50	Aha1 domain-containing protein	Phvul.007G26 PTHR13009 - IPhvul.007G26
51	EAP30/Vps36 family protein	Phvul.011G18K12190 - ESCFPhvul.011G18
52	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
53	RNA-binding ASCH domain protein	Phvul.005G15 PTHR34204:SiPhvul.005G15
54	protein phosphatase X 2	Phvul.008G27K15423 - serirPhvul.008G27
55	Protein of unknown function (DUF2921)	Phvul.005G06 PF11145 - ProPhvul.005G06
56	pumilio 7	Phvul.006G20 PTHR12537:SiPhvul.006G20
57	DNA-binding bromodomain-containing protein	Phvul.006G04 PTHR22881:SiPhvul.006G04
58		0 0 0 Phvul.008G21
59	embryo defective 1923	0 0 0 Phvul.011G11
60	hexokinase 2	Phvul.010G14 PTHR19443//IPhvul.010G14

1				
2	myb domain protein 105			Phvul.002G08PTHR10641:SiPhvul.002G08
3	MOS4-associated complex 3B			Phvul.007G27K10599 - pre-iPhvul.007G27
4				0 Phvul.001G06PTHR34194:SiPhvul.001G06
5				0 Phvul.010G11PF08167 - rRNPhvul.010G11
6				0 Phvul.010G11PF08167 - rRNPhvul.010G11
7				0 Phvul.010G11PF08167 - rRNPhvul.010G11
8	tracheary element differentiation-related 7	0	0	Phvul.001G05
9	cellulose synthase like E1			Phvul.008G27PTHR13301//IPhvul.008G27
10	ubiquitin-specific protease 26			Phvul.009G10K11858 - ubiq Phvul.009G10
11	ubiquitin-specific protease 26			Phvul.009G10K11858 - ubiq Phvul.009G10
12	ubiquitin-specific protease 26			Phvul.009G10K11858 - ubiq Phvul.009G10
13	ubiquitin-specific protease 26			Phvul.009G10K11858 - ubiq Phvul.009G10
14	ubiquitin-specific protease 26			Phvul.009G10K11858 - ubiq Phvul.009G10
15	ubiquitin-specific protease 26			Phvul.009G10K11858 - ubiq Phvul.009G10
16	tracheary element differentiation-related 6	0	0	Phvul.001G07
17	Protein of unknown function (DUF2921)			Phvul.010G15PF11145 - ProPhvul.010G15
18		0	0	0 Phvul.011G10
19		0	0	0 Phvul.006G14
20		0	0	0 Phvul.006G14
21		0	0	0 Phvul.006G14
22				
23	Calcium-binding endonuclease/exonuclease/phc			Phvul.010G12PTHR12121//IPhvul.010G12
24	Calcium-binding endonuclease/exonuclease/phc			Phvul.010G12PTHR12121//IPhvul.010G12
25	K <sup>+</sup> efflux antiporter 5			Phvul.004G12PTHR16254:SiPhvul.004G12
26	Pentatricopeptide repeat (PPR) superfamily prot			Phvul.002G04PF01535//PF1Phvul.002G04
27	FAD-binding Berberine family protein			Phvul.007G11PF01565//PFCPhvul.007G11
28				0 Phvul.006G02PF14577 - SievPhvul.006G02
29				
30	Phox (PX) domain-containing protein			Phvul.009G17PTHR12326 - IPhvul.009G17
31	ATP binding cassette subfamily B1			Phvul.007G14PTHR24221:SiPhvul.007G14
32	DNAJ heat shock family protein			Phvul.003G17PTHR24078:SiPhvul.003G17
33	RNA-binding ASCH domain protein			Phvul.005G15PTHR34204:SiPhvul.005G15
34	RNA-binding ASCH domain protein			Phvul.005G15PTHR34204:SiPhvul.005G15
35	myb domain protein 56			Phvul.001G10PTHR10641:SiPhvul.001G10
36	Aha1 domain-containing protein			Phvul.007G26PTHR13009 - IPhvul.007G26
37	Aha1 domain-containing protein			Phvul.007G26PTHR13009 - IPhvul.007G26
38	EAP30/Vps36 family protein			Phvul.011G18K12190 - ESCFPhvul.011G18
39	RNA-binding ASCH domain protein			Phvul.005G15PTHR34204:SiPhvul.005G15
40	protein phosphatase X 2			Phvul.008G27K15423 - serirPhvul.008G27
41	Protein of unknown function (DUF2921)			Phvul.005G06PF11145 - ProPhvul.005G06
42	pumilio 7			Phvul.006G20PTHR12537:SiPhvul.006G20
43	DNA-binding bromodomain-containing protein			Phvul.006G04PTHR22881:SiPhvul.006G04
44		0	0	0 Phvul.008G21
45				
46	embryo defective 1923		0	0 Phvul.011G11
47	hexokinase 2			Phvul.010G14PTHR19443//IPhvul.010G14
48	myb domain protein 105			Phvul.002G08PTHR10641:SiPhvul.002G08
49	MOS4-associated complex 3B			Phvul.007G27K10599 - pre-iPhvul.007G27
50				0 Phvul.001G06PTHR34194:SiPhvul.001G06
51				0 Phvul.001G06PTHR34194:SiPhvul.001G06
52		0	0	0 Phvul.011G13
53		0	0	0 Phvul.011G13
54		0	0	0 Phvul.011G13
55				
56				
57				
58				
59				
60				



1				
2		0	0	0 Phvul.011G13
3		0	0	0 Phvul.011G13
4		0	0	0 Phvul.011G13
5				
6	TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:Si	Phvul.004G01
7	TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:Si	Phvul.004G01
8		0	0	0 Phvul.009G10
9		0	0	0 Phvul.009G10
10		0	0	0 Phvul.009G10
11		0	0	0 Phvul.009G10
12	Glycosyl hydrolase family protein with chitinase	Phvul.003G15	PTHR11177://I	Phvul.003G15
13	related to AP2 11	Phvul.006G17	PTHR31194://I	Phvul.006G17
14		0	0	0 Phvul.002G18
15		0	0	0 Phvul.011G10
16				
17	Integrase-type DNA-binding superfamily protein	Phvul.007G02	PTHR31194://I	Phvul.007G02
18	Plant protein of unknown function (DUF946)	Phvul.005G04	PTHR17204:Si	Phvul.005G04
19		0	0	0 Phvul.006G14
20				
21	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.011G06	PF01535://PF1	Phvul.011G06
22	pumilio 7	Phvul.006G20	PTHR12537:Si	Phvul.006G20
23	Translation initiation factor 2, small GTP-binding	Phvul.005G05	PTHR23115:Si	Phvul.005G05
24	P-loop containing nucleoside triphosphate hydr	Phvul.001G02	K10395 - kine	Phvul.001G02
25	MATE efflux family protein	Phvul.008G06	PTHR11206:Si	Phvul.008G06
26	MAP kinase kinase 9	Phvul.004G14	PTHR24361:Si	Phvul.004G14
27	fibrillarlin 1	Phvul.001G05	K14563 - rRN	Phvul.001G05
28	CTC-interacting domain 12	Phvul.009G04	PF00076://PFC	Phvul.009G04
29		0	0	0 Phvul.011G13
30				
31	TOXICOS EN LEVADURA 2	Phvul.008G11	PTHR14155:Si	Phvul.008G11
32	TOXICOS EN LEVADURA 63	Phvul.006G07	PTHR14155:Si	Phvul.006G07
33	spermidine hydroxycinnamoyl transferase	Phvul.L00168	PTHR31642:Si	Phvul.L00168
34	glycine-rich RNA-binding protein 3	Phvul.008G03	K12741 - hete	Phvul.008G03
35	RING/U-box superfamily protein	Phvul.008G03	PTHR13139 - I	Phvul.008G03
36	protein arginine methyltransferase 10	Phvul.009G19	PTHR11006:Si	Phvul.009G19
37	RING/U-box superfamily protein	Phvul.008G03	PTHR13139 - I	Phvul.008G03
38	spermidine hydroxycinnamoyl transferase	Phvul.006G03	K13065 - shiki	Phvul.006G03
39	tetratricopeptide repeat (TPR)-containing protei	Phvul.001G20	PTHR17130:Si	Phvul.001G20
40	RNA-binding (RRM/RBD/RNP motifs) family prot	Phvul.011G15	PTHR24012:Si	Phvul.011G15
41	plastidic GLC translocator	Phvul.004G06	PTHR23500:Si	Phvul.004G06
42	Eukaryotic aspartyl protease family protein	Phvul.006G04	PTHR13683:Si	Phvul.006G04
43		0	0	0 Phvul.009G00
44				
45	TCP family transcription factor 4	Phvul.005G06	PTHR31072:Si	Phvul.005G06
46		0	0	0 Phvul.011G13
47		0	0	0 Phvul.011G13
48		0	0	0 Phvul.011G13
49		0	0	0 Phvul.011G13
50		0	0	0 Phvul.011G13
51		0	0	0 Phvul.011G13
52		0	0	0 Phvul.011G13
53		0	0	0 Phvul.011G13
54		0	0	0 Phvul.011G13
55		0	0	0 Phvul.011G13
56		0	0	0 Phvul.011G13
57		0	0	0 Phvul.011G13
58		0	0	0 Phvul.011G13
59		0	0	0 Phvul.011G13
60	related to AP2 11	Phvul.006G17	PTHR31194://I	Phvul.006G17
		0	0	0 Phvul.002G18

1			
2	Plant protein of unknown function (DUF946)	Phvul.005G04PTHR17204:Si	Phvul.005G04
3	TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01PTHR32285:Si	Phvul.004G01
4	TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01PTHR32285:Si	Phvul.004G01
5			
6	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.011G06PF01535//PF1	Phvul.011G06
7	HSP20-like chaperones superfamily protein	Phvul.002G23PTHR11527:Si	Phvul.002G23
8	spermidine hydroxycinnamoyl transferase	Phvul.L00168;PTHR31642:Si	Phvul.L00168;
9			
10		0	0
11	spermidine hydroxycinnamoyl transferase	Phvul.006G03K13065 - shiki	Phvul.006G03
12		0	0
13		0	0
14		0	0
15		0	0
16	Glycosyl hydrolase family protein with chitinase	Phvul.003G15PTHR11177//I	Phvul.003G15
17	fibrillarlin 1	Phvul.001G05K14563 - rRN	Phvul.001G05
18			
19	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.004G05PF01535//PF1	Phvul.004G05
20	Integrase-type DNA-binding superfamily protein	Phvul.007G02PTHR31194//I	Phvul.007G02
21			
22	phospholipase A 2A	Phvul.009G06KOG0513 - Ca	Phvul.009G06
23	MATE efflux family protein	Phvul.008G06PTHR11206:Si	Phvul.008G06
24	Cyclin D6;1	Phvul.011G11K18812 - cycli	Phvul.011G11
25	Major facilitator superfamily protein	Phvul.010G00PTHR11654//I	Phvul.010G00
26			
27	phospholipase A 2A	Phvul.009G06KOG0513 - Ca	Phvul.009G06
28	pumilio 7	Phvul.006G20PTHR12537:Si	Phvul.006G20
29	Translation initiation factor 2, small GTP-binding	Phvul.005G05PTHR23115:Si	Phvul.005G05
30			
31	P-loop containing nucleoside triphosphate hydr	Phvul.001G02K10395 - kine	Phvul.001G02
32	Acyl-CoA N-acyltransferases (NAT) superfamily p	Phvul.006G09PTHR13256:Si	Phvul.006G09
33	Acyl-CoA N-acyltransferases (NAT) superfamily p	Phvul.006G09PTHR13256:Si	Phvul.006G09
34			
35	glycine-rich RNA-binding protein 3	Phvul.008G03K12741 - hete	Phvul.008G03
36	Metal-dependent phosphohydrolase	Phvul.011G02K06950 - unch	Phvul.011G02
37			
38	RING/U-box superfamily protein	Phvul.008G03PTHR13139 - I	Phvul.008G03
39	RING/U-box superfamily protein	Phvul.008G03PTHR13139 - I	Phvul.008G03
40	plastidic GLC translocator	Phvul.004G06PTHR23500:Si	Phvul.004G06
41	Eukaryotic aspartyl protease family protein	Phvul.006G04PTHR13683:Si	Phvul.006G04
42			
43	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:Si	Phvul.007G15
44		0	0
45		0	0
46		0	0
47		0	0
48		0	0
49		0	0
50		0	0
51		0	0
52	related to AP2 11	Phvul.006G17PTHR31194//I	Phvul.006G17
53		0	0
54			
55	Plant protein of unknown function (DUF946)	Phvul.005G04PTHR17204:Si	Phvul.005G04
56	TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01PTHR32285:Si	Phvul.004G01
57	TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01PTHR32285:Si	Phvul.004G01
58			
59	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.011G06PF01535//PF1	Phvul.011G06
60	HSP20-like chaperones superfamily protein	Phvul.002G23PTHR11527:Si	Phvul.002G23
	spermidine hydroxycinnamoyl transferase	Phvul.L00168;PTHR31642:Si	Phvul.L00168;



1				
2		0	0	0 Phvul.011G10
3	spermidine hydroxycinnamoyl transferase	Phvul.006G03K13065 - shiki	Phvul.006G03	
4		0	0	0 Phvul.009G10
5		0	0	0 Phvul.009G10
6		0	0	0 Phvul.009G10
7		0	0	0 Phvul.009G10
8	Glycosyl hydrolase family protein with chitinase	Phvul.003G15PTHR11177//I	Phvul.003G15	
9	fibrillarlin 1	Phvul.001G05K14563 - rRN	Phvul.001G05	
10	Pentatricopeptide repeat (PPR) superfamily prot	Phvul.004G05PF01535//PF1	Phvul.004G05	
11	Integrase-type DNA-binding superfamily protein	Phvul.007G02PTHR31194//I	Phvul.007G02	
12	phospholipase A 2A	Phvul.009G06KOG0513 - Ca	Phvul.009G06	
13	MATE efflux family protein	Phvul.008G06PTHR11206:Si	Phvul.008G06	
14	Cyclin D6;1	Phvul.011G11K18812 - cycli	Phvul.011G11	
15	Major facilitator superfamily protein	Phvul.010G00PTHR11654//I	Phvul.010G00	
16	phospholipase A 2A	Phvul.009G06KOG0513 - Ca	Phvul.009G06	
17	pumilio 7	Phvul.006G20PTHR12537:Si	Phvul.006G20	
18	Translation initiation factor 2, small GTP-binding	Phvul.005G05PTHR23115:Si	Phvul.005G05	
19	P-loop containing nucleoside triphosphate hydr	Phvul.001G02K10395 - kine	Phvul.001G02	
20	Acyl-CoA N-acyltransferases (NAT) superfamily p	Phvul.006G09PTHR13256:Si	Phvul.006G09	
21	Acyl-CoA N-acyltransferases (NAT) superfamily p	Phvul.006G09PTHR13256:Si	Phvul.006G09	
22	glycine-rich RNA-binding protein 3	Phvul.008G03K12741 - hete	Phvul.008G03	
23	Metal-dependent phosphohydrolase	Phvul.011G02K06950 - unch	Phvul.011G02	
24	RING/U-box superfamily protein	Phvul.008G03PTHR13139 - I	Phvul.008G03	
25	RING/U-box superfamily protein	Phvul.008G03PTHR13139 - I	Phvul.008G03	
26	plastidic GLC translocator	Phvul.004G06PTHR23500:Si	Phvul.004G06	
27	Eukaryotic aspartyl protease family protein	Phvul.006G04PTHR13683:Si	Phvul.006G04	
28	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:Si	Phvul.007G15	
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2	not assigned.ε	(original description: pacid=37161909 transcript=Phvul.004G064100.1 locus=Phvul.C
3	not assigned.r	no hits & (original description: pacid=37150946 transcript=Phvul.009G096000.1 locu
4	Cell wall organ	KDO-8-phosphate synthase (original description: pacid=37161420 transcript=Phvul.0
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11	not assigned.r	no hits & (original description: pacid=37148987 transcript=Phvul.009G196100.1 locu
12	not assigned.ε	(original description: pacid=37159372 transcript=Phvul.008G199900.1 locus=Phvul.C
13	not assigned.r	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
14	not assigned.r	no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
15	not assigned.ε	(original description: pacid=37163516 transcript=Phvul.004G038100.1 locus=Phvul.C
16	RNA biosynth	transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011
17	RNA biosynth	transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011
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21	not assigned.ε	(original description: pacid=37162066 transcript=Phvul.004G160700.1 locus=Phvul.C
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40	not assigned.ε	(original description: pacid=37159372 transcript=Phvul.008G199900.1 locus=Phvul.C
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54	not assigned.r	no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl
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60	RNA biosynth	transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011

1 RNA biosynth transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011  
2 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00  
3 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00  
4 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00  
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6 not assigned.ε (original description: pacid=37174808 transcript=Phvul.002G041900.1 locus=Phvul.C  
7 Protein biosyr assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv  
8 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu  
9 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172  
10 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172  
11 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172  
12 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172  
13 Protein home class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t  
14 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1  
15 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1  
16 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1  
17 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1  
18 Protein modif CPL phosphatase (original description: pacid=37178354 transcript=Phvul.002G22690  
19 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1  
20 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1  
21 not assigned.r no hits & (original description: pacid=37164826 transcript=Phvul.007G222000.1 locu  
22 not assigned.r no hits & (original description: pacid=37165981 transcript=Phvul.007G029200.1 locu  
23 not assigned.ε (original description: pacid=37146336 transcript=Phvul.003G058400.1 locus=Phvul.C  
24 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37174  
25 not assigned.ε (original description: pacid=37163186 transcript=Phvul.004G028100.1 locus=Phvul.C  
26 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu  
27 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu  
28 Protein biosyr component RPL27 of LSU proteome component (original description: pacid=371773C  
29 Enzyme classii Laccase-15 OS=Arabidopsis thaliana (sp|q84j37|lac15\_arath : 554.0) & Enzyme classi  
30 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript  
31 not assigned.ε (original description: pacid=37153077 transcript=Phvul.005G102100.2 locus=Phvul.C  
32 not assigned.ε (original description: pacid=37153077 transcript=Phvul.005G102100.2 locus=Phvul.C  
33 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00  
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38 Protein biosyr assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv  
39 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172  
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46 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00  
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1 Solute transp  
2 solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00  
3 not assigned.ε (original description: pacid=37174808 transcript=Phvul.002G041900.1 locus=Phvul.C  
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15 C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript  
16 Cell wall orgar  
17 TED-type cellulose synthase CSC-interactive protein (original description: pacid=3717  
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20 **Protein home**  
21 **deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G**  
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32 Solute transp  
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46 Enzyme classii  
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58 Solute transp  
59 monosaccharide transporter (STP) (original description: pacid=37167067 transcript=f  
60 Solute transp  
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1 Solute transp:monosaccharide transporter (STP) (original description: pacid=37166808 transcript=f  
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4 Protein modif catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3  
5 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu  
6 not assigned.ε (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C  
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8 RNA processir component MAC3 of non-snRNP MOS4-associated complex (original description: pac  
9 Solute transp:proton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran  
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13 Cell wall orgarTED-type cellulose synthase CSC-interactive protein (original description: pacid=3717  
14 not assigned.ε (original description: pacid=37161159 transcript=Phvul.008G279750.1 locus=Phvul.C  
15 Protein home:deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G  
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26 Solute transp:proton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran  
27 not assigned.ε (original description: pacid=37176369 transcript=Phvul.002G044500.1 locus=Phvul.C  
28 Enzyme classiiEnzyme classification.EC\_1 oxidoreductases.EC\_1.1 oxidoreductase acting on CH-OH  
29 not assigned.ε (original description: pacid=37172660 transcript=Phvul.006G021500.1 locus=Phvul.C  
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31 Solute transp:subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.C  
32 Protein home:co-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1  
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38 Vesicle trafficl component VPS36 of ESCRT-II complex (original description: pacid=37155231 transcr  
39 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu  
40 Protein modif catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3  
41 not assigned.r no hits & (original description: pacid=37152330 transcript=Phvul.005G065300.1 locu  
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45 not assigned.r no hits & (original description: pacid=37157005 transcript=Phvul.011G111800.1 locu  
46 Carbohydrate hexokinase (original description: pacid=37142381 transcript=Phvul.010G144900.1 lo

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19 Solute transpcproton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran  
20 not assigned.ε (original description: pacid=37176369 transcript=Phvul.002G044500.1 locus=Phvul.C  
21 Enzyme classiiEnzyme classification.EC\_1 oxidoreductases.EC\_1.1 oxidoreductase acting on CH-OH  
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8 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu  
9 Enzyme classii no description available(sp|a0a072ur65|cht5b\_medtr : 395.0) & Enzyme classificati  
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18 Protein biosyr IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv  
19 Cytoskeleton imotor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001  
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22 Protein biosyr methyltransferase component Nop1/fibrillarlin of snoRNP rRNA methylation complex  
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36 Protein homee pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G04  
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47 not assigned.r no hits & (original description: pacid=37177963 transcript=Phvul.002G183700.1 locu



1 not assigned.r no hits & (original description: pacid=37153363 transcript=Phvul.005G043000.2 locu  
2 not assigned.ε (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C  
3 not assigned.ε (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C  
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5 Protein home class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t  
6 Enzyme classiiEnzyme classification.EC\_2 transferases.EC\_2.3 acyltransferase(50.2.3 : 24.7) (origina  
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12 Enzyme classii no description available(sp|a0a072ur65|cht5b\_medtr : 395.0) & Enzyme classificati  
13 Protein biosyr methyltransferase component Nop1/fibrillarlin of snoRNP rRNA methylation complex  
14 not assigned.ε (original description: pacid=37162384 transcript=Phvul.004G057900.1 locus=Phvul.C  
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16 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(  
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18 Cell cycle orgacyclin (CYCD) (original description: pacid=37157024 transcript=Phvul.011G110000.1 |  
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21 not assigned.ε (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C  
22 Protein biosyr IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv  
23 Cytoskeleton motor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001  
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28 Protein home RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G  
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45 Protein home class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t  
46 Enzyme classiiEnzyme classification.EC\_2 transferases.EC\_2.3 acyltransferase(50.2.3 : 24.7) (origina

1 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu  
2 Enzyme classiiSpermidine hydroxycinnamoyl transferase OS=Arabidopsis thaliana (sp|o64470|sht\_  
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6 Enzyme classii no description available(sp|a0a072ur65|cht5b\_medtr : 395.0) & Enzyme classificac  
7 Protein biosyr methyltransferase component Nop1/fibrillarlin of snoRNP rRNA methylation complex  
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9 RNA biosynthtranscription factor (ERF) (original description: pacid=37164213 transcript=Phvul.007  
10 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(  
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12 Cell cycle orgacyclin (CYCD) (original description: pacid=37157024 transcript=Phvul.011G110000.1 |  
13 Solute transp anion transporter (NRT1/PTR) (original description: pacid=37143370 transcript=Phvu  
14 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(  
15 not assigned.ε (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C  
16 Protein biosyr IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv  
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22 Protein homee RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G  
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16 J04G038100 ID=Phvul.004G038100.1.v2.1 annot-version=v2.1) & O-fucosyltransferase 30 OS=Arabi  
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26 & Phvul.002G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
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40 & Phvul.006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor  
41 & Phvul.006G045600 ID=Phvul.006G045600.1.v2.1 annot-version=v2.1)  
42 & Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)  
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17 010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |  
18 010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |  
19 ript=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=  
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44 us=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
45 us=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
46 us=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)



1 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
2 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
3 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
4 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
5 004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-  
6 004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-  
7 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)  
8 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)  
9 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)  
10 on.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr  
11 006G173500.1 locus=Phvul.006G173500 ID=Phvul.006G173500.1.v2.1 annot-version=v2.1) &  
12 js=Phvul.002G183700 ID=Phvul.002G183700.1.v2.1 annot-version=v2.1)  
13 js=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)  
14 007G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &  
15 js=Phvul.005G043000 ID=Phvul.005G043000.2.v2.1 annot-version=v2.1)  
16 js=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)  
17 011G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat  
18 006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor  
19 ul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &  
20 001G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &  
21 008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &  
22 004G147900.1 locus=Phvul.004G147900 ID=Phvul.004G147900.1.v2.1 annot-version=v2.1) &  
23 < (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID  
24 009G046200 ID=Phvul.009G046200.1.v2.1 annot-version=v2.1) & Polyadenylate-binding protein-int  
25 js=Phvul.011G133400 ID=Phvul.011G133400.1.v2.1 annot-version=v2.1)  
26 008G111100.1 locus=Phvul.008G111100 ID=Phvul.008G111100.1.v2.1 annot-version=v2.1) &  
27 006G070000.2 locus=Phvul.006G070000 ID=Phvul.006G070000.2.v2.1 annot-version=v2.1) &  
28 al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687  
29 008G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &  
30 008G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &  
31 009G198900 ID=Phvul.009G198900.1.v2.1 annot-version=v2.1) & Protein arginine N-methyltransfer  
32 008G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &  
33 \_arath : 311.0) & Enzyme classification.EC\_2 transferases.EC\_2.3 acyltransferase(50.2.3 : 22.0) (origi  
34 ript=Phvul.001G205600.1 locus=Phvul.001G205600 ID=Phvul.001G205600.1.v2.1 annot-version=v2  
35 011G159400 ID=Phvul.011G159400.1.v2.1 annot-version=v2.1) & UBP1-associated protein 2C OS=A  
36 ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &  
37 006G048000.1 locus=Phvul.006G048000 ID=Phvul.006G048000.1.v2.1 annot-version=v2.1) &  
38 js=Phvul.009G007900 ID=Phvul.009G007900.1.v2.1 annot-version=v2.1)  
39 005G067950.1 locus=Phvul.005G067950 ID=Phvul.005G067950.1.v2.1 annot-version=v2.1) &  
40 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
41 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
42 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
43 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
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46 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
47 006G173500.1 locus=Phvul.006G173500 ID=Phvul.006G173500.1.v2.1 annot-version=v2.1) &  
48 js=Phvul.002G183700 ID=Phvul.002G183700.1.v2.1 annot-version=v2.1)

1 js=Phvul.005G043000 ID=Phvul.005G043000.2.v2.1 annot-version=v2.1)  
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3 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-  
4 J11G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat  
5 transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi  
6 al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687  
7 js=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)  
8 arath : 311.0) & Enzyme classification.EC\_2 transferases.EC\_2.3 acyltransferase(50.2.3 : 22.0) (origi  
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11 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)  
12 on.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr  
13 < (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID  
14 J04G057900 ID=Phvul.004G057900.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
15 7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &  
16 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &  
17 l.008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &  
18 locus=Phvul.011G110000 ID=Phvul.011G110000.1.v2.1 annot-version=v2.1) &  
19 il.010G003800.1 locus=Phvul.010G003800 ID=Phvul.010G003800.1.v2.1 annot-version=v2.1) &  
20 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &  
21 J06G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor  
22 ul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &  
23 1G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &  
24 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)  
25 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)  
26 08G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &  
27 js=Phvul.011G028900 ID=Phvul.011G028900.1.v2.1 annot-version=v2.1)  
28 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &  
29 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &  
30 ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &  
31 48000.1 locus=Phvul.006G048000 ID=Phvul.006G048000.1.v2.1 annot-version=v2.1) &  
32 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)  
33 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
34 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
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36 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
37 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
38 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
39 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
40 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)  
41 06G173500.1 locus=Phvul.006G173500 ID=Phvul.006G173500.1.v2.1 annot-version=v2.1) &  
42 js=Phvul.002G183700 ID=Phvul.002G183700.1.v2.1 annot-version=v2.1)  
43 js=Phvul.005G043000 ID=Phvul.005G043000.2.v2.1 annot-version=v2.1)  
44 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-  
45 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-  
46 J11G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat  
47 transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi  
48 al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687

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2 js=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)  
3 \_arath : 311.0) & Enzyme classification.EC\_2 transferases.EC\_2.3 acyltransferase(50.2.3 : 22.0) (origi  
4 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)  
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6 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)  
7 on.EC\_3 hydrolases.EC\_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr  
8 < (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 IC  
9 004G057900 ID=Phvul.004G057900.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
10 7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &  
11 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &  
12 l.008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &  
13 locus=Phvul.011G110000 ID=Phvul.011G110000.1.v2.1 annot-version=v2.1) &  
14 il.010G003800.1 locus=Phvul.010G003800 ID=Phvul.010G003800.1.v2.1 annot-version=v2.1) &  
15 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &  
16 006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor  
17 ul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &  
18 1G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &  
19 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)  
20 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)  
21 08G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &  
22 js=Phvul.011G028900 ID=Phvul.011G028900.1.v2.1 annot-version=v2.1)  
23 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &  
24 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &  
25 ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &  
26 48000.1 locus=Phvul.006G048000 ID=Phvul.006G048000.1.v2.1 annot-version=v2.1) &  
27 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)  
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3 thaliana (sp|p42814|rns2\_arath : 111.0)  
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7 thaliana (sp|p42814|rns2\_arath : 111.0)  
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10 thaliana (sp|p42814|rns2\_arath : 111.0)  
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14 NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3\_arath : 384.0)  
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18 idopsis thaliana (sp|q1jpm5|oft30\_arath : 545.0)  
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26 OS=Arabidopsis thaliana (sp|q8vxz0|nud20\_arath : 429.0)  
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36 NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3\_arath : 384.0)  
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39 OS=Arabidopsis thaliana (sp|q8vxz0|nud20\_arath : 429.0)  
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45 idopsis thaliana (sp|q1jpm5|oft30\_arath : 545.0)  
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51 NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3\_arath : 384.0)  
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53 OS=Arabidopsis thaliana (sp|q8vxz0|nud20\_arath : 429.0)  
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7 ina (sp|q9xip8|cdi\_arath : 441.0)

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11 -version=v2.1) &

12 -version=v2.1) &

13 -version=v2.1) &

14 -version=v2.1) &

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29 ce 37 OS=Arabidopsis thaliana (sp|o22960|tbl37\_arath : 515.0)

30 -version=v2.1) &

31 elicase DExH18, mitochondrial OS=Arabidopsis thaliana (sp|f4kfv7|suv3l\_arath : 1000.0)

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36 -version=v2.1) &

37 donor(50.1.10 : 222.3) (original description: pacid=37161921 transcript=Phvul.004G087000.1 locus:

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39 23|fly1\_arath : 853.0)

40 23|fly1\_arath : 853.0)

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46 ina (sp|q9xip8|cdi\_arath : 441.0)

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51 -version=v2.1) &

52 -version=v2.1) &

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3 ina (sp|q9xip8|cdi\_arath : 441.0)  
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7 -version=v2.1) &

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25 it-version=v2.1) &

26 i OS=*Oryza sativa* subsp. *japonica* (sp|q651x6|csle6\_orysj : 667.0)

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29 DN B OS=*Arabidopsis thaliana* (sp|q9ss87|seob\_arath : 193.0)  
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40 .1) &

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44 ing protein At4g14820 OS=*Arabidopsis thaliana* (sp|o23337|pp311\_arath : 842.0)

45 o : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007)

46 roplastic OS=*Arabidopsis thaliana* (sp|q9c9r6|pum7\_arath : 433.0)  
47  
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56 *Arabidopsis thaliana* (sp|q9lvz8|lor12\_arath : 212.0)  
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6 nnot-version=v2.1) &

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8 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22\_arath : 560.0)

9 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22\_arath : 560.0)

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11 2.1 annot-version=v2.1) &

12 v2.1) &

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14 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1\_solbu : 363.0)

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17 it-version=v2.1) &

18 i OS=Oryza sativa subsp. japonica (sp|q651x6|csle6\_orysj : 667.0)

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25 it-version=v2.1) &

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32 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22\_arath : 560.0)

33 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22\_arath : 560.0)

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35 v2.1) &

36 ing protein At4g14820 OS=Arabidopsis thaliana (sp|o23337|pp311\_arath : 842.0)

37 oso : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007G113300.1)

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39 ON B OS=Arabidopsis thaliana (sp|q9ss87|seob\_arath : 193.0)

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53 nnot-version=v2.1) &

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56 roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7\_arath : 433.0)

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3 2.1 annot-version=v2.1) &  
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8 t-version=v2.1) &  
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10 i OS=*Oryza sativa* subsp. *japonica* (sp|q651x6|csle6\_orysj : 667.0)  
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16 t-version=v2.1) &  
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23 protein At1g02270 OS=*Arabidopsis thaliana* (sp|o81916|yc22\_arath : 560.0)

24 protein At1g02270 OS=*Arabidopsis thaliana* (sp|o81916|yc22\_arath : 560.0)

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27 ing protein At4g14820 OS=*Arabidopsis thaliana* (sp|o23337|pp311\_arath : 842.0)

28 o : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007G113300.1)

29 ON B OS=*Arabidopsis thaliana* (sp|q9ss87|seob\_arath : 193.0)  
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41 .1) &  
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44 nnot-version=v2.1) &  
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47 roplastic OS=*Arabidopsis thaliana* (sp|q9c9r6|pum7\_arath : 433.0)  
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54 2.1 annot-version=v2.1) &  
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6 like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22\_arath : 415.0)

7 like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22\_arath : 415.0)

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12 ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.  
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21 t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5\_arath : 632.0)

22 roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7\_arath : 433.0)

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29 D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &

30 teracting protein 12 OS=Arabidopsis thaliana (sp|q9s7n9|cid12\_arath : 405.0)

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36 '.1.v2.1 annot-version=v2.1) &

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40 rase PRMT10 OS=Arabidopsis thaliana (sp|q9mat5|anm10\_arath : 573.0)

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42 inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phvul.006G037000.1.v2.1) &

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44 rabadopsis thaliana (sp|q9lka4|uba2c\_arath : 315.0)

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like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22\_arath : 415.0)

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t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5\_arath : 632.0)  
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inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phvi

ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.  
D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &

ing protein At1g79490, mitochondrial OS=Arabidopsis thaliana (sp|q9sak0|pp132\_arath : 1241.0)

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8 ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.1  
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10 D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &

11 ing protein At1g79490, mitochondrial OS=Arabidopsis thaliana (sp|q9sak0|pp132\_arath : 1241.0)  
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20 roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7\_arath : 433.0)  
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	miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end
1						
2						
3	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
4	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
5	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
6	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
7	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
8	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
9	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
10	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
11	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
12	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
13	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
14	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
15	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
16	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
17	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
18	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
19	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
20	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
21	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
22	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
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25	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
26	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
27	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
28	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
29	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
30	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
31	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
32	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
33	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
34	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
35	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
36	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
37	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
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41	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
42	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
43	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
44	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
45	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
46	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
47	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
48	uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	22
49	uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	22
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51	uggagaagcagg	Phvul.005G074500.1	1	-1	1	21
52	uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
53	uggagaagcagg	Phvul.005G055400.1	1	-1	1	21
54	uggagaagcagg	Phvul.005G074500.1	1	-1	1	21
55	uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
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60	uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
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50	uggagaagcagg Phvul.005G055400.1	1	-1	1	21
51	uggagaagcagg Phvul.005G074500.1	1	-1	1	21
52	uggagaagcagg Phvul.011G160400.1	1	-1	1	21
53	uggagaagcagg Phvul.005G055400.1	1	-1	1	21
54	uggagaagcagg Phvul.005G074500.1	1	-1	1	21
55	uggagaagcagg Phvul.011G160400.1	1	-1	1	21
56	uggagaagcagg Phvul.005G055400.1	1	-1	1	21
57	uggagaagcagg Phvul.005G074500.1	1	-1	1	22
58	uggagaagcagg Phvul.011G160400.1	1	-1	1	22
59	uggagaagcagg Phvul.005G055400.1	1	-1	1	22
60	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21



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2	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
3	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
4	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
5					
6	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
7	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	21
8	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
9					
10	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
11	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
12	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
13					
14	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
15	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	21
16	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
17					
18	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
19	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
20	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
21					
22	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
23	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	21
24	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
25					
26	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
27	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
28	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
29					
30	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
31	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	21
32	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
33					
34	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
35	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
36	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
37					
38	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
39	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	21
40	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
41					
42	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
43	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
44	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
45					
46	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
47	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	21
48	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
49					
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51	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
52	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
53					
54	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
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56	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
57					
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59	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
60	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21

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3	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
4	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
5					
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7	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
8	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
9					
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11	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
12	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
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15	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
16	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
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19	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
20	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
21					
22	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
23	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
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27	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
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29					
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33					
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36	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
37					
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47	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	21
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5	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	21
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7	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	21
8	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
9	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	21
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11	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	21
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14	uggagaagcagg Phvul.006G169300.1	2.5	-1	1	22
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16	uggagaagcagg Phvul.007G164800.1	2.5	-1	1	22
17	uggagaagcagg Phvul.011G065700.1	2.5	-1	1	22
18	uggagaagcagg Phvul.011G065700.3	2.5	-1	1	22
19	uggagaagcagg Phvul.011G065700.2	2.5	-1	1	22
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21	uggagaagcagg Phvul.004G172600.1	2.5	-1	1	22
22	uggagaagcagg Phvul.010G089100.2	3	-1	1	21
23	uggagaagcagg Phvul.002G325300.2	3	-1	1	21
24	uggagaagcagg Phvul.004G139200.1	3	-1	1	21
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26	uggagaagcagg Phvul.005G001200.1	3	-1	1	21
27	uggagaagcagg Phvul.008G147100.2	3	-1	1	21
28	uggagaagcagg Phvul.008G147100.4	3	-1	1	21
29	uggagaagcagg Phvul.008G147100.4	3	-1	1	21
30	uggagaagcagg Phvul.008G147100.3	3	-1	1	21
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32	uggagaagcagg Phvul.010G128500.1	3	-1	1	21
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4	uggagaagcagg Phvul.008G147100.3	3	-1	1	21
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6	uggagaagcagg Phvul.010G128500.1	3	-1	1	21
7	uggagaagcagg Phvul.010G089100.2	3	-1	1	21
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9	uggagaagcagg Phvul.004G139200.1	3	-1	1	21
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13	uggagaagcagg Phvul.008G147100.3	3	-1	1	21
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36	uggagaagcagg Phvul.008G147100.2	3	-1	1	21
37					
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5					
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9					
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11	uggagaagcagg Phvul.008G147100.2	3	-1	1	21
12	uggagaagcagg Phvul.008G147100.4	3	-1	1	21
13	uggagaagcagg Phvul.008G147100.3	3	-1	1	21
14	uggagaagcagg Phvul.006G086200.1	3	-1	1	21
15	uggagaagcagg Phvul.010G128500.1	3	-1	1	21
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48	uggagaagcagg Phvul.008G277800.1	3.5	-1	1	21
49	uggagaagcagg Phvul.003G067000.1	3.5	-1	1	21
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51	uggagaagcagg Phvul.001G240500.1	3.5	-1	1	21
52	uggagaagcagg Phvul.008G061000.1	3.5	-1	1	21
53	uggagaagcagg Phvul.003G246400.1	3.5	-1	1	21
54					
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57	uggagaagcagg Phvul.009G130000.1	3.5	-1	1	21
58					
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	uggagaagcagg Phvul.007G083500.1	3.5	-1	1	21

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8	uggagaagcagg Phvul.005G005200.1	3.5	-1	1	21
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59	uggagaagcagg Phvul.002G157300.1	4	-1	1	21
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7	uggagaagcagg Phvul.002G271400.1	4.5	-1	1	21
8	uggagaagcagg Phvul.011G166200.1	4.5	-1	1	21
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16	uggagaagcagg Phvul.010G115000.1	4.5	-1	1	21
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25					
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27	uggagaagcagg Phvul.008G017200.2	4.5	-1	1	21
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33					
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12	uggagaagcagg Phvul.006G047000.1	4.5	-1	1	21
13					
14	uggagaagcagg Phvul.005G001000.1	4.5	-1	1	21
15	uggagaagcagg Phvul.003G056900.1	4.5	-1	1	21
16	uggagaagcagg Phvul.003G056900.2	4.5	-1	1	21
17					
18	uggagaagcagg Phvul.008G017200.1	4.5	-1	1	21
19	uggagaagcagg Phvul.008G017200.2	4.5	-1	1	21
20	uggagaagcagg Phvul.003G056900.3	4.5	-1	1	21
21					
22	uggagaagcagg Phvul.007G106300.1	4.5	-1	1	21
23	uggagaagcagg Phvul.009G034400.1	4.5	-1	1	21
24	uggagaagcagg Phvul.L002444.2	4.5	-1	1	21
25					
26	uggagaagcagg Phvul.L002444.1	4.5	-1	1	21
27	uggagaagcagg Phvul.008G070000.1	4.5	-1	1	21
28	uggagaagcagg Phvul.010G156200.1	4.5	-1	1	21
29					
30	uggagaagcagg Phvul.009G217000.1	4.5	-1	1	21
31	uggagaagcagg Phvul.008G043500.1	4.5	-1	1	21
32	uggagaagcagg Phvul.009G079400.3	4.5	-1	1	21
33					
34	uggagaagcagg Phvul.001G193000.3	4.5	-1	1	21
35	uggagaagcagg Phvul.001G193000.4	4.5	-1	1	21
36	uggagaagcagg Phvul.003G154400.1	4.5	-1	1	21
37					
38	uggagaagcagg Phvul.009G030200.1	4.5	-1	1	21
39	uggagaagcagg Phvul.004G166100.1	4.5	-1	1	21
40	uggagaagcagg Phvul.009G160200.1	4.5	-1	1	21
41	uggagaagcagg Phvul.002G119600.1	4.5	-1	1	21
42					
43	uggagaagcagg Phvul.002G150800.1	4.5	-1	1	21
44	uggagaagcagg Phvul.002G271400.1	4.5	-1	1	21
45	uggagaagcagg Phvul.011G166200.1	4.5	-1	1	21
46					
47	uggagaagcagg Phvul.001G110100.1	4.5	-1	1	21
48	uggagaagcagg Phvul.002G037500.1	4.5	-1	1	21
49	uggagaagcagg Phvul.002G017700.2	4.5	-1	1	21
50					
51	uggagaagcagg Phvul.002G017700.1	4.5	-1	1	21
52	uggagaagcagg Phvul.007G022500.3	4.5	-1	1	21
53	uggagaagcagg Phvul.010G115000.1	4.5	-1	1	21
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56	uggagaagcagg Phvul.006G154900.1	4.5	-1	1	21
57	uggagaagcagg Phvul.006G047000.1	4.5	-1	1	21
58					
59	uggagaagcagg Phvul.005G001000.1	4.5	-1	1	21
60	uggagaagcagg Phvul.003G056900.1	4.5	-1	1	21
	uggagaagcagg Phvul.003G056900.2	4.5	-1	1	21



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3	uggagaagcagg Phvul.008G017200.2	4.5	-1	1	21
4	uggagaagcagg Phvul.003G056900.3	4.5	-1	1	21
5					
6	uggagaagcagg Phvul.007G106300.1	4.5	-1	1	21
7	uggagaagcagg Phvul.009G034400.1	4.5	-1	1	21
8	uggagaagcagg Phvul.L002444.2	4.5	-1	1	21
9					
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11	uggagaagcagg Phvul.008G070000.1	4.5	-1	1	21
12	uggagaagcagg Phvul.010G156200.1	4.5	-1	1	21
13					
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15	uggagaagcagg Phvul.008G043500.1	4.5	-1	1	21
16	uggagaagcagg Phvul.009G079400.3	4.5	-1	1	21
17					
18	uggagaagcagg Phvul.001G193000.3	4.5	-1	1	21
19	uggagaagcagg Phvul.001G193000.4	4.5	-1	1	21
20	uggagaagcagg Phvul.003G154400.1	4.5	-1	1	21
21					
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23	uggagaagcagg Phvul.004G166100.1	4.5	-1	1	21
24	uggagaagcagg Phvul.009G160200.1	4.5	-1	1	21
25					
26	uggagaagcagg Phvul.002G119600.1	4.5	-1	1	21
27	uggagaagcagg Phvul.002G150800.1	4.5	-1	1	21
28	uggagaagcagg Phvul.002G271400.1	4.5	-1	1	21
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31	uggagaagcagg Phvul.001G110100.1	4.5	-1	1	21
32	uggagaagcagg Phvul.002G037500.1	4.5	-1	1	21
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35	uggagaagcagg Phvul.002G017700.1	4.5	-1	1	21
36	uggagaagcagg Phvul.007G022500.3	4.5	-1	1	21
37	uggagaagcagg Phvul.010G115000.1	4.5	-1	1	21
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41	uggagaagcagg Phvul.006G047000.1	4.5	-1	1	21
42					
43	uggagaagcagg Phvul.005G001000.1	4.5	-1	1	21
44	uggagaagcagg Phvul.003G056900.1	4.5	-1	1	21
45	uggagaagcagg Phvul.003G056900.2	4.5	-1	1	21
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47	uggagaagcagg Phvul.008G017200.1	4.5	-1	1	21
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49	uggagaagcagg Phvul.003G056900.3	4.5	-1	1	21
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52	uggagaagcagg Phvul.009G034400.1	4.5	-1	1	21
53	uggagaagcagg Phvul.L002444.2	4.5	-1	1	21
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56	uggagaagcagg Phvul.008G070000.1	4.5	-1	1	21
57	uggagaagcagg Phvul.010G156200.1	4.5	-1	1	21
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60	uggagaagcagg Phvul.008G043500.1	4.5	-1	1	21
	uggagaagcagg Phvul.009G079400.3	4.5	-1	1	21



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7	uggagaagcagg Phvul.004G166100.1	4.5	-1	1	21
8	uggagaagcagg Phvul.009G160200.1	4.5	-1	1	21
9					
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11	uggagaagcagg Phvul.002G150800.1	4.5	-1	1	21
12	uggagaagcagg Phvul.002G271400.1	4.5	-1	1	21
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16	uggagaagcagg Phvul.002G037500.1	4.5	-1	1	21
17					
18	uggagaagcagg Phvul.002G017700.2	4.5	-1	1	21
19	uggagaagcagg Phvul.002G017700.1	4.5	-1	1	21
20	uggagaagcagg Phvul.007G022500.3	4.5	-1	1	21
21					
22	uggagaagcagg Phvul.010G115000.1	4.5	-1	1	21
23	uggagaagcagg Phvul.010G115000.2	4.5	-1	1	21
24	uggagaagcagg Phvul.006G154900.1	4.5	-1	1	21
25					
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27	uggagaagcagg Phvul.005G001000.1	4.5	-1	1	21
28	uggagaagcagg Phvul.003G056900.1	4.5	-1	1	21
29					
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31	uggagaagcagg Phvul.008G017200.1	4.5	-1	1	21
32	uggagaagcagg Phvul.008G017200.2	4.5	-1	1	21
33					
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35	uggagaagcagg Phvul.007G106300.1	4.5	-1	1	21
36	uggagaagcagg Phvul.009G034400.1	4.5	-1	1	21
37					
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39	uggagaagcagg Phvul.L002444.1	4.5	-1	1	21
40	uggagaagcagg Phvul.008G070000.1	4.5	-1	1	21
41	uggagaagcagg Phvul.010G156200.1	4.5	-1	1	21
42					
43	uggagaagcagg Phvul.009G217000.1	4.5	-1	1	21
44	uggagaagcagg Phvul.008G043500.1	4.5	-1	1	21
45	uggagaagcagg Phvul.009G079400.3	4.5	-1	1	21
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49	uggagaagcagg Phvul.003G154400.1	4.5	-1	1	21
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52	uggagaagcagg Phvul.004G166100.1	4.5	-1	1	21
53	uggagaagcagg Phvul.009G160200.1	4.5	-1	1	21
54					
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56	uggagaagcagg Phvul.002G150800.1	4.5	-1	1	21
57	uggagaagcagg Phvul.002G271400.1	4.5	-1	1	21
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60	uggagaagcagg Phvul.001G110100.1	4.5	-1	1	21
	uggagaagcagg Phvul.002G037500.1	4.5	-1	1	21

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3	uggagaagcagg Phvul.002G017700.1	4.5	-1	1	21
4	uggagaagcagg Phvul.007G022500.3	4.5	-1	1	21
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7	uggagaagcagg Phvul.010G115000.2	4.5	-1	1	21
8	uggagaagcagg Phvul.006G154900.1	4.5	-1	1	21
9					
10	uggagaagcagg Phvul.006G047000.1	4.5	-1	1	21
11	uggagaagcagg Phvul.005G001000.1	4.5	-1	1	21
12	uggagaagcagg Phvul.003G056900.1	4.5	-1	1	21
13					
14	uggagaagcagg Phvul.003G056900.2	4.5	-1	1	21
15	uggagaagcagg Phvul.008G017200.1	4.5	-1	1	21
16	uggagaagcagg Phvul.008G017200.2	4.5	-1	1	21
17					
18	uggagaagcagg Phvul.003G056900.3	4.5	-1	1	21
19	uggagaagcagg Phvul.007G106300.1	4.5	-1	1	21
20	uggagaagcagg Phvul.009G034400.1	4.5	-1	1	21
21					
22	uggagaagcagg Phvul.L002444.2	4.5	-1	1	21
23	uggagaagcagg Phvul.L002444.1	4.5	-1	1	21
24	uggagaagcagg Phvul.008G070000.1	4.5	-1	1	21
25					
26	uggagaagcagg Phvul.010G156200.1	4.5	-1	1	22
27	uggagaagcagg Phvul.009G160200.1	4.5	-1	1	22
28	uggagaagcagg Phvul.009G217000.1	4.5	-1	1	22
29					
30	uggagaagcagg Phvul.007G022500.3	4.5	-1	1	22
31	uggagaagcagg Phvul.008G043500.1	4.5	-1	1	22
32	uggagaagcagg Phvul.009G079400.3	4.5	-1	1	22
33					
34	uggagaagcagg Phvul.001G193000.3	4.5	-1	1	22
35	uggagaagcagg Phvul.001G193000.4	4.5	-1	1	22
36	uggagaagcagg Phvul.009G167700.2	4.5	-1	1	22
37	uggagaagcagg Phvul.003G154400.1	4.5	-1	1	22
38					
39	uggagaagcagg Phvul.L003746.2	4.5	-1	1	22
40	uggagaagcagg Phvul.L003746.1	4.5	-1	1	22
41					
42	uggagaagcagg Phvul.009G030200.1	4.5	-1	1	22
43	uggagaagcagg Phvul.004G166100.1	4.5	-1	1	22
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45	uggagaagcagg Phvul.002G150800.1	4.5	-1	1	22
46					
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48	uggagaagcagg Phvul.011G166200.1	4.5	-1	1	22
49	uggagaagcagg Phvul.006G067900.1	4.5	-1	1	22
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52	uggagaagcagg Phvul.002G037500.1	4.5	-1	1	22
53	uggagaagcagg Phvul.010G115000.1	4.5	-1	1	22
54	uggagaagcagg Phvul.010G115000.2	4.5	-1	1	22
55	uggagaagcagg Phvul.002G157000.1	4.5	-1	1	22
56					
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60	uggagaagcagg Phvul.003G181900.1	5	-1	1	21

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4	uggagaagcagg Phvul.003G121200.2	5	-1	1	21
5					
6	uggagaagcagg Phvul.006G075600.1	5	-1	1	21
7	uggagaagcagg Phvul.008G284900.1	5	-1	1	21
8	uggagaagcagg Phvul.007G163400.1	5	-1	1	21
9					
10	uggagaagcagg Phvul.001G266600.1	5	-1	1	21
11	uggagaagcagg Phvul.006G091100.2	5	-1	1	21
12	uggagaagcagg Phvul.006G091100.1	5	-1	1	21
13					
14	uggagaagcagg Phvul.003G037500.1	5	-1	1	21
15	uggagaagcagg Phvul.009G007300.1	5	-1	1	21
16	uggagaagcagg Phvul.003G100200.1	5	-1	1	21
17					
18	uggagaagcagg Phvul.003G100200.2	5	-1	1	21
19	uggagaagcagg Phvul.002G262600.1	5	-1	1	21
20	uggagaagcagg Phvul.002G262600.2	5	-1	1	21
21					
22	uggagaagcagg Phvul.002G299004.1	5	-1	1	21
23	uggagaagcagg Phvul.002G299004.3	5	-1	1	21
24	uggagaagcagg Phvul.007G156200.1	5	-1	1	21
25					
26	uggagaagcagg Phvul.002G006400.1	5	-1	1	21
27	uggagaagcagg Phvul.002G006400.3	5	-1	1	21
28	uggagaagcagg Phvul.005G001000.1	5	-1	1	21
29					
30	uggagaagcagg Phvul.002G006400.2	5	-1	1	21
31	uggagaagcagg Phvul.008G243700.1	5	-1	1	21
32	uggagaagcagg Phvul.007G201400.1	5	-1	1	21
33					
34	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
35	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
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37					
38	uggagaagcagg Phvul.007G157500.1	5	-1	1	21
39	uggagaagcagg Phvul.003G181600.1	5	-1	1	21
40	uggagaagcagg Phvul.007G157500.5	5	-1	1	21
41					
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43	uggagaagcagg Phvul.006G164800.1	5	-1	1	21
44	uggagaagcagg Phvul.007G157500.3	5	-1	1	21
45	uggagaagcagg Phvul.007G157500.3	5	-1	1	21
46					
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49	uggagaagcagg Phvul.007G157500.4	5	-1	1	21
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52	uggagaagcagg Phvul.002G116800.1	5	-1	1	21
53	uggagaagcagg Phvul.008G103100.1	5	-1	1	21
54					
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56	uggagaagcagg Phvul.003G262800.1	5	-1	1	21
57	uggagaagcagg Phvul.008G072300.1	5	-1	1	21
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4	uggagaagcagg Phvul.005G155100.1	5	-1	1	21
5					
6	uggagaagcagg Phvul.005G155100.3	5	-1	1	21
7	uggagaagcagg Phvul.009G201600.2	5	-1	1	21
8	uggagaagcagg Phvul.004G088300.4	5	-1	1	21
9					
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11	uggagaagcagg Phvul.002G106900.1	5	-1	1	21
12	uggagaagcagg Phvul.005G099500.1	5	-1	1	21
13					
14	uggagaagcagg Phvul.003G181900.1	5	-1	1	21
15	uggagaagcagg Phvul.003G181900.2	5	-1	1	21
16	uggagaagcagg Phvul.003G121200.1	5	-1	1	21
17					
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19	uggagaagcagg Phvul.006G075600.1	5	-1	1	21
20	uggagaagcagg Phvul.008G284900.1	5	-1	1	21
21					
22	uggagaagcagg Phvul.007G163400.1	5	-1	1	21
23	uggagaagcagg Phvul.001G266600.1	5	-1	1	21
24	uggagaagcagg Phvul.006G091100.2	5	-1	1	21
25					
26	uggagaagcagg Phvul.006G091100.1	5	-1	1	21
27	uggagaagcagg Phvul.003G037500.1	5	-1	1	21
28	uggagaagcagg Phvul.009G007300.1	5	-1	1	21
29					
30	uggagaagcagg Phvul.003G100200.1	5	-1	1	21
31	uggagaagcagg Phvul.003G100200.2	5	-1	1	21
32	uggagaagcagg Phvul.002G262600.1	5	-1	1	21
33					
34	uggagaagcagg Phvul.002G262600.2	5	-1	1	21
35	uggagaagcagg Phvul.002G299004.1	5	-1	1	21
36	uggagaagcagg Phvul.002G299004.3	5	-1	1	21
37					
38	uggagaagcagg Phvul.007G156200.1	5	-1	1	21
39	uggagaagcagg Phvul.002G006400.1	5	-1	1	21
40	uggagaagcagg Phvul.002G006400.3	5	-1	1	21
41					
42	uggagaagcagg Phvul.005G001000.1	5	-1	1	21
43	uggagaagcagg Phvul.002G006400.2	5	-1	1	21
44	uggagaagcagg Phvul.008G243700.1	5	-1	1	21
45	uggagaagcagg Phvul.007G201400.1	5	-1	1	21
46					
47	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
48	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
49	uggagaagcagg Phvul.007G157500.1	5	-1	1	21
50					
51	uggagaagcagg Phvul.007G157500.1	5	-1	1	21
52	uggagaagcagg Phvul.003G181600.1	5	-1	1	21
53					
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56	uggagaagcagg Phvul.006G164800.1	5	-1	1	21
57	uggagaagcagg Phvul.007G157500.3	5	-1	1	21
58					
59	uggagaagcagg Phvul.007G157500.3	5	-1	1	21
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	uggagaagcagg Phvul.007G157500.4	5	-1	1	21

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3	uggagaagcagg Phvul.005G059500.1	5	-1	1	21
4	uggagaagcagg Phvul.002G116800.1	5	-1	1	21
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7	uggagaagcagg Phvul.008G075300.1	5	-1	1	21
8	uggagaagcagg Phvul.003G262800.1	5	-1	1	21
9					
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11	uggagaagcagg Phvul.008G072300.2	5	-1	1	21
12	uggagaagcagg Phvul.004G088300.1	5	-1	1	21
13	uggagaagcagg Phvul.004G088300.3	5	-1	1	21
14	uggagaagcagg Phvul.004G088300.2	5	-1	1	21
15	uggagaagcagg Phvul.009G201600.1	5	-1	1	21
16	uggagaagcagg Phvul.005G155100.1	5	-1	1	21
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18	uggagaagcagg Phvul.009G201600.2	5	-1	1	21
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21	uggagaagcagg Phvul.002G106900.1	5	-1	1	21
22	uggagaagcagg Phvul.005G099500.1	5	-1	1	21
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26	uggagaagcagg Phvul.003G121200.2	5	-1	1	21
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28	uggagaagcagg Phvul.008G284900.1	5	-1	1	21
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31	uggagaagcagg Phvul.006G091100.2	5	-1	1	21
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35	uggagaagcagg Phvul.003G100200.1	5	-1	1	21
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38	uggagaagcagg Phvul.002G262600.2	5	-1	1	21
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46	uggagaagcagg Phvul.008G243700.1	5	-1	1	21
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8	uggagaagcagg Phvul.006G164800.1	5	-1	1	21
9					
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8	uggagaagcagg Phvul.002G006400.2	5	-1	1	21
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32	uggagaagcagg Phvul.008G103100.1	5	-1	1	21
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57	uggagaagcagg Phvul.007G163400.1	5	-1	1	21
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25					
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7	uggagaagcagg Phvul.004G088300.2	5	-1	1	21
8					
9	uggagaagcagg Phvul.009G201600.1	5	-1	1	21
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11	uggagaagcagg Phvul.005G155100.3	5	-1	1	21
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13					
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32	uggagaagcagg Phvul.007G163400.1	5	-1	1	21
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34	uggagaagcagg Phvul.001G266600.1	5	-1	1	21
35	uggagaagcagg Phvul.006G091100.2	5	-1	1	21
36	uggagaagcagg Phvul.006G091100.1	5	-1	1	21
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38	uggagaagcagg Phvul.003G037500.1	5	-1	1	21
39	uggagaagcagg Phvul.009G007300.1	5	-1	1	21
40	uggagaagcagg Phvul.003G100200.1	5	-1	1	21
41	uggagaagcagg Phvul.003G100200.2	5	-1	1	21
42					
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44	uggagaagcagg Phvul.002G262600.2	5	-1	1	21
45	uggagaagcagg Phvul.002G299004.1	5	-1	1	21
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57	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
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35	uggagaagcagg Phvul.002G006400.3	5	-1	1	21
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44	uggagaagcagg Phvul.003G181600.1	5	-1	1	21
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47	uggagaagcagg Phvul.006G164800.1	5	-1	1	21
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28	uggagaagcagg Phvul.005G099500.1	5	-1	1	21
29					
30	uggagaagcagg Phvul.003G181900.1	5	-1	1	21
31	uggagaagcagg Phvul.003G181900.2	5	-1	1	21
32	uggagaagcagg Phvul.003G121200.1	5	-1	1	21
33					
34	uggagaagcagg Phvul.003G121200.2	5	-1	1	21
35	uggagaagcagg Phvul.006G075600.1	5	-1	1	21
36	uggagaagcagg Phvul.008G284900.1	5	-1	1	21
37	uggagaagcagg Phvul.007G163400.1	5	-1	1	21
38					
39	uggagaagcagg Phvul.001G266600.1	5	-1	1	21
40	uggagaagcagg Phvul.006G091100.2	5	-1	1	21
41	uggagaagcagg Phvul.006G091100.1	5	-1	1	21
42					
43	uggagaagcagg Phvul.003G037500.1	5	-1	1	21
44	uggagaagcagg Phvul.009G007300.1	5	-1	1	21
45	uggagaagcagg Phvul.003G100200.1	5	-1	1	21
46					
47	uggagaagcagg Phvul.003G100200.2	5	-1	1	21
48	uggagaagcagg Phvul.002G262600.1	5	-1	1	21
49	uggagaagcagg Phvul.002G262600.2	5	-1	1	21
50					
51	uggagaagcagg Phvul.002G299004.1	5	-1	1	21
52	uggagaagcagg Phvul.002G299004.3	5	-1	1	21
53	uggagaagcagg Phvul.007G156200.1	5	-1	1	21
54					
55	uggagaagcagg Phvul.002G006400.1	5	-1	1	21
56	uggagaagcagg Phvul.002G006400.3	5	-1	1	21
57	uggagaagcagg Phvul.005G001000.1	5	-1	1	21
58					
59	uggagaagcagg Phvul.002G006400.2	5	-1	1	21
60	uggagaagcagg Phvul.008G243700.1	5	-1	1	21
	uggagaagcagg Phvul.007G201400.1	5	-1	1	21

1					
2	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
3	uggagaagcagg Phvul.007G157500.2	5	-1	1	21
4	uggagaagcagg Phvul.007G157500.1	5	-1	1	21
5					
6	uggagaagcagg Phvul.007G157500.1	5	-1	1	21
7	uggagaagcagg Phvul.003G181600.1	5	-1	1	21
8	uggagaagcagg Phvul.007G157500.5	5	-1	1	21
9					
10	uggagaagcagg Phvul.007G157500.5	5	-1	1	21
11	uggagaagcagg Phvul.006G164800.1	5	-1	1	21
12	uggagaagcagg Phvul.007G157500.3	5	-1	1	21
13					
14	uggagaagcagg Phvul.007G157500.3	5	-1	1	21
15	uggagaagcagg Phvul.005G059700.1	5	-1	1	21
16	uggagaagcagg Phvul.007G157500.4	5	-1	1	21
17					
18	uggagaagcagg Phvul.007G157500.4	5	-1	1	21
19	uggagaagcagg Phvul.005G059500.1	5	-1	1	21
20	uggagaagcagg Phvul.002G116800.1	5	-1	1	21
21					
22	uggagaagcagg Phvul.008G103100.1	5	-1	1	21
23	uggagaagcagg Phvul.008G075300.1	5	-1	1	21
24	uggagaagcagg Phvul.003G262800.1	5	-1	1	21
25					
26	uggagaagcagg Phvul.008G072300.1	5	-1	1	21
27	uggagaagcagg Phvul.008G072300.2	5	-1	1	21
28	uggagaagcagg Phvul.004G088300.1	5	-1	1	21
29					
30	uggagaagcagg Phvul.004G088300.3	5	-1	1	21
31	uggagaagcagg Phvul.004G088300.2	5	-1	1	21
32	uggagaagcagg Phvul.009G201600.1	5	-1	1	21
33					
34	uggagaagcagg Phvul.005G155100.1	5	-1	1	21
35	uggagaagcagg Phvul.005G155100.3	5	-1	1	21
36	uggagaagcagg Phvul.009G201600.2	5	-1	1	21
37					
38	uggagaagcagg Phvul.004G088300.4	5	-1	1	21
39	uggagaagcagg Phvul.006G075600.1	5	-1	1	22
40	uggagaagcagg Phvul.008G284900.1	5	-1	1	22
41					
42	uggagaagcagg Phvul.006G091100.2	5	-1	1	22
43	uggagaagcagg Phvul.009G222600.1	5	-1	1	22
44	uggagaagcagg Phvul.006G091100.1	5	-1	1	22
45					
46	uggagaagcagg Phvul.002G106900.1	5	-1	1	22
47	uggagaagcagg Phvul.005G099500.1	5	-1	1	22
48	uggagaagcagg Phvul.003G181900.1	5	-1	1	22
49	uggagaagcagg Phvul.003G181900.2	5	-1	1	22
50					
51	uggagaagcagg Phvul.003G121200.1	5	-1	1	22
52	uggagaagcagg Phvul.003G121200.2	5	-1	1	22
53	uggagaagcagg Phvul.005G059700.1	5	-1	1	22
54					
55	uggagaagcagg Phvul.005G059500.1	5	-1	1	22
56	uggagaagcagg Phvul.008G072300.1	5	-1	1	22
57	uggagaagcagg Phvul.008G072300.2	5	-1	1	22
58					
59	uggagaagcagg Phvul.009G201600.1	5	-1	1	22
60	uggagaagcagg Phvul.005G155100.1	5	-1	1	22
	uggagaagcagg Phvul.005G155100.3	5	-1	1	22

1					
2	uggagaagcagg Phvul.009G201600.2	5	-1	1	22
3	uggagaagcagg Phvul.005G155100.2	5	-1	1	22
4	uggagaagcagg Phvul.009G114400.1	5	-1	1	22
5					
6	uggagaagcagg Phvul.003G240100.1	5	-1	1	22
7	uggagaagcagg Phvul.002G283000.3	5	-1	1	22
8	uggagaagcagg Phvul.002G283000.1	5	-1	1	22
9					
10	uggagaagcagg Phvul.002G283000.2	5	-1	1	22
11	uggagaagcagg Phvul.003G170100.1	5	-1	1	22
12	uggagaagcagg Phvul.011G173600.1	5	-1	1	22
13					
14	uggagaagcagg Phvul.003G283500.1	5	-1	1	22
15	uggagaagcagg Phvul.007G163400.1	5	-1	1	22
16	uggagaagcagg Phvul.003G037500.1	5	-1	1	22
17					
18	uggagaagcagg Phvul.001G266600.1	5	-1	1	22
19	uggagaagcagg Phvul.001G243500.2	5	-1	1	22
20	uggagaagcagg Phvul.006G067900.1	5	-1	1	22
21					
22	uggagaagcagg Phvul.008G140600.1	5	-1	1	22
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not distribute



1				
2	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
3	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
4	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
5				
6	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
7	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
8	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
9				
10	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
11	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
12	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
13				
14	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
15	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
16	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
17				
18	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
19	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
20	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
21				
22	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
23	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
24	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
25				
26	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
27	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
28	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
29				
30	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
31	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
32	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
33				
34	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
35	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
36	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
37				
38	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
39	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
40	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
41				
42	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
43	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
44	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
45				
46	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
47	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
48	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
49				
50	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
51	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
52	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
53				
54	1273	1293 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371528
55	973	993 UGGAGAAGC/	AGCACGUGU( Cleavage	pacid=371560
56	727	747 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371538
57				
58	1272	1293 UGGAGAAGC/	GAGCACGUGI( Cleavage	pacid=371528
59	972	993 UGGAGAAGC/	GAGCACGUGI( Cleavage	pacid=371560
60	726	747 UGGAGAAGC/	GAGCAAGUG( Cleavage	pacid=371538
	191	211 UGGAGAAGC/	AGCAAGUGCC( Cleavage	pacid=371718





1				
2	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
3	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
4	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
5	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
6	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
7	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
8				
9				
10	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
11	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
12	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
13	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
14	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
15	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
16				
17				
18	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
19	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
20	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
21	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
22	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
23	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
24				
25				
26	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
27	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
28	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
29	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
30	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
31	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
32				
33				
34	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
35	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
36	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
37	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
38	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
39	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
40				
41				
42	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
43	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
44	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
45	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
46	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
47	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
48				
49				
50	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
51	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
52	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
53	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
54	351	371 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
55	349	369 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574
56				
57				
58	213	233 UGGAGAAGC/	:: : ::::::::::: CACACUUCCC Cleavage	pacid=371629
59	191	211 UGGAGAAGC/	:: ::::::::::: AGCAAGUGCC Cleavage	pacid=371718
60	496	516 UGGAGAAGC/	::::::::::: : CCCGCGUGCC Cleavage	pacid=371641
	876	896 UGGAGAAGC/	.. ::::::::::: CUUGCUUGU  Cleavage	pacid=371574





1				
2	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
3	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
4	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
5	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
6	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
7	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
8	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
9	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
10	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
11	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
12	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
13	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
14	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
15	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
16	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
17	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
18	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
19	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
20	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
21	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
22	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
23	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
24	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
25	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
26	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
27	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
28	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
29	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
30	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
31	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
32	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
33	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
34	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
35	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
36	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
37	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
38	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
39	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
40	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
41	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
42	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
43	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
44	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
45	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
46	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
47	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
48	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
49	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
50	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
51	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
52	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
53	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
54	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
55	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
56	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
57	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
58	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
59	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
60	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578

1				
2	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
3	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
4	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
5	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
6	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
7	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
8	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUI Cleavage	pacid=371619
9	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
10	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
11	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
12	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
13	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
14	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
15	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
16	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
17	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
18	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUI Cleavage	pacid=371619
19	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
20	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
21	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
22	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
23	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
24	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
25	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
26	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
27	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
28	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUI Cleavage	pacid=371619
29	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
30	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
31	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
32	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
33	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
34	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
35	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
36	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
37	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
38	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUI Cleavage	pacid=371619
39	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
40	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
41	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
42	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
43	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
44	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
45	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
46	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
47	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
48	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUI Cleavage	pacid=371619
49	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
50	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
51	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
52	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
53	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
54	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
55	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
56	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
57	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
58	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUI Cleavage	pacid=371619
59	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
60	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578

1				
2	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
3	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
4	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
5	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
6	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
7	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
8				
9	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
10	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
11	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
12	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
13	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
14	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
15	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
16	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
17	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
18	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
19	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
20	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
21	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
22	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
23	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
24	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
25	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
26	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
27	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
28	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
29	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
30	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
31	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
32	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
33	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
34	180	200 UGGAGAAGC/	:: ::::: UGCACGUGCC Cleavage	pacid=371438
35	508	528 UGGAGAAGC/	:: ::::: ACUCCGUCCC Cleavage	pacid=371767
36	186	206 UGGAGAAGC/	:: ::::: CUCACGUUUL Cleavage	pacid=371619
37	340	360 UGGAGAAGC/	:: ::::: AACAGGUGCC Translation	pacid=371542
38	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
39	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
40	182	202 UGGAGAAGC/	:: ::::: GACACUUGCL Cleavage	pacid=371578
41	286	306 UGGAGAAGC/	:: ::::: ACCAUUGGCL Cleavage	pacid=371732
42	79	98 UGGAGAAGC/	:: ::::: CACAC-UGCU Cleavage	pacid=371439
43	179	200 UGGAGAAGC/	:: ::::: GUGCACGUG Cleavage	pacid=371438
44	507	528 UGGAGAAGC/	:: ::::: AACUCCGUCC Cleavage	pacid=371767
45	185	206 UGGAGAAGC/	:: ::::: UCUCACGUUL Cleavage	pacid=371619
46	339	360 UGGAGAAGC/	:: ::::: CAACAGGUG Translation	pacid=371542
47	181	202 UGGAGAAGC/	:: ::::: GGACACUUG Cleavage	pacid=371578
48	181	202 UGGAGAAGC/	:: ::::: GGACACUUG Cleavage	pacid=371578
49	181	202 UGGAGAAGC/	:: ::::: GGACACUUG Cleavage	pacid=371578
50	1540	1560 UGGAGAAGC/	:: ::::: UGCAGCUGCL Cleavage	pacid=371672
51	1459	1479 UGGAGAAGC/	:: ::::: UGCAGCUGCL Cleavage	pacid=371672
52	3334	3354 UGGAGAAGC/	:: ::::: UUAUGUGC Cleavage	pacid=371569
53	395	415 UGGAGAAGC/	:: ::::: CCAACGUGUC Cleavage	pacid=371597
54	349	369 UGGAGAAGC/	:: ::::: CUCGCGUGCC Cleavage	pacid=371564
55	398	418 UGGAGAAGC/	:: ::::: CCAACGUGCL Cleavage	pacid=371609
56	2339	2359 UGGAGAAGC/	:: ::::: AACACGUGCC Cleavage	pacid=371543
57	512	532 UGGAGAAGC/	:: ::::: GCCACGUGCA Cleavage	pacid=371586
58	749	769 UGGAGAAGC/	:: ::::: CACAUGUGU Cleavage	pacid=371470
59				
60				

1				
2	134	154 UGGAGAAGC/	... : ::::: GGUGCAUUC(Cleavage	pacid=371704
3	6862	6882 UGGAGAAGC/	. : ::::: UCAGCAUGU(Cleavage	pacid=371594
4	1550	1570 UGGAGAAGC/	:: ::::: CUCACUUGCC Cleavage	pacid=371472
5	1368	1388 UGGAGAAGC/	:: ::::: ACCACUUGUC Cleavage	pacid=371488
6	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
7	904	924 UGGAGAAGC/	. : : : ACUAUGUUU(Cleavage	pacid=371508
8				
9	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
10				
11	3330	3350 UGGAGAAGC/	: : : : UCUACAUUC Cleavage	pacid=371560
12	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC Cleavage	pacid=371672
13				
14	1459	1479 UGGAGAAGC/	::: : : UGCAGCUGC Cleavage	pacid=371672
15	3334	3354 UGGAGAAGC/	: : : : UUAUGUGC(Cleavage	pacid=371569
16	395	415 UGGAGAAGC/	::: : : CCAACGUGUC Cleavage	pacid=371597
17	349	369 UGGAGAAGC/	::: : : CUCGCGUGCC Cleavage	pacid=371564
18	398	418 UGGAGAAGC/	::: : : CCAACGUGC Cleavage	pacid=371609
19				
20	2339	2359 UGGAGAAGC/	: : : : AACACGUGCC Cleavage	pacid=371543
21				
22	512	532 UGGAGAAGC/	::: : : GCCACGUGC Cleavage	pacid=371586
23	749	769 UGGAGAAGC/	::: : : CACAUGUGU(Cleavage	pacid=371470
24	134	154 UGGAGAAGC/	... : ::::: GGUGCAUUC(Cleavage	pacid=371704
25				
26	6862	6882 UGGAGAAGC/	. : ::::: UCAGCAUGU(Cleavage	pacid=371594
27	1550	1570 UGGAGAAGC/	:: ::::: CUCACUUGCC Cleavage	pacid=371472
28	1368	1388 UGGAGAAGC/	:: ::::: ACCACUUGUC Cleavage	pacid=371488
29	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
30	904	924 UGGAGAAGC/	. : : : ACUAUGUUU(Cleavage	pacid=371508
31	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
32				
33	3330	3350 UGGAGAAGC/	: : : : UCUACAUUC Cleavage	pacid=371560
34				
35	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC Cleavage	pacid=371672
36	1459	1479 UGGAGAAGC/	::: : : UGCAGCUGC Cleavage	pacid=371672
37				
38	3334	3354 UGGAGAAGC/	: : : : UUAUGUGC(Cleavage	pacid=371569
39	395	415 UGGAGAAGC/	::: : : CCAACGUGUC Cleavage	pacid=371597
40	349	369 UGGAGAAGC/	::: : : CUCGCGUGCC Cleavage	pacid=371564
41	398	418 UGGAGAAGC/	::: : : CCAACGUGC Cleavage	pacid=371609
42				
43	2339	2359 UGGAGAAGC/	: : : : AACACGUGCC Cleavage	pacid=371543
44	512	532 UGGAGAAGC/	::: : : GCCACGUGC Cleavage	pacid=371586
45	749	769 UGGAGAAGC/	::: : : CACAUGUGU(Cleavage	pacid=371470
46				
47	134	154 UGGAGAAGC/	... : ::::: GGUGCAUUC(Cleavage	pacid=371704
48	6862	6882 UGGAGAAGC/	. : ::::: UCAGCAUGU(Cleavage	pacid=371594
49	1550	1570 UGGAGAAGC/	:: ::::: CUCACUUGCC Cleavage	pacid=371472
50	1368	1388 UGGAGAAGC/	:: ::::: ACCACUUGUC Cleavage	pacid=371488
51	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
52	904	924 UGGAGAAGC/	. : : : ACUAUGUUU(Cleavage	pacid=371508
53	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
54				
55	3330	3350 UGGAGAAGC/	: : : : UCUACAUUC Cleavage	pacid=371560
56	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC Cleavage	pacid=371672
57				
58	1459	1479 UGGAGAAGC/	::: : : UGCAGCUGC Cleavage	pacid=371672
59	3334	3354 UGGAGAAGC/	: : : : UUAUGUGC(Cleavage	pacid=371569
60	395	415 UGGAGAAGC/	::: : : CCAACGUGUC Cleavage	pacid=371597



1					
2	349	369	UGGAGAAGC/	:::.....: CUCGCGUGCC Cleavage	pacid=371564
3	398	418	UGGAGAAGC/	:::.....: CCAACGUGCL Cleavage	pacid=371609
4	2339	2359	UGGAGAAGC/	:::.....: AACACGUGCC Cleavage	pacid=371543
5	512	532	UGGAGAAGC/	:::.....: GCCACGUGCA Cleavage	pacid=371586
6	749	769	UGGAGAAGC/	:::.....: CACAUGUGU( Cleavage	pacid=371470
7	134	154	UGGAGAAGC/	:::.....: GGUGCAUUC( Cleavage	pacid=371704
8	6862	6882	UGGAGAAGC/	:::.....: UCAGCAUGU( Cleavage	pacid=371594
9	1550	1570	UGGAGAAGC/	:::.....: CUCACUUGCC Cleavage	pacid=371472
10	1368	1388	UGGAGAAGC/	:::.....: ACCACUUGUC Cleavage	pacid=371488
11	609	629	UGGAGAAGC/	:::.....: GUCACGUUU(Translation	pacid=371524
12	904	924	UGGAGAAGC/	:::.....: ACUAUGUUU( Cleavage	pacid=371508
13	335	355	UGGAGAAGC/	:::.....: CCCACGUCCU Cleavage	pacid=371552
14	3330	3350	UGGAGAAGC/	:::.....: UCUACAUUC Cleavage	pacid=371560
15	1540	1560	UGGAGAAGC/	:::.....: UGCAGCUGCL Cleavage	pacid=371672
16	1459	1479	UGGAGAAGC/	:::.....: UGCAGCUGCL Cleavage	pacid=371672
17	3334	3354	UGGAGAAGC/	:::.....: UUAUGUGC( Cleavage	pacid=371569
18	395	415	UGGAGAAGC/	:::.....: CCAACGUGUC Cleavage	pacid=371597
19	349	369	UGGAGAAGC/	:::.....: CUCGCGUGCC Cleavage	pacid=371564
20	398	418	UGGAGAAGC/	:::.....: CCAACGUGCL Cleavage	pacid=371609
21	2339	2359	UGGAGAAGC/	:::.....: AACACGUGCC Cleavage	pacid=371543
22	512	532	UGGAGAAGC/	:::.....: GCCACGUGCA Cleavage	pacid=371586
23	749	769	UGGAGAAGC/	:::.....: CACAUGUGU( Cleavage	pacid=371470
24	134	154	UGGAGAAGC/	:::.....: GGUGCAUUC( Cleavage	pacid=371704
25	6862	6882	UGGAGAAGC/	:::.....: UCAGCAUGU( Cleavage	pacid=371594
26	1550	1570	UGGAGAAGC/	:::.....: CUCACUUGCC Cleavage	pacid=371472
27	1368	1388	UGGAGAAGC/	:::.....: ACCACUUGUC Cleavage	pacid=371488
28	609	629	UGGAGAAGC/	:::.....: GUCACGUUU(Translation	pacid=371524
29	904	924	UGGAGAAGC/	:::.....: ACUAUGUUU( Cleavage	pacid=371508
30	335	355	UGGAGAAGC/	:::.....: CCCACGUCCU Cleavage	pacid=371552
31	3330	3350	UGGAGAAGC/	:::.....: UCUACAUUC Cleavage	pacid=371560
32	1540	1560	UGGAGAAGC/	:::.....: UGCAGCUGCL Cleavage	pacid=371672
33	1459	1479	UGGAGAAGC/	:::.....: UGCAGCUGCL Cleavage	pacid=371672
34	3334	3354	UGGAGAAGC/	:::.....: UUAUGUGC( Cleavage	pacid=371569
35	395	415	UGGAGAAGC/	:::.....: CCAACGUGUC Cleavage	pacid=371597
36	349	369	UGGAGAAGC/	:::.....: CUCGCGUGCC Cleavage	pacid=371564
37	398	418	UGGAGAAGC/	:::.....: CCAACGUGCL Cleavage	pacid=371609
38	2339	2359	UGGAGAAGC/	:::.....: AACACGUGCC Cleavage	pacid=371543
39	512	532	UGGAGAAGC/	:::.....: GCCACGUGCA Cleavage	pacid=371586
40	749	769	UGGAGAAGC/	:::.....: CACAUGUGU( Cleavage	pacid=371470
41	134	154	UGGAGAAGC/	:::.....: GGUGCAUUC( Cleavage	pacid=371704
42	6862	6882	UGGAGAAGC/	:::.....: UCAGCAUGU( Cleavage	pacid=371594
43	1550	1570	UGGAGAAGC/	:::.....: CUCACUUGCC Cleavage	pacid=371472
44	1368	1388	UGGAGAAGC/	:::.....: ACCACUUGUC Cleavage	pacid=371488
45	609	629	UGGAGAAGC/	:::.....: GUCACGUUU(Translation	pacid=371524
46	904	924	UGGAGAAGC/	:::.....: ACUAUGUUU( Cleavage	pacid=371508
47	335	355	UGGAGAAGC/	:::.....: CCCACGUCCU Cleavage	pacid=371552
48	3330	3350	UGGAGAAGC/	:::.....: UCUACAUUC Cleavage	pacid=371560
49	1540	1560	UGGAGAAGC/	:::.....: UGCAGCUGCL Cleavage	pacid=371672
50	1459	1479	UGGAGAAGC/	:::.....: UGCAGCUGCL Cleavage	pacid=371672
51	3334	3354	UGGAGAAGC/	:::.....: UUAUGUGC( Cleavage	pacid=371569
52	395	415	UGGAGAAGC/	:::.....: CCAACGUGUC Cleavage	pacid=371597
53	349	369	UGGAGAAGC/	:::.....: CUCGCGUGCC Cleavage	pacid=371564
54	398	418	UGGAGAAGC/	:::.....: CCAACGUGCL Cleavage	pacid=371609
55	2339	2359	UGGAGAAGC/	:::.....: AACACGUGCC Cleavage	pacid=371543
56	512	532	UGGAGAAGC/	:::.....: GCCACGUGCA Cleavage	pacid=371586
57	749	769	UGGAGAAGC/	:::.....: CACAUGUGU( Cleavage	pacid=371470
58	134	154	UGGAGAAGC/	:::.....: GGUGCAUUC( Cleavage	pacid=371704
59	6862	6882	UGGAGAAGC/	:::.....: UCAGCAUGU( Cleavage	pacid=371594
60	1550	1570	UGGAGAAGC/	:::.....: CUCACUUGCC Cleavage	pacid=371472
61	1368	1388	UGGAGAAGC/	:::.....: ACCACUUGUC Cleavage	pacid=371488
62	609	629	UGGAGAAGC/	:::.....: GUCACGUUU(Translation	pacid=371524
63	904	924	UGGAGAAGC/	:::.....: ACUAUGUUU( Cleavage	pacid=371508
64	335	355	UGGAGAAGC/	:::.....: CCCACGUCCU Cleavage	pacid=371552





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2	1550	1570 UGGAGAAGC/	::: ::::::::::: CUCACUUGCC Cleavage	pacid=371472
3	1368	1388 UGGAGAAGC/	::: ::::::::::: ACCACUUGUC Cleavage	pacid=371488
4	609	629 UGGAGAAGC/	::: ::::::::::: GUCACGUUU(Translation	pacid=371524
5	904	924 UGGAGAAGC/	::: ::::::::::: ACUAUGUUU  Cleavage	pacid=371508
6	335	355 UGGAGAAGC/	::: ::::::::::: CCCACGUCCU Cleavage	pacid=371552
7	3330	3350 UGGAGAAGC/	::: ::::::::::: UCUACAUUC  Cleavage	pacid=371560
8	1540	1560 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
9	1459	1479 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
10	3334	3354 UGGAGAAGC/	::: ::::::::::: UUAUGUGC  Cleavage	pacid=371569
11	395	415 UGGAGAAGC/	::: ::::::::::: CCAACGUGUC Cleavage	pacid=371597
12	349	369 UGGAGAAGC/	::: ::::::::::: CUCGCGUGCC Cleavage	pacid=371564
13	398	418 UGGAGAAGC/	::: ::::::::::: CCAACGUGC  Cleavage	pacid=371609
14	2339	2359 UGGAGAAGC/	::: ::::::::::: AACACGUGCC Cleavage	pacid=371543
15	512	532 UGGAGAAGC/	::: ::::::::::: GCCACGUGC  Cleavage	pacid=371586
16	749	769 UGGAGAAGC/	::: ::::::::::: CACAUGUGU( Cleavage	pacid=371470
17	134	154 UGGAGAAGC/	::: ::::::::::: GGUGCAUUC( Cleavage	pacid=371704
18	6862	6882 UGGAGAAGC/	::: ::::::::::: UCAGCAUGU( Cleavage	pacid=371594
19	1550	1570 UGGAGAAGC/	::: ::::::::::: CUCACUUGCC Cleavage	pacid=371472
20	1368	1388 UGGAGAAGC/	::: ::::::::::: ACCACUUGUC Cleavage	pacid=371488
21	609	629 UGGAGAAGC/	::: ::::::::::: GUCACGUUU(Translation	pacid=371524
22	904	924 UGGAGAAGC/	::: ::::::::::: ACUAUGUUU  Cleavage	pacid=371508
23	335	355 UGGAGAAGC/	::: ::::::::::: CCCACGUCCU Cleavage	pacid=371552
24	3330	3350 UGGAGAAGC/	::: ::::::::::: UCUACAUUC  Cleavage	pacid=371560
25	1540	1560 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
26	1459	1479 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
27	3334	3354 UGGAGAAGC/	::: ::::::::::: UUAUGUGC  Cleavage	pacid=371569
28	395	415 UGGAGAAGC/	::: ::::::::::: CCAACGUGUC Cleavage	pacid=371597
29	349	369 UGGAGAAGC/	::: ::::::::::: CUCGCGUGCC Cleavage	pacid=371564
30	398	418 UGGAGAAGC/	::: ::::::::::: CCAACGUGC  Cleavage	pacid=371609
31	2339	2359 UGGAGAAGC/	::: ::::::::::: AACACGUGCC Cleavage	pacid=371543
32	512	532 UGGAGAAGC/	::: ::::::::::: GCCACGUGC  Cleavage	pacid=371586
33	749	769 UGGAGAAGC/	::: ::::::::::: CACAUGUGU( Cleavage	pacid=371470
34	134	154 UGGAGAAGC/	::: ::::::::::: GGUGCAUUC( Cleavage	pacid=371704
35	6862	6882 UGGAGAAGC/	::: ::::::::::: UCAGCAUGU( Cleavage	pacid=371594
36	1550	1570 UGGAGAAGC/	::: ::::::::::: CUCACUUGCC Cleavage	pacid=371472
37	1368	1388 UGGAGAAGC/	::: ::::::::::: ACCACUUGUC Cleavage	pacid=371488
38	609	629 UGGAGAAGC/	::: ::::::::::: GUCACGUUU(Translation	pacid=371524
39	904	924 UGGAGAAGC/	::: ::::::::::: ACUAUGUUU  Cleavage	pacid=371508
40	335	355 UGGAGAAGC/	::: ::::::::::: CCCACGUCCU Cleavage	pacid=371552
41	3330	3350 UGGAGAAGC/	::: ::::::::::: UCUACAUUC  Cleavage	pacid=371560
42	1540	1560 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
43	1459	1479 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
44	3334	3354 UGGAGAAGC/	::: ::::::::::: UUAUGUGC  Cleavage	pacid=371569
45	395	415 UGGAGAAGC/	::: ::::::::::: CCAACGUGUC Cleavage	pacid=371597
46	349	369 UGGAGAAGC/	::: ::::::::::: CUCGCGUGCC Cleavage	pacid=371564
47	398	418 UGGAGAAGC/	::: ::::::::::: CCAACGUGC  Cleavage	pacid=371609
48	2339	2359 UGGAGAAGC/	::: ::::::::::: AACACGUGCC Cleavage	pacid=371543
49	512	532 UGGAGAAGC/	::: ::::::::::: GCCACGUGC  Cleavage	pacid=371586
50	749	769 UGGAGAAGC/	::: ::::::::::: CACAUGUGU( Cleavage	pacid=371470
51	134	154 UGGAGAAGC/	::: ::::::::::: GGUGCAUUC( Cleavage	pacid=371704
52	6862	6882 UGGAGAAGC/	::: ::::::::::: UCAGCAUGU( Cleavage	pacid=371594
53	1550	1570 UGGAGAAGC/	::: ::::::::::: CUCACUUGCC Cleavage	pacid=371472
54	1368	1388 UGGAGAAGC/	::: ::::::::::: ACCACUUGUC Cleavage	pacid=371488
55	609	629 UGGAGAAGC/	::: ::::::::::: GUCACGUUU(Translation	pacid=371524
56	904	924 UGGAGAAGC/	::: ::::::::::: ACUAUGUUU  Cleavage	pacid=371508
57	335	355 UGGAGAAGC/	::: ::::::::::: CCCACGUCCU Cleavage	pacid=371552
58	3330	3350 UGGAGAAGC/	::: ::::::::::: UCUACAUUC  Cleavage	pacid=371560
59	1540	1560 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
60	1459	1479 UGGAGAAGC/	::: ::::::::::: UGCAGCUGC  Cleavage	pacid=371672
61	3334	3354 UGGAGAAGC/	::: ::::::::::: UUAUGUGC  Cleavage	pacid=371569
62	395	415 UGGAGAAGC/	::: ::::::::::: CCAACGUGUC Cleavage	pacid=371597
63	349	369 UGGAGAAGC/	::: ::::::::::: CUCGCGUGCC Cleavage	pacid=371564
64	398	418 UGGAGAAGC/	::: ::::::::::: CCAACGUGC  Cleavage	pacid=371609

1				
2	2339	2359 UGGAGAAGC/	::: ::: : AACACGUGCC Cleavage	pacid=371543
3	512	532 UGGAGAAGC/	::: : : GCCACGUGCA Cleavage	pacid=371586
4	749	769 UGGAGAAGC/	::: : : CACAUGUGU( Cleavage	pacid=371470
5	134	154 UGGAGAAGC/	::: : : GGUGCAUUC( Cleavage	pacid=371704
6	6862	6882 UGGAGAAGC/	::: : : UCAGCAUGU( Cleavage	pacid=371594
7	1550	1570 UGGAGAAGC/	::: : : CUCACUUGCC Cleavage	pacid=371472
8	1368	1388 UGGAGAAGC/	::: : : ACCACUUGUC Cleavage	pacid=371488
9	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
10	904	924 UGGAGAAGC/	::: : : ACUAUGUUU( Cleavage	pacid=371508
11	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
12	3330	3350 UGGAGAAGC/	::: : : UCUACAUUC( Cleavage	pacid=371560
13	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672
14	1459	1479 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672
15	3334	3354 UGGAGAAGC/	::: : : UUAUGUGC( Cleavage	pacid=371569
16	395	415 UGGAGAAGC/	::: : : CCAACGUGUC Cleavage	pacid=371597
17	349	369 UGGAGAAGC/	::: : : CUCGCGUGCC Cleavage	pacid=371564
18	398	418 UGGAGAAGC/	::: : : CCAACGUGC( Cleavage	pacid=371609
19	2339	2359 UGGAGAAGC/	::: ::: : AACACGUGCC Cleavage	pacid=371543
20	512	532 UGGAGAAGC/	::: : : GCCACGUGCA Cleavage	pacid=371586
21	749	769 UGGAGAAGC/	::: : : CACAUGUGU( Cleavage	pacid=371470
22	134	154 UGGAGAAGC/	::: : : GGUGCAUUC( Cleavage	pacid=371704
23	6862	6882 UGGAGAAGC/	::: : : UCAGCAUGU( Cleavage	pacid=371594
24	1550	1570 UGGAGAAGC/	::: : : CUCACUUGCC Cleavage	pacid=371472
25	1368	1388 UGGAGAAGC/	::: : : ACCACUUGUC Cleavage	pacid=371488
26	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
27	904	924 UGGAGAAGC/	::: : : ACUAUGUUU( Cleavage	pacid=371508
28	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
29	3330	3350 UGGAGAAGC/	::: : : UCUACAUUC( Cleavage	pacid=371560
30	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672
31	1459	1479 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672
32	3334	3354 UGGAGAAGC/	::: : : UUAUGUGC( Cleavage	pacid=371569
33	395	415 UGGAGAAGC/	::: : : CCAACGUGUC Cleavage	pacid=371597
34	349	369 UGGAGAAGC/	::: : : CUCGCGUGCC Cleavage	pacid=371564
35	398	418 UGGAGAAGC/	::: : : CCAACGUGC( Cleavage	pacid=371609
36	2339	2359 UGGAGAAGC/	::: ::: : AACACGUGCC Cleavage	pacid=371543
37	512	532 UGGAGAAGC/	::: : : GCCACGUGCA Cleavage	pacid=371586
38	749	769 UGGAGAAGC/	::: : : CACAUGUGU( Cleavage	pacid=371470
39	134	154 UGGAGAAGC/	::: : : GGUGCAUUC( Cleavage	pacid=371704
40	6862	6882 UGGAGAAGC/	::: : : UCAGCAUGU( Cleavage	pacid=371594
41	1550	1570 UGGAGAAGC/	::: : : CUCACUUGCC Cleavage	pacid=371472
42	1368	1388 UGGAGAAGC/	::: : : ACCACUUGUC Cleavage	pacid=371488
43	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
44	904	924 UGGAGAAGC/	::: : : ACUAUGUUU( Cleavage	pacid=371508
45	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
46	3330	3350 UGGAGAAGC/	::: : : UCUACAUUC( Cleavage	pacid=371560
47	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672
48	1459	1479 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672
49	3334	3354 UGGAGAAGC/	::: : : UUAUGUGC( Cleavage	pacid=371569
50	395	415 UGGAGAAGC/	::: : : CCAACGUGUC Cleavage	pacid=371597
51	349	369 UGGAGAAGC/	::: : : CUCGCGUGCC Cleavage	pacid=371564
52	398	418 UGGAGAAGC/	::: : : CCAACGUGC( Cleavage	pacid=371609
53	2339	2359 UGGAGAAGC/	::: ::: : AACACGUGCC Cleavage	pacid=371543
54	512	532 UGGAGAAGC/	::: : : GCCACGUGCA Cleavage	pacid=371586
55	749	769 UGGAGAAGC/	::: : : CACAUGUGU( Cleavage	pacid=371470
56	134	154 UGGAGAAGC/	::: : : GGUGCAUUC( Cleavage	pacid=371704
57	6862	6882 UGGAGAAGC/	::: : : UCAGCAUGU( Cleavage	pacid=371594
58	1550	1570 UGGAGAAGC/	::: : : CUCACUUGCC Cleavage	pacid=371472
59	1368	1388 UGGAGAAGC/	::: : : ACCACUUGUC Cleavage	pacid=371488
60	609	629 UGGAGAAGC/	::: : : GUCACGUUU(Translation	pacid=371524
61	904	924 UGGAGAAGC/	::: : : ACUAUGUUU( Cleavage	pacid=371508
62	335	355 UGGAGAAGC/	::: : : CCCACGUCCU Cleavage	pacid=371552
63	3330	3350 UGGAGAAGC/	::: : : UCUACAUUC( Cleavage	pacid=371560
64	1540	1560 UGGAGAAGC/	::: : : UGCAGCUGC( Cleavage	pacid=371672

1				
2	1459	1479 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
3	3334	3354 UGGAGAAGC/	UUA AUGUGC( Cleavage	pacid=371569
4	395	415 UGGAGAAGC/	CCAACGUGUC( Cleavage	pacid=371597
5	349	369 UGGAGAAGC/	CUCGCGUGCC( Cleavage	pacid=371564
6	398	418 UGGAGAAGC/	CCAACGUGC( Cleavage	pacid=371609
7	2339	2359 UGGAGAAGC/	AACACGUGCC( Cleavage	pacid=371543
8	512	532 UGGAGAAGC/	GCCACGUGC( Cleavage	pacid=371586
9	749	769 UGGAGAAGC/	CACAUGUGU( Cleavage	pacid=371470
10	134	154 UGGAGAAGC/	GGUGCAUUC( Cleavage	pacid=371704
11	6862	6882 UGGAGAAGC/	UCAGCAUGU( Cleavage	pacid=371594
12	1550	1570 UGGAGAAGC/	CUCACUUGCC( Cleavage	pacid=371472
13	1368	1388 UGGAGAAGC/	ACCACUUGUC( Cleavage	pacid=371488
14	609	629 UGGAGAAGC/	GUCACGUUU( Translation	pacid=371524
15	904	924 UGGAGAAGC/	ACUAUGUUU( Cleavage	pacid=371508
16	335	355 UGGAGAAGC/	CCCACGUCCU( Cleavage	pacid=371552
17	3330	3350 UGGAGAAGC/	UCUACAUUC( Cleavage	pacid=371560
18	1540	1560 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
19	1459	1479 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
20	3334	3354 UGGAGAAGC/	UUA AUGUGC( Cleavage	pacid=371569
21	395	415 UGGAGAAGC/	CCAACGUGUC( Cleavage	pacid=371597
22	349	369 UGGAGAAGC/	CUCGCGUGCC( Cleavage	pacid=371564
23	398	418 UGGAGAAGC/	CCAACGUGC( Cleavage	pacid=371609
24	2339	2359 UGGAGAAGC/	AACACGUGCC( Cleavage	pacid=371543
25	512	532 UGGAGAAGC/	GCCACGUGC( Cleavage	pacid=371586
26	749	769 UGGAGAAGC/	CACAUGUGU( Cleavage	pacid=371470
27	134	154 UGGAGAAGC/	GGUGCAUUC( Cleavage	pacid=371704
28	6862	6882 UGGAGAAGC/	UCAGCAUGU( Cleavage	pacid=371594
29	1550	1570 UGGAGAAGC/	CUCACUUGCC( Cleavage	pacid=371472
30	1368	1388 UGGAGAAGC/	ACCACUUGUC( Cleavage	pacid=371488
31	609	629 UGGAGAAGC/	GUCACGUUU( Translation	pacid=371524
32	904	924 UGGAGAAGC/	ACUAUGUUU( Cleavage	pacid=371508
33	335	355 UGGAGAAGC/	CCCACGUCCU( Cleavage	pacid=371552
34	3330	3350 UGGAGAAGC/	UCUACAUUC( Cleavage	pacid=371560
35	1540	1560 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
36	1459	1479 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
37	3334	3354 UGGAGAAGC/	UUA AUGUGC( Cleavage	pacid=371569
38	395	415 UGGAGAAGC/	CCAACGUGUC( Cleavage	pacid=371597
39	349	369 UGGAGAAGC/	CUCGCGUGCC( Cleavage	pacid=371564
40	398	418 UGGAGAAGC/	CCAACGUGC( Cleavage	pacid=371609
41	2339	2359 UGGAGAAGC/	AACACGUGCC( Cleavage	pacid=371543
42	512	532 UGGAGAAGC/	GCCACGUGC( Cleavage	pacid=371586
43	749	769 UGGAGAAGC/	CACAUGUGU( Cleavage	pacid=371470
44	134	154 UGGAGAAGC/	GGUGCAUUC( Cleavage	pacid=371704
45	6862	6882 UGGAGAAGC/	UCAGCAUGU( Cleavage	pacid=371594
46	1550	1570 UGGAGAAGC/	CUCACUUGCC( Cleavage	pacid=371472
47	1368	1388 UGGAGAAGC/	ACCACUUGUC( Cleavage	pacid=371488
48	609	629 UGGAGAAGC/	GUCACGUUU( Translation	pacid=371524
49	904	924 UGGAGAAGC/	ACUAUGUUU( Cleavage	pacid=371508
50	335	355 UGGAGAAGC/	CCCACGUCCU( Cleavage	pacid=371552
51	3330	3350 UGGAGAAGC/	UCUACAUUC( Cleavage	pacid=371560
52	1540	1560 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
53	1459	1479 UGGAGAAGC/	UGCAGCUGC( Cleavage	pacid=371672
54	3334	3354 UGGAGAAGC/	UUA AUGUGC( Cleavage	pacid=371569
55	395	415 UGGAGAAGC/	CCAACGUGUC( Cleavage	pacid=371597
56	349	369 UGGAGAAGC/	CUCGCGUGCC( Cleavage	pacid=371564
57	398	418 UGGAGAAGC/	CCAACGUGC( Cleavage	pacid=371609
58	2339	2359 UGGAGAAGC/	AACACGUGCC( Cleavage	pacid=371543
59	512	532 UGGAGAAGC/	GCCACGUGC( Cleavage	pacid=371586
60	749	769 UGGAGAAGC/	CACAUGUGU( Cleavage	pacid=371470
61	134	154 UGGAGAAGC/	GGUGCAUUC( Cleavage	pacid=371704
62	6862	6882 UGGAGAAGC/	UCAGCAUGU( Cleavage	pacid=371594
63	1550	1570 UGGAGAAGC/	CUCACUUGCC( Cleavage	pacid=371472
64	1368	1388 UGGAGAAGC/	ACCACUUGUC( Cleavage	pacid=371488

1				
2	609	629 UGGAGAAGC/	::: : : ::::: GUCACGUUU(Translation	pacid=371524
3	904	924 UGGAGAAGC/	::: : : ::::: ACUAUGUUU Cleavage	pacid=371508
4	335	355 UGGAGAAGC/	::: : : ::::: CCCACGUCCU Cleavage	pacid=371552
5				
6	3330	3350 UGGAGAAGC/	::: : : ::::: UCUACAUUC Cleavage	pacid=371560
7	1539	1560 UGGAGAAGC/	::: : : ::::: CUGCAGCUG Cleavage	pacid=371672
8	1458	1479 UGGAGAAGC/	::: : : ::::: CUGCAGCUG Cleavage	pacid=371672
9				
10	3333	3354 UGGAGAAGC/	::: : : ::::: GUUAAUGUG Cleavage	pacid=371569
11	3329	3350 UGGAGAAGC/	::: : : ::::: UUCUACAUU Cleavage	pacid=371560
12	394	415 UGGAGAAGC/	::: : : ::::: UCCAACGUG Cleavage	pacid=371597
13				
14	348	369 UGGAGAAGC/	::: : : ::::: UCUCGCGUG Cleavage	pacid=371564
15	397	418 UGGAGAAGC/	::: : : ::::: UCCAACGUG Cleavage	pacid=371609
16	2338	2359 UGGAGAAGC/	::: : : ::::: GAACACGUG Cleavage	pacid=371543
17				
18	440	461 UGGAGAAGC/	::: : : ::::: UUCCCUAUG Cleavage	pacid=371782
19	412	433 UGGAGAAGC/	::: : : ::::: UUCCCUUUG Cleavage	pacid=371745
20	354	375 UGGAGAAGC/	::: : : ::::: UUCCCUUUG Cleavage	pacid=371745
21				
22	511	532 UGGAGAAGC/	::: : : ::::: AGCCACGUG Cleavage	pacid=371586
23	748	769 UGGAGAAGC/	::: : : ::::: CCACAUGUG Cleavage	pacid=371470
24	133	154 UGGAGAAGC/	::: : : ::::: GGGUGCAUU Cleavage	pacid=371704
25				
26	6861	6882 UGGAGAAGC/	::: : : ::::: AUCAGCAUG Cleavage	pacid=371594
27	1549	1570 UGGAGAAGC/	::: : : ::::: ACUCACUUG Cleavage	pacid=371472
28	1367	1388 UGGAGAAGC/	::: : : ::::: UACCACUUG Cleavage	pacid=371488
29				
30	21	41 UGGAGAAGC/	::: : : ::::: UGCACUUCU Cleavage	pacid=371620
31	1501	1521 UGGAGAAGC/	::: : : ::::: GGCAUGUGG Cleavage	pacid=371757
32	432	452 UGGAGAAGC/	::: : : ::::: GGUGCGUGC Translation	pacid=371502
33				
34	1178	1198 UGGAGAAGC/	::: : : ::::: CGUACGUGG Cleavage	pacid=371566
35	406	426 UGGAGAAGC/	::: : : ::::: GGUGUGUGC Cleavage	pacid=371737
36	525	545 UGGAGAAGC/	::: : : ::::: UGCACCUUCC Cleavage	pacid=371721
37				
38	1996	2015 UGGAGAAGC/	::: : : ::::: UGCAUG-GUC Cleavage	pacid=371696
39	898	918 UGGAGAAGC/	::: : : ::::: AGCAAGUGC Cleavage	pacid=371646
40	129	149 UGGAGAAGC/	::: : : ::::: GAGAUGUGU Cleavage	pacid=371632
41	129	149 UGGAGAAGC/	::: : : ::::: GAGAUGUGU Cleavage	pacid=371632
42				
43	431	451 UGGAGAAGC/	::: : : ::::: AGCAUGGGU Cleavage	pacid=371640
44	322	342 UGGAGAAGC/	::: : : ::::: AGCAUGGGU Cleavage	pacid=371664
45	1774	1794 UGGAGAAGC/	::: : : ::::: UUCACGUGU Cleavage	pacid=371661
46				
47	1651	1671 UGGAGAAGC/	::: : : ::::: AGCAUGGGU Cleavage	pacid=371610
48	1516	1536 UGGAGAAGC/	::: : : ::::: UUUUCGUGU Cleavage	pacid=371543
49	66	86 UGGAGAAGC/	::: : : ::::: GAGAUGUGC Cleavage	pacid=371692
50				
51	2150	2170 UGGAGAAGC/	::: : : ::::: AAAAUGUGC Cleavage	pacid=371627
52	2011	2031 UGGAGAAGC/	::: : : ::::: AAAAUGUGC Cleavage	pacid=371627
53	1437	1457 UGGAGAAGC/	::: : : ::::: CUCACGUGCC Cleavage	pacid=371647
54				
55	96	116 UGGAGAAGC/	::: : : ::::: GUUGUGUGC Cleavage	pacid=371508
56	1414	1434 UGGAGAAGC/	::: : : ::::: UUUUAUGUGC Cleavage	pacid=371727
57	1417	1437 UGGAGAAGC/	::: : : ::::: UUUUAUGUGC Cleavage	pacid=371727
58				
59	391	411 UGGAGAAGC/	::: : : ::::: CAUGCGUGG Cleavage	pacid=371424
60	391	411 UGGAGAAGC/	::: : : ::::: CAUGCGUGG Cleavage	pacid=371424
	238	258 UGGAGAAGC/	::: : : ::::: UUCAUGUGU Cleavage	pacid=371581





1				
2	1651	1671 UGGAGAAGC/	::: : ..:::..... AGCAUGGGUICleavage	pacid=371610
3	1516	1536 UGGAGAAGC/	::: : ..:::..... UUUUCGUGU Cleavage	pacid=371543
4	66	86 UGGAGAAGC/	::: : ..:::..... GAGAUGUGC(Cleavage	pacid=371692
5	2150	2170 UGGAGAAGC/	::: : ..:::..... : AAAAUGUGC(Cleavage	pacid=371627
6	2011	2031 UGGAGAAGC/	::: : ..:::..... : AAAAUGUGC(Cleavage	pacid=371627
7	1437	1457 UGGAGAAGC/	::: : ..:::..... : CUCACGUGCC Cleavage	pacid=371647
8	96	116 UGGAGAAGC/	::: : ..:::..... GUUGUGUGC Cleavage	pacid=371508
9	1414	1434 UGGAGAAGC/	::: : ..:::..... UUUUAUGUGC Cleavage	pacid=371727
10	1417	1437 UGGAGAAGC/	::: : ..:::..... UUUUAUGUGC Cleavage	pacid=371727
11	391	411 UGGAGAAGC/	::: : ..:::..... CAUGCGUGG(Cleavage	pacid=371424
12	391	411 UGGAGAAGC/	::: : ..:::..... CAUGCGUGG(Cleavage	pacid=371424
13	238	258 UGGAGAAGC/	::: : ..:::..... : UUCAUGUGU Cleavage	pacid=371581
14	360	380 UGGAGAAGC/	::: : ..:::..... : AUCAUGUGC(Translation	pacid=371680
15	112	132 UGGAGAAGC/	::: : ..:::..... UUGACGUAU(Cleavage	pacid=371766
16	1338	1358 UGGAGAAGC/	::: : ..:::..... : AGGACAUGCC Cleavage	pacid=371602
17	622	642 UGGAGAAGC/	::: : ..:::..... : UUCUUGUGC(Cleavage	pacid=371502
18	21	41 UGGAGAAGC/	::: : ..:::..... UGCACUUCU(Cleavage	pacid=371620
19	1501	1521 UGGAGAAGC/	::: : ..:::..... : GGCAUGUGG(Cleavage	pacid=371757
20	432	452 UGGAGAAGC/	::: : ..:::..... GGUGCGUGC(Translation	pacid=371502
21	1178	1198 UGGAGAAGC/	::: : ..:::..... CGUACGUGG(Cleavage	pacid=371566
22	406	426 UGGAGAAGC/	::: : ..:::..... : GGUGUGUGC Cleavage	pacid=371737
23	525	545 UGGAGAAGC/	::: : ..:::..... UGCACCUUCC Cleavage	pacid=371721
24	1996	2015 UGGAGAAGC/	::: : ..:::..... : UGCAUG-GUC Cleavage	pacid=371696
25	898	918 UGGAGAAGC/	::: : ..:::..... AGCAAGUGCC Cleavage	pacid=371646
26	129	149 UGGAGAAGC/	::: : ..:::..... GAGAUGUGU Cleavage	pacid=371632
27	129	149 UGGAGAAGC/	::: : ..:::..... GAGAUGUGU Cleavage	pacid=371632
28	431	451 UGGAGAAGC/	::: : ..:::..... AGCAUGGGU(Cleavage	pacid=371640
29	322	342 UGGAGAAGC/	::: : ..:::..... AGCAUGGGU(Cleavage	pacid=371664
30	1774	1794 UGGAGAAGC/	::: : ..:::..... UUCACGUGUICleavage	pacid=371661
31	1651	1671 UGGAGAAGC/	::: : ..:::..... AGCAUGGGUICleavage	pacid=371610
32	1516	1536 UGGAGAAGC/	::: : ..:::..... UUUUCGUGU Cleavage	pacid=371543
33	66	86 UGGAGAAGC/	::: : ..:::..... GAGAUGUGC(Cleavage	pacid=371692
34	2150	2170 UGGAGAAGC/	::: : ..:::..... : AAAAUGUGC(Cleavage	pacid=371627
35	2011	2031 UGGAGAAGC/	::: : ..:::..... : AAAAUGUGC(Cleavage	pacid=371627
36	1437	1457 UGGAGAAGC/	::: : ..:::..... : CUCACGUGCC Cleavage	pacid=371647
37	96	116 UGGAGAAGC/	::: : ..:::..... GUUGUGUGC Cleavage	pacid=371508
38	1414	1434 UGGAGAAGC/	::: : ..:::..... UUUUAUGUGC Cleavage	pacid=371727
39	1417	1437 UGGAGAAGC/	::: : ..:::..... UUUUAUGUGC Cleavage	pacid=371727
40	391	411 UGGAGAAGC/	::: : ..:::..... CAUGCGUGG(Cleavage	pacid=371424
41	391	411 UGGAGAAGC/	::: : ..:::..... CAUGCGUGG(Cleavage	pacid=371424
42	238	258 UGGAGAAGC/	::: : ..:::..... : UUCAUGUGU Cleavage	pacid=371581
43	360	380 UGGAGAAGC/	::: : ..:::..... : AUCAUGUGC(Translation	pacid=371680
44	112	132 UGGAGAAGC/	::: : ..:::..... UUGACGUAU(Cleavage	pacid=371766
45	1338	1358 UGGAGAAGC/	::: : ..:::..... : AGGACAUGCC Cleavage	pacid=371602
46	622	642 UGGAGAAGC/	::: : ..:::..... : UUCUUGUGC(Cleavage	pacid=371502
47	21	41 UGGAGAAGC/	::: : ..:::..... UGCACUUCU(Cleavage	pacid=371620

1				
2	1501	1521 UGGAGAAGC/	::: :: GGCAUGUGG(Cleavage	pacid=371757
3	432	452 UGGAGAAGC/	::: :: GGUGCGUGC(Translation	pacid=371502
4	1178	1198 UGGAGAAGC/	::: :: CGUACGUGG(Cleavage	pacid=371566
5				
6	406	426 UGGAGAAGC/	::: :: GGUGUGUGC Cleavage	pacid=371737
7	525	545 UGGAGAAGC/	::: :: UGCACCUUCC Cleavage	pacid=371721
8				
9	1996	2015 UGGAGAAGC/	::: :: UGCAUG-GUC Cleavage	pacid=371696
10	898	918 UGGAGAAGC/	::: :: AGCAAGUGCC Cleavage	pacid=371646
11	129	149 UGGAGAAGC/	::: :: GAGAUGUGU Cleavage	pacid=371632
12	129	149 UGGAGAAGC/	::: :: GAGAUGUGU Cleavage	pacid=371632
13				
14	431	451 UGGAGAAGC/	::: :: AGCAUGGGU(Cleavage	pacid=371640
15	322	342 UGGAGAAGC/	::: :: AGCAUGGGU(Cleavage	pacid=371664
16	1774	1794 UGGAGAAGC/	::: :: UUCACGUGU(Cleavage	pacid=371661
17				
18	1651	1671 UGGAGAAGC/	::: :: AGCAUGGGU(Cleavage	pacid=371610
19	1516	1536 UGGAGAAGC/	::: :: UUUUCGUGU Cleavage	pacid=371543
20	66	86 UGGAGAAGC/	::: :: GAGAUGUGC(Cleavage	pacid=371692
21				
22	2150	2170 UGGAGAAGC/	::: :: AAAAUGUGC(Cleavage	pacid=371627
23	2011	2031 UGGAGAAGC/	::: :: AAAAUGUGC(Cleavage	pacid=371627
24	1437	1457 UGGAGAAGC/	::: :: CUCACGUGCC Cleavage	pacid=371647
25				
26	96	116 UGGAGAAGC/	::: :: GUUGUGUGC Cleavage	pacid=371508
27	1414	1434 UGGAGAAGC/	::: :: UUUUUGUGC Cleavage	pacid=371727
28	1417	1437 UGGAGAAGC/	::: :: UUUUUGUGC Cleavage	pacid=371727
29				
30	391	411 UGGAGAAGC/	::: :: CAUGCGUGG(Cleavage	pacid=371424
31	391	411 UGGAGAAGC/	::: :: CAUGCGUGG(Cleavage	pacid=371424
32	238	258 UGGAGAAGC/	::: :: UUCAUGUGU Cleavage	pacid=371581
33				
34	360	380 UGGAGAAGC/	::: :: AUCAUGUGC(Translation	pacid=371680
35	112	132 UGGAGAAGC/	::: :: UUGACGUAU(Cleavage	pacid=371766
36	1338	1358 UGGAGAAGC/	::: :: AGGACAUGCC Cleavage	pacid=371602
37	622	642 UGGAGAAGC/	::: :: UUCUUGUGC(Cleavage	pacid=371502
38				
39	21	41 UGGAGAAGC/	::: :: UGCACUUCU(Cleavage	pacid=371620
40	1501	1521 UGGAGAAGC/	::: :: GGCAUGUGG(Cleavage	pacid=371757
41	432	452 UGGAGAAGC/	::: :: GGUGCGUGC(Translation	pacid=371502
42	1178	1198 UGGAGAAGC/	::: :: CGUACGUGG(Cleavage	pacid=371566
43				
44	406	426 UGGAGAAGC/	::: :: GGUGUGUGC Cleavage	pacid=371737
45	525	545 UGGAGAAGC/	::: :: UGCACCUUCC Cleavage	pacid=371721
46				
47	1996	2015 UGGAGAAGC/	::: :: UGCAUG-GUC Cleavage	pacid=371696
48	898	918 UGGAGAAGC/	::: :: AGCAAGUGCC Cleavage	pacid=371646
49	129	149 UGGAGAAGC/	::: :: GAGAUGUGU Cleavage	pacid=371632
50	129	149 UGGAGAAGC/	::: :: GAGAUGUGU Cleavage	pacid=371632
51	431	451 UGGAGAAGC/	::: :: AGCAUGGGU(Cleavage	pacid=371640
52	322	342 UGGAGAAGC/	::: :: AGCAUGGGU(Cleavage	pacid=371664
53	1774	1794 UGGAGAAGC/	::: :: UUCACGUGU(Cleavage	pacid=371661
54				
55	1651	1671 UGGAGAAGC/	::: :: AGCAUGGGU(Cleavage	pacid=371610
56	1516	1536 UGGAGAAGC/	::: :: UUUUCGUGU Cleavage	pacid=371543
57	66	86 UGGAGAAGC/	::: :: GAGAUGUGC(Cleavage	pacid=371692
58				
59	2150	2170 UGGAGAAGC/	::: :: AAAAUGUGC(Cleavage	pacid=371627
60	2011	2031 UGGAGAAGC/	::: :: AAAAUGUGC(Cleavage	pacid=371627



1				
2	1437	1457 UGGAGAAGC/	:::~::~: :: CUCACGUGCC Cleavage	pacid=371647
3	96	116 UGGAGAAGC/	.....: GUUGUGUGC Cleavage	pacid=371508
4	1414	1434 UGGAGAAGC/	:.....: UUU AUGUGC Cleavage	pacid=371727
5	1417	1437 UGGAGAAGC/	:.....: UUU AUGUGC Cleavage	pacid=371727
6	391	411 UGGAGAAGC/	.....: CAUGCUGG(Cleavage	pacid=371424
7	391	411 UGGAGAAGC/	.....: CAUGCUGG(Cleavage	pacid=371424
8	238	258 UGGAGAAGC/	:.....: UUCAUGUGU Cleavage	pacid=371581
9	360	380 UGGAGAAGC/	:.....: AUCAUGUGC(Translation	pacid=371680
10	112	132 UGGAGAAGC/	:.....: UUGACGUAU(Cleavage	pacid=371766
11	1338	1358 UGGAGAAGC/	:.....: AGGACAUGCC Cleavage	pacid=371602
12	622	642 UGGAGAAGC/	:.....: UUCUUGUGC(Cleavage	pacid=371502
13	21	41 UGGAGAAGC/	:.....: UGCACUUCU(Cleavage	pacid=371620
14	1501	1521 UGGAGAAGC/	:.....: GGCAUGUGG(Cleavage	pacid=371757
15	432	452 UGGAGAAGC/	.....: GGUGCGUGC(Translation	pacid=371502
16	1178	1198 UGGAGAAGC/	:.....: CGUACGUGG(Cleavage	pacid=371566
17	406	426 UGGAGAAGC/	:.....: GGUGUGUGC Cleavage	pacid=371737
18	525	545 UGGAGAAGC/	:.....: UGCACCUUCC Cleavage	pacid=371721
19	1996	2015 UGGAGAAGC/	:.....: UGCAUG-GUC Cleavage	pacid=371696
20	898	918 UGGAGAAGC/	:.....: AGCAAGUGCC Cleavage	pacid=371646
21	129	149 UGGAGAAGC/	:.....: GAGAUGUGU Cleavage	pacid=371632
22	129	149 UGGAGAAGC/	:.....: GAGAUGUGU Cleavage	pacid=371632
23	431	451 UGGAGAAGC/	:.....: AGCAUGGGU(Cleavage	pacid=371640
24	322	342 UGGAGAAGC/	:.....: AGCAUGGGU(Cleavage	pacid=371664
25	1774	1794 UGGAGAAGC/	:.....: UUCACGUGU(Cleavage	pacid=371661
26	1651	1671 UGGAGAAGC/	:.....: AGCAUGGGU(Cleavage	pacid=371610
27	1516	1536 UGGAGAAGC/	:.....: UUUUCGUGU Cleavage	pacid=371543
28	66	86 UGGAGAAGC/	:.....: GAGAUGUGC(Cleavage	pacid=371692
29	2150	2170 UGGAGAAGC/	:.....: AAAAUGUGC(Cleavage	pacid=371627
30	2011	2031 UGGAGAAGC/	:.....: AAAAUGUGC(Cleavage	pacid=371627
31	1437	1457 UGGAGAAGC/	:::~::~: :: CUCACGUGCC Cleavage	pacid=371647
32	96	116 UGGAGAAGC/	.....: GUUGUGUGC Cleavage	pacid=371508
33	1414	1434 UGGAGAAGC/	:.....: UUU AUGUGC Cleavage	pacid=371727
34	1417	1437 UGGAGAAGC/	:.....: UUU AUGUGC Cleavage	pacid=371727
35	391	411 UGGAGAAGC/	.....: CAUGCUGG(Cleavage	pacid=371424
36	391	411 UGGAGAAGC/	.....: CAUGCUGG(Cleavage	pacid=371424
37	238	258 UGGAGAAGC/	:.....: UUCAUGUGU Cleavage	pacid=371581
38	360	380 UGGAGAAGC/	:.....: AUCAUGUGC(Translation	pacid=371680
39	112	132 UGGAGAAGC/	:.....: UUGACGUAU(Cleavage	pacid=371766
40	1338	1358 UGGAGAAGC/	:.....: AGGACAUGCC Cleavage	pacid=371602
41	622	642 UGGAGAAGC/	:.....: UUCUUGUGC(Cleavage	pacid=371502
42	21	41 UGGAGAAGC/	:.....: UGCACUUCU(Cleavage	pacid=371620
43	1501	1521 UGGAGAAGC/	:.....: GGCAUGUGG(Cleavage	pacid=371757
44	432	452 UGGAGAAGC/	.....: GGUGCGUGC(Translation	pacid=371502
45	1178	1198 UGGAGAAGC/	:.....: CGUACGUGG(Cleavage	pacid=371566
46	406	426 UGGAGAAGC/	:.....: GGUGUGUGC Cleavage	pacid=371737
47	525	545 UGGAGAAGC/	:.....: UGCACCUUCC Cleavage	pacid=371721
48				
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1				
2	1996	2015 UGGAGAAGC/	UGCAUG-GUC Cleavage	pacid=371696
3	898	918 UGGAGAAGC/	AGCAAGUGCC Cleavage	pacid=371646
4	129	149 UGGAGAAGC/	GAGAUUGUGU Cleavage	pacid=371632
5	129	149 UGGAGAAGC/	GAGAUUGUGU Cleavage	pacid=371632
6	431	451 UGGAGAAGC/	AGCAUGGGU(Cleavage	pacid=371640
7	322	342 UGGAGAAGC/	AGCAUGGGU(Cleavage	pacid=371664
8				
9	1774	1794 UGGAGAAGC/	UUCACGUGUI Cleavage	pacid=371661
10	1651	1671 UGGAGAAGC/	AGCAUGGGU(Cleavage	pacid=371610
11	1516	1536 UGGAGAAGC/	UUUUCGUGU Cleavage	pacid=371543
12				
13	66	86 UGGAGAAGC/	GAGAUUGUC(Cleavage	pacid=371692
14	2150	2170 UGGAGAAGC/	AAAAUGUGCC Cleavage	pacid=371627
15	2011	2031 UGGAGAAGC/	AAAAUGUGCC Cleavage	pacid=371627
16	1437	1457 UGGAGAAGC/	CUCACGUGCC Cleavage	pacid=371647
17	96	116 UGGAGAAGC/	GUUGUGUGC Cleavage	pacid=371508
18	1414	1434 UGGAGAAGC/	UUUAUGUGC Cleavage	pacid=371727
19	1417	1437 UGGAGAAGC/	UUUAUGUGC Cleavage	pacid=371727
20	391	411 UGGAGAAGC/	CAUGCUGGC(Cleavage	pacid=371424
21	391	411 UGGAGAAGC/	CAUGCUGGC(Cleavage	pacid=371424
22	238	258 UGGAGAAGC/	UUCAUGUGU Cleavage	pacid=371581
23	360	380 UGGAGAAGC/	AUCAUGUGCC(Translation	pacid=371680
24	112	132 UGGAGAAGC/	UUGACGUAU(Cleavage	pacid=371766
25	1338	1358 UGGAGAAGC/	AGGACAUGCC Cleavage	pacid=371602
26	622	642 UGGAGAAGC/	UUCUUGUGC(Cleavage	pacid=371502
27	21	41 UGGAGAAGC/	UGCACUUCU(Cleavage	pacid=371620
28	1501	1521 UGGAGAAGC/	GGCAUGUGGC Cleavage	pacid=371757
29	432	452 UGGAGAAGC/	GGUGCGUGC(Translation	pacid=371502
30	1178	1198 UGGAGAAGC/	CGUACGUGGC(Cleavage	pacid=371566
31	406	426 UGGAGAAGC/	GGUGUGUGC Cleavage	pacid=371737
32	525	545 UGGAGAAGC/	UGCACCUUCC Cleavage	pacid=371721
33	1996	2015 UGGAGAAGC/	UGCAUG-GUC Cleavage	pacid=371696
34	898	918 UGGAGAAGC/	AGCAAGUGCC Cleavage	pacid=371646
35	129	149 UGGAGAAGC/	GAGAUUGUGU Cleavage	pacid=371632
36	129	149 UGGAGAAGC/	GAGAUUGUGU Cleavage	pacid=371632
37	431	451 UGGAGAAGC/	AGCAUGGGU(Cleavage	pacid=371640
38	322	342 UGGAGAAGC/	AGCAUGGGU(Cleavage	pacid=371664
39	1774	1794 UGGAGAAGC/	UUCACGUGUI Cleavage	pacid=371661
40	1651	1671 UGGAGAAGC/	AGCAUGGGU(Cleavage	pacid=371610
41	1516	1536 UGGAGAAGC/	UUUUCGUGU Cleavage	pacid=371543
42	66	86 UGGAGAAGC/	GAGAUUGUC(Cleavage	pacid=371692
43	2150	2170 UGGAGAAGC/	AAAAUGUGCC Cleavage	pacid=371627
44	2011	2031 UGGAGAAGC/	AAAAUGUGCC Cleavage	pacid=371627
45	1437	1457 UGGAGAAGC/	CUCACGUGCC Cleavage	pacid=371647
46	96	116 UGGAGAAGC/	GUUGUGUGC Cleavage	pacid=371508
47	1414	1434 UGGAGAAGC/	UUUAUGUGC Cleavage	pacid=371727
48	1417	1437 UGGAGAAGC/	UUUAUGUGC Cleavage	pacid=371727
49	391	411 UGGAGAAGC/	CAUGCUGGC(Cleavage	pacid=371424
50				
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2	391	411 UGGAGAAGC/	.....: CAUGCUGUGG(Cleavage	pacid=371424
3	238	258 UGGAGAAGC/	.....: UUCAUGUGU Cleavage	pacid=371581
4	360	380 UGGAGAAGC/	.....: AUCAUGUGC(Translation	pacid=371680
5	112	132 UGGAGAAGC/	.....: UUGACGUAI(Cleavage	pacid=371766
6	1338	1358 UGGAGAAGC/	.....: AGGACAUGCC(Cleavage	pacid=371602
7	622	642 UGGAGAAGC/	.....: UUCUUGUGC(Cleavage	pacid=371502
8	21	41 UGGAGAAGC/	.....: UGCACUUCU(Cleavage	pacid=371620
9	1501	1521 UGGAGAAGC/	.....: GGCAUGUGG(Cleavage	pacid=371757
10	432	452 UGGAGAAGC/	.....: GGUGCGUGC(Translation	pacid=371502
11	1178	1198 UGGAGAAGC/	.....: CGUACGUGG(Cleavage	pacid=371566
12	406	426 UGGAGAAGC/	.....: GGUGUGUGC Cleavage	pacid=371737
13	525	545 UGGAGAAGC/	.....: UGCACCUUCC Cleavage	pacid=371721
14	1996	2015 UGGAGAAGC/	.....: UGCAUG-GUC Cleavage	pacid=371696
15	898	918 UGGAGAAGC/	.....: AGCAAGUGCC(Cleavage	pacid=371646
16	129	149 UGGAGAAGC/	.....: GAGAUGUGU Cleavage	pacid=371632
17	129	149 UGGAGAAGC/	.....: GAGAUGUGU Cleavage	pacid=371632
18	431	451 UGGAGAAGC/	.....: AGCAUGGGU(Cleavage	pacid=371640
19	322	342 UGGAGAAGC/	.....: AGCAUGGGU(Cleavage	pacid=371664
20	1774	1794 UGGAGAAGC/	.....: UUCACGUGU(Cleavage	pacid=371661
21	1651	1671 UGGAGAAGC/	.....: AGCAUGGGU(Cleavage	pacid=371610
22	1516	1536 UGGAGAAGC/	.....: UUUUCGUGU Cleavage	pacid=371543
23	66	86 UGGAGAAGC/	.....: GAGAUGUGC(Cleavage	pacid=371692
24	2150	2170 UGGAGAAGC/	.....: AAAAUGUGC(Cleavage	pacid=371627
25	2011	2031 UGGAGAAGC/	.....: AAAAUGUGC(Cleavage	pacid=371627
26	1437	1457 UGGAGAAGC/	.....: CUCACGUGCC Cleavage	pacid=371647
27	96	116 UGGAGAAGC/	.....: GUUGUGUGC Cleavage	pacid=371508
28	1414	1434 UGGAGAAGC/	.....: UUUUUGUGC Cleavage	pacid=371727
29	1417	1437 UGGAGAAGC/	.....: UUUUUGUGC Cleavage	pacid=371727
30	391	411 UGGAGAAGC/	.....: CAUGCUGUGG(Cleavage	pacid=371424
31	391	411 UGGAGAAGC/	.....: CAUGCUGUGG(Cleavage	pacid=371424
32	238	258 UGGAGAAGC/	.....: UUCAUGUGU Cleavage	pacid=371581
33	360	380 UGGAGAAGC/	.....: AUCAUGUGC(Translation	pacid=371680
34	112	132 UGGAGAAGC/	.....: UUGACGUAI(Cleavage	pacid=371766
35	1338	1358 UGGAGAAGC/	.....: AGGACAUGCC(Cleavage	pacid=371602
36	622	642 UGGAGAAGC/	.....: UUCUUGUGC(Cleavage	pacid=371502
37	21	41 UGGAGAAGC/	.....: UGCACUUCU(Cleavage	pacid=371620
38	1501	1521 UGGAGAAGC/	.....: GGCAUGUGG(Cleavage	pacid=371757
39	432	452 UGGAGAAGC/	.....: GGUGCGUGC(Translation	pacid=371502
40	1178	1198 UGGAGAAGC/	.....: CGUACGUGG(Cleavage	pacid=371566
41	406	426 UGGAGAAGC/	.....: GGUGUGUGC Cleavage	pacid=371737
42	525	545 UGGAGAAGC/	.....: UGCACCUUCC Cleavage	pacid=371721
43	1996	2015 UGGAGAAGC/	.....: UGCAUG-GUC Cleavage	pacid=371696
44	898	918 UGGAGAAGC/	.....: AGCAAGUGCC(Cleavage	pacid=371646
45	129	149 UGGAGAAGC/	.....: GAGAUGUGU Cleavage	pacid=371632
46	129	149 UGGAGAAGC/	.....: GAGAUGUGU Cleavage	pacid=371632
47	431	451 UGGAGAAGC/	.....: AGCAUGGGU(Cleavage	pacid=371640

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2	322	342 UGGAGAAGC/	::: : :::::..... AGCAUGGGU(Cleavage	pacid=371664
3	1774	1794 UGGAGAAGC/	: :::::.....: UUCACGUGU(Cleavage	pacid=371661
4	1651	1671 UGGAGAAGC/	::: : :::::..... AGCAUGGGU(Cleavage	pacid=371610
5	1516	1536 UGGAGAAGC/	: ::::: : ::::: UUUUCGUGU Cleavage	pacid=371543
6	66	86 UGGAGAAGC/	: ::::: : ::::: GAGAUGUGC(Cleavage	pacid=371692
7	2150	2170 UGGAGAAGC/	: :::::.....: AAAAUGUGC(Cleavage	pacid=371627
8	2011	2031 UGGAGAAGC/	: :::::.....: AAAAUGUGC(Cleavage	pacid=371627
9	1437	1457 UGGAGAAGC/	: :::::.....: CUCACGUGCC Cleavage	pacid=371647
10	96	116 UGGAGAAGC/	: :::::.....: GUUGUGUGC Cleavage	pacid=371508
11	1414	1434 UGGAGAAGC/	: :::::.....: UUAUGUGC Cleavage	pacid=371727
12	1417	1437 UGGAGAAGC/	: :::::.....: UUAUGUGC Cleavage	pacid=371727
13	391	411 UGGAGAAGC/	: ::::: : ::::: CAUGCGUGG(Cleavage	pacid=371424
14	391	411 UGGAGAAGC/	: ::::: : ::::: CAUGCGUGG(Cleavage	pacid=371424
15	238	258 UGGAGAAGC/	: :::::.....: UUCAUGUGU Cleavage	pacid=371581
16	360	380 UGGAGAAGC/	: ::::: : ::::: AUCAUGUGC(Translation	pacid=371680
17	112	132 UGGAGAAGC/	: ::: : ::::: UUGACGUAU(Cleavage	pacid=371766
18	1338	1358 UGGAGAAGC/	: : ::::: : ::::: AGGACAUGCC Cleavage	pacid=371602
19	622	642 UGGAGAAGC/	: : ::::: : ::::: UUCUUGUGC(Cleavage	pacid=371502
20	21	41 UGGAGAAGC/	: ::::: : ::::: UGCACUUCU(Cleavage	pacid=371620
21	1501	1521 UGGAGAAGC/	: ::::: : ::::: : GGCAUGUGG(Cleavage	pacid=371757
22	432	452 UGGAGAAGC/	: ::::: : ::::: : GGUGCGUGC(Translation	pacid=371502
23	1178	1198 UGGAGAAGC/	: ::::: : : ::::: CGUACGUGG(Cleavage	pacid=371566
24	406	426 UGGAGAAGC/	: :::::.....: GGUGUGUGC Cleavage	pacid=371737
25	525	545 UGGAGAAGC/	: ::::: : : ::::: UGCACCUUCC Cleavage	pacid=371721
26	1996	2015 UGGAGAAGC/	: ::::: : ::::: : UGCAUG-GUC Cleavage	pacid=371696
27	898	918 UGGAGAAGC/	: : :::::.....: AGCAAGUGC(Cleavage	pacid=371646
28	129	149 UGGAGAAGC/	: :::::.....: GAGAUGUGU Cleavage	pacid=371632
29	129	149 UGGAGAAGC/	: :::::.....: GAGAUGUGU Cleavage	pacid=371632
30	431	451 UGGAGAAGC/	: ::: : :::::..... AGCAUGGGU(Cleavage	pacid=371640
31	322	342 UGGAGAAGC/	: ::: : :::::..... AGCAUGGGU(Cleavage	pacid=371664
32	1774	1794 UGGAGAAGC/	: :::::.....: UUCACGUGU(Cleavage	pacid=371661
33	1651	1671 UGGAGAAGC/	: ::: : :::::..... AGCAUGGGU(Cleavage	pacid=371610
34	1516	1536 UGGAGAAGC/	: ::::: : ::::: UUUUCGUGU Cleavage	pacid=371543
35	66	86 UGGAGAAGC/	: ::::: : ::::: GAGAUGUGC(Cleavage	pacid=371692
36	2150	2170 UGGAGAAGC/	: :::::.....: AAAAUGUGC(Cleavage	pacid=371627
37	2011	2031 UGGAGAAGC/	: :::::.....: AAAAUGUGC(Cleavage	pacid=371627
38	1437	1457 UGGAGAAGC/	: :::::.....: CUCACGUGCC Cleavage	pacid=371647
39	96	116 UGGAGAAGC/	: :::::.....: GUUGUGUGC Cleavage	pacid=371508
40	1414	1434 UGGAGAAGC/	: :::::.....: UUAUGUGC Cleavage	pacid=371727
41	1417	1437 UGGAGAAGC/	: :::::.....: UUAUGUGC Cleavage	pacid=371727
42	391	411 UGGAGAAGC/	: ::::: : ::::: CAUGCGUGG(Cleavage	pacid=371424
43	391	411 UGGAGAAGC/	: ::::: : ::::: CAUGCGUGG(Cleavage	pacid=371424
44	238	258 UGGAGAAGC/	: :::::.....: UUCAUGUGU Cleavage	pacid=371581
45	360	380 UGGAGAAGC/	: ::::: : ::::: AUCAUGUGC(Translation	pacid=371680
46	112	132 UGGAGAAGC/	: ::: : ::::: UUGACGUAU(Cleavage	pacid=371766
47	1338	1358 UGGAGAAGC/	: : ::::: : ::::: AGGACAUGCC Cleavage	pacid=371602















1				
2	49	69 UGGAGAAGC/	::: ::::: ::::: GGUACAUGUICleavage	pacid=371422
3	3477	3497 UGGAGAAGC/	::: ::::: ::::: GGGCUGUGCICleavage	pacid=371724
4	372	392 UGGAGAAGC/	::: ::::: ::::: AGCGUUUGCICleavage	pacid=371721
5	304	324 UGGAGAAGC/	::: ::::: ::::: UCUCGUGCICleavage	pacid=371530
6	2017	2037 UGGAGAAGC/	::: ::::: ::::: GGCAUGUCUICleavage	pacid=371461
7	1749	1769 UGGAGAAGC/	::: ::::: ::::: GGCAUGUCUICleavage	pacid=371461
8	151	171 UGGAGAAGC/	::: ::::: ::::: GCCGCUUGCICleavage	pacid=371589
9	151	171 UGGAGAAGC/	::: ::::: ::::: GCCGCUUGCICleavage	pacid=371589
10	1700	1720 UGGAGAAGC/	::: ::::: ::::: GGCAUGUCUICleavage	pacid=371461
11	1369	1389 UGGAGAAGC/	::: ::::: ::::: CGCAUCUGCCCleavage	pacid=371646
12	775	795 UGGAGAAGC/	::: ::::: ::::: AGUUCGUGU Translation	pacid=371518
13	1011	1031 UGGAGAAGC/	::: ::::: ::::: AGUACGGGC/Cleavage	pacid=371742
14	879	899 UGGAGAAGC/	::: ::::: ::::: AGUACGGGC/Cleavage	pacid=371742
15	772	792 UGGAGAAGC/	::: ::::: ::::: AGUGCAUGCCCleavage	pacid=371577
16	526	546 UGGAGAAGC/	::: ::::: ::::: UGCAUGUGCICleavage	pacid=371422
17	220	240 UGGAGAAGC/	::: ::::: ::::: ACCACGUGCICleavage	pacid=371515
18	1359	1379 UGGAGAAGC/	::: ::::: ::::: UGCACUUGGICleavage	pacid=371586
19	1415	1435 UGGAGAAGC/	::: ::::: ::::: UGUUUGUGUCleavage	pacid=371487
20	1237	1257 UGGAGAAGC/	::: ::::: ::::: UGUUCGUGCITranslation	pacid=371708
21	1208	1228 UGGAGAAGC/	::: ::::: ::::: UGUUCGUGCITranslation	pacid=371708
22	238	257 UGGAGAAGC/	::: ::::: ::::: CGCACGUGCCCleavage	pacid=371484
23	182	202 UGGAGAAGC/	::: ::::: ::::: GGU AUGUGC.Cleavage	pacid=371500
24	210	230 UGGAGAAGC/	::: ::::: ::::: ... AGCACGUGCC Translation	pacid=371623
25	676	696 UGGAGAAGC/	::: ::::: ::::: UGCAGGGUICleavage	pacid=371516
26	1409	1429 UGGAGAAGC/	::: ::::: ::::: UGCUGGUGCICleavage	pacid=371770
27	480	500 UGGAGAAGC/	::: ::::: ::::: UGCAAGUUUICleavage	pacid=371764
28	876	896 UGGAGAAGC/	::: ::::: ::::: UGCAGUUGCITranslation	pacid=371754
29	1302	1321 UGGAGAAGC/	::: ::::: ::::: AGCAUGUGCCCleavage	pacid=371566
30	1139	1159 UGGAGAAGC/	::: ::::: ::::: UGCACUGGCCCleavage	pacid=371699
31	998	1018 UGGAGAAGC/	::: ::::: ::::: UGUAGGAGCICleavage	pacid=371749
32	564	584 UGGAGAAGC/	::: ::::: ::::: CGAACGUGCCCleavage	pacid=371759
33	564	584 UGGAGAAGC/	::: ::::: ::::: CGAACGUGCCCleavage	pacid=371759
34	78	97 UGGAGAAGC/	::: ::::: ::::: UGCAUGU-UCleavage	pacid=371675
35	49	69 UGGAGAAGC/	::: ::::: ::::: GGUACAUGUICleavage	pacid=371422
36	49	69 UGGAGAAGC/	::: ::::: ::::: GGUACAUGUICleavage	pacid=371422
37	3477	3497 UGGAGAAGC/	::: ::::: ::::: GGGCUGUGCICleavage	pacid=371724
38	372	392 UGGAGAAGC/	::: ::::: ::::: AGCGUUUGCICleavage	pacid=371721
39	304	324 UGGAGAAGC/	::: ::::: ::::: UCUCGUGCICleavage	pacid=371530
40	2017	2037 UGGAGAAGC/	::: ::::: ::::: GGCAUGUCUICleavage	pacid=371461
41	1749	1769 UGGAGAAGC/	::: ::::: ::::: GGCAUGUCUICleavage	pacid=371461
42	151	171 UGGAGAAGC/	::: ::::: ::::: GCCGCUUGCICleavage	pacid=371589
43	151	171 UGGAGAAGC/	::: ::::: ::::: GCCGCUUGCICleavage	pacid=371589
44	1700	1720 UGGAGAAGC/	::: ::::: ::::: GGCAUGUCUICleavage	pacid=371461
45	1369	1389 UGGAGAAGC/	::: ::::: ::::: CGCAUCUGCCCleavage	pacid=371646
46	775	795 UGGAGAAGC/	::: ::::: ::::: AGUUCGUGU Translation	pacid=371518
47	1011	1031 UGGAGAAGC/	::: ::::: ::::: AGUACGGGC/Cleavage	pacid=371742







1				
2	372	392 UGGAGAAGC/	... :..... :... AGCGUUUGC(Cleavage	pacid=371721
3	304	324 UGGAGAAGC/	..... :... UCUCGUGC(Cleavage	pacid=371530
4	2017	2037 UGGAGAAGC/	..... :... GGCAUGUCU(Cleavage	pacid=371461
5	1749	1769 UGGAGAAGC/	..... :... GGCAUGUCU(Cleavage	pacid=371461
6	151	171 UGGAGAAGC/	.. :..... :... GCCGCUUGC(Cleavage	pacid=371589
7	151	171 UGGAGAAGC/	.. :..... :... GCCGCUUGC(Cleavage	pacid=371589
8	1700	1720 UGGAGAAGC/	..... :... GGCAUGUCU(Cleavage	pacid=371461
9	1369	1389 UGGAGAAGC/	... :..... :... CGCAUCUGCC(Cleavage	pacid=371646
10	775	795 UGGAGAAGC/	. :..... :... AGUUCGUGU(Translation	pacid=371518
11	1011	1031 UGGAGAAGC/	..... :... AGUACGGGC(Cleavage	pacid=371742
12	879	899 UGGAGAAGC/	..... :... AGUACGGGC(Cleavage	pacid=371742
13	772	792 UGGAGAAGC/	... :..... :... AGUGCAUGC(Cleavage	pacid=371577
14	526	546 UGGAGAAGC/	..... :... UGCAUGUGC(Cleavage	pacid=371422
15	220	240 UGGAGAAGC/	..... :... ACCACGUGC(Cleavage	pacid=371515
16	1359	1379 UGGAGAAGC/	..... :... UGCACUUGG(Cleavage	pacid=371586
17	1415	1435 UGGAGAAGC/	... :..... :... UGUUUGUGU(Cleavage	pacid=371487
18	1237	1257 UGGAGAAGC/	... :..... :... UGUUCGUGC(Translation	pacid=371708
19	1208	1228 UGGAGAAGC/	... :..... :... UGUUCGUGC(Translation	pacid=371708
20	238	257 UGGAGAAGC/	..... :... CGCACGUGCC(Cleavage	pacid=371484
21	182	202 UGGAGAAGC/	..... :... GGU AUGUGC(Cleavage	pacid=371500
22	210	230 UGGAGAAGC/	..... :... AGCACGUGCC(Translation	pacid=371623
23	676	696 UGGAGAAGC/	... :..... :... UGCGAGGUG(Cleavage	pacid=371516
24	1409	1429 UGGAGAAGC/	..... :... UGCUGGUGC(Cleavage	pacid=371770
25	480	500 UGGAGAAGC/	..... :... UGCAAGUUU(Cleavage	pacid=371764
26	876	896 UGGAGAAGC/	..... :... UGCAGUUGC(Translation	pacid=371754
27	1302	1321 UGGAGAAGC/	..... :... AGCAUGUGC(Cleavage	pacid=371566
28	1139	1159 UGGAGAAGC/	..... :... UGCACUGGC(Cleavage	pacid=371699
29	998	1018 UGGAGAAGC/	..... :... UGUAGGAGC(Cleavage	pacid=371749
30	564	584 UGGAGAAGC/	..... :... CGAACGUGCC(Cleavage	pacid=371759
31	564	584 UGGAGAAGC/	..... :... CGAACGUGCC(Cleavage	pacid=371759
32	78	97 UGGAGAAGC/	..... :... UGCAUGU-UC(Cleavage	pacid=371675
33	49	69 UGGAGAAGC/	... :... :... GGUACAUGU(Cleavage	pacid=371422
34	49	69 UGGAGAAGC/	... :... :... GGUACAUGU(Cleavage	pacid=371422
35	3477	3497 UGGAGAAGC/	..... :... GGGCUGUGC(Cleavage	pacid=371724
36	372	392 UGGAGAAGC/	... :..... :... AGCGUUUGC(Cleavage	pacid=371721
37	304	324 UGGAGAAGC/	..... :... UCUCGUGC(Cleavage	pacid=371530
38	2017	2037 UGGAGAAGC/	..... :... GGCAUGUCU(Cleavage	pacid=371461
39	1749	1769 UGGAGAAGC/	..... :... GGCAUGUCU(Cleavage	pacid=371461
40	151	171 UGGAGAAGC/	.. :..... :... GCCGCUUGC(Cleavage	pacid=371589
41	151	171 UGGAGAAGC/	.. :..... :... GCCGCUUGC(Cleavage	pacid=371589
42	1700	1720 UGGAGAAGC/	..... :... GGCAUGUCU(Cleavage	pacid=371461
43	1369	1389 UGGAGAAGC/	... :..... :... CGCAUCUGCC(Cleavage	pacid=371646
44	775	795 UGGAGAAGC/	. :..... :... AGUUCGUGU(Translation	pacid=371518
45	1011	1031 UGGAGAAGC/	..... :... AGUACGGGC(Cleavage	pacid=371742
46	879	899 UGGAGAAGC/	..... :... AGUACGGGC(Cleavage	pacid=371742
47	772	792 UGGAGAAGC/	... :..... :... AGUGCAUGC(Cleavage	pacid=371577

1			
2	526	546 UGGAGAAGC/ ::::::::::: ::... UGCAUGUGC Cleavage	pacid=371422
3	220	240 UGGAGAAGC/ ::::::::::: ACCACGUGCL Cleavage	pacid=371515
4	1359	1379 UGGAGAAGC/ ::::: : : : ::::: UGCACUUGG Cleavage	pacid=371586
5	1415	1435 UGGAGAAGC/ :. : ::::::::::: UGUUUGUGU Cleavage	pacid=371487
6	1237	1257 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation	pacid=371708
7	1208	1228 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation	pacid=371708
8			
9	238	257 UGGAGAAGC/ ::::::::::: ::::: CGCACGUGCC Cleavage	pacid=371484
10	182	202 UGGAGAAGC/ : ::::: : : ::::: GGU AUGUGC. Cleavage	pacid=371500
11	210	230 UGGAGAAGC/ ::::::::::: ::::: ... AGCACGUGCC Translation	pacid=371623
12	676	696 UGGAGAAGC/ :. : : ::::::::::: UGCGAGGGU Cleavage	pacid=371516
13	1409	1429 UGGAGAAGC/ : : : ::::::::::: : UGCUGGUGC Cleavage	pacid=371770
14	480	500 UGGAGAAGC/ : : : : ::::: : : UGCAAGUUU Cleavage	pacid=371764
15	876	896 UGGAGAAGC/ : : : : ::::: : : UGCAGUUGC Translation	pacid=371754
16	1302	1321 UGGAGAAGC/ : ::::::::::: : : : AGCAUGUGC Cleavage	pacid=371566
17	1139	1159 UGGAGAAGC/ : : : : ::::: : : UGCACUGGCC Cleavage	pacid=371699
18	998	1018 UGGAGAAGC/ : : : : ::::::::::: UGUAGGAGC Cleavage	pacid=371749
19	564	584 UGGAGAAGC/ : ::::::::::: : CGAACGUGCC Cleavage	pacid=371759
20	564	584 UGGAGAAGC/ : ::::::::::: : CGAACGUGCC Cleavage	pacid=371759
21	78	97 UGGAGAAGC/ : : : : ::::: : : UGCAUGU-UC Cleavage	pacid=371675
22	49	69 UGGAGAAGC/ : : : : ::::: : : GGUACAUGU Cleavage	pacid=371422
23	49	69 UGGAGAAGC/ : : : : ::::: : : GGUACAUGU Cleavage	pacid=371422
24	3477	3497 UGGAGAAGC/ : ::::::::::: : : : GGCUGUGC Cleavage	pacid=371724
25	372	392 UGGAGAAGC/ :. : ::::::::::: : AGCGUUUGC Cleavage	pacid=371721
26	304	324 UGGAGAAGC/ : ::::::::::: : : UCUCGUGCL Cleavage	pacid=371530
27	2017	2037 UGGAGAAGC/ : : : : ::::: : : GGCAUGUCU Cleavage	pacid=371461
28	1749	1769 UGGAGAAGC/ : : : : ::::: : : GGCAUGUCU Cleavage	pacid=371461
29	151	171 UGGAGAAGC/ : : ::::::::::: : GCCGCUUGCL Cleavage	pacid=371589
30	151	171 UGGAGAAGC/ : : ::::::::::: : GCCGCUUGCL Cleavage	pacid=371589
31	1700	1720 UGGAGAAGC/ : : : : ::::: : : GGCAUGUCU Cleavage	pacid=371461
32	1369	1389 UGGAGAAGC/ :. : ::::::::::: : CGCAUCUGCC Cleavage	pacid=371646
33	775	795 UGGAGAAGC/ :. : ::::: : ::::: AGUUCGUGU Translation	pacid=371518
34	1011	1031 UGGAGAAGC/ : : : : ::::::::::: AGUACGGGC Cleavage	pacid=371742
35	879	899 UGGAGAAGC/ : : : : ::::::::::: AGUACGGGC Cleavage	pacid=371742
36	772	792 UGGAGAAGC/ :. : ::::::::::: : AGUGCAUGC Cleavage	pacid=371577
37	526	546 UGGAGAAGC/ ::::::::::: : :... UGCAUGUGC Cleavage	pacid=371422
38	220	240 UGGAGAAGC/ ::::::::::: : ACCACGUGCL Cleavage	pacid=371515
39	1359	1379 UGGAGAAGC/ ::::: : : : ::::: UGCACUUGG Cleavage	pacid=371586
40	1415	1435 UGGAGAAGC/ :. : ::::::::::: UGUUUGUGU Cleavage	pacid=371487
41	1237	1257 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation	pacid=371708
42	1208	1228 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation	pacid=371708
43			
44	238	257 UGGAGAAGC/ ::::::::::: : : : CGCACGUGCC Cleavage	pacid=371484
45	182	202 UGGAGAAGC/ : ::::: : : ::::: GGU AUGUGC. Cleavage	pacid=371500
46	210	230 UGGAGAAGC/ ::::::::::: : : ... AGCACGUGCC Translation	pacid=371623
47	676	696 UGGAGAAGC/ :. : : ::::::::::: UGCGAGGGU Cleavage	pacid=371516
48	1409	1429 UGGAGAAGC/ : : : ::::::::::: : UGCUGGUGC Cleavage	pacid=371770
49	480	500 UGGAGAAGC/ : : : : ::::: : : UGCAAGUUU Cleavage	pacid=371764
50			
51			
52			
53			
54			
55			
56			
57			
58			
59			
60			



1			
2	876	896 UGGAGAAGC/ :::: : :::: : :::: : UGCAGUUGCI Translation	pacid=371754
3	1302	1321 UGGAGAAGC/ :::: : :::: : :::: : AGCAUGUGC( Cleavage	pacid=371566
4	1139	1159 UGGAGAAGC/ :::: : :::: : :::: : UGCACUGGCC( Cleavage	pacid=371699
5			
6	998	1018 UGGAGAAGC/ :::: : :::: : :::: : UGUAGGAGCI Cleavage	pacid=371749
7	564	584 UGGAGAAGC/ : :::: : :::: : : CGAACGUGCC Cleavage	pacid=371759
8	564	584 UGGAGAAGC/ : :::: : :::: : : CGAACGUGCC Cleavage	pacid=371759
9			
10	78	97 UGGAGAAGC/ :::: : :::: : :::: : UGCAUGU-UC Cleavage	pacid=371675
11	49	69 UGGAGAAGC/ :::: : :::: : :::: : GGUACAUGUI Cleavage	pacid=371422
12	49	69 UGGAGAAGC/ :::: : :::: : :::: : GGUACAUGUI Cleavage	pacid=371422
13			
14	3477	3497 UGGAGAAGC/ :::: : :::: : :::: : GGGCUGUGC( Cleavage	pacid=371724
15	372	392 UGGAGAAGC/ :::: : :::: : :::: : AGCGUUUGC( Cleavage	pacid=371721
16	304	324 UGGAGAAGC/ :::: : :::: : :::: : UCUCGUGCL Cleavage	pacid=371530
17			
18	2017	2037 UGGAGAAGC/ :::: : :::: : :::: : GGCAUGUCU( Cleavage	pacid=371461
19	1749	1769 UGGAGAAGC/ :::: : :::: : :::: : GGCAUGUCU( Cleavage	pacid=371461
20	151	171 UGGAGAAGC/ :::: : :::: : :::: : GCCGCUUGCL Cleavage	pacid=371589
21	151	171 UGGAGAAGC/ :::: : :::: : :::: : GCCGCUUGCL Cleavage	pacid=371589
22			
23	1700	1720 UGGAGAAGC/ :::: : :::: : :::: : GGCAUGUCU( Cleavage	pacid=371461
24	1369	1389 UGGAGAAGC/ :::: : :::: : :::: : CGCAUCUGCC Cleavage	pacid=371646
25			
26	775	795 UGGAGAAGC/ : :::: : :::: : : AGUUCGUGU Translation	pacid=371518
27	1011	1031 UGGAGAAGC/ :::: : :::: : :::: : AGUACGGGC/ Cleavage	pacid=371742
28	879	899 UGGAGAAGC/ :::: : :::: : :::: : AGUACGGGC/ Cleavage	pacid=371742
29	772	792 UGGAGAAGC/ :::: : :::: : :::: : AGUGCAUGC( Cleavage	pacid=371577
30			
31	526	546 UGGAGAAGC/ :::: : :::: : :::: : UGCAUGUGCI Cleavage	pacid=371422
32	220	240 UGGAGAAGC/ :::: : :::: : :::: : ACCACGUGCL Cleavage	pacid=371515
33			
34	1359	1379 UGGAGAAGC/ :::: : :::: : :::: : UGCACUUGC( Cleavage	pacid=371586
35	1415	1435 UGGAGAAGC/ :::: : :::: : :::: : UGUUUGUGU Cleavage	pacid=371487
36	1237	1257 UGGAGAAGC/ :::: : :::: : :::: : UGUUCGUGCI Translation	pacid=371708
37			
38	1208	1228 UGGAGAAGC/ :::: : :::: : :::: : UGUUCGUGCI Translation	pacid=371708
39	238	257 UGGAGAAGC/ :::: : :::: : :::: : CGCACGUGCC Cleavage	pacid=371484
40	182	202 UGGAGAAGC/ :::: : :::: : :::: : GGUUAUGUGC. Cleavage	pacid=371500
41	210	230 UGGAGAAGC/ :::: : :::: : :::: : AGCACGUGCC Translation	pacid=371623
42			
43	676	696 UGGAGAAGC/ :::: : :::: : :::: : UGCGAGGGU( Cleavage	pacid=371516
44	1409	1429 UGGAGAAGC/ :::: : :::: : :::: : UGCUGGUGCI Cleavage	pacid=371770
45	480	500 UGGAGAAGC/ :::: : :::: : :::: : UGCAAGUUU( Cleavage	pacid=371764
46			
47	876	896 UGGAGAAGC/ :::: : :::: : :::: : UGCAGUUGCI Translation	pacid=371754
48	1302	1321 UGGAGAAGC/ :::: : :::: : :::: : AGCAUGUGC( Cleavage	pacid=371566
49	1139	1159 UGGAGAAGC/ :::: : :::: : :::: : UGCACUGGCC( Cleavage	pacid=371699
50			
51	998	1018 UGGAGAAGC/ :::: : :::: : :::: : UGUAGGAGCI Cleavage	pacid=371749
52	564	584 UGGAGAAGC/ : :::: : :::: : : CGAACGUGCC Cleavage	pacid=371759
53	564	584 UGGAGAAGC/ : :::: : :::: : : CGAACGUGCC Cleavage	pacid=371759
54			
55	78	97 UGGAGAAGC/ :::: : :::: : :::: : UGCAUGU-UC Cleavage	pacid=371675
56	49	69 UGGAGAAGC/ :::: : :::: : :::: : GGUACAUGUI Cleavage	pacid=371422
57	49	69 UGGAGAAGC/ :::: : :::: : :::: : GGUACAUGUI Cleavage	pacid=371422
58			
59	3477	3497 UGGAGAAGC/ :::: : :::: : :::: : GGGCUGUGC( Cleavage	pacid=371724
60	372	392 UGGAGAAGC/ :::: : :::: : :::: : AGCGUUUGC( Cleavage	pacid=371721
	304	324 UGGAGAAGC/ :::: : :::: : :::: : UCUCGUGCL Cleavage	pacid=371530

1				
2	2017	2037 UGGAGAAGC/	::: :: :: GGCAUGUCU(Cleavage	pacid=371461
3	1749	1769 UGGAGAAGC/	::: :: :: GGCAUGUCU(Cleavage	pacid=371461
4	151	171 UGGAGAAGC/	:: ::::: GCCGCUUGCL Cleavage	pacid=371589
5	151	171 UGGAGAAGC/	:: ::::: GCCGCUUGCL Cleavage	pacid=371589
6	1700	1720 UGGAGAAGC/	::: :: :: GGCAUGUCU(Cleavage	pacid=371461
7	1369	1389 UGGAGAAGC/	:: ::::: CGCAUCUGCC Cleavage	pacid=371646
8	775	795 UGGAGAAGC/	:: ::::: AGUUCGUGU Translation	pacid=371518
9	1011	1031 UGGAGAAGC/	::: :: ::::: AGUACGGGC/ Cleavage	pacid=371742
10	879	899 UGGAGAAGC/	::: :: ::::: AGUACGGGC/ Cleavage	pacid=371742
11	772	792 UGGAGAAGC/	::: ::::: AGUGCAUGC(Cleavage	pacid=371577
12	526	546 UGGAGAAGC/	::: ::::: UGCAUGUGC(Cleavage	pacid=371422
13	220	240 UGGAGAAGC/	::: ::::: ACCACGUGCL Cleavage	pacid=371515
14	1359	1379 UGGAGAAGC/	::: :: ::::: UGCACUUGG(Cleavage	pacid=371586
15	1415	1435 UGGAGAAGC/	::: ::::: UGUUUGUGU Cleavage	pacid=371487
16	1237	1257 UGGAGAAGC/	::: ::::: UGUUCGUGC(Translation	pacid=371708
17	1208	1228 UGGAGAAGC/	::: ::::: UGUUCGUGC(Translation	pacid=371708
18	238	257 UGGAGAAGC/	::: ::::: CGCACGUGCC Cleavage	pacid=371484
19	182	202 UGGAGAAGC/	::: ::::: GUAUGUGC Cleavage	pacid=371500
20	210	230 UGGAGAAGC/	::: ::::: AGCACGUGCC Translation	pacid=371623
21	676	696 UGGAGAAGC/	::: ::::: UGCGAGGGU(Cleavage	pacid=371516
22	1409	1429 UGGAGAAGC/	::: ::::: UGCUUGUGC(Cleavage	pacid=371770
23	480	500 UGGAGAAGC/	::: ::::: UGCAAGUUU(Cleavage	pacid=371764
24	876	896 UGGAGAAGC/	::: ::::: UGCAGUUGC(Translation	pacid=371754
25	1302	1321 UGGAGAAGC/	::: ::::: AGCAUGUGC(Cleavage	pacid=371566
26	1139	1159 UGGAGAAGC/	::: ::::: UGCACUGCC Cleavage	pacid=371699
27	998	1018 UGGAGAAGC/	::: ::::: UGUAGGAGC(Cleavage	pacid=371749
28	564	584 UGGAGAAGC/	::: ::::: CGAACGUGCC Cleavage	pacid=371759
29	564	584 UGGAGAAGC/	::: ::::: CGAACGUGCC Cleavage	pacid=371759
30	78	97 UGGAGAAGC/	::: ::::: UGCAUGU-UC Cleavage	pacid=371675
31	49	69 UGGAGAAGC/	::: ::::: GUAUGU(Cleavage	pacid=371422
32	49	69 UGGAGAAGC/	::: ::::: GUAUGU(Cleavage	pacid=371422
33	3477	3497 UGGAGAAGC/	::: ::::: GGCUGUGC(Cleavage	pacid=371724
34	372	392 UGGAGAAGC/	::: ::::: AGCGUUUGC(Cleavage	pacid=371721
35	304	324 UGGAGAAGC/	::: ::::: UCUCGUGCL Cleavage	pacid=371530
36	2017	2037 UGGAGAAGC/	::: :: :: GGCAUGUCU(Cleavage	pacid=371461
37	1749	1769 UGGAGAAGC/	::: :: :: GGCAUGUCU(Cleavage	pacid=371461
38	151	171 UGGAGAAGC/	:: ::::: GCCGCUUGCL Cleavage	pacid=371589
39	151	171 UGGAGAAGC/	:: ::::: GCCGCUUGCL Cleavage	pacid=371589
40	1700	1720 UGGAGAAGC/	::: :: :: GGCAUGUCU(Cleavage	pacid=371461
41	1369	1389 UGGAGAAGC/	:: ::::: CGCAUCUGCC Cleavage	pacid=371646
42	775	795 UGGAGAAGC/	:: ::::: AGUUCGUGU Translation	pacid=371518
43	1011	1031 UGGAGAAGC/	::: :: ::::: AGUACGGGC/ Cleavage	pacid=371742
44	879	899 UGGAGAAGC/	::: :: ::::: AGUACGGGC/ Cleavage	pacid=371742
45	772	792 UGGAGAAGC/	::: ::::: AGUGCAUGC(Cleavage	pacid=371577
46	526	546 UGGAGAAGC/	::: ::::: UGCAUGUGC(Cleavage	pacid=371422
47	220	240 UGGAGAAGC/	::: ::::: ACCACGUGCL Cleavage	pacid=371515





1					
2	151	171 UGGAGAAGC/	:: ::::: GCCGCUUGCL	Cleavage	pacid=371589
3	151	171 UGGAGAAGC/	:: ::::: GCCGCUUGCL	Cleavage	pacid=371589
4	1700	1720 UGGAGAAGC/	::: :::: :::: GGCAUGUCU	(Cleavage	pacid=371461
5	1369	1389 UGGAGAAGC/	::: :::: :::: CGCAUCUGCC	Cleavage	pacid=371646
6	775	795 UGGAGAAGC/	: :::: :::: AGUUCGUGU	Translation	pacid=371518
7	1011	1031 UGGAGAAGC/	::: :::: :::: AGUACGGGC/	Cleavage	pacid=371742
8	879	899 UGGAGAAGC/	::: :::: :::: AGUACGGGC/	Cleavage	pacid=371742
9	772	792 UGGAGAAGC/	::: :::: :::: AGUGCAUGCC	(Cleavage	pacid=371577
10	526	546 UGGAGAAGC/	::: :::: :::: UGCAUGUGCI	Cleavage	pacid=371422
11	220	240 UGGAGAAGC/	::: :::: :::: ACCACGUGCL	Cleavage	pacid=371515
12	1359	1379 UGGAGAAGC/	::: :::: :::: UGCACUUGG	(Cleavage	pacid=371586
13	1415	1435 UGGAGAAGC/	::: :::: :::: UGUUUGUGU	Cleavage	pacid=371487
14	1237	1257 UGGAGAAGC/	::: :::: :::: UGUUCGUGC	(Translation	pacid=371708
15	1208	1228 UGGAGAAGC/	::: :::: :::: UGUUCGUGC	(Translation	pacid=371708
16	238	257 UGGAGAAGC/	::: :::: :::: CGCACGUGCC	Cleavage	pacid=371484
17	182	202 UGGAGAAGC/	::: :::: :::: GGU AUGUGC	Cleavage	pacid=371500
18	210	230 UGGAGAAGC/	::: :::: :::: ... AGCACGUGCC	Translation	pacid=371623
19	676	696 UGGAGAAGC/	::: :::: :::: UGCGAGGGU	(Cleavage	pacid=371516
20	1409	1429 UGGAGAAGC/	::: :::: :::: UGCUGGUGCI	Cleavage	pacid=371770
21	480	500 UGGAGAAGC/	::: :::: :::: UGCAAGUUU	(Cleavage	pacid=371764
22	876	896 UGGAGAAGC/	::: :::: :::: UGCAGUUGC	(Translation	pacid=371754
23	1302	1321 UGGAGAAGC/	::: :::: :::: AGCAUGUGC	(Cleavage	pacid=371566
24	1139	1159 UGGAGAAGC/	::: :::: :::: UGCACUGGC	(Cleavage	pacid=371699
25	998	1018 UGGAGAAGC/	::: :::: :::: UGUAGGAGC	(Cleavage	pacid=371749
26	564	584 UGGAGAAGC/	::: :::: :::: CGAACGUGCC	Cleavage	pacid=371759
27	564	584 UGGAGAAGC/	::: :::: :::: CGAACGUGCC	Cleavage	pacid=371759
28	78	97 UGGAGAAGC/	::: :::: :::: UGCAUGU-UC	Cleavage	pacid=371675
29	49	69 UGGAGAAGC/	::: :::: :::: GGUACAUGU	(Cleavage	pacid=371422
30	49	69 UGGAGAAGC/	::: :::: :::: GGUACAUGU	(Cleavage	pacid=371422
31	3477	3497 UGGAGAAGC/	::: :::: :::: GGGCUGUGC	(Cleavage	pacid=371724
32	372	392 UGGAGAAGC/	::: :::: :::: AGCGUUUGC	(Cleavage	pacid=371721
33	304	324 UGGAGAAGC/	::: :::: :::: UCUCGUGCL	Cleavage	pacid=371530
34	2017	2037 UGGAGAAGC/	::: :::: :::: GGCAUGUCU	(Cleavage	pacid=371461
35	1749	1769 UGGAGAAGC/	::: :::: :::: GGCAUGUCU	(Cleavage	pacid=371461
36	151	171 UGGAGAAGC/	::: :::: :::: GCCGCUUGCL	Cleavage	pacid=371589
37	151	171 UGGAGAAGC/	::: :::: :::: GCCGCUUGCL	Cleavage	pacid=371589
38	1700	1720 UGGAGAAGC/	::: :::: :::: GGCAUGUCU	(Cleavage	pacid=371461
39	1369	1389 UGGAGAAGC/	::: :::: :::: CGCAUCUGCC	Cleavage	pacid=371646
40	775	795 UGGAGAAGC/	: :::: :::: AGUUCGUGU	Translation	pacid=371518
41	1011	1031 UGGAGAAGC/	::: :::: :::: AGUACGGGC/	Cleavage	pacid=371742
42	879	899 UGGAGAAGC/	::: :::: :::: AGUACGGGC/	Cleavage	pacid=371742
43	772	792 UGGAGAAGC/	::: :::: :::: AGUGCAUGCC	(Cleavage	pacid=371577
44	526	546 UGGAGAAGC/	::: :::: :::: UGCAUGUGCI	Cleavage	pacid=371422
45	220	240 UGGAGAAGC/	::: :::: :::: ACCACGUGCL	Cleavage	pacid=371515
46	1359	1379 UGGAGAAGC/	::: :::: :::: UGCACUUGG	(Cleavage	pacid=371586
47	1415	1435 UGGAGAAGC/	::: :::: :::: UGUUUGUGU	Cleavage	pacid=371487





1				
2	564	584 UGGAGAAGC/ : ::::: : . CGAACGUGCC Cleavage	pacid=371759	
3	564	584 UGGAGAAGC/ : ::::: : . CGAACGUGCC Cleavage	pacid=371759	
4	78	97 UGGAGAAGC/ ::::: : : : : : : : UGCAUGU-UC Cleavage	pacid=371675	
5	49	69 UGGAGAAGC/ : : : : : : : : : : GGUACAUGU Cleavage	pacid=371422	
6	49	69 UGGAGAAGC/ : : : : : : : : : : GGUACAUGU Cleavage	pacid=371422	
7	49	69 UGGAGAAGC/ : : : : : : : : : : GGUACAUGU Cleavage	pacid=371422	
8	3477	3497 UGGAGAAGC/ : : : : : : : : : : GGCUGUGC Cleavage	pacid=371724	
9	372	392 UGGAGAAGC/ : : : : : : : : : : AGCGUUUGC Cleavage	pacid=371721	
10	304	324 UGGAGAAGC/ : : : : : : : : : : UCUCGUGC Cleavage	pacid=371530	
11	2017	2037 UGGAGAAGC/ : : : : : : : : : : GGCAUGUCU Cleavage	pacid=371461	
12	1749	1769 UGGAGAAGC/ : : : : : : : : : : GGCAUGUCU Cleavage	pacid=371461	
13	151	171 UGGAGAAGC/ : : : : : : : : : : GCCGCUUGC Cleavage	pacid=371589	
14	151	171 UGGAGAAGC/ : : : : : : : : : : GCCGCUUGC Cleavage	pacid=371589	
15	1700	1720 UGGAGAAGC/ : : : : : : : : : : GGCAUGUCU Cleavage	pacid=371461	
16	1369	1389 UGGAGAAGC/ : : : : : : : : : : CGCAUCUGCC Cleavage	pacid=371646	
17	775	795 UGGAGAAGC/ : : : : : : : : : : AGUUCGUGU Translation	pacid=371518	
18	1011	1031 UGGAGAAGC/ : : : : : : : : : : AGUACGGGC Cleavage	pacid=371742	
19	879	899 UGGAGAAGC/ : : : : : : : : : : AGUACGGGC Cleavage	pacid=371742	
20	772	792 UGGAGAAGC/ : : : : : : : : : : AGUGCAUGC Cleavage	pacid=371577	
21	525	546 UGGAGAAGC/ : : : : : : : : : : AUGCAUGUG Cleavage	pacid=371422	
22	675	696 UGGAGAAGC/ : : : : : : : : : : UUGCGAGGG Cleavage	pacid=371516	
23	219	240 UGGAGAAGC/ : : : : : : : : : : AACCAGUGC Cleavage	pacid=371515	
24	77	97 UGGAGAAGC/ : : : : : : : : : : UUGCAUGU-L Cleavage	pacid=371675	
25	1358	1379 UGGAGAAGC/ : : : : : : : : : : CUGCACUUG Cleavage	pacid=371586	
26	1414	1435 UGGAGAAGC/ : : : : : : : : : : CUGUUUGUG Cleavage	pacid=371487	
27	1236	1257 UGGAGAAGC/ : : : : : : : : : : AUGUUCGUG Translation	pacid=371708	
28	1207	1228 UGGAGAAGC/ : : : : : : : : : : AUGUUCGUG Translation	pacid=371708	
29	784	805 UGGAGAAGC/ : : : : : : : : : : UUCCACGUG Translation	pacid=371513	
30	237	257 UGGAGAAGC/ : : : : : : : : : : ACGCACGUG Cleavage	pacid=371484	
31	819	839 UGGAGAAGC/ : : : : : : : : : : UUGCACCU-C Cleavage	pacid=371743	
32	819	839 UGGAGAAGC/ : : : : : : : : : : UUGCACCU-C Cleavage	pacid=371743	
33	181	202 UGGAGAAGC/ : : : : : : : : : : CGGUAUGUG Cleavage	pacid=371500	
34	209	230 UGGAGAAGC/ : : : : : : : : : : ...AAGCACGUG Translation	pacid=371623	
35	1408	1429 UGGAGAAGC/ : : : : : : : : : : CUGCUGGUG Cleavage	pacid=371770	
36	479	500 UGGAGAAGC/ : : : : : : : : : : CUGCAAGUUI Cleavage	pacid=371764	
37	875	896 UGGAGAAGC/ : : : : : : : : : : GUGCAGUUG Translation	pacid=371754	
38	1301	1321 UGGAGAAGC/ : : : : : : : : : : CAGCAUGUG Cleavage	pacid=371566	
39	1222	1243 UGGAGAAGC/ : : : : : : : : : : AACC GGUGI Cleavage	pacid=371718	
40	1138	1159 UGGAGAAGC/ : : : : : : : : : : CUGCACUGG Cleavage	pacid=371699	
41	997	1018 UGGAGAAGC/ : : : : : : : : : : CUGUAGGAG Cleavage	pacid=371749	
42	48	69 UGGAGAAGC/ : : : : : : : : : : UGGUACAUGI Cleavage	pacid=371422	
43	48	69 UGGAGAAGC/ : : : : : : : : : : UGGUACAUGI Cleavage	pacid=371422	
44	3461	3482 UGGAGAAGC/ : : : : : : : : : : UUCUAUCUG Cleavage	pacid=371775	
45	890	911 UGGAGAAGC/ : : : : : : : : : : UGCACUGCC Translation	pacid=371489	
46	273	293 UGGAGAAGC/ : : : : : : : : : : UGUGUGUGU Cleavage	pacid=371747	
47	894	914 UGGAGAAGC/ : : : : : : : : : : UGCAUGUGU Translation	pacid=371531	
48	81	100 UGGAGAAGC/ : : : : : : : : : : UGCAUGUG Cleavage	pacid=371483	



1				
2	81	100 UGGAGAAGC/	UGCAUGUGC(Translation	pacid=371483
3	210	229 UGGAGAAGC/	UGCACGUGCC Cleavage	pacid=371445
4	210	229 UGGAGAAGC/	UGCACGUGCC Cleavage	pacid=371445
5				
6	67	88 UGGAGAAGC/	UGCAACGUGI Cleavage	pacid=371715
7	2692	2712 UGGAGAAGC/	UGCAUCUGU(Cleavage	pacid=371592
8	1441	1461 UGGAGAAGC/	UGCUGUGU Translation	pacid=371656
9				
10	393	413 UGGAGAAGC/	UGUCUGUGU Cleavage	pacid=371678
11	1867	1887 UGGAGAAGC/	UGUAUUUGC.Cleavage	pacid=371738
12	1795	1815 UGGAGAAGC/	UGUAUUUGC.Cleavage	pacid=371738
13				
14	2809	2829 UGGAGAAGC/	GGCACGUGCC(Translation	pacid=371462
15	639	659 UGGAGAAGC/	UAGACGUGUI Cleavage	pacid=371520
16	1429	1450 UGGAGAAGC/	UGCUCAGUG(Cleavage	pacid=371468
17				
18	1429	1450 UGGAGAAGC/	UGCUCAGUG(Cleavage	pacid=371468
19	1946	1966 UGGAGAAGC/	UGCAGUUGC(Cleavage	pacid=371764
20	1712	1732 UGGAGAAGC/	UGCAGUUGC(Cleavage	pacid=371764
21				
22	4127	4147 UGGAGAAGC/	ACCAUGUGCC Cleavage	pacid=371756
23	3713	3733 UGGAGAAGC/	ACCAUGUGCC Cleavage	pacid=371756
24	2142	2165 UGGAGAAGC/	GGCACGUCCC Cleavage	pacid=371647
25				
26	729	749 UGGAGAAGC/	AGCAUGUGU(Cleavage	pacid=371776
27	729	749 UGGAGAAGC/	AGCAUGUGU(Cleavage	pacid=371776
28	1576	1596 UGGAGAAGC/	UUCUCUUGCI Translation	pacid=371530
29				
30	549	569 UGGAGAAGC/	AGCAUGUGU(Cleavage	pacid=371777
31	444	464 UGGAGAAGC/	GACAUGUGC(Translation	pacid=371607
32	449	469 UGGAGAAGC/	AGCAUGUGCI Cleavage	pacid=371663
33				
34	417	437 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
35	1075	1095 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
36	331	351 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
37				
38	989	1009 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
39	1100	1120 UGGAGAAGC/	AACACGUGU(Cleavage	pacid=371470
40	99	119 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
41				
42	977	997 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
43	278	298 UGGAGAAGC/	UGCACCUCCC Cleavage	pacid=371740
44	249	269 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
45				
46	907	927 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
47	420	440 UGGAGAAGC/	UGCUCUGCC Cleavage	pacid=371532
48	161	181 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
49				
50	819	839 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
51	285	305 UGGAGAAGC/	UGCUCUGCC Cleavage	pacid=371528
52	501	521 UGGAGAAGC/	AGCAUGUGC(Cleavage	pacid=371779
53				
54	611	631 UGGAGAAGC/	UGCAAGUCUI Cleavage	pacid=371590
55	205	225 UGGAGAAGC/	AGCAUGUGCI Cleavage	pacid=371599
56	179	200 UGGAGAAGC/	ACCACGUGAC Cleavage	pacid=371457
57	4269	4289 UGGAGAAGC/	UGAACAUGA(Cleavage	pacid=371579
58				
59	4266	4286 UGGAGAAGC/	UGAACAUGA(Cleavage	pacid=371579
60	1610	1630 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
	1571	1591 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622

1			
2	1531	1551 UGGAGAAGC/::: :: :..... UGCAGCUGC/ Cleavage	pacid=371622
3	3830	3850 UGGAGAAGC/:: : :..... UGAACAUGUI Cleavage	pacid=371514
4	2950	2970 UGGAGAAGC/:: . :..... UGUUUGGGU Cleavage	pacid=371537
5	2890	2910 UGGAGAAGC/:: . :..... UGUUUGGGU Cleavage	pacid=371537
6	3661	3681 UGGAGAAGC/:: : :..... UGAACAUGUI Cleavage	pacid=371514
7	1224	1244 UGGAGAAGC/::: :: :..... UGCAGCUGC/ Cleavage	pacid=371622
8	890	911 UGGAGAAGC/::: : :..... UGCACCUGCC Translation	pacid=371489
9	273	293 UGGAGAAGC/::..... :..... UGUGUGUGU Cleavage	pacid=371747
10	894	914 UGGAGAAGC/:::..... :..... UGCAUGUGU Translation	pacid=371531
11	81	100 UGGAGAAGC/:::..... :..... UGCAUGUGC(Translation	pacid=371483
12	81	100 UGGAGAAGC/:::..... :..... UGCAUGUGC(Translation	pacid=371483
13	210	229 UGGAGAAGC/:::..... :..... UGCACGUGCC Cleavage	pacid=371445
14	210	229 UGGAGAAGC/:::..... :..... UGCACGUGCC Cleavage	pacid=371445
15	67	88 UGGAGAAGC/::: :..... UGCAACGUGI Cleavage	pacid=371715
16	2692	2712 UGGAGAAGC/::: . :..... UGCAUCUGU( Cleavage	pacid=371592
17	1441	1461 UGGAGAAGC/:: :..... :..... UGCUUGUGU Translation	pacid=371656
18	393	413 UGGAGAAGC/:: . :..... UGUCUGUGU Cleavage	pacid=371678
19	1867	1887 UGGAGAAGC/::.. : :..... UGUUUUUGC Cleavage	pacid=371738
20	1795	1815 UGGAGAAGC/::.. : :..... UGUUUUUGC Cleavage	pacid=371738
21	2809	2829 UGGAGAAGC/ :..... :..... GGCACGUGCC Translation	pacid=371462
22	639	659 UGGAGAAGC/ :..... :..... UAGACGUGUI Cleavage	pacid=371520
23	1429	1450 UGGAGAAGC/:: : :..... UGCUCAGUG( Cleavage	pacid=371468
24	1429	1450 UGGAGAAGC/:: : :..... UGCUCAGUG( Cleavage	pacid=371468
25	1946	1966 UGGAGAAGC/::: :..... : UGCAGUUGC( Cleavage	pacid=371764
26	1712	1732 UGGAGAAGC/::: :..... : UGCAGUUGC( Cleavage	pacid=371764
27	4127	4147 UGGAGAAGC/ :..... :..... ACCAUGUGCC Cleavage	pacid=371756
28	3713	3733 UGGAGAAGC/ :..... :..... ACCAUGUGCC Cleavage	pacid=371756
29	2142	2165 UGGAGAAGC/ :..... :..... GGCACGUCCC Cleavage	pacid=371647
30	729	749 UGGAGAAGC/ :..... :..... AGCAUGUGU( Cleavage	pacid=371776
31	729	749 UGGAGAAGC/ :..... :..... AGCAUGUGU( Cleavage	pacid=371776
32	1576	1596 UGGAGAAGC/:: : :..... UUCUCUUGC( Translation	pacid=371530
33	549	569 UGGAGAAGC/ :..... :..... AGCAUGUGU( Cleavage	pacid=371777
34	444	464 UGGAGAAGC/ :..... :..... GACAUGUGC( Translation	pacid=371607
35	449	469 UGGAGAAGC/ :..... :..... AGCAUGUGC( Cleavage	pacid=371663
36	417	437 UGGAGAAGC/ :..... :..... AGCACGUGU( Cleavage	pacid=371656
37	1075	1095 UGGAGAAGC/ :..... :..... ACAACGUGC( Cleavage	pacid=371656
38	331	351 UGGAGAAGC/ :..... :..... AGCACGUGU( Cleavage	pacid=371656
39	989	1009 UGGAGAAGC/ :..... :..... ACAACGUGC( Cleavage	pacid=371656
40	1100	1120 UGGAGAAGC/ :..... :..... AACACGUGU( Cleavage	pacid=371470
41	99	119 UGGAGAAGC/ :..... :..... AGCACGUGU( Cleavage	pacid=371656
42	977	997 UGGAGAAGC/ :..... :..... ACAACGUGC( Cleavage	pacid=371656
43	278	298 UGGAGAAGC/::: : :..... UGCACCUCCC Cleavage	pacid=371740
44	249	269 UGGAGAAGC/ :..... :..... AGCACGUGU( Cleavage	pacid=371656
45	907	927 UGGAGAAGC/ :..... :..... ACAACGUGC( Cleavage	pacid=371656
46	420	440 UGGAGAAGC/:: : :..... : UGCUCUGCC Cleavage	pacid=371532
47	161	181 UGGAGAAGC/ :..... :..... AGCACGUGU( Cleavage	pacid=371656

1				
2	819	839 UGGAGAAGC/	.....: :... ACAACGUGCL Cleavage	pacid=371656
3	285	305 UGGAGAAGC/	::: : : : : : : : : : UGCUCCUGCC Cleavage	pacid=371528
4	501	521 UGGAGAAGC/	.....: : : : : : : : : : AGCAUGUGC( Cleavage	pacid=371779
5	611	631 UGGAGAAGC/	::: : : : : : : : : : : UGCAAGUCUI Cleavage	pacid=371590
6	205	225 UGGAGAAGC/	.....: : : : : : : : : : AGCAUGUGC( Cleavage	pacid=371599
7	179	200 UGGAGAAGC/	.....: : : : : : : : : : ACCACGUGAC Cleavage	pacid=371457
8				
9				
10	4269	4289 UGGAGAAGC/	::: : : : : : : : : : : UGAACAUGA( Cleavage	pacid=371579
11	4266	4286 UGGAGAAGC/	::: : : : : : : : : : : UGAACAUGA( Cleavage	pacid=371579
12	1610	1630 UGGAGAAGC/	::: : : : : : : : : : : UGCAGCUGC/ Cleavage	pacid=371622
13				
14	1571	1591 UGGAGAAGC/	::: : : : : : : : : : : UGCAGCUGC/ Cleavage	pacid=371622
15	1531	1551 UGGAGAAGC/	::: : : : : : : : : : : UGCAGCUGC/ Cleavage	pacid=371622
16	3830	3850 UGGAGAAGC/	::: : : : : : : : : : : UGAACAUGUI Cleavage	pacid=371514
17				
18	2950	2970 UGGAGAAGC/	::: : : : : : : : : : : UGUUUGGGU Cleavage	pacid=371537
19	2890	2910 UGGAGAAGC/	::: : : : : : : : : : : UGUUUGGGU Cleavage	pacid=371537
20	3661	3681 UGGAGAAGC/	::: : : : : : : : : : : UGAACAUGUI Cleavage	pacid=371514
21				
22	1224	1244 UGGAGAAGC/	::: : : : : : : : : : : UGCAGCUGC/ Cleavage	pacid=371622
23	890	911 UGGAGAAGC/	.....: : : : : : : : : : UGCACCUGCC Translation	pacid=371489
24	273	293 UGGAGAAGC/	.....: : : : : : : : : : UGUGUGUGU Cleavage	pacid=371747
25				
26	894	914 UGGAGAAGC/	.....: : : : : : : : : : UGCAUGUGU( Translation	pacid=371531
27	81	100 UGGAGAAGC/	.....: : : : : : : : : : UGCAUGUGC( Translation	pacid=371483
28	81	100 UGGAGAAGC/	.....: : : : : : : : : : UGCAUGUGC( Translation	pacid=371483
29				
30	210	229 UGGAGAAGC/	.....: : : : : : : : : : UGCACGUGC( Cleavage	pacid=371445
31	210	229 UGGAGAAGC/	.....: : : : : : : : : : UGCACGUGC( Cleavage	pacid=371445
32	67	88 UGGAGAAGC/	.....: : : : : : : : : : UGCAACGUG( Cleavage	pacid=371715
33				
34	2692	2712 UGGAGAAGC/	::: : : : : : : : : : : UGCAUCUGU( Cleavage	pacid=371592
35	1441	1461 UGGAGAAGC/	::: : : : : : : : : : : UGCUUGUGU Translation	pacid=371656
36	393	413 UGGAGAAGC/	::: : : : : : : : : : : UGUCUGUGU Cleavage	pacid=371678
37				
38	1867	1887 UGGAGAAGC/	::: : : : : : : : : : : UGUUUUUGC( Cleavage	pacid=371738
39	1795	1815 UGGAGAAGC/	::: : : : : : : : : : : UGUUUUUGC( Cleavage	pacid=371738
40	2809	2829 UGGAGAAGC/	.....: : : : : : : : : : GGCACGUGC( Translation	pacid=371462
41	639	659 UGGAGAAGC/	.....: : : : : : : : : : UAGACGUGUI Cleavage	pacid=371520
42				
43	1429	1450 UGGAGAAGC/	::: : : : : : : : : : : UGCUCAGUG( Cleavage	pacid=371468
44	1429	1450 UGGAGAAGC/	::: : : : : : : : : : : UGCUCAGUG( Cleavage	pacid=371468
45	1946	1966 UGGAGAAGC/	::: : : : : : : : : : : UGCAGUUGC( Cleavage	pacid=371764
46				
47	1712	1732 UGGAGAAGC/	::: : : : : : : : : : : UGCAGUUGC( Cleavage	pacid=371764
48	4127	4147 UGGAGAAGC/	.....: : : : : : : : : : ACCAUGUGCC Cleavage	pacid=371756
49	3713	3733 UGGAGAAGC/	.....: : : : : : : : : : ACCAUGUGCC Cleavage	pacid=371756
50				
51	2142	2165 UGGAGAAGC/	.....: : : : : : : : : : GGCACGUCCC Cleavage	pacid=371647
52	729	749 UGGAGAAGC/	.....: : : : : : : : : : AGCAUGUGU( Cleavage	pacid=371776
53	729	749 UGGAGAAGC/	.....: : : : : : : : : : AGCAUGUGU( Cleavage	pacid=371776
54				
55	1576	1596 UGGAGAAGC/	::: : : : : : : : : : : UUCUCUUGC( Translation	pacid=371530
56	549	569 UGGAGAAGC/	.....: : : : : : : : : : AGCAUGUGU( Cleavage	pacid=371777
57	444	464 UGGAGAAGC/	.....: : : : : : : : : : GACAUGUGC( Translation	pacid=371607
58				
59	449	469 UGGAGAAGC/	.....: : : : : : : : : : AGCAUGUGC( Cleavage	pacid=371663
60	417	437 UGGAGAAGC/	.....: : : : : : : : : : AGCACGUGU( Cleavage	pacid=371656
	1075	1095 UGGAGAAGC/	.....: : : : : : : : : : ACAACGUGCL Cleavage	pacid=371656

1				
2	331	351 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
3	989	1009 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
4	1100	1120 UGGAGAAGC/	AACACGUGU(Cleavage	pacid=371470
5				
6	99	119 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
7	977	997 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
8	278	298 UGGAGAAGC/	UGCACCUCCC Cleavage	pacid=371740
9				
10	249	269 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
11	907	927 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
12	420	440 UGGAGAAGC/	UGCUCUGCC Cleavage	pacid=371532
13				
14	161	181 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
15	819	839 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
16	285	305 UGGAGAAGC/	UGCUCUGCC Cleavage	pacid=371528
17				
18	501	521 UGGAGAAGC/	AGCAUGUGC(Cleavage	pacid=371779
19	611	631 UGGAGAAGC/	UGCAAGUCUI Cleavage	pacid=371590
20	205	225 UGGAGAAGC/	AGCAUGUGC Cleavage	pacid=371599
21				
22	179	200 UGGAGAAGC/	ACCACGUGAC Cleavage	pacid=371457
23	4269	4289 UGGAGAAGC/	UGAACAUGA(Cleavage	pacid=371579
24	4266	4286 UGGAGAAGC/	UGAACAUGA(Cleavage	pacid=371579
25				
26	1610	1630 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
27	1571	1591 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
28	1531	1551 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
29				
30	3830	3850 UGGAGAAGC/	UGAACAUGUI Cleavage	pacid=371514
31	2950	2970 UGGAGAAGC/	UGUUUGGGU Cleavage	pacid=371537
32	2890	2910 UGGAGAAGC/	UGUUUGGGU Cleavage	pacid=371537
33				
34	3661	3681 UGGAGAAGC/	UGAACAUGUI Cleavage	pacid=371514
35	1224	1244 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
36	890	911 UGGAGAAGC/	UGCACCUGCC Translation	pacid=371489
37				
38	273	293 UGGAGAAGC/	UGUGUGUGU Cleavage	pacid=371747
39	894	914 UGGAGAAGC/	UGCAUGUGU Translation	pacid=371531
40	81	100 UGGAGAAGC/	UGCAUGUGC(Translation	pacid=371483
41	81	100 UGGAGAAGC/	UGCAUGUGC(Translation	pacid=371483
42				
43	210	229 UGGAGAAGC/	UGCACGUGCC Cleavage	pacid=371445
44	210	229 UGGAGAAGC/	UGCACGUGCC Cleavage	pacid=371445
45	67	88 UGGAGAAGC/	UGCAACGUGI Cleavage	pacid=371715
46				
47	2692	2712 UGGAGAAGC/	UGCAUCUGU(Cleavage	pacid=371592
48	1441	1461 UGGAGAAGC/	UGCUUGUGU Translation	pacid=371656
49	393	413 UGGAGAAGC/	UGUCUGUGU Cleavage	pacid=371678
50				
51	1867	1887 UGGAGAAGC/	UGUAUUUGC Cleavage	pacid=371738
52	1795	1815 UGGAGAAGC/	UGUAUUUGC Cleavage	pacid=371738
53	2809	2829 UGGAGAAGC/	GGCACGUGCC Translation	pacid=371462
54				
55	639	659 UGGAGAAGC/	UAGACGUGUI Cleavage	pacid=371520
56	1429	1450 UGGAGAAGC/	UGCUCAGUG(Cleavage	pacid=371468
57	1429	1450 UGGAGAAGC/	UGCUCAGUG(Cleavage	pacid=371468
58				
59	1946	1966 UGGAGAAGC/	UGCAGUUGC(Cleavage	pacid=371764
60	1712	1732 UGGAGAAGC/	UGCAGUUGC(Cleavage	pacid=371764
	4127	4147 UGGAGAAGC/	ACCAUGUGCC Cleavage	pacid=371756

1					
2	3713	3733 UGGAGAAGC/	:::.....: :::::	ACCAUGUGCC Cleavage	pacid=371756
3	2142	2165 UGGAGAAGC/	.....: :::::	GGCACGUCCC Cleavage	pacid=371647
4	729	749 UGGAGAAGC/	.....: : .....	AGCAUGUGU(Cleavage	pacid=371776
5	729	749 UGGAGAAGC/	.....: : .....	AGCAUGUGU(Cleavage	pacid=371776
6	1576	1596 UGGAGAAGC/	:::.....: .....	UUCUCUUGC(Translation	pacid=371530
7	549	569 UGGAGAAGC/	.....: : .....	AGCAUGUGU(Cleavage	pacid=371777
8	444	464 UGGAGAAGC/	.....: :::::	GACAUGUGC(Translation	pacid=371607
9	449	469 UGGAGAAGC/	.....: .....	AGCAUGUGC(Translation	pacid=371663
10	417	437 UGGAGAAGC/	.....: :::::	AGCACGUGU(Cleavage	pacid=371656
11	1075	1095 UGGAGAAGC/	.....: .....	ACAACGUGC(Translation	pacid=371656
12	331	351 UGGAGAAGC/	.....: .....	AGCACGUGU(Cleavage	pacid=371656
13	989	1009 UGGAGAAGC/	.....: .....	ACAACGUGC(Translation	pacid=371656
14	1100	1120 UGGAGAAGC/	.....: : .....	AACACGUGU(Cleavage	pacid=371470
15	99	119 UGGAGAAGC/	.....: .....	AGCACGUGU(Cleavage	pacid=371656
16	977	997 UGGAGAAGC/	.....: .....	ACAACGUGC(Translation	pacid=371656
17	278	298 UGGAGAAGC/	.....: .....	UGCACCUCCC Cleavage	pacid=371740
18	249	269 UGGAGAAGC/	.....: .....	AGCACGUGU(Cleavage	pacid=371656
19	907	927 UGGAGAAGC/	.....: .....	ACAACGUGC(Translation	pacid=371656
20	420	440 UGGAGAAGC/	.....: : .....	UGCUCUGCC Cleavage	pacid=371532
21	161	181 UGGAGAAGC/	.....: .....	AGCACGUGU(Cleavage	pacid=371656
22	819	839 UGGAGAAGC/	.....: .....	ACAACGUGC(Translation	pacid=371656
23	285	305 UGGAGAAGC/	.....: : .....	UGCUCUGCC Cleavage	pacid=371528
24	501	521 UGGAGAAGC/	.....: : .....	AGCAUGUGC(Translation	pacid=371779
25	611	631 UGGAGAAGC/	.....: : .....	UGCAAGUCU(Cleavage	pacid=371590
26	205	225 UGGAGAAGC/	.....: : .....	AGCAUGUGC(Translation	pacid=371599
27	179	200 UGGAGAAGC/	.....: .....	ACCACGUGAC Cleavage	pacid=371457
28	4269	4289 UGGAGAAGC/	.....: : .....	UGAACAUGA(Cleavage	pacid=371579
29	4266	4286 UGGAGAAGC/	.....: : .....	UGAACAUGA(Cleavage	pacid=371579
30	1610	1630 UGGAGAAGC/	.....: : .....	UGCAGCUGC(Translation	pacid=371622
31	1571	1591 UGGAGAAGC/	.....: : .....	UGCAGCUGC(Translation	pacid=371622
32	1531	1551 UGGAGAAGC/	.....: : .....	UGCAGCUGC(Translation	pacid=371622
33	3830	3850 UGGAGAAGC/	.....: : .....	UGAACAUGU(Cleavage	pacid=371514
34	2950	2970 UGGAGAAGC/	.....: : .....	UGUUUGGGU Cleavage	pacid=371537
35	2890	2910 UGGAGAAGC/	.....: : .....	UGUUUGGGU Cleavage	pacid=371537
36	3661	3681 UGGAGAAGC/	.....: : .....	UGAACAUGU(Cleavage	pacid=371514
37	1224	1244 UGGAGAAGC/	.....: : .....	UGCAGCUGC(Translation	pacid=371622
38	890	911 UGGAGAAGC/	.....: : .....	UGCACCUCCC Translation	pacid=371489
39	273	293 UGGAGAAGC/	.....: : .....	UGUGUGUGU Cleavage	pacid=371747
40	894	914 UGGAGAAGC/	.....: : .....	UGCAUGUGU(Translation	pacid=371531
41	81	100 UGGAGAAGC/	.....: .....	UGCAUGUGC(Translation	pacid=371483
42	81	100 UGGAGAAGC/	.....: .....	UGCAUGUGC(Translation	pacid=371483
43	210	229 UGGAGAAGC/	.....: .....	UGCACGUGC(Translation	pacid=371445
44	210	229 UGGAGAAGC/	.....: .....	UGCACGUGC(Translation	pacid=371445
45	67	88 UGGAGAAGC/	.....: .....	UGCAACGUG(Translation	pacid=371715
46	2692	2712 UGGAGAAGC/	.....: : .....	UGCAUCUGU(Cleavage	pacid=371592
47	1441	1461 UGGAGAAGC/	.....: .....	UGCUCUGUGU Translation	pacid=371656



1			
2	393	413 UGGAGAAGC/ :: : ::::: : UGUCUGUGU Cleavage	pacid=371678
3	1867	1887 UGGAGAAGC/ : : : : : UGUUUUUGC Cleavage	pacid=371738
4	1795	1815 UGGAGAAGC/ : : : : : UGUUUUUGC Cleavage	pacid=371738
5			
6	2809	2829 UGGAGAAGC/ : : : : : GGCACGUGCC Translation	pacid=371462
7	639	659 UGGAGAAGC/ : : : : : UAGACGUGU Cleavage	pacid=371520
8	1429	1450 UGGAGAAGC/ : : : : : UGCUCAGUG( Cleavage	pacid=371468
9			
10	1429	1450 UGGAGAAGC/ : : : : : UGCUCAGUG( Cleavage	pacid=371468
11	1946	1966 UGGAGAAGC/ : : : : : UGCAGUUGC( Cleavage	pacid=371764
12	1712	1732 UGGAGAAGC/ : : : : : UGCAGUUGC( Cleavage	pacid=371764
13			
14	4127	4147 UGGAGAAGC/ : : : : : ACCAUGUGCC Cleavage	pacid=371756
15	3713	3733 UGGAGAAGC/ : : : : : ACCAUGUGCC Cleavage	pacid=371756
16	2142	2165 UGGAGAAGC/ : : : : : GGCACGUCCC Cleavage	pacid=371647
17			
18	729	749 UGGAGAAGC/ : : : : : AGCAUGUGU( Cleavage	pacid=371776
19	729	749 UGGAGAAGC/ : : : : : AGCAUGUGU( Cleavage	pacid=371776
20	1576	1596 UGGAGAAGC/ : : : : : UUCUCUUGC( Translation	pacid=371530
21			
22	549	569 UGGAGAAGC/ : : : : : AGCAUGUGU( Cleavage	pacid=371777
23	444	464 UGGAGAAGC/ : : : : : GACAUGUGCC Translation	pacid=371607
24	449	469 UGGAGAAGC/ : : : : : AGCAUGUGU( Cleavage	pacid=371663
25			
26	417	437 UGGAGAAGC/ : : : : : AGCACGUGU( Cleavage	pacid=371656
27	1075	1095 UGGAGAAGC/ : : : : : ACAACGUGU( Cleavage	pacid=371656
28	331	351 UGGAGAAGC/ : : : : : AGCACGUGU( Cleavage	pacid=371656
29			
30	989	1009 UGGAGAAGC/ : : : : : ACAACGUGU( Cleavage	pacid=371656
31	1100	1120 UGGAGAAGC/ : : : : : AACACGUGU( Cleavage	pacid=371470
32	99	119 UGGAGAAGC/ : : : : : AGCACGUGU( Cleavage	pacid=371656
33			
34	977	997 UGGAGAAGC/ : : : : : ACAACGUGU( Cleavage	pacid=371656
35	278	298 UGGAGAAGC/ : : : : : UGCACCUCCC Cleavage	pacid=371740
36	249	269 UGGAGAAGC/ : : : : : AGCACGUGU( Cleavage	pacid=371656
37			
38	907	927 UGGAGAAGC/ : : : : : ACAACGUGU( Cleavage	pacid=371656
39	420	440 UGGAGAAGC/ : : : : : UGCUCUGCC Cleavage	pacid=371532
40	161	181 UGGAGAAGC/ : : : : : AGCACGUGU( Cleavage	pacid=371656
41	819	839 UGGAGAAGC/ : : : : : ACAACGUGU( Cleavage	pacid=371656
42			
43	285	305 UGGAGAAGC/ : : : : : UGCUCUGCC Cleavage	pacid=371528
44	501	521 UGGAGAAGC/ : : : : : AGCAUGUGU( Cleavage	pacid=371779
45	611	631 UGGAGAAGC/ : : : : : UGCAAGUCU( Cleavage	pacid=371590
46			
47	205	225 UGGAGAAGC/ : : : : : AGCAUGUGU( Cleavage	pacid=371599
48	179	200 UGGAGAAGC/ : : : : : ACCACGUGAC Cleavage	pacid=371457
49	4269	4289 UGGAGAAGC/ : : : : : UGAACAUGA( Cleavage	pacid=371579
50	4266	4286 UGGAGAAGC/ : : : : : UGAACAUGA( Cleavage	pacid=371579
51			
52	1610	1630 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage	pacid=371622
53	1571	1591 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage	pacid=371622
54			
55	1531	1551 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage	pacid=371622
56	3830	3850 UGGAGAAGC/ : : : : : UGAACAUGU( Cleavage	pacid=371514
57	2950	2970 UGGAGAAGC/ : : : : : UGUUUGGGU Cleavage	pacid=371537
58			
59	2890	2910 UGGAGAAGC/ : : : : : UGUUUGGGU Cleavage	pacid=371537
60	3661	3681 UGGAGAAGC/ : : : : : UGAACAUGU( Cleavage	pacid=371514
	1224	1244 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage	pacid=371622

1			
2	890	911 UGGAGAAGC/::::: ::::: ::::: UGCACCUGCC Translation	pacid=371489
3	273	293 UGGAGAAGC/::.....: ::::: UGUGUGUGU Cleavage	pacid=371747
4	894	914 UGGAGAAGC/::::: ::::: UGCAUGUGU Translation	pacid=371531
5			
6	81	100 UGGAGAAGC/::::: ::::: UGCAUGUGC(Translation	pacid=371483
7	81	100 UGGAGAAGC/::::: ::::: UGCAUGUGC(Translation	pacid=371483
8			
9	210	229 UGGAGAAGC/::::: ::::: UGCACGUGCC Cleavage	pacid=371445
10	210	229 UGGAGAAGC/::::: ::::: UGCACGUGCC Cleavage	pacid=371445
11	67	88 UGGAGAAGC/::::: ::::: UGCAACGUGI Cleavage	pacid=371715
12	2692	2712 UGGAGAAGC/::::: ::::: UGCAUCUGU(Cleavage	pacid=371592
13			
14	1441	1461 UGGAGAAGC/::: :::: UGCUUGUGU Translation	pacid=371656
15	393	413 UGGAGAAGC/::: :::: UGUCUGUGU Cleavage	pacid=371678
16	1867	1887 UGGAGAAGC/::: :::: UGUUUUUGC.Cleavage	pacid=371738
17			
18	1795	1815 UGGAGAAGC/::: :::: UGUUUUUGC.Cleavage	pacid=371738
19	2809	2829 UGGAGAAGC/::::: ::::: GGCACGUGCC Translation	pacid=371462
20	639	659 UGGAGAAGC/::::: ::::: UAGACGUGU(Cleavage	pacid=371520
21			
22	1429	1450 UGGAGAAGC/::: :::: UGCUCAGUG(Cleavage	pacid=371468
23	1429	1450 UGGAGAAGC/::: :::: UGCUCAGUG(Cleavage	pacid=371468
24	1946	1966 UGGAGAAGC/::: :::: UGCAGUUGC(Cleavage	pacid=371764
25			
26	1712	1732 UGGAGAAGC/::: :::: UGCAGUUGC(Cleavage	pacid=371764
27	4127	4147 UGGAGAAGC/::::: ::::: ACCAUGUGCC Cleavage	pacid=371756
28	3713	3733 UGGAGAAGC/::::: ::::: ACCAUGUGCC Cleavage	pacid=371756
29			
30	2142	2165 UGGAGAAGC/::::: ::::: GGCACGUCCC Cleavage	pacid=371647
31	729	749 UGGAGAAGC/::::: ::::: AGCAUGUGU(Cleavage	pacid=371776
32	729	749 UGGAGAAGC/::::: ::::: AGCAUGUGU(Cleavage	pacid=371776
33			
34	1576	1596 UGGAGAAGC/::: :::: UUCUCUUGC(Translation	pacid=371530
35	549	569 UGGAGAAGC/::::: ::::: AGCAUGUGU(Cleavage	pacid=371777
36	444	464 UGGAGAAGC/::::: ::::: GACAUGUGC(Translation	pacid=371607
37			
38	449	469 UGGAGAAGC/::::: ::::: AGCAUGUGC( Cleavage	pacid=371663
39	417	437 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage	pacid=371656
40	1075	1095 UGGAGAAGC/::::: ::::: ACAACGUGC( Cleavage	pacid=371656
41			
42	331	351 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage	pacid=371656
43	989	1009 UGGAGAAGC/::::: ::::: ACAACGUGC( Cleavage	pacid=371656
44	1100	1120 UGGAGAAGC/::::: ::::: AACACGUGU(Cleavage	pacid=371470
45			
46	99	119 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage	pacid=371656
47	977	997 UGGAGAAGC/::::: ::::: ACAACGUGC( Cleavage	pacid=371656
48	278	298 UGGAGAAGC/::::: ::::: UGCACCUCCC Cleavage	pacid=371740
49	249	269 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage	pacid=371656
50			
51	907	927 UGGAGAAGC/::::: ::::: ACAACGUGC( Cleavage	pacid=371656
52	420	440 UGGAGAAGC/::: :::: UGCUCCUGCC Cleavage	pacid=371532
53			
54	161	181 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage	pacid=371656
55	819	839 UGGAGAAGC/::::: ::::: ACAACGUGC( Cleavage	pacid=371656
56	285	305 UGGAGAAGC/::: :::: UGCUCCUGCC Cleavage	pacid=371528
57	501	521 UGGAGAAGC/::::: ::::: AGCAUGUGC( Cleavage	pacid=371779
58			
59	611	631 UGGAGAAGC/::: :::: UGCAAGUCU( Cleavage	pacid=371590
60	205	225 UGGAGAAGC/::::: ::::: AGCAUGUGC( Cleavage	pacid=371599
	179	200 UGGAGAAGC/::::: ::::: ACCACGUGAC Cleavage	pacid=371457



1			
2	4269	4289 UGGAGAAGC/:: :: :: :: :: :: :: :: UGAACAUGA(Cleavage	pacid=371579
3	4266	4286 UGGAGAAGC/:: :: :: :: :: :: :: :: UGAACAUGA(Cleavage	pacid=371579
4	1610	1630 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAGCUGC(Cleavage	pacid=371622
5	1571	1591 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAGCUGC(Cleavage	pacid=371622
6	1531	1551 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAGCUGC(Cleavage	pacid=371622
7	3830	3850 UGGAGAAGC/:: :: :: :: :: :: :: :: UGAACAUGU(Cleavage	pacid=371514
8	2950	2970 UGGAGAAGC/:: :: :: :: :: :: :: :: UGUUUGGGU(Cleavage	pacid=371537
9	2890	2910 UGGAGAAGC/:: :: :: :: :: :: :: :: UGUUUGGGU(Cleavage	pacid=371537
10	3661	3681 UGGAGAAGC/:: :: :: :: :: :: :: :: UGAACAUGU(Cleavage	pacid=371514
11	1224	1244 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAGCUGC(Cleavage	pacid=371622
12	890	911 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCACCUGCC(Translation	pacid=371489
13	273	293 UGGAGAAGC/:: :: :: :: :: :: :: :: UGUGUGUGU(Cleavage	pacid=371747
14	894	914 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAUGUGU(Translation	pacid=371531
15	81	100 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAUGUGC(Translation	pacid=371483
16	81	100 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAUGUGC(Translation	pacid=371483
17	210	229 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCACGUGCC(Cleavage	pacid=371445
18	210	229 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCACGUGCC(Cleavage	pacid=371445
19	67	88 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAACGUGU(Cleavage	pacid=371715
20	2692	2712 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAUCUGU(Cleavage	pacid=371592
21	1441	1461 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCUUGUGU(Translation	pacid=371656
22	393	413 UGGAGAAGC/:: :: :: :: :: :: :: :: UGUCUGUGU(Cleavage	pacid=371678
23	1867	1887 UGGAGAAGC/:: :: :: :: :: :: :: :: UGUUUUGC(Cleavage	pacid=371738
24	1795	1815 UGGAGAAGC/:: :: :: :: :: :: :: :: UGUUUUGC(Cleavage	pacid=371738
25	2809	2829 UGGAGAAGC/:: :: :: :: :: :: :: :: GGCACGUGCC(Translation	pacid=371462
26	639	659 UGGAGAAGC/:: :: :: :: :: :: :: :: UAGACGUGU(Cleavage	pacid=371520
27	1429	1450 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCUCAGUG(Cleavage	pacid=371468
28	1429	1450 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCUCAGUG(Cleavage	pacid=371468
29	1946	1966 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAGUUGC(Cleavage	pacid=371764
30	1712	1732 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCAGUUGC(Cleavage	pacid=371764
31	4127	4147 UGGAGAAGC/:: :: :: :: :: :: :: :: ACCAUGUGCC(Cleavage	pacid=371756
32	3713	3733 UGGAGAAGC/:: :: :: :: :: :: :: :: ACCAUGUGCC(Cleavage	pacid=371756
33	2142	2165 UGGAGAAGC/:: :: :: :: :: :: :: :: GGCACGUCCC(Cleavage	pacid=371647
34	729	749 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCAUGUGU(Cleavage	pacid=371776
35	729	749 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCAUGUGU(Cleavage	pacid=371776
36	1576	1596 UGGAGAAGC/:: :: :: :: :: :: :: :: UUCUCUUGU(Translation	pacid=371530
37	549	569 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCAUGUGU(Cleavage	pacid=371777
38	444	464 UGGAGAAGC/:: :: :: :: :: :: :: :: GACAUGUGU(Translation	pacid=371607
39	449	469 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCAUGUGU(Cleavage	pacid=371663
40	417	437 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCACGUGU(Cleavage	pacid=371656
41	1075	1095 UGGAGAAGC/:: :: :: :: :: :: :: :: ACAACGUGU(Cleavage	pacid=371656
42	331	351 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCACGUGU(Cleavage	pacid=371656
43	989	1009 UGGAGAAGC/:: :: :: :: :: :: :: :: ACAACGUGU(Cleavage	pacid=371656
44	1100	1120 UGGAGAAGC/:: :: :: :: :: :: :: :: AACACGUGU(Cleavage	pacid=371470
45	99	119 UGGAGAAGC/:: :: :: :: :: :: :: :: AGCACGUGU(Cleavage	pacid=371656
46	977	997 UGGAGAAGC/:: :: :: :: :: :: :: :: ACAACGUGU(Cleavage	pacid=371656
47	278	298 UGGAGAAGC/:: :: :: :: :: :: :: :: UGCACCUCCC(Cleavage	pacid=371740

1			
2	249	269 UGGAGAAGC/ ::::::::::: ::::: AGCACGUGU(Cleavage	pacid=371656
3	907	927 UGGAGAAGC/ ::::::::::: ::::: ACAACGUGCL Cleavage	pacid=371656
4	420	440 UGGAGAAGC/ :::: : ::::::::::: : UGCUCCUGCC Cleavage	pacid=371532
5	161	181 UGGAGAAGC/ ::::::::::: ::::: AGCACGUGU(Cleavage	pacid=371656
6	819	839 UGGAGAAGC/ ::::::::::: ::::: ACAACGUGCL Cleavage	pacid=371656
7	285	305 UGGAGAAGC/ :::: : ::::::::::: : UGCUCCUGCC Cleavage	pacid=371528
8	501	521 UGGAGAAGC/ ::::::::::: :: : AGCAUGUGC(Cleavage	pacid=371779
9	611	631 UGGAGAAGC/ :::: : ..::::::::: UGCAAGUCUI Cleavage	pacid=371590
10	205	225 UGGAGAAGC/ ::::::::::: . ::::: AGCAUGUGCL Cleavage	pacid=371599
11	179	200 UGGAGAAGC/ ::::: ::::::::::: ACCACGUGAC Cleavage	pacid=371457
12	4269	4289 UGGAGAAGC/ :::: : : ::::::::::: : UGAACAUGA(Cleavage	pacid=371579
13	4266	4286 UGGAGAAGC/ :::: : : ::::::::::: : UGAACAUGA(Cleavage	pacid=371579
14	1610	1630 UGGAGAAGC/ ::::: :: : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
15	1571	1591 UGGAGAAGC/ ::::: :: : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
16	1531	1551 UGGAGAAGC/ ::::: :: : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
17	3830	3850 UGGAGAAGC/ :: : : ..::::::::: UGAACAUGUI Cleavage	pacid=371514
18	2950	2970 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU Cleavage	pacid=371537
19	2890	2910 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU Cleavage	pacid=371537
20	3661	3681 UGGAGAAGC/ :: : : ..::::::::: UGAACAUGUI Cleavage	pacid=371514
21	1224	1244 UGGAGAAGC/ ::::: :: : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
22	890	911 UGGAGAAGC/ ::::: ::::: ::::::::::: UGCACCUGCC Translation	pacid=371489
23	273	293 UGGAGAAGC/ ::.....: ::::::::::: UGUGUGUGU Cleavage	pacid=371747
24	894	914 UGGAGAAGC/ ::::.....: ::::::::::: UGCAUGUGU Translation	pacid=371531
25	81	100 UGGAGAAGC/ ::::.....: ::::::::::: UGCAUGUGC(Translation	pacid=371483
26	81	100 UGGAGAAGC/ ::::.....: ::::::::::: UGCAUGUGC(Translation	pacid=371483
27	210	229 UGGAGAAGC/ ::::.....: ::::::::::: UGCACGUGCC Cleavage	pacid=371445
28	210	229 UGGAGAAGC/ ::::.....: ::::::::::: UGCACGUGCC Cleavage	pacid=371445
29	67	88 UGGAGAAGC/ ::::: ..::::::::: UGCAACGUGI Cleavage	pacid=371715
30	2692	2712 UGGAGAAGC/ ::::: . ::::::::::: UGCAUCUGU(Cleavage	pacid=371592
31	1441	1461 UGGAGAAGC/ ::: ..::: ..::::::::: UGCUUGUGU Translation	pacid=371656
32	393	413 UGGAGAAGC/ :: . ::.....: ..::::::::: UGUCUGUGU Cleavage	pacid=371678
33	1867	1887 UGGAGAAGC/ ::.. : : ::::::::::: UGUUUUUGC Cleavage	pacid=371738
34	1795	1815 UGGAGAAGC/ ::.. : : ::::::::::: UGUUUUUGC Cleavage	pacid=371738
35	2809	2829 UGGAGAAGC/ ::::.....: ..::: GGCACGUGCC(Translation	pacid=371462
36	639	659 UGGAGAAGC/ ::::.....: ::::::::::: UAGACGUGUI Cleavage	pacid=371520
37	1429	1450 UGGAGAAGC/ ::::: ..::::::::: UGCUCAGUG(Cleavage	pacid=371468
38	1429	1450 UGGAGAAGC/ ::::: ..::::::::: UGCUCAGUG(Cleavage	pacid=371468
39	1946	1966 UGGAGAAGC/ ::::: ..::::::::: UGCAGUUGC(Cleavage	pacid=371764
40	1712	1732 UGGAGAAGC/ ::::: ..::::::::: UGCAGUUGC(Cleavage	pacid=371764
41	4127	4147 UGGAGAAGC/ ::::.....: ::::: ACCAUGUGCC Cleavage	pacid=371756
42	3713	3733 UGGAGAAGC/ ::::.....: ::::: ACCAUGUGCC Cleavage	pacid=371756
43	2142	2165 UGGAGAAGC/ ::::: ..::::::::: GGCACGUCCC Cleavage	pacid=371647
44	729	749 UGGAGAAGC/ ::::.....: : ::::: AGCAUGUGU(Cleavage	pacid=371776
45	729	749 UGGAGAAGC/ ::::.....: : ::::: AGCAUGUGU(Cleavage	pacid=371776
46	1576	1596 UGGAGAAGC/ :: : : ..::: ..::::::::: UUCUCUUGCI Translation	pacid=371530
47	549	569 UGGAGAAGC/ ::::.....: : ::::: AGCAUGUGU(Cleavage	pacid=371777

1				
2	444	464 UGGAGAAGC/	::: ::: : GACAUGUGC(Translation	pacid=371607
3	449	469 UGGAGAAGC/	::: ::: : AGCAUGUGC( Cleavage	pacid=371663
4	417	437 UGGAGAAGC/	::: ::: : AGCACGUGU( Cleavage	pacid=371656
5				
6	1075	1095 UGGAGAAGC/	::: ::: : ACAACGUGC( Cleavage	pacid=371656
7	331	351 UGGAGAAGC/	::: ::: : AGCACGUGU( Cleavage	pacid=371656
8	989	1009 UGGAGAAGC/	::: ::: : ACAACGUGC( Cleavage	pacid=371656
9				
10	1100	1120 UGGAGAAGC/	::: ::: : AACACGUGU( Cleavage	pacid=371470
11	99	119 UGGAGAAGC/	::: ::: : AGCACGUGU( Cleavage	pacid=371656
12	977	997 UGGAGAAGC/	::: ::: : ACAACGUGC( Cleavage	pacid=371656
13				
14	278	298 UGGAGAAGC/	::: : ::: : UGCACCUCCC Cleavage	pacid=371740
15	249	269 UGGAGAAGC/	::: ::: : AGCACGUGU( Cleavage	pacid=371656
16	907	927 UGGAGAAGC/	::: ::: : ACAACGUGC( Cleavage	pacid=371656
17				
18	420	440 UGGAGAAGC/	::: : ::: : UGCUCCUGCC Cleavage	pacid=371532
19	161	181 UGGAGAAGC/	::: ::: : AGCACGUGU( Cleavage	pacid=371656
20	819	839 UGGAGAAGC/	::: ::: : ACAACGUGC( Cleavage	pacid=371656
21				
22	285	305 UGGAGAAGC/	::: : ::: : UGCUCCUGCC Cleavage	pacid=371528
23	501	521 UGGAGAAGC/	::: ::: : AGCAUGUGC( Cleavage	pacid=371779
24	611	631 UGGAGAAGC/	::: : ::: : UGCAAGUCU( Cleavage	pacid=371590
25				
26	205	225 UGGAGAAGC/	::: ::: : AGCAUGUGC( Cleavage	pacid=371599
27	179	200 UGGAGAAGC/	::: : ::: : ACCACGUGAC Cleavage	pacid=371457
28	4269	4289 UGGAGAAGC/	::: : ::: : UGAACAUGA( Cleavage	pacid=371579
29				
30	4266	4286 UGGAGAAGC/	::: : ::: : UGAACAUGA( Cleavage	pacid=371579
31	1610	1630 UGGAGAAGC/	::: : ::: : UGCAGCUGC/ Cleavage	pacid=371622
32	1571	1591 UGGAGAAGC/	::: : ::: : UGCAGCUGC/ Cleavage	pacid=371622
33				
34	1531	1551 UGGAGAAGC/	::: : ::: : UGCAGCUGC/ Cleavage	pacid=371622
35	3830	3850 UGGAGAAGC/	::: : ::: : UGAACAUGU( Cleavage	pacid=371514
36	2950	2970 UGGAGAAGC/	::: : ::: : UGUUUGGGU( Cleavage	pacid=371537
37				
38	2890	2910 UGGAGAAGC/	::: : ::: : UGUUUGGGU( Cleavage	pacid=371537
39	3661	3681 UGGAGAAGC/	::: : ::: : UGAACAUGU( Cleavage	pacid=371514
40	1224	1244 UGGAGAAGC/	::: : ::: : UGCAGCUGC/ Cleavage	pacid=371622
41				
42	890	911 UGGAGAAGC/	::: : ::: : UGCACCUGCC( Translation	pacid=371489
43	273	293 UGGAGAAGC/	::: ::: : UGUGUGUGU( Cleavage	pacid=371747
44	894	914 UGGAGAAGC/	::: ::: : UGCAUGUGU( Translation	pacid=371531
45	81	100 UGGAGAAGC/	::: ::: : UGCAUGUGC( Translation	pacid=371483
46				
47	81	100 UGGAGAAGC/	::: ::: : UGCAUGUGC( Translation	pacid=371483
48	210	229 UGGAGAAGC/	::: ::: : UGCACGUGC( Cleavage	pacid=371445
49	210	229 UGGAGAAGC/	::: ::: : UGCACGUGC( Cleavage	pacid=371445
50				
51	67	88 UGGAGAAGC/	::: : ::: : UGCAACGUG( Cleavage	pacid=371715
52	2692	2712 UGGAGAAGC/	::: : ::: : UGCAUCUGU( Cleavage	pacid=371592
53	1441	1461 UGGAGAAGC/	::: : ::: : UGCUUGUGU( Translation	pacid=371656
54				
55	393	413 UGGAGAAGC/	::: : ::: : UGUCUGUGU( Cleavage	pacid=371678
56	1867	1887 UGGAGAAGC/	::: : ::: : UGUUUUGC( Cleavage	pacid=371738
57	1795	1815 UGGAGAAGC/	::: : ::: : UGUUUUGC( Cleavage	pacid=371738
58				
59	2809	2829 UGGAGAAGC/	::: ::: : GGCACGUGC( Translation	pacid=371462
60	639	659 UGGAGAAGC/	::: ::: : UAGACGUGU( Cleavage	pacid=371520
	1429	1450 UGGAGAAGC/	::: : ::: : UGCUCAGUG( Cleavage	pacid=371468



1				
2	210	229 UGGAGAAGC/ ::::::::::: :::::	UGCACGUGCC Cleavage	pacid=371445
3	67	88 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAACGUGI Cleavage	pacid=371715
4	2692	2712 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAUCUGU( Cleavage	pacid=371592
5	1441	1461 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCUUGUGU Translation	pacid=371656
6	393	413 UGGAGAAGC/ ::: ::::: ::::: :::::	UGUCUGUGU Cleavage	pacid=371678
7	1867	1887 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGUAUUUGC. Cleavage	pacid=371738
8	1795	1815 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGUAUUUGC. Cleavage	pacid=371738
9	2809	2829 UGGAGAAGC/ ::::::::::: :::::	GGCACGUGCC Translation	pacid=371462
10	639	659 UGGAGAAGC/ ::::::::::: :::::	UAGACGUGUI Cleavage	pacid=371520
11	1429	1450 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCUCAGUG( Cleavage	pacid=371468
12	1429	1450 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCUCAGUG( Cleavage	pacid=371468
13	1946	1966 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAGUUGC( Cleavage	pacid=371764
14	1712	1732 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAGUUGC( Cleavage	pacid=371764
15	4127	4147 UGGAGAAGC/ ::::::::::: :::::	ACCAUGUGCC Cleavage	pacid=371756
16	3713	3733 UGGAGAAGC/ ::::::::::: :::::	ACCAUGUGCC Cleavage	pacid=371756
17	2142	2165 UGGAGAAGC/ ::::: ::::: ::::: :::::	GGCACGUCCC Cleavage	pacid=371647
18	729	749 UGGAGAAGC/ ::::::::::: :::::	AGCAUGUGUI Cleavage	pacid=371776
19	729	749 UGGAGAAGC/ ::::::::::: :::::	AGCAUGUGUI Cleavage	pacid=371776
20	1576	1596 UGGAGAAGC/ ::::: ::::: ::::: :::::	UUCUCUUGCI Translation	pacid=371530
21	549	569 UGGAGAAGC/ ::::::::::: :::::	AGCAUGUGUI Cleavage	pacid=371777
22	444	464 UGGAGAAGC/ ::::::::::: :::::	GACAUGUGC( Translation	pacid=371607
23	449	469 UGGAGAAGC/ ::::::::::: :::::	AGCAUGUGCI Cleavage	pacid=371663
24	417	437 UGGAGAAGC/ ::::::::::: :::::	AGCACGUGU( Cleavage	pacid=371656
25	1075	1095 UGGAGAAGC/ ::::::::::: :::::	ACAACGUGCL Cleavage	pacid=371656
26	331	351 UGGAGAAGC/ ::::::::::: :::::	AGCACGUGU( Cleavage	pacid=371656
27	989	1009 UGGAGAAGC/ ::::::::::: :::::	ACAACGUGCL Cleavage	pacid=371656
28	1100	1120 UGGAGAAGC/ ::::::::::: :::::	AACACGUGU( Cleavage	pacid=371470
29	99	119 UGGAGAAGC/ ::::::::::: :::::	AGCACGUGU( Cleavage	pacid=371656
30	977	997 UGGAGAAGC/ ::::::::::: :::::	ACAACGUGCL Cleavage	pacid=371656
31	278	298 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCACCUCCC Cleavage	pacid=371740
32	249	269 UGGAGAAGC/ ::::::::::: :::::	AGCACGUGU( Cleavage	pacid=371656
33	907	927 UGGAGAAGC/ ::::::::::: :::::	ACAACGUGCL Cleavage	pacid=371656
34	420	440 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCUCUGCC Cleavage	pacid=371532
35	161	181 UGGAGAAGC/ ::::::::::: :::::	AGCACGUGU( Cleavage	pacid=371656
36	819	839 UGGAGAAGC/ ::::::::::: :::::	ACAACGUGCL Cleavage	pacid=371656
37	285	305 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCUCUGCC Cleavage	pacid=371528
38	501	521 UGGAGAAGC/ ::::::::::: :::::	AGCAUGUGC( Cleavage	pacid=371779
39	611	631 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAAGUCUI Cleavage	pacid=371590
40	205	225 UGGAGAAGC/ ::::::::::: :::::	AGCAUGUGCI Cleavage	pacid=371599
41	179	200 UGGAGAAGC/ ::::: ::::: ::::: :::::	ACCACGUGAC Cleavage	pacid=371457
42	4269	4289 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGAACAUGA( Cleavage	pacid=371579
43	4266	4286 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGAACAUGA( Cleavage	pacid=371579
44	1610	1630 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAGCUGC/ Cleavage	pacid=371622
45	1571	1591 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAGCUGC/ Cleavage	pacid=371622
46	1531	1551 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGCAGCUGC/ Cleavage	pacid=371622
47	3830	3850 UGGAGAAGC/ ::::: ::::: ::::: :::::	UGAACAUGUI Cleavage	pacid=371514





1			
2	501	521 UGGAGAAGC/ ::::::::::: :: : AGCAUGUGC( Cleavage	pacid=371779
3	611	631 UGGAGAAGC/ :::: : ..::::::::: UGCAAGUCU( Cleavage	pacid=371590
4	205	225 UGGAGAAGC/ ::::::::::: . ::::: AGCAUGUGC( Cleavage	pacid=371599
5	179	200 UGGAGAAGC/ ::::: ::::::::::: ACCACGUGAC( Cleavage	pacid=371457
6	4269	4289 UGGAGAAGC/ :: : : ::::::::::: :: UGAACAUGA( Cleavage	pacid=371579
7	4266	4286 UGGAGAAGC/ :: : : ::::::::::: :: UGAACAUGA( Cleavage	pacid=371579
8	1610	1630 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
9	1571	1591 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
10	1531	1551 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
11	3830	3850 UGGAGAAGC/ :: : : ..::::::::: UGAACAUGU( Cleavage	pacid=371514
12	2950	2970 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU( Cleavage	pacid=371537
13	2890	2910 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU( Cleavage	pacid=371537
14	3661	3681 UGGAGAAGC/ :: : : ..::::::::: UGAACAUGU( Cleavage	pacid=371514
15	1224	1244 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage	pacid=371622
16	890	911 UGGAGAAGC/ ::::: ::::: ::::::::::: UGCACCUGCC( Translation	pacid=371489
17	273	293 UGGAGAAGC/ ::::: ..::::::::: UGUGUGUGU( Cleavage	pacid=371747
18	894	914 UGGAGAAGC/ ::::: ..::::::::: UGCAUGUGU( Translation	pacid=371531
19	81	100 UGGAGAAGC/ ::::: ..::::::::: UGCAUGUGC( Translation	pacid=371483
20	81	100 UGGAGAAGC/ ::::: ..::::::::: UGCAUGUGC( Translation	pacid=371483
21	210	229 UGGAGAAGC/ ::::::::::: ..::: UGCACGUGCC( Cleavage	pacid=371445
22	210	229 UGGAGAAGC/ ::::::::::: ..::: UGCACGUGCC( Cleavage	pacid=371445
23	67	88 UGGAGAAGC/ ::::: ..::::::::: UGCAACGUG( Cleavage	pacid=371715
24	2692	2712 UGGAGAAGC/ ::::: ..::::::::: . UGCAUCUGU( Cleavage	pacid=371592
25	1441	1461 UGGAGAAGC/ :: : ..::: ..::::::::: UGCUUGUGU( Translation	pacid=371656
26	393	413 UGGAGAAGC/ :: . : ..::::::::: UGUCUGUGU( Cleavage	pacid=371678
27	1867	1887 UGGAGAAGC/ ::.. : : ::::::::::: UGUUUUGC( Cleavage	pacid=371738
28	1795	1815 UGGAGAAGC/ ::.. : : ::::::::::: UGUUUUGC( Cleavage	pacid=371738
29	2809	2829 UGGAGAAGC/ ::::::::::: ..::: GGCACGUGCC( Translation	pacid=371462
30	639	659 UGGAGAAGC/ ::::::::::: ..::: UAGACGUGU( Cleavage	pacid=371520
31	1429	1450 UGGAGAAGC/ :: : : ..::::::::: UGCUCAGUG( Cleavage	pacid=371468
32	1429	1450 UGGAGAAGC/ :: : : ..::::::::: UGCUCAGUG( Cleavage	pacid=371468
33	1946	1966 UGGAGAAGC/ :::: : ::::::::::: :: UGCAGUUGC( Cleavage	pacid=371764
34	1712	1732 UGGAGAAGC/ :::: : ::::::::::: :: UGCAGUUGC( Cleavage	pacid=371764
35	4127	4147 UGGAGAAGC/ ::::::::::: ..::: ACCAUGUGCC( Cleavage	pacid=371756
36	3713	3733 UGGAGAAGC/ ::::::::::: ..::: ACCAUGUGCC( Cleavage	pacid=371756
37	2142	2165 UGGAGAAGC/ ::::: ..::::::::: GGCACGUCCC( Cleavage	pacid=371647
38	729	749 UGGAGAAGC/ ::::::::::: : ..::: AGCAUGUGU( Cleavage	pacid=371776
39	729	749 UGGAGAAGC/ ::::::::::: : ..::: AGCAUGUGU( Cleavage	pacid=371776
40	1576	1596 UGGAGAAGC/ :: : ..::: ..::::::::: UUCUCUUGC( Translation	pacid=371530
41	549	569 UGGAGAAGC/ ::::::::::: : ..::: AGCAUGUGU( Cleavage	pacid=371777
42	444	464 UGGAGAAGC/ ::::: ..::::::::: GACAUGUGC( Translation	pacid=371607
43	449	469 UGGAGAAGC/ ::::::::::: ..::: AGCAUGUGC( Cleavage	pacid=371663
44	417	437 UGGAGAAGC/ ::::::::::: ..::: AGCACGUGU( Cleavage	pacid=371656
45	1075	1095 UGGAGAAGC/ ::::::::::: ..::: ACAACGUGC( Cleavage	pacid=371656
46	331	351 UGGAGAAGC/ ::::::::::: ..::: AGCACGUGU( Cleavage	pacid=371656
47	989	1009 UGGAGAAGC/ ::::::::::: ..::: ACAACGUGC( Cleavage	pacid=371656



1				
2	1100	1120 UGGAGAAGC/	::: :: AACACGUGU(Cleavage	pacid=371470
3	99	119 UGGAGAAGC/	::: :: AGCACGUGU(Cleavage	pacid=371656
4	977	997 UGGAGAAGC/	::: :: ACAACGUGU(Cleavage	pacid=371656
5	278	298 UGGAGAAGC/	::: :: UGCACCUCCC(Cleavage	pacid=371740
6	249	269 UGGAGAAGC/	::: :: AGCACGUGU(Cleavage	pacid=371656
7	907	927 UGGAGAAGC/	::: :: ACAACGUGU(Cleavage	pacid=371656
8	420	440 UGGAGAAGC/	::: :: UGCUCUGCC(Cleavage	pacid=371532
9	161	181 UGGAGAAGC/	::: :: AGCACGUGU(Cleavage	pacid=371656
10	819	839 UGGAGAAGC/	::: :: ACAACGUGU(Cleavage	pacid=371656
11	285	305 UGGAGAAGC/	::: :: UGCUCUGCC(Cleavage	pacid=371528
12	501	521 UGGAGAAGC/	::: :: AGCAUGUGU(Cleavage	pacid=371779
13	611	631 UGGAGAAGC/	::: :: UGCAAGUCU(Cleavage	pacid=371590
14	205	225 UGGAGAAGC/	::: :: AGCAUGUGU(Cleavage	pacid=371599
15	179	200 UGGAGAAGC/	::: :: ACCACGUGU(Cleavage	pacid=371457
16	4269	4289 UGGAGAAGC/	::: :: UGAACAUGU(Cleavage	pacid=371579
17	4266	4286 UGGAGAAGC/	::: :: UGAACAUGU(Cleavage	pacid=371579
18	1610	1630 UGGAGAAGC/	::: :: UGCAGCUGU(Cleavage	pacid=371622
19	1571	1591 UGGAGAAGC/	::: :: UGCAGCUGU(Cleavage	pacid=371622
20	1531	1551 UGGAGAAGC/	::: :: UGCAGCUGU(Cleavage	pacid=371622
21	3830	3850 UGGAGAAGC/	::: :: UGAACAUGU(Cleavage	pacid=371514
22	2950	2970 UGGAGAAGC/	::: :: UGUUUGGU(Cleavage	pacid=371537
23	2890	2910 UGGAGAAGC/	::: :: UGUUUGGU(Cleavage	pacid=371537
24	3661	3681 UGGAGAAGC/	::: :: UGAACAUGU(Cleavage	pacid=371514
25	1224	1244 UGGAGAAGC/	::: :: UGCAGCUGU(Cleavage	pacid=371622
26	890	911 UGGAGAAGC/	::: :: UGCACCUCC(Translation	pacid=371489
27	273	293 UGGAGAAGC/	::: :: UGUGUGUGU(Cleavage	pacid=371747
28	894	914 UGGAGAAGC/	::: :: UGCAUGUGU(Translation	pacid=371531
29	81	100 UGGAGAAGC/	::: :: UGCAUGUGU(Translation	pacid=371483
30	81	100 UGGAGAAGC/	::: :: UGCAUGUGU(Translation	pacid=371483
31	210	229 UGGAGAAGC/	::: :: UGCACGUGU(Cleavage	pacid=371445
32	210	229 UGGAGAAGC/	::: :: UGCACGUGU(Cleavage	pacid=371445
33	67	88 UGGAGAAGC/	::: :: UGCAACGUGU(Cleavage	pacid=371715
34	2692	2712 UGGAGAAGC/	::: :: UGCAUCUGU(Cleavage	pacid=371592
35	1441	1461 UGGAGAAGC/	::: :: UGCUUGUGU(Translation	pacid=371656
36	393	413 UGGAGAAGC/	::: :: UGUCUGUGU(Cleavage	pacid=371678
37	1867	1887 UGGAGAAGC/	::: :: UGUUUUGU(Cleavage	pacid=371738
38	1795	1815 UGGAGAAGC/	::: :: UGUUUUGU(Cleavage	pacid=371738
39	2809	2829 UGGAGAAGC/	::: :: GGCACGUGU(Translation	pacid=371462
40	639	659 UGGAGAAGC/	::: :: UAGACGUGU(Cleavage	pacid=371520
41	1429	1450 UGGAGAAGC/	::: :: UGCUCAGUG(Cleavage	pacid=371468
42	1429	1450 UGGAGAAGC/	::: :: UGCUCAGUG(Cleavage	pacid=371468
43	1946	1966 UGGAGAAGC/	::: :: UGCAGUUGU(Cleavage	pacid=371764
44	1712	1732 UGGAGAAGC/	::: :: UGCAGUUGU(Cleavage	pacid=371764
45	4127	4147 UGGAGAAGC/	::: :: ACCAUGUGU(Cleavage	pacid=371756
46	3713	3733 UGGAGAAGC/	::: :: ACCAUGUGU(Cleavage	pacid=371756
47	2142	2165 UGGAGAAGC/	::: :: GGCACGUCCC(Cleavage	pacid=371647

1			
2	729	749 UGGAGAAGC/ ::::: : : : : AGCAUGUGU(Cleavage	pacid=371776
3	729	749 UGGAGAAGC/ ::::: : : : : AGCAUGUGU(Cleavage	pacid=371776
4	1576	1596 UGGAGAAGC/ : : : : : : : : : : UUCUCUUGC(Translation	pacid=371530
5	549	569 UGGAGAAGC/ ::::: : : : : AGCAUGUGU(Cleavage	pacid=371777
6	444	464 UGGAGAAGC/ ::::: : : : : GACAUGUGC(Translation	pacid=371607
7	449	469 UGGAGAAGC/ ::::: : : : : : AGCAUGUGC(Cleavage	pacid=371663
8	417	437 UGGAGAAGC/ ::::: : : : : : AGCACGUGU(Cleavage	pacid=371656
9	1075	1095 UGGAGAAGC/ ::::: : : : : : ACAACGUGC(Cleavage	pacid=371656
10	331	351 UGGAGAAGC/ ::::: : : : : : AGCACGUGU(Cleavage	pacid=371656
11	989	1009 UGGAGAAGC/ ::::: : : : : : ACAACGUGC(Cleavage	pacid=371656
12	1100	1120 UGGAGAAGC/ ::::: : : : : : AACACGUGU(Cleavage	pacid=371470
13	99	119 UGGAGAAGC/ ::::: : : : : : AGCACGUGU(Cleavage	pacid=371656
14	977	997 UGGAGAAGC/ ::::: : : : : : ACAACGUGC(Cleavage	pacid=371656
15	278	298 UGGAGAAGC/ : : : : : : : : : : UGCACCUCCC(Cleavage	pacid=371740
16	249	269 UGGAGAAGC/ ::::: : : : : : AGCACGUGU(Cleavage	pacid=371656
17	907	927 UGGAGAAGC/ ::::: : : : : : ACAACGUGC(Cleavage	pacid=371656
18	420	440 UGGAGAAGC/ : : : : : : : : : : UGCUCCUGC(Cleavage	pacid=371532
19	161	181 UGGAGAAGC/ ::::: : : : : : AGCACGUGU(Cleavage	pacid=371656
20	819	839 UGGAGAAGC/ ::::: : : : : : ACAACGUGC(Cleavage	pacid=371656
21	285	305 UGGAGAAGC/ : : : : : : : : : : UGCUCCUGC(Cleavage	pacid=371528
22	501	521 UGGAGAAGC/ ::::: : : : : : : : AGCAUGUGC(Cleavage	pacid=371779
23	611	631 UGGAGAAGC/ : : : : : : : : : : UGCAAGUCU(Cleavage	pacid=371590
24	205	225 UGGAGAAGC/ ::::: : : : : : : : AGCAUGUGC(Cleavage	pacid=371599
25	179	200 UGGAGAAGC/ ::::: : : : : : : : ACCACGUGAC(Cleavage	pacid=371457
26	4269	4289 UGGAGAAGC/ : : : : : : : : : : UGAACAUGA(Cleavage	pacid=371579
27	4266	4286 UGGAGAAGC/ : : : : : : : : : : UGAACAUGA(Cleavage	pacid=371579
28	1610	1630 UGGAGAAGC/ : : : : : : : : : : UGCAGCUGC(Cleavage	pacid=371622
29	1571	1591 UGGAGAAGC/ : : : : : : : : : : UGCAGCUGC(Cleavage	pacid=371622
30	1531	1551 UGGAGAAGC/ : : : : : : : : : : UGCAGCUGC(Cleavage	pacid=371622
31	3830	3850 UGGAGAAGC/ : : : : : : : : : : UGAACAUGU(Cleavage	pacid=371514
32	2950	2970 UGGAGAAGC/ : : : : : : : : : : UGUUUGGGU(Cleavage	pacid=371537
33	2890	2910 UGGAGAAGC/ : : : : : : : : : : UGUUUGGGU(Cleavage	pacid=371537
34	3661	3681 UGGAGAAGC/ : : : : : : : : : : UGAACAUGU(Cleavage	pacid=371514
35	1224	1244 UGGAGAAGC/ : : : : : : : : : : UGCAGCUGC(Cleavage	pacid=371622
36	890	911 UGGAGAAGC/ : : : : : : : : : : UGCACCUGCC(Translation	pacid=371489
37	273	293 UGGAGAAGC/ : : : : : : : : : : UGUGUGUGU(Cleavage	pacid=371747
38	894	914 UGGAGAAGC/ : : : : : : : : : : UGCAUGUGU(Translation	pacid=371531
39	81	100 UGGAGAAGC/ : : : : : : : : : : UGCAUGUGC(Translation	pacid=371483
40	81	100 UGGAGAAGC/ : : : : : : : : : : UGCAUGUGC(Translation	pacid=371483
41	210	229 UGGAGAAGC/ : : : : : : : : : : UGCACGUGC(Cleavage	pacid=371445
42	210	229 UGGAGAAGC/ : : : : : : : : : : UGCACGUGC(Cleavage	pacid=371445
43	67	88 UGGAGAAGC/ : : : : : : : : : : UGCAACGUG(Cleavage	pacid=371715
44	2692	2712 UGGAGAAGC/ : : : : : : : : : : UGCAUCUGU(Cleavage	pacid=371592
45	1441	1461 UGGAGAAGC/ : : : : : : : : : : UGCUUGUGU(Translation	pacid=371656
46	393	413 UGGAGAAGC/ : : : : : : : : : : UGUCUGUGU(Cleavage	pacid=371678
47	1867	1887 UGGAGAAGC/ : : : : : : : : : : UGUUUUGC(Cleavage	pacid=371738

1				
2	1795	1815 UGGAGAAGC/ ::.. :: .....	UGUAUUUGC.Cleavage	pacid=371738
3	2809	2829 UGGAGAAGC/ ::..... ::...	GGCACGUGCC Translation	pacid=371462
4	639	659 UGGAGAAGC/ ::..... ::.....	UAGACGUGUI Cleavage	pacid=371520
5				
6	1429	1450 UGGAGAAGC/ :: : .....	UGCUCAGUG( Cleavage	pacid=371468
7	1429	1450 UGGAGAAGC/ :: : .....	UGCUCAGUG( Cleavage	pacid=371468
8				
9	1946	1966 UGGAGAAGC/ ::.. : .....	UGCAGUUGC( Cleavage	pacid=371764
10	1712	1732 UGGAGAAGC/ ::.. : .....	UGCAGUUGC( Cleavage	pacid=371764
11	4127	4147 UGGAGAAGC/ ::..... : .....	ACCAUGUGCC Cleavage	pacid=371756
12	3713	3733 UGGAGAAGC/ ::..... : .....	ACCAUGUGCC Cleavage	pacid=371756
13				
14	2142	2165 UGGAGAAGC/ ::.. : .....	GGCACGUCCC Cleavage	pacid=371647
15	729	749 UGGAGAAGC/ ::..... : .....	AGCAUGUGUI Cleavage	pacid=371776
16	729	749 UGGAGAAGC/ ::..... : .....	AGCAUGUGUI Cleavage	pacid=371776
17				
18	1576	1596 UGGAGAAGC/ :: : .....	UUCUCUUGC( Translation	pacid=371530
19	549	569 UGGAGAAGC/ ::..... : .....	AGCAUGUGUI Cleavage	pacid=371777
20	444	464 UGGAGAAGC/ ::..... : .....	GACAUGUGCC( Translation	pacid=371607
21				
22	449	469 UGGAGAAGC/ ::..... : .....	AGCAUGUGC( Cleavage	pacid=371663
23	417	437 UGGAGAAGC/ ::..... : .....	AGCACGUGU( Cleavage	pacid=371656
24	1075	1095 UGGAGAAGC/ ::..... : .....	ACAACGUGC( Cleavage	pacid=371656
25				
26	331	351 UGGAGAAGC/ ::..... : .....	AGCACGUGU( Cleavage	pacid=371656
27	989	1009 UGGAGAAGC/ ::..... : .....	ACAACGUGC( Cleavage	pacid=371656
28	1100	1120 UGGAGAAGC/ ::..... : .....	AACACGUGU( Cleavage	pacid=371470
29				
30	99	119 UGGAGAAGC/ ::..... : .....	AGCACGUGU( Cleavage	pacid=371656
31	977	997 UGGAGAAGC/ ::..... : .....	ACAACGUGC( Cleavage	pacid=371656
32	278	298 UGGAGAAGC/ ::.. : .....	UGCACCUCCC Cleavage	pacid=371740
33				
34	249	269 UGGAGAAGC/ ::..... : .....	AGCACGUGU( Cleavage	pacid=371656
35	907	927 UGGAGAAGC/ ::..... : .....	ACAACGUGC( Cleavage	pacid=371656
36	420	440 UGGAGAAGC/ :: : .....	UGCUCUGCC Cleavage	pacid=371532
37				
38	161	181 UGGAGAAGC/ ::..... : .....	AGCACGUGU( Cleavage	pacid=371656
39	819	839 UGGAGAAGC/ ::..... : .....	ACAACGUGC( Cleavage	pacid=371656
40	285	305 UGGAGAAGC/ :: : .....	UGCUCUGCC Cleavage	pacid=371528
41	501	521 UGGAGAAGC/ ::..... : .....	AGCAUGUGC( Cleavage	pacid=371779
42				
43	611	631 UGGAGAAGC/ :: : .....	UGCAAGUCUI Cleavage	pacid=371590
44	205	225 UGGAGAAGC/ ::..... : .....	AGCAUGUGC( Cleavage	pacid=371599
45	179	200 UGGAGAAGC/ ::.. : .....	ACCACGUGAC Cleavage	pacid=371457
46				
47	4269	4289 UGGAGAAGC/ :: : .....	UGAACAUGA( Cleavage	pacid=371579
48	4266	4286 UGGAGAAGC/ :: : .....	UGAACAUGA( Cleavage	pacid=371579
49	1610	1630 UGGAGAAGC/ ::.. : .....	UGCAGCUGC/ Cleavage	pacid=371622
50				
51	1571	1591 UGGAGAAGC/ ::.. : .....	UGCAGCUGC/ Cleavage	pacid=371622
52	1531	1551 UGGAGAAGC/ ::.. : .....	UGCAGCUGC/ Cleavage	pacid=371622
53	3830	3850 UGGAGAAGC/ :: : .....	UGAACAUGUI Cleavage	pacid=371514
54				
55	2950	2970 UGGAGAAGC/ :: : .....	UGUUUGGGU Cleavage	pacid=371537
56	2890	2910 UGGAGAAGC/ :: : .....	UGUUUGGGU Cleavage	pacid=371537
57	3661	3681 UGGAGAAGC/ :: : .....	UGAACAUGUI Cleavage	pacid=371514
58				
59	1224	1244 UGGAGAAGC/ ::.. : .....	UGCAGCUGC/ Cleavage	pacid=371622
60	890	911 UGGAGAAGC/ ::.. : .....	UGCACCUGCC Translation	pacid=371489
	273	293 UGGAGAAGC/ ::..... : .....	UGUGUGUGU Cleavage	pacid=371747



1				
2	1610	1630 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage		pacid=371622
3	1571	1591 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage		pacid=371622
4	1531	1551 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage		pacid=371622
5				
6	3830	3850 UGGAGAAGC/:: : :.....: UGAACAUGUI Cleavage		pacid=371514
7	2950	2970 UGGAGAAGC/:: . :.....: UGUUUGGGU Cleavage		pacid=371537
8	2890	2910 UGGAGAAGC/:: . :.....: UGUUUGGGU Cleavage		pacid=371537
9				
10	3661	3681 UGGAGAAGC/:: : :.....: UGAACAUGUI Cleavage		pacid=371514
11	1224	1244 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage		pacid=371622
12	890	911 UGGAGAAGC/::: : :.....: UGCACCUGCC Translation		pacid=371489
13				
14	273	293 UGGAGAAGC/::.....: :.....: UGUGUGUGU Cleavage		pacid=371747
15	894	914 UGGAGAAGC/::: : :.....: UGCAUGUGU Translation		pacid=371531
16	81	100 UGGAGAAGC/::: : :.....: UGCAUGUGC( Translation		pacid=371483
17				
18	81	100 UGGAGAAGC/::: : :.....: UGCAUGUGC( Translation		pacid=371483
19	210	229 UGGAGAAGC/::: : :.....: UGCACGUGCC Cleavage		pacid=371445
20	210	229 UGGAGAAGC/::: : :.....: UGCACGUGCC Cleavage		pacid=371445
21				
22	67	88 UGGAGAAGC/::: : :.....: UGCAACGUGI Cleavage		pacid=371715
23	2692	2712 UGGAGAAGC/::: . :.....: UGCAUCUGU( Cleavage		pacid=371592
24	1441	1461 UGGAGAAGC/:: : :.....: UGCUUGUGU Translation		pacid=371656
25				
26	393	413 UGGAGAAGC/:: . :.....: UGUCUGUGU Cleavage		pacid=371678
27	1867	1887 UGGAGAAGC/::.. : :.....: UGUUUUUGC Cleavage		pacid=371738
28	1795	1815 UGGAGAAGC/::.. : :.....: UGUUUUUGC Cleavage		pacid=371738
29				
30	2809	2829 UGGAGAAGC/ : : :.....: GGCACGUGCC Translation		pacid=371462
31	639	659 UGGAGAAGC/ : : :.....: UAGACGUGUI Cleavage		pacid=371520
32	1429	1450 UGGAGAAGC/:: : :.....: UGCUCAGUG( Cleavage		pacid=371468
33				
34	1429	1450 UGGAGAAGC/:: : :.....: UGCUCAGUG( Cleavage		pacid=371468
35	1946	1966 UGGAGAAGC/::: : :.....: UGCAGUUGC( Cleavage		pacid=371764
36	1712	1732 UGGAGAAGC/::: : :.....: UGCAGUUGC( Cleavage		pacid=371764
37				
38	4127	4147 UGGAGAAGC/ : : :.....: ACCAUGUGCC Cleavage		pacid=371756
39	3713	3733 UGGAGAAGC/ : : :.....: ACCAUGUGCC Cleavage		pacid=371756
40	2142	2165 UGGAGAAGC/ : : :.....: GGCACGUCCC Cleavage		pacid=371647
41				
42	729	749 UGGAGAAGC/ : : :.....: AGCAUGUGUI Cleavage		pacid=371776
43	729	749 UGGAGAAGC/ : : :.....: AGCAUGUGUI Cleavage		pacid=371776
44	1576	1596 UGGAGAAGC/:: : :.....: UUCUCUUGCI Translation		pacid=371530
45	549	569 UGGAGAAGC/ : : :.....: AGCAUGUGUI Cleavage		pacid=371777
46				
47	444	464 UGGAGAAGC/ : : :.....: GACAUGUGC( Translation		pacid=371607
48	449	469 UGGAGAAGC/ : : :.....: AGCAUGUGCI Cleavage		pacid=371663
49	417	437 UGGAGAAGC/ : : :.....: AGCACGUGU( Cleavage		pacid=371656
50				
51	1075	1095 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage		pacid=371656
52	331	351 UGGAGAAGC/ : : :.....: AGCACGUGU( Cleavage		pacid=371656
53	989	1009 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage		pacid=371656
54				
55	1100	1120 UGGAGAAGC/ : : :.....: AACACGUGU( Cleavage		pacid=371470
56	99	119 UGGAGAAGC/ : : :.....: AGCACGUGU( Cleavage		pacid=371656
57	977	997 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage		pacid=371656
58				
59	278	298 UGGAGAAGC/ : : :.....: UGCACCUCCC Cleavage		pacid=371740
60	249	269 UGGAGAAGC/ : : :.....: AGCACGUGU( Cleavage		pacid=371656
	907	927 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage		pacid=371656



1				
2	420	440 UGGAGAAGC/ :: : ::::: : : UGCUCCUGCC Cleavage	pacid=371532	
3	161	181 UGGAGAAGC/ ::::: : : : AGCACGUGU( Cleavage	pacid=371656	
4	819	839 UGGAGAAGC/ ::::: : : : ACAACGUGCL Cleavage	pacid=371656	
5	285	305 UGGAGAAGC/ :: : : ::::: : : UGCUCCUGCC Cleavage	pacid=371528	
6	501	521 UGGAGAAGC/ ::::: : : : : AGCAUGUGCC Cleavage	pacid=371779	
7	611	631 UGGAGAAGC/ ::::: : : : : UGCAAGUCU( Cleavage	pacid=371590	
8	205	225 UGGAGAAGC/ ::::: : : : : AGCAUGUGC( Cleavage	pacid=371599	
9	179	200 UGGAGAAGC/ ::::: : : : : ACCACGUGAC Cleavage	pacid=371457	
10	4269	4289 UGGAGAAGC/ :: : : : ::::: : : UGAACAUGA( Cleavage	pacid=371579	
11	4266	4286 UGGAGAAGC/ :: : : : ::::: : : UGAACAUGA( Cleavage	pacid=371579	
12	1610	1630 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage	pacid=371622	
13	1571	1591 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage	pacid=371622	
14	1531	1551 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage	pacid=371622	
15	3830	3850 UGGAGAAGC/ :: : : : : : UGAACAUGU( Cleavage	pacid=371514	
16	2950	2970 UGGAGAAGC/ :: : : : : : UGUUUGGGU Cleavage	pacid=371537	
17	2890	2910 UGGAGAAGC/ :: : : : : : UGUUUGGGU Cleavage	pacid=371537	
18	3661	3681 UGGAGAAGC/ :: : : : : : UGAACAUGU( Cleavage	pacid=371514	
19	1224	1244 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage	pacid=371622	
20	890	911 UGGAGAAGC/ ::::: : : : : UGCACCUGCC Translation	pacid=371489	
21	273	293 UGGAGAAGC/ ::::: : : : : UGUGUGUGU Cleavage	pacid=371747	
22	894	914 UGGAGAAGC/ ::::: : : : : UGCAUGUGU( Translation	pacid=371531	
23	81	100 UGGAGAAGC/ ::::: : : : : UGCAUGUGC( Translation	pacid=371483	
24	81	100 UGGAGAAGC/ ::::: : : : : UGCAUGUGC( Translation	pacid=371483	
25	210	229 UGGAGAAGC/ ::::: : : : : UGCACGUGCC Cleavage	pacid=371445	
26	210	229 UGGAGAAGC/ ::::: : : : : UGCACGUGCC Cleavage	pacid=371445	
27	67	88 UGGAGAAGC/ ::::: : : : : UGCAACGUG( Cleavage	pacid=371715	
28	2692	2712 UGGAGAAGC/ ::::: : : : : UGCAUCUGU( Cleavage	pacid=371592	
29	1441	1461 UGGAGAAGC/ :: : : : : : UGCUUGUGU Translation	pacid=371656	
30	393	413 UGGAGAAGC/ :: : : : : : UGUCUGUGU Cleavage	pacid=371678	
31	1867	1887 UGGAGAAGC/ :: : : : : : UGUUUUUGC Cleavage	pacid=371738	
32	1795	1815 UGGAGAAGC/ :: : : : : : UGUUUUUGC Cleavage	pacid=371738	
33	2809	2829 UGGAGAAGC/ ::::: : : : : GGCACGUGCC Translation	pacid=371462	
34	639	659 UGGAGAAGC/ ::::: : : : : UAGACGUGU( Cleavage	pacid=371520	
35	1429	1450 UGGAGAAGC/ :: : : : : : UGCUCAGUG( Cleavage	pacid=371468	
36	1429	1450 UGGAGAAGC/ :: : : : : : UGCUCAGUG( Cleavage	pacid=371468	
37	1946	1966 UGGAGAAGC/ ::::: : : : : UGCAGUUGC( Cleavage	pacid=371764	
38	1712	1732 UGGAGAAGC/ ::::: : : : : UGCAGUUGC( Cleavage	pacid=371764	
39	4127	4147 UGGAGAAGC/ ::::: : : : : ACCAUGUGCC Cleavage	pacid=371756	
40	3713	3733 UGGAGAAGC/ ::::: : : : : ACCAUGUGCC Cleavage	pacid=371756	
41	2142	2165 UGGAGAAGC/ ::::: : : : : GGCACGUCCC Cleavage	pacid=371647	
42	729	749 UGGAGAAGC/ ::::: : : : : AGCAUGUGU( Cleavage	pacid=371776	
43	729	749 UGGAGAAGC/ ::::: : : : : AGCAUGUGU( Cleavage	pacid=371776	
44	1576	1596 UGGAGAAGC/ :: : : : : : UUCUCUUGC( Translation	pacid=371530	
45	549	569 UGGAGAAGC/ ::::: : : : : AGCAUGUGU( Cleavage	pacid=371777	
46	444	464 UGGAGAAGC/ ::::: : : : : GACAUGUGC( Translation	pacid=371607	
47	449	469 UGGAGAAGC/ ::::: : : : : AGCAUGUGC( Cleavage	pacid=371663	

1				
2	417	437 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
3	1075	1095 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
4	331	351 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
5	989	1009 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
6	1100	1120 UGGAGAAGC/	AACACGUGU(Cleavage	pacid=371470
7	99	119 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
8	977	997 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
9	278	298 UGGAGAAGC/	UGCACCUCCC Cleavage	pacid=371740
10	249	269 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
11	907	927 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
12	420	440 UGGAGAAGC/	UGCUCUGCC Cleavage	pacid=371532
13	161	181 UGGAGAAGC/	AGCACGUGU(Cleavage	pacid=371656
14	819	839 UGGAGAAGC/	ACAACGUGCL Cleavage	pacid=371656
15	285	305 UGGAGAAGC/	UGCUCUGCC Cleavage	pacid=371528
16	501	521 UGGAGAAGC/	AGCAUGUGC(Cleavage	pacid=371779
17	611	631 UGGAGAAGC/	UGCAAGUCUI Cleavage	pacid=371590
18	205	225 UGGAGAAGC/	AGCAUGUGCL Cleavage	pacid=371599
19	179	200 UGGAGAAGC/	ACCACGUGAC Cleavage	pacid=371457
20	4269	4289 UGGAGAAGC/	UGAACAUGA(Cleavage	pacid=371579
21	4266	4286 UGGAGAAGC/	UGAACAUGA(Cleavage	pacid=371579
22	1610	1630 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
23	1571	1591 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
24	1531	1551 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
25	3830	3850 UGGAGAAGC/	UGAACAUGUI Cleavage	pacid=371514
26	2950	2970 UGGAGAAGC/	UGUUUGGGU Cleavage	pacid=371537
27	2890	2910 UGGAGAAGC/	UGUUUGGGU Cleavage	pacid=371537
28	3661	3681 UGGAGAAGC/	UGAACAUGUI Cleavage	pacid=371514
29	1224	1244 UGGAGAAGC/	UGCAGCUGC/ Cleavage	pacid=371622
30	66	88 UGGAGAAGC/	UUGCAACGU(Cleavage	pacid=371715
31	2691	2712 UGGAGAAGC/	UUGCAUCUGI Cleavage	pacid=371592
32	1866	1887 UGGAGAAGC/	UUGUAUUUG Cleavage	pacid=371738
33	889	911 UGGAGAAGC/	AUGCACCUGC Translation	pacid=371489
34	1794	1815 UGGAGAAGC/	UUGUAUUUG Cleavage	pacid=371738
35	272	293 UGGAGAAGC/	CUGUGUGUG Cleavage	pacid=371747
36	893	914 UGGAGAAGC/	CUGCAUGUGI Translation	pacid=371531
37	80	100 UGGAGAAGC/	CUGCAUGUG(Translation	pacid=371483
38	80	100 UGGAGAAGC/	CUGCAUGUG(Translation	pacid=371483
39	209	229 UGGAGAAGC/	CUGCACGUG(Cleavage	pacid=371445
40	209	229 UGGAGAAGC/	CUGCACGUG(Cleavage	pacid=371445
41	419	440 UGGAGAAGC/	UUGCUCUG(Cleavage	pacid=371532
42	284	305 UGGAGAAGC/	UUGCUCUG(Cleavage	pacid=371528
43	4268	4289 UGGAGAAGC/	UUGAACAUG/ Cleavage	pacid=371579
44	4265	4286 UGGAGAAGC/	UUGAACAUG/ Cleavage	pacid=371579
45	3829	3850 UGGAGAAGC/	UUGAACAUGI Cleavage	pacid=371514
46	2949	2970 UGGAGAAGC/	UUGUUUGGG Cleavage	pacid=371537
47	2889	2910 UGGAGAAGC/	UUGUUUGGG Cleavage	pacid=371537









1					
2	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
3	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
4	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
5					
6	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
7	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
8	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
9					
10	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
11	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
12	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
13					
14	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
15	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
16	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
17					
18	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
19	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
20	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
21					
22	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
23	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
24	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
25					
26	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
27	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
28	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
29					
30	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
31	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
32	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
33					
34	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
35	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
36	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
37					
38	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
39	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
40	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
41					
42	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
43	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
44	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
45					
46	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
47	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
48	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
49					
50	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
51	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
52	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
53					
54	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
55	1 Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663	
56	1 Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup>	0
57					
58	1 Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup>	0
59	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
60	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0
	1 Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup>	0

1					
2	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
3	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
4	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
5					
6	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
7	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
8	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
9					
10	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
11	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
12	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
13					
14	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
15	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
16	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
17	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
18	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
19	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
20	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
21					
22	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
23	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
24	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
25	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
26	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
27	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
28	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
29					
30	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
31	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
32	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
33	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
34	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
35	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
36	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
37					
38	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
39	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
40	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
41	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
42	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
43	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
44	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
45					
46	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
47	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
48	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
49	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
50	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
51	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
52	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
53					
54	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
55	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
56	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
57	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
58	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
59	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
60	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0



1					
2	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
3	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
4	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
5	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
6	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
7	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
8	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
9	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
10	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
11	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
12	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
13	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
14	1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P <sup>-</sup> 0
15	1	Phvul.007G164800	Phvul.007G164800		0 PTHR33448,P <sup>-</sup> 0
16	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
17	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
18	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
19	1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P <sup>-</sup> 0
20	1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P <sup>-</sup> KOG1663
21	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
22	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
23	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
24	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
25	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
26	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
27	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
28	1	Phvul.008G147100	Phvul.008G147100		0 0 0
29	1	Phvul.008G147100	Phvul.008G147100		0 0 0
30	1	Phvul.008G147100	Phvul.008G147100		0 0 0
31	1	Phvul.008G147100	Phvul.008G147100		0 0 0
32	1	Phvul.006G086200	Phvul.006G086200		0 PTHR32133 0
33	1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup> KOG2399
34	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
35	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
36	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
37	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
38	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
39	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
40	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
41	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
42	1	Phvul.008G147100	Phvul.008G147100		0 0 0
43	1	Phvul.008G147100	Phvul.008G147100		0 0 0
44	1	Phvul.008G147100	Phvul.008G147100		0 0 0
45	1	Phvul.008G147100	Phvul.008G147100		0 0 0
46	1	Phvul.006G086200	Phvul.006G086200		0 PTHR32133 0
47	1	Phvul.006G086200	Phvul.006G086200		0 PTHR32133 0
48	1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup> KOG2399
49	1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup> KOG2399
50	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
51	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
52	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
53	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
54	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
55	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
56	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
57	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
58	1	Phvul.008G147100	Phvul.008G147100		0 0 0
59	1	Phvul.008G147100	Phvul.008G147100		0 0 0
60	1	Phvul.008G147100	Phvul.008G147100		0 0 0
61	1	Phvul.006G086200	Phvul.006G086200		0 PTHR32133 0
62	1	Phvul.006G086200	Phvul.006G086200		0 PTHR32133 0
63	1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup> KOG2399
64	1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup> KOG2399
65	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
66	1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup> 0
67	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
68	1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup> 0
69	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
70	1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup> 0
71	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0
72	1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup> 0

1					
2	1 Phvul.008G147100	Phvul.008G147100	0	0	0
3	1 Phvul.008G147100	Phvul.008G147100	0	0	0
4	1 Phvul.008G147100	Phvul.008G147100	0	0	0
5					
6	1 Phvul.006G086200	Phvul.006G086200	0 PTHR32133		0
7	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
8	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
9					
10	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
11	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
12	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
13					
14	1 Phvul.008G147100	Phvul.008G147100	0	0	0
15	1 Phvul.008G147100	Phvul.008G147100	0	0	0
16	1 Phvul.008G147100	Phvul.008G147100	0	0	0
17					
18	1 Phvul.006G086200	Phvul.006G086200	0 PTHR32133		0
19	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
20	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
21					
22	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
23	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
24	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
25					
26	1 Phvul.008G147100	Phvul.008G147100	0	0	0
27	1 Phvul.008G147100	Phvul.008G147100	0	0	0
28	1 Phvul.008G147100	Phvul.008G147100	0	0	0
29					
30	1 Phvul.006G086200	Phvul.006G086200	0 PTHR32133		0
31	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
32	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
33					
34	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
35	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
36	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
37					
38	1 Phvul.008G147100	Phvul.008G147100	0	0	0
39	1 Phvul.008G147100	Phvul.008G147100	0	0	0
40	1 Phvul.008G147100	Phvul.008G147100	0	0	0
41					
42	1 Phvul.006G086200	Phvul.006G086200	0 PTHR32133		0
43	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
44	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
45					
46	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
47	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
48	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
49					
50	1 Phvul.008G147100	Phvul.008G147100	0	0	0
51	1 Phvul.008G147100	Phvul.008G147100	0	0	0
52	1 Phvul.008G147100	Phvul.008G147100	0	0	0
53					
54	1 Phvul.006G086200	Phvul.006G086200	0 PTHR32133		0
55	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
56	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
57					
58	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
59	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
60	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
	1 Phvul.008G147100	Phvul.008G147100	0	0	0



1					
2	1 Phvul.008G147100	Phvul.008G147100	0	0	0
3	1 Phvul.008G147100	Phvul.008G147100	0	0	0
4	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
5					
6	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
7	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
8	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
9					
10	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
11	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
12	1 Phvul.008G147100	Phvul.008G147100	0	0	0
13					
14	1 Phvul.008G147100	Phvul.008G147100	0	0	0
15	1 Phvul.008G147100	Phvul.008G147100	0	0	0
16	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
17					
18	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
19	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
20	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
21					
22	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
23	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
24	1 Phvul.008G147100	Phvul.008G147100	0	0	0
25					
26	1 Phvul.008G147100	Phvul.008G147100	0	0	0
27	1 Phvul.008G147100	Phvul.008G147100	0	0	0
28	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
29					
30	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
31	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
32	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
33					
34	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
35	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
36	1 Phvul.008G147100	Phvul.008G147100	0	0	0
37	1 Phvul.008G147100	Phvul.008G147100	0	0	0
38					
39	1 Phvul.008G147100	Phvul.008G147100	0	0	0
40	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
41					
42	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
43	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
44	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
45					
46	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
47	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
48	1 Phvul.008G147100	Phvul.008G147100	0	0	0
49	1 Phvul.008G147100	Phvul.008G147100	0	0	0
50					
51	1 Phvul.008G147100	Phvul.008G147100	0	0	0
52	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
53					
54	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
55	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
56	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
57					
58	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
59	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
60	1 Phvul.008G147100	Phvul.008G147100	0	0	0
	1 Phvul.008G147100	Phvul.008G147100	0	0	0

1					
2	1 Phvul.008G147100	Phvul.008G147100	0	0	0
3	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
4	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
5	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
6	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
7	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
8	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
9	1 Phvul.008G147100	Phvul.008G147100	0	0	0
10	1 Phvul.008G147100	Phvul.008G147100	0	0	0
11	1 Phvul.008G147100	Phvul.008G147100	0	0	0
12	1 Phvul.008G147100	Phvul.008G147100	0	0	0
13	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
14	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
15	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
16	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
17	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
18	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
19	1 Phvul.008G147100	Phvul.008G147100	0	0	0
20	1 Phvul.008G147100	Phvul.008G147100	0	0	0
21	1 Phvul.008G147100	Phvul.008G147100	0	0	0
22	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
23	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
24	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
25	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
26	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
27	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
28	1 Phvul.008G147100	Phvul.008G147100	0	0	0
29	1 Phvul.008G147100	Phvul.008G147100	0	0	0
30	1 Phvul.008G147100	Phvul.008G147100	0	0	0
31	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
32	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
33	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
34	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
35	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
36	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
37	1 Phvul.008G147100	Phvul.008G147100	0	0	0
38	1 Phvul.008G147100	Phvul.008G147100	0	0	0
39	1 Phvul.008G147100	Phvul.008G147100	0	0	0
40	1 Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
41	1 Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P <sup>-</sup>	KOG2399
42	1 Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P <sup>-</sup>	0
43	1 Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P <sup>-</sup>	0
44	1 Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P <sup>-</sup>	0
45	1 Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P <sup>-</sup>	0
46	1 Phvul.008G147100	Phvul.008G147100	0	0	0
47	1 Phvul.008G147100	Phvul.008G147100	0	0	0
48	1 Phvul.008G147100	Phvul.008G147100	0	0	0
49	1 Phvul.008G147100	Phvul.008G147100	0	0	0
50	1 Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P <sup>-</sup>	0
51	1 Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P <sup>-</sup>	0
52	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P <sup>-</sup>	0
53	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
54	1 Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P <sup>-</sup>	0
55	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
56	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00	PTHR11689,P <sup>-</sup>	0
57	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P <sup>-</sup>	KOG4750
58	1 Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P <sup>-</sup>	0

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2	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
3	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
4	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P		KOG0546
5	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
6	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
7	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P		KOG0014
8	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
9	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
10	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
11	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
12	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
13	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002		KOG1187
14	1 Phvul.011G110300	Phvul.011G110300		0 PTHR34056,P	0
15	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
16	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
17	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P		KOG4750
18	1 Phvul.003G067000	Phvul.003G067000		0 PTHR34222,P	0
19	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
20	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
21	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P		KOG0546
22	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
23	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
24	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P		KOG0014
25	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
26	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
27	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
28	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
29	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
30	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002		KOG1187
31	1 Phvul.011G110300	Phvul.011G110300		0 PTHR34056,P	0
32	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
33	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
34	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P		KOG4750
35	1 Phvul.003G067000	Phvul.003G067000		0 PTHR34222,P	0
36	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
37	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
38	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P		KOG0546
39	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
40	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
41	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P		KOG0014
42	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
43	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
44	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
45	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
46	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
47	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002		KOG1187
48	1 Phvul.011G110300	Phvul.011G110300		0 PTHR34056,P	0
49	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
50	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
51	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P		KOG4750
52	1 Phvul.003G067000	Phvul.003G067000		0 PTHR34222,P	0
53	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
54	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
55	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P		KOG0546
56	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
57	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
58	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P		KOG0014
59	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
60	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
61	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
62	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
63	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
64	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002		KOG1187

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2	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P		0
3	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099		0
4	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
5					
6	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P	KOG4750	
7	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P		0
8	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P	KOG0769	
9					
10	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
11	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P	KOG0546	
12	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P		0
13					
14	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P		0
15	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P	KOG0014	
16	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P		0
17					
18	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
19	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P		0
20	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P		0
21					
22	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
23	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187	
24	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P		0
25					
26	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099		0
27	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
28	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P	KOG4750	
29	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P		0
30	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P	KOG0769	
31	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
32	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P	KOG0546	
33	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P		0
34					
35	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P		0
36	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P	KOG0014	
37					
38	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P		0
39	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
40	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P		0
41	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P		0
42					
43	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
44	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187	
45	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P		0
46	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099		0
47	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
48	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P	KOG4750	
49	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P		0
50	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P	KOG0769	
51	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
52	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P	KOG0546	
53	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P		0
54					
55	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P		0
56	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P	KOG0014	
57	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P		0
58					
59					
60					

1				
2	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
3	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
4	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
5				
6	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P'	0
7	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
8	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P'	0
9				
10	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
11	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P'	0
12	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P' KOG4750	
13				
14	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P'	0
15	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P' KOG0769	
16	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P'	0
17				
18	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P' KOG0546	
19	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P'	0
20	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P'	0
21				
22	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P' KOG0014	
23	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P'	0
24	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
25				
26	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
27	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
28	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P'	0
29	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
30	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P'	0
31	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
32	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P'	0
33				
34	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P' KOG4750	
35	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P'	0
36	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P' KOG0769	
37	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P'	0
38	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P' KOG0546	
39	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P'	0
40	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P'	0
41				
42	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P' KOG0014	
43	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P'	0
44	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
45	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
46	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
47	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P'	0
48	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
49	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P'	0
50	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
51	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P'	0
52	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P' KOG4750	
53	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P'	0
54	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P' KOG0769	
55	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P'	0
56	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P' KOG0546	
57	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P'	0
58	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P'	0
59				
60	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P' KOG0014	
	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P'	0
	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P'	0
	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P'	0
	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P'	0
	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P'	0
	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P' KOG4750	
	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P'	0
	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P' KOG0769	
	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P'	0



1					
2	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P	KOG0546	
3	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
4	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
5					
6	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P	KOG0014	
7	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
8	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
9					
10	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
11	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
12	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
13					
14	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187	
15	1 Phvul.011G110300	Phvul.011G110300		0 PTHR34056,P	0
16	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
17					
18	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
19	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P	KOG4750	
20	1 Phvul.003G067000	Phvul.003G067000		0 PTHR34222,P	0
21					
22	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
23	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
24	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P	KOG0546	
25	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
26	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
27	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P	KOG0014	
28	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
29	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
30	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
31	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
32	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
33	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187	
34	1 Phvul.011G110300	Phvul.011G110300		0 PTHR34056,P	0
35	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
36	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P		0
37	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P	KOG4750	
38	1 Phvul.003G067000	Phvul.003G067000		0 PTHR34222,P	0
39	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
40	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P		0
41	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P	KOG0546	
42	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
43	1 Phvul.005G087600	Phvul.005G087600		0 PTHR34379,P	0
44	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P	KOG0014	
45	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
46	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
47	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
48	1 Phvul.007G083500	Phvul.007G083500		0 PTHR36319,P	0
49	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P		0
50	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187	
51	1 Phvul.011G110300	Phvul.011G110300		0 PTHR34056,P	0
52	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0

1				
2	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
3	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup>	KOG4750
4	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
5				
6	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup>	KOG0769
7	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
8	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup>	KOG0546
9				
10	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0
11	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>	0
12	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup>	KOG0014
13	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P <sup>-</sup>	0
14	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
15	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
16	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
17	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
18	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>	0
19	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187
20	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>	0
21	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
22	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
23	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
24	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup>	KOG4750
25	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
26	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup>	KOG0769
27	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
28	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup>	KOG0546
29	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0
30	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>	0
31	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup>	KOG0014
32	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P <sup>-</sup>	0
33	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
34	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
35	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
36	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>	0
37	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187
38	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>	0
39	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
40	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
41	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup>	KOG4750
42	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
43	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup>	KOG0769
44	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
45	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup>	KOG0546
46	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0
47	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>	0
48	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup>	KOG0014
49	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P <sup>-</sup>	0
50	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
51	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
52	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
53	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>	0
54	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187
55	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>	0
56	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
57	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
58	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup>	KOG4750
59	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
60	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup>	KOG0769
61	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
62	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup>	KOG0546
63	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0
64	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>	0
65	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup>	KOG0014
66	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P <sup>-</sup>	0
67	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
68	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0



1				
2	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
3	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>	0
4	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
5				
6	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>	0
7	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
8	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
9				
10	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup> KOG4750	
11	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
12	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup> KOG0769	
13				
14	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
15	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup> KOG0546	
16	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0
17				
18	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>	0
19	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup> KOG0014	
20	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P <sup>-</sup>	0
21				
22	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
23				
24	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
25				
26	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>	0
27	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
28	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>	0
29				
30	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
31	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
32	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup> KOG4750	
33				
34	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
35	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup> KOG0769	
36	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
37				
38	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup> KOG0546	
39	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0
40	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>	0
41				
42	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup> KOG0014	
43	1 Phvul.011G108000	Phvul.011G108000	PF08241 PTHR10108,P <sup>-</sup>	0
44	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069	0
45				
46	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
47	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>	0
48	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>	0
49	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002 KOG1187	
50				
51	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>	0
52	1 Phvul.008G077700	Phvul.008G077700	PF01657 PTHR32099	0
53				
54	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>	0
55	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup> KOG4750	
56	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>	0
57	1 Phvul.001G240500	Phvul.001G240500	PF00153 PTHR24089,P <sup>-</sup> KOG0769	
58	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>	0
59				
60	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup> KOG0546	
	1 Phvul.009G132000	Phvul.009G132000	PF03141 PTHR10108,P <sup>-</sup>	0

1					
2	1 Phvul.005G087600	Phvul.005G087600	0 PTHR34379,P <sup>-</sup>		0
3	1 Phvul.009G130000	Phvul.009G130000	PF01486,PF00PTHR11945,P <sup>-</sup>	KOG0014	
4	1 Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P <sup>-</sup>	0
5					
6	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
7	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>		0
8	1 Phvul.007G083500	Phvul.007G083500	0 PTHR36319,P <sup>-</sup>		0
9					
10	1 Phvul.011G079800	Phvul.011G079800	PF00046,PF08PTHR24326,P <sup>-</sup>		0
11	1 Phvul.011G054900	Phvul.011G054900	PF01695,PF00PTHR23069		0
12	1 Phvul.008G077800	Phvul.008G077800	PF01657,PF07PTHR27002	KOG1187	
13					
14	1 Phvul.011G110300	Phvul.011G110300	0 PTHR34056,P <sup>-</sup>		0
15	1 Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
16	1 Phvul.005G005200	Phvul.005G005200	PF00571,PF00PTHR11689,P <sup>-</sup>		0
17					
18	1 Phvul.002G073200	Phvul.002G073200	PF00892	PTHR31218,P <sup>-</sup>	KOG4510
19	1 Phvul.002G073100	Phvul.002G073100	PF00892	PTHR31218,P <sup>-</sup>	KOG4510
20	1 Phvul.002G073100	Phvul.002G073100	PF00892	PTHR31218,P <sup>-</sup>	KOG4510
21					
22	1 Phvul.008G277800	Phvul.008G277800	PF00132,PF06PTHR23416,P <sup>-</sup>	KOG4750	
23	1 Phvul.003G067000	Phvul.003G067000	0 PTHR34222,P <sup>-</sup>		0
24	1 Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P <sup>-</sup>	KOG0769
25					
26	1 Phvul.008G061000	Phvul.008G061000	PF04851,PF08PTHR10799,P <sup>-</sup>		0
27	1 Phvul.003G246400	Phvul.003G246400	PF07719,PF00PTHR11071,P <sup>-</sup>	KOG0546	
28	1 Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P <sup>-</sup>	0
29	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P <sup>-</sup>	KOG0472	
30					
31	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
32	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup>	KOG1476
33	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup>	KOG0254
34					
35	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
36	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
37	1 Phvul.001G151600	Phvul.001G151600	0 PTHR34798,P <sup>-</sup>		0
38					
39	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P <sup>-</sup>	KOG3181	
40	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
41	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
42					
43	1 Phvul.007G156900	Phvul.007G156900	0 PTHR33981,P <sup>-</sup>		0
44	1 Phvul.007G157000	Phvul.007G157000	0 PTHR33981,P <sup>-</sup>		0
45	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P <sup>-</sup>		0
46					
47	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
48	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
49	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P <sup>-</sup>		0
50					
51	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
52	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
53	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup>	KOG0223
54					
55	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
56	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
57	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
58					
59	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
60	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
	1 Phvul.008G127800	Phvul.008G127800	0	0	0

1						
2	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P		0
3	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339	
4	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P			0
5	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000		KOG1187	
6	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P		KOG0472	
7	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P		0
8	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476	
9	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254	
10	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P		0
11	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339	
12	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P		0
13	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P		KOG3181	
14	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P		KOG1187	
15	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P		KOG1187	
16	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P		0
17	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P		0
18	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P			0
19	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P		0
20	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P		0
21	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P			0
22	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
23	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
24	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223	
25	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P		0
26	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
27	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
28	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
29	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
30	1 Phvul.008G127800	Phvul.008G127800		0	0	0
31	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P		0
32	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339	
33	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P			0
34	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000		KOG1187	
35	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P		KOG0472	
36	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P		0
37	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476	
38	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254	
39	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P		0
40	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339	
41	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P		0
42	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P		KOG3181	
43	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P		KOG1187	
44	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P		KOG1187	
45	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P		0
46	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P		0
47	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P			0

1					
2	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
3	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
4	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P <sup>-</sup>	0
5					
6	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
7	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
8	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup>	KOG0223
9					
10	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
11	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
12	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
13					
14	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
15	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
16	1 Phvul.008G127800	Phvul.008G127800		0 0	0
17					
18	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
19	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
20	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
21					
22	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
23	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup>	KOG0472
24	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
25					
26	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup>	KOG1476
27	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup>	KOG0254
28	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
29	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
30					
31	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
32	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P <sup>-</sup>	KOG3181
33	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup>	KOG1187
34	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup>	KOG1187
35	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
36	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
37					
38	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P <sup>-</sup>	0
39	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
40	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
41	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P <sup>-</sup>	0
42	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
43	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
44	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup>	KOG0223
45	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
46	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
47	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
48	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
49	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
50					
51	1 Phvul.008G127800	Phvul.008G127800		0 0	0
52	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
53	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
54	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
55	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
56	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup>	KOG0472
57					
58					
59					
60					

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2	1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
3	1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup> KOG1476	
4	1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup> KOG0254	
5						
6	1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
7	1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
8	1	Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
9						
10	1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P <sup>-</sup>	KOG3181	
11	1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
12	1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
13						
14	1	Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
15	1	Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
16	1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P <sup>-</sup>		0
17	1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
18	1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
19	1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P <sup>-</sup>		0
20	1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
21	1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
22						
23	1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup> KOG0223	
24	1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
25	1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
26	1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
27	1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
28	1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
29	1	Phvul.008G127800	Phvul.008G127800		0 0	0
30	1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
31	1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
32	1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P <sup>-</sup>		0
33	1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000	KOG1187	
34	1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P <sup>-</sup>	KOG0472	
35	1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
36	1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup> KOG1476	
37	1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup> KOG0254	
38	1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
39	1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
40	1	Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
41	1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P <sup>-</sup>	KOG3181	
42	1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
43	1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
44	1	Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
45	1	Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
46	1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P <sup>-</sup>		0
47	1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
48	1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
49	1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P <sup>-</sup>		0
50	1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
51	1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0



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2	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup>	KOG0223
3	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
4	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
5	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
6	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
7	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
8	1 Phvul.008G127800	Phvul.008G127800		0	0
9	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
10	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
11	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
12	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
13	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup>	KOG0472
14	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
15	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup>	KOG1476
16	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup>	KOG0254
17	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
18	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
19	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
20	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P <sup>-</sup>	KOG3181
21	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup>	KOG1187
22	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup>	KOG1187
23	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
24	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
25	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P <sup>-</sup>	0
26	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
27	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
28	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P <sup>-</sup>	0
29	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
30	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
31	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup>	KOG0223
32	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
33	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
34	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
35	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
36	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
37	1 Phvul.008G127800	Phvul.008G127800		0	0
38	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
39	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
40	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
41	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
42	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup>	KOG0472
43	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
44	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup>	KOG1476
45	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup>	KOG0254
46	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
47	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup>	KOG1339

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2	1 Phvul.001G151600	Phvul.001G151600	0 PTHR34798,P		0
3	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P	KOG3181	
4	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
5	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
6	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
7	1 Phvul.007G156900	Phvul.007G156900	0 PTHR33981,P		0
8	1 Phvul.007G157000	Phvul.007G157000	0 PTHR33981,P		0
9					
10	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P		0
11	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
12	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
13					
14	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P		0
15	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
16	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
17					
18	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
19	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
20	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
21					
22	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
23	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
24	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
25					
26	1 Phvul.008G127800	Phvul.008G127800	0	0	0
27	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
28	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
29					
30	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P		0
31	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000	KOG1187	
32	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P	KOG0472	
33					
34	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
35	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
36	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
37					
38	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
39	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
40	1 Phvul.001G151600	Phvul.001G151600	0 PTHR34798,P		0
41	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P	KOG3181	
42					
43	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
44	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
45	1 Phvul.007G156900	Phvul.007G156900	0 PTHR33981,P		0
46	1 Phvul.007G157000	Phvul.007G157000	0 PTHR33981,P		0
47					
48	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P		0
49	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
50					
51	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
52	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P		0
53					
54	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
55	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
56	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
57	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
58	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
59	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
60	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0



1					
2	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
3	1 Phvul.008G127800	Phvul.008G127800		0 0	0
4	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
5	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
6	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
7	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000 KOG1187	
8	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup> KOG0472	
9	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
10	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup> KOG1476	
11	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup> KOG0254	
12	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
13	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
14	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
15	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P <sup>-</sup> KOG3181	
16	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup> KOG1187	
17	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup> KOG1187	
18	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
19	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
20	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P <sup>-</sup>	0
21	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
22	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
23	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P <sup>-</sup>	0
24	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
25	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
26	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup> KOG0223	
27	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
28	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
29	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
30	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
31	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
32	1 Phvul.008G127800	Phvul.008G127800		0 0	0
33	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
34	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
35	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
36	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000 KOG1187	
37	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup> KOG0472	
38	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
39	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup> KOG1476	
40	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup> KOG0254	
41	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
42	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
43	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
44	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P <sup>-</sup> KOG3181	
45	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup> KOG1187	
46	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup> KOG1187	
47	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0

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2	1 Phvul.007G157000	Phvul.007G157000	0 PTHR33981,P		0
3	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P		0
4	1 Phvul.008G159000	Phvul.008G159000	PF10250 PTHR31741,P		0
5					
6	1 Phvul.005G114000	Phvul.005G114000	PF05634 PTHR10388,P		0
7	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P		0
8	1 Phvul.004G041500	Phvul.004G041500	PF02005 PTHR10631		0
9					
10	1 Phvul.004G041500	Phvul.004G041500	PF02005 PTHR10631		0
11	1 Phvul.007G084000	Phvul.007G084000	PF00230 PTHR19139,P KOG0223		
12	1 Phvul.009G119100	Phvul.009G119100	PF13386 PTHR33876,P		0
13					
14	1 Phvul.006G102900	Phvul.006G102900	PF06886 PTHR31358,P		0
15	1 Phvul.006G102900	Phvul.006G102900	PF06886 PTHR31358,P		0
16	1 Phvul.010G079200	Phvul.010G079200	PF04690 PTHR31675,P		0
17					
18	1 Phvul.010G079200	Phvul.010G079200	PF04690 PTHR31675,P		0
19	1 Phvul.008G127800	Phvul.008G127800	0 0		0
20	1 Phvul.001G038000	Phvul.001G038000	PF01843 PTHR13140,P		0
21					
22	1 Phvul.002G105200	Phvul.002G105200	PF00026 PTHR13683,P KOG1339		
23	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P		0
24	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000 KOG1187		
25					
26	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P KOG0472		
27	1 Phvul.002G157300	Phvul.002G157300	PF03479 PTHR31500,P		0
28	1 Phvul.009G146400	Phvul.009G146400	PF03360 PTHR10896,P KOG1476		
29	1 Phvul.011G046800	Phvul.011G046800	PF00083 PTHR23500,P KOG0254		
30					
31	1 Phvul.006G023000	Phvul.006G023000	PF00657 PTHR22835,P		0
32	1 Phvul.006G093600	Phvul.006G093600	PF00026 PTHR13683,P KOG1339		
33					
34	1 Phvul.001G151600	Phvul.001G151600	0 PTHR34798,P		0
35	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P KOG3181		
36	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P KOG1187		
37					
38	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P KOG1187		
39	1 Phvul.007G156900	Phvul.007G156900	0 PTHR33981,P		0
40	1 Phvul.007G157000	Phvul.007G157000	0 PTHR33981,P		0
41	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P		0
42					
43	1 Phvul.008G159000	Phvul.008G159000	PF10250 PTHR31741,P		0
44	1 Phvul.005G114000	Phvul.005G114000	PF05634 PTHR10388,P		0
45					
46	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P		0
47	1 Phvul.004G041500	Phvul.004G041500	PF02005 PTHR10631		0
48	1 Phvul.004G041500	Phvul.004G041500	PF02005 PTHR10631		0
49	1 Phvul.007G084000	Phvul.007G084000	PF00230 PTHR19139,P KOG0223		
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51	1 Phvul.009G119100	Phvul.009G119100	PF13386 PTHR33876,P		0
52	1 Phvul.006G102900	Phvul.006G102900	PF06886 PTHR31358,P		0
53					
54	1 Phvul.006G102900	Phvul.006G102900	PF06886 PTHR31358,P		0
55	1 Phvul.010G079200	Phvul.010G079200	PF04690 PTHR31675,P		0
56	1 Phvul.010G079200	Phvul.010G079200	PF04690 PTHR31675,P		0
57					
58	1 Phvul.008G127800	Phvul.008G127800	0 0		0
59	1 Phvul.001G038000	Phvul.001G038000	PF01843 PTHR13140,P		0
60	1 Phvul.002G105200	Phvul.002G105200	PF00026 PTHR13683,P KOG1339		
	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P		0

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2	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000	KOG1187	
3	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P	KOG0472	
4	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
5					
6	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
7	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
8					
9	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
10	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
11	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P	0
12	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P	KOG3181	
13					
14	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
15	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
16	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P	0
17					
18	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
19	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P		0
20	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
21					
22	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
23	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P		0
24	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
25					
26	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
27	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
28	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
29					
30	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
31	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
32	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
33					
34	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
35	1 Phvul.008G127800	Phvul.008G127800		0	0
36	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
37					
38	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
39	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P		0
40	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000	KOG1187	
41	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P	KOG0472	
42					
43	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
44	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
45	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
46					
47	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
48	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
49	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P	0
50					
51	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P	KOG3181	
52	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
53	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P	KOG1187	
54					
55	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P	0
56	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
57	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P		0
58					
59	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
60	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P		0

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2	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
3	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
4	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
5					
6	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
7	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
8	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
9					
10	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
11	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
12	1 Phvul.008G127800	Phvul.008G127800		0 0	0
13					
14	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
15	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
16	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
17					
18	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
19	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
20	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
21					
22	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
23	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
24	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
25					
26	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
27	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P	0
28	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
29	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
30					
31	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
32	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P	0
33	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P	0
34					
35	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
36	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
37	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
38					
39	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
40	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
41	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
42					
43	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
44	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
45	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
46	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
47	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
48	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
49					
50					
51	1 Phvul.008G127800	Phvul.008G127800		0 0	0
52	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
53	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
54					
55	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
56	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
57	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
58					
59	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
60	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254

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2	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
3	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
4	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
5					
6	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P <sup>-</sup>	KOG3181	
7	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
8					
9	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
10	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
11	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
12					
13	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P <sup>-</sup>		0
14	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
15	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
16	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P <sup>-</sup>		0
17					
18	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
19	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
20	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup> KOG0223	
21					
22	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
23	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
24	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
25					
26	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
27	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
28	1 Phvul.008G127800	Phvul.008G127800		0 0	0
29					
30	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
31	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
32	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16PTHR31413,P <sup>-</sup>		0
33					
34	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00PTHR27000	KOG1187	
35	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00PTHR27004,P <sup>-</sup>	KOG0472	
36	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
37	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup> KOG1476	
38					
39	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup> KOG0254	
40	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
41	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup> KOG1339	
42					
43	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
44	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00PTHR11760,P <sup>-</sup>	KOG3181	
45	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
46					
47	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00PTHR27000,P <sup>-</sup>	KOG1187	
48	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
49	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
50					
51	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00PTHR21499,P <sup>-</sup>		0
52	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
53					
54	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
55	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08PTHR31602,P <sup>-</sup>		0
56	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
57	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
58					
59	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup> KOG0223	
60	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0



1					
2	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
3	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
4	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
5					
6	1 Phvul.008G127800	Phvul.008G127800		0 0	0
7	1 Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P <sup>-</sup>	0
8	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
9					
10	1 Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P <sup>-</sup>	0
11	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
12	1 Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P <sup>-</sup>	0
13					
14	1 Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P <sup>-</sup>	KOG0254
15	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
16	1 Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P <sup>-</sup>	0
17					
18	1 Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P <sup>-</sup>	0
19	1 Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P <sup>-</sup>	KOG0472
20	1 Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P <sup>-</sup>	0
21					
22	1 Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P <sup>-</sup>	KOG1476
23	1 Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
24	1 Phvul.001G151600	Phvul.001G151600		0 PTHR34798,P <sup>-</sup>	0
25					
26	1 Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
27	1 Phvul.009G121200	Phvul.009G121200	PF02493,PF01	PTHR23086,P <sup>-</sup>	KOG0229
28	1 Phvul.009G121200	Phvul.009G121200	PF02493,PF01	PTHR23086,P <sup>-</sup>	KOG0229
29					
30	1 Phvul.007G156900	Phvul.007G156900		0 PTHR33981,P <sup>-</sup>	0
31	1 Phvul.007G157000	Phvul.007G157000		0 PTHR33981,P <sup>-</sup>	0
32	1 Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P <sup>-</sup>	0
33					
34	1 Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P <sup>-</sup>	KOG3181
35	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup>	KOG1187
36	1 Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P <sup>-</sup>	KOG1187
37					
38	1 Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P <sup>-</sup>	0
39	1 Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P <sup>-</sup>	0
40	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
41	1 Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
42					
43	1 Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P <sup>-</sup>	KOG1339
44	1 Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P <sup>-</sup>	KOG0223
45	1 Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P <sup>-</sup>	0
46					
47	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
48	1 Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P <sup>-</sup>	0
49	1 Phvul.008G127800	Phvul.008G127800		0 0	0
50					
51	1 Phvul.007G029900	Phvul.007G029900	PF00560,PF08	PTHR27008,P <sup>-</sup>	KOG1187
52	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
53	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
54					
55	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
56	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
57	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
58					
59	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
60	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>	0
	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0



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2	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541	
3	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193		0
4	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>		0
5	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>		0
6	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>		0
7	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906		0
8	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup>	KOG1594	
9	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130		0
10	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>		0
11	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>		0
12	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>		0
13	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>		0
14	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>		0
15	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>		0
16	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>-</sup>		0
17	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>		0
18	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243		0
19	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243		0
20	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383	
21	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383	
22	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243		0
23	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156	
24	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>		0
25	1 Phvul.L002444	Phvul.L002444		0 PTHR33401		0
26	1 Phvul.L002444	Phvul.L002444		0 PTHR33401		0
27	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473	
28	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600	
29	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>		0
30	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>		0
31	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329		0
32	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064		0
33	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064		0
34	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>		0
35	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>		0
36	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541	
37	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193		0
38	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>		0
39	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>		0
40	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>		0
41	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906		0
42	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup>	KOG1594	
43	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130		0
44	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>		0
45	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>		0
46	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>		0
47	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>		0

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2	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>	0
3	1 Phvul.006G154900	Phvul.006G154900	0 PTHR33739,P <sup>-</sup>	0
4	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>	0
5				
6	2 Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P <sup>-</sup>	0
7	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243	0
8	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243	0
9				
10	1 Phvul.008G017200	Phvul.008G017200	PF00282 PTHR11999,P <sup>-</sup> KOG1383	
11	1 Phvul.008G017200	Phvul.008G017200	PF00282 PTHR11999,P <sup>-</sup> KOG1383	
12	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243	0
13				
14	1 Phvul.007G106300	Phvul.007G106300	PF00067 PTHR24298,P <sup>-</sup> KOG0156	
15	1 Phvul.009G034400	Phvul.009G034400	PF16913 PTHR31376,P <sup>-</sup>	0
16	1 Phvul.L002444	Phvul.L002444	0 PTHR33401	0
17				
18	1 Phvul.L002444	Phvul.L002444	0 PTHR33401	0
19	1 Phvul.008G070000	Phvul.008G070000	PF01988 PTHR31851,P <sup>-</sup> KOG4473	
20	1 Phvul.010G156200	Phvul.010G156200	PF00487 PTHR11351,P <sup>-</sup> KOG1600	
21				
22	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04PTHR21450,P <sup>-</sup>	0
23	1 Phvul.008G043500	Phvul.008G043500	PF00847 PTHR32467,P <sup>-</sup>	0
24	1 Phvul.009G079400	Phvul.009G079400	PF05254 PTHR21329	0
25				
26	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064	0
27	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064	0
28	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14PTHR24015,P <sup>-</sup>	0
29	1 Phvul.009G030200	Phvul.009G030200	PF08241 PTHR10108,P <sup>-</sup>	0
30	1 Phvul.004G166100	Phvul.004G166100	PF00578 PTHR10430 KOG0541	
31	1 Phvul.009G160200	Phvul.009G160200	PF13414 PTHR16193	0
32	1 Phvul.002G119600	Phvul.002G119600	PF11443 PTHR31373,P <sup>-</sup>	0
33	1 Phvul.002G150800	Phvul.002G150800	PF00155 PTHR11751,P <sup>-</sup>	0
34	1 Phvul.002G271400	Phvul.002G271400	PF00266 PTHR11601,P <sup>-</sup>	0
35				
36	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00PTHR10906	0
37	1 Phvul.001G110100	Phvul.001G110100	0 PTHR11122,P <sup>-</sup> KOG1594	
38	1 Phvul.002G037500	Phvul.002G037500	0 PTHR17130	0
39				
40	1 Phvul.002G017700	Phvul.002G017700	PF00069 PTHR27001,P <sup>-</sup>	0
41	1 Phvul.002G017700	Phvul.002G017700	PF00069 PTHR27001,P <sup>-</sup>	0
42	1 Phvul.007G022500	Phvul.007G022500	PF00111 PTHR19370,P <sup>-</sup>	0
43	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>	0
44	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>	0
45	1 Phvul.006G154900	Phvul.006G154900	0 PTHR33739,P <sup>-</sup>	0
46	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>	0
47	2 Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P <sup>-</sup>	0
48	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243	0
49	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243	0
50				
51	1 Phvul.008G017200	Phvul.008G017200	PF00282 PTHR11999,P <sup>-</sup> KOG1383	
52	1 Phvul.008G017200	Phvul.008G017200	PF00282 PTHR11999,P <sup>-</sup> KOG1383	
53	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243	0
54	1 Phvul.007G106300	Phvul.007G106300	PF00067 PTHR24298,P <sup>-</sup> KOG0156	
55	1 Phvul.009G034400	Phvul.009G034400	PF16913 PTHR31376,P <sup>-</sup>	0
56	1 Phvul.L002444	Phvul.L002444	0 PTHR33401	0
57				
58				
59				
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1					
2	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
3	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>+</sup> KOG4473	
4	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>+</sup> KOG1600	
5					
6	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>+</sup>	0
7	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>+</sup>	0
8	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
9					
10	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
11	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
12	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>+</sup>	0
13					
14	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>+</sup>	0
15	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
16	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
17					
18	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>+</sup>	0
19	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>+</sup>	0
20	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>+</sup>	0
21					
22	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
23	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>+</sup> KOG1594	
24	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
25					
26	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>+</sup>	0
27	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>+</sup>	0
28	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>+</sup>	0
29					
30	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>+</sup>	0
31	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>+</sup>	0
32	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>+</sup>	0
33					
34	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>+</sup>	0
35	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>+</sup>	0
36	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
37	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
38					
39	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>+</sup> KOG1383	
40	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>+</sup> KOG1383	
41					
42	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
43	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>+</sup> KOG0156	
44	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>+</sup>	0
45					
46	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
47	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
48	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>+</sup> KOG4473	
49	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>+</sup> KOG1600	
50					
51	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>+</sup>	0
52	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>+</sup>	0
53	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
54					
55	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
56	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
57	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>+</sup>	0
58	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>+</sup>	0
59	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
60	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0

1					
2	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
3	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
4	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
5					
6	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
7	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup>	KOG1594
8	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
9					
10	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
11	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
12	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
13					
14	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
15	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
16	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0
17					
18	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>-</sup>	0
19	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
20	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
21					
22	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
23	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
24	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
25					
26	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
27	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
28	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
29					
30	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
31	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
32	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473
33	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
34					
35	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
36	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
37	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
38					
39	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
40	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
41					
42	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>	0
43	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
44	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
45	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
46					
47	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
48	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
49	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
50					
51	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
52	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup>	KOG1594
53	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
54					
55	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
56	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
57	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
58					
59	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
60	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0

1					
2	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>		0
3	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
4	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
5					
6	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
7	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
8	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
9					
10	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
11	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup> KOG0156	
12	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
13					
14	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
15	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
16	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup> KOG4473	
17	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup> KOG1600	
18					
19	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04PTHR21450,P <sup>-</sup>		0
20	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
21					
22	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
23	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
24	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
25					
26	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14PTHR24015,P <sup>-</sup>		0
27	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
28	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
29	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
30					
31	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
32	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
33	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
34					
35	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00PTHR10906		0
36	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup> KOG1594	
37	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
38					
39	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
40	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
41	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
42					
43	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
44	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
45	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0
46					
47	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>		0
48	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
49	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
50					
51	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
52	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
53	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
54					
55	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
56	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup> KOG0156	
57	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
58					
59	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
60	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup> KOG4473	



1					
2	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
3	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
4	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
5					
6	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
7	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
8	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
9					
10	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>	0
11	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
12	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
13					
14	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
15	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
16	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
17					
18	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
19	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
20	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup>	KOG1594
21					
22	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
23	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
24	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
25					
26	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
27	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
28	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
29					
30	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0
31	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>-</sup>	0
32	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
33					
34	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
35	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
36	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
37	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
38					
39	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
40	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
41	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
42					
43	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
44	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
45					
46	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473
47	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
48	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
49	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
50					
51	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
52	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
53	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
54					
55	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>	0
56	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
57	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
58					
59	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
60	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0



1					
2	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
3	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
4	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P	KOG1594
5					
6	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
7	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
8	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
9					
10	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
11	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
12	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
13					
14	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P	0
15	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P	0
16	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
17					
18	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
19	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
20	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
21	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
22					
23	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
24	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
25					
26	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
27	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
28	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
29					
30	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
31	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
32	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
33	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
34					
35	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
36	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
37	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
38					
39	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
40	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
41	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
42					
43	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
44	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
45	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
46					
47	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
48	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
49	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P	KOG1594
50					
51	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
52	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
53	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
54					
55	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
56	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
57	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
58					
59	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P	0
60	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P	0
	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0

1					
2	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
3	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
4	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
5	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
6	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
7	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
8	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
9	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
10	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
11	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
12	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
13	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
14	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473
15	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
16	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
17	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
18	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
19	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
20	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
21	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064		0
22	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064		0
23	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>	0
24	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
25	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
26	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
27	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
28	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
29	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
30	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
31	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
32	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
33	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
34	1 Phvul.001G110100	Phvul.001G110100	0 PTHR11122,P <sup>-</sup>	KOG1594	
35	1 Phvul.002G037500	Phvul.002G037500	0 PTHR17130		0
36	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
37	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
38	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
39	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
40	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
41	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
42	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
43	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
44	1 Phvul.006G154900	Phvul.006G154900	0 PTHR33739,P <sup>-</sup>		0
45	1 Phvul.006G154900	Phvul.006G154900	0 PTHR33739,P <sup>-</sup>		0
46	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>-</sup>	0
47	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
48	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
49	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
50	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
51	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
52	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
53	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
54	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
55	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
56	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
57	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
58	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
59	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
60	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
61	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473
62	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473
63	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
64	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
65	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0

1					
2	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P'	0
3	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
4	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
5					
6	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
7	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P'	0
8	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P'	0
9					
10	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
11	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
12	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P'	0
13					
14	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P'	0
15	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P'	0
16	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
17					
18	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P' KOG1594	
19	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
20	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P'	0
21					
22	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P'	0
23	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P'	0
24	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P'	0
25					
26	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P'	0
27	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P'	0
28	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P'	0
29					
30	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P'	0
31	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
32	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
33					
34	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P' KOG1383	
35	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P' KOG1383	
36	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
37	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P' KOG0156	
38					
39	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P'	0
40	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
41					
42	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
43	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P' KOG4473	
44	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P' KOG1600	
45	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P'	0
46					
47	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P'	0
48	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
49	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
50					
51	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
52	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P'	0
53	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P'	0
54					
55	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
56	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
57	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P'	0
58					
59	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P'	0
60	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P'	0
	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0

1					
2	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup> KOG1594	
3	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
4	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
5	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
6	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
7	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
8	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
9	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0
10	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>		0
11	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
12	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
13	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
14	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
15	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
16	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
17	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup> KOG0156	
18	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
19	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
20	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
21	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup> KOG4473	
22	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup> KOG1600	
23	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04PTHR21450,P <sup>-</sup>		0
24	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
25	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
26	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
27	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
28	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14PTHR24015,P <sup>-</sup>		0
29	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
30	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
31	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
32	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
33	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
34	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
35	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00PTHR10906		0
36	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup> KOG1594	
37	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
38	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
39	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
40	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
41	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
42	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
43	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0
44	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>		0
45	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
46	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
47	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0

1					
2	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>+</sup> KOG1383	
3	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>+</sup> KOG1383	
4	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
5					
6	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>+</sup> KOG0156	
7	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>+</sup>	0
8	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
9					
10	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
11	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>+</sup> KOG4473	
12	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>+</sup> KOG1600	
13					
14	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>+</sup>	0
15	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>+</sup>	0
16	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
17					
18	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
19	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
20	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>+</sup>	0
21	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>+</sup>	0
22					
23	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
24	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
25					
26	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>+</sup>	0
27	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>+</sup>	0
28	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>+</sup>	0
29					
30	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
31	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>+</sup> KOG1594	
32	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
33					
34	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>+</sup>	0
35	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>+</sup>	0
36	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>+</sup>	0
37	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>+</sup>	0
38					
39	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>+</sup>	0
40	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>+</sup>	0
41	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>+</sup>	0
42					
43	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>+</sup>	0
44	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
45	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
46					
47	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>+</sup> KOG1383	
48	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>+</sup> KOG1383	
49	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
50					
51	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>+</sup> KOG0156	
52	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>+</sup>	0
53	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
54					
55	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
56	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>+</sup> KOG4473	
57	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>+</sup> KOG1600	
58					
59	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>+</sup>	0
60	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>+</sup>	0
	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0



1					
2	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064		0
3	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064		0
4	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14PTHR24015,P <sup>-</sup>		0
5	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
6	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
7	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
8	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
9	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
10	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
11	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
12	1 Phvul.001G110100	Phvul.001G110100	0 PTHR11122,P <sup>-</sup>	KOG1594	
13	1 Phvul.002G037500	Phvul.002G037500	0 PTHR17130		0
14	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
15	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
16	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
17	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
18	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P <sup>-</sup>	0
19	1 Phvul.006G154900	Phvul.006G154900	0 PTHR33739,P <sup>-</sup>		0
20	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P <sup>-</sup>	0
21	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
22	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
23	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
24	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
25	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup>	KOG1383
26	1 Phvul.003G056900	Phvul.003G056900	0 PTHR37243		0
27	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup>	KOG0156
28	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
29	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
30	1 Phvul.L002444	Phvul.L002444	0 PTHR33401		0
31	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup>	KOG4473
32	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup>	KOG1600
33	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
34	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
35	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
36	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064		0
37	1 Phvul.001G193000	Phvul.001G193000	0 PTHR36064		0
38	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P <sup>-</sup>	0
39	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
40	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
41	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
42	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
43	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
44	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
45	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
46	1 Phvul.001G110100	Phvul.001G110100	0 PTHR11122,P <sup>-</sup>	KOG1594	
47	1 Phvul.002G037500	Phvul.002G037500	0 PTHR17130		0



1					
2	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
3	1 Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P <sup>-</sup>	0
4	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
5					
6	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
7	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
8	1 Phvul.006G154900	Phvul.006G154900		0 PTHR33739,P <sup>-</sup>	0
9					
10	1 Phvul.006G047000	Phvul.006G047000	PF02922,PF00PTHR10357,P <sup>-</sup>		0
11	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
12	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
13					
14	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
15	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
16	1 Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P <sup>-</sup> KOG1383	
17					
18	1 Phvul.003G056900	Phvul.003G056900		0 PTHR37243	0
19	1 Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P <sup>-</sup> KOG0156	
20	1 Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P <sup>-</sup>	0
21					
22	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
23	1 Phvul.L002444	Phvul.L002444		0 PTHR33401	0
24					
25	1 Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P <sup>-</sup> KOG4473	
26	1 Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P <sup>-</sup> KOG1600	
27	1 Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
28	1 Phvul.009G217000	Phvul.009G217000	PF04783,PF04PTHR21450,P <sup>-</sup>		0
29	1 Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P <sup>-</sup>	0
30					
31	1 Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P <sup>-</sup>	0
32	1 Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
33					
34	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
35	1 Phvul.001G193000	Phvul.001G193000		0 PTHR36064	0
36	1 Phvul.009G167700	Phvul.009G167700	PF13193,PF00PTHR24096,P <sup>-</sup> KOG1176		
37	1 Phvul.003G154400	Phvul.003G154400	PF12854,PF14PTHR24015,P <sup>-</sup>		0
38					
39	1 Phvul.L003746	Phvul.L003746	PF01823	PTHR33199,P <sup>-</sup>	0
40	1 Phvul.L003746	Phvul.L003746	PF01823	PTHR33199,P <sup>-</sup>	0
41					
42	1 Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P <sup>-</sup>	0
43	1 Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430 KOG0541	
44	1 Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P <sup>-</sup>	0
45	1 Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P <sup>-</sup>	0
46					
47	1 Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P <sup>-</sup>	0
48	1 Phvul.011G166200	Phvul.011G166200	PF10559,PF00PTHR10906		0
49	2 Phvul.006G067900	Phvul.006G067900	PF01699	PTHR31503,P <sup>-</sup> KOG1397	
50					
51	1 Phvul.001G110100	Phvul.001G110100		0 PTHR11122,P <sup>-</sup> KOG1594	
52	1 Phvul.002G037500	Phvul.002G037500		0 PTHR17130	0
53					
54	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
55	1 Phvul.010G115000	Phvul.010G115000	PF00400,PF12PTHR13950,P <sup>-</sup>		0
56	1 Phvul.002G157000	Phvul.002G157000	PF08372,PF00PTHR10024,P <sup>-</sup>		0
57	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P <sup>-</sup>		0
58					
59	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P <sup>-</sup>		0
60	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0

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2	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
3	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
4	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
5					
6	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
7	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
8	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
9					
10	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
11	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764	
12	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764	
13					
14	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>-</sup>	KOG2381
15	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
16	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>		0
17	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>		0
18	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>		0
19	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>		0
20	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>		0
21	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>		0
22					
23	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P <sup>-</sup>	0
24	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup>	KOG4172
25	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup>	KOG4172
26	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
27	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup>	KOG4172
28	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>-</sup>	0
29	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P <sup>-</sup>	KOG0773	
30	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
31	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
32	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
33	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
34	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P <sup>-</sup>	0
35	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
36	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
37	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P <sup>-</sup>	0
38	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
39	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
40	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P <sup>-</sup>	0
41	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
42	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
43	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P <sup>-</sup>	0
44	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup>	KOG4551
45	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P <sup>-</sup>		0
46	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
47	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
48	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
49	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
50	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
51	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0

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2	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
3	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
4	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
5	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
6	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
7	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
8	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
9	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P		0
10	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P		0
11	1 Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P		0
12	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
13	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
14	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0
15	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0
16	1 Phvul.006G075600	Phvul.006G075600	PF00141 PTHR31388,P		0
17	1 Phvul.008G284900	Phvul.008G284900	PF08801 PTHR13405,P		0
18	1 Phvul.007G163400	Phvul.007G163400	PF00632 PTHR11254,P		0
19	1 Phvul.001G266600	Phvul.001G266600	PF00464 PTHR11680,P		0
20	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
21	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
22	1 Phvul.003G037500	Phvul.003G037500	PF00454 PTHR15245,P	KOG2381	
23	1 Phvul.009G007300	Phvul.009G007300	0 PTHR35993		0
24	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
25	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
26	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
27	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
28	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
29	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
30	1 Phvul.007G156200	Phvul.007G156200	PF00010 PTHR12565,P		0
31	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
32	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
33	2 Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P		0
34	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
35	1 Phvul.008G243700	Phvul.008G243700	PF01764 PTHR21493,P		0
36	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
37	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
38	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
39	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
40	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
41	1 Phvul.003G181600	Phvul.003G181600	PF13639 PTHR22763,P		0
42	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
43	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
44	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
45	1 Phvul.006G164800	Phvul.006G164800	PF04765 PTHR12956,P		0
46	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
47	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
48	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
49	1 Phvul.005G059700	Phvul.005G059700	PF00141 PTHR31235,P		0
50	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
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2	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
3	1	Phvul.005G059500	Phvul.005G059500	PF00141 PTHR31235,P <sup>-</sup>	0
4	1	Phvul.002G116800	Phvul.002G116800	PF10181 PTHR15231,P <sup>-</sup>	KOG4551
5					
6	1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P <sup>-</sup>	0
7	1	Phvul.008G075300	Phvul.008G075300	0 PTHR33601,P <sup>-</sup>	0
8	1	Phvul.003G262800	Phvul.003G262800	PF02519 PTHR31374,P <sup>-</sup>	0
9					
10	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P <sup>-</sup>	KOG4658
11	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P <sup>-</sup>	KOG4658
12	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
13					
14	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
15	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
16	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>	0
17	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>	0
18	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>	0
19	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>	0
20	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>	0
21					
22	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
23	1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P <sup>-</sup>	0
24	1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P <sup>-</sup>	0
25					
26	1	Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P <sup>-</sup>	0
27	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P <sup>-</sup>	0
28	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P <sup>-</sup>	0
29	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P <sup>-</sup>	0
30	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P <sup>-</sup>	0
31	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P <sup>-</sup>	0
32	1	Phvul.006G075600	Phvul.006G075600	PF00141 PTHR31388,P <sup>-</sup>	0
33	1	Phvul.008G284900	Phvul.008G284900	PF08801 PTHR13405,P <sup>-</sup>	0
34	1	Phvul.007G163400	Phvul.007G163400	PF00632 PTHR11254,P <sup>-</sup>	0
35	1	Phvul.001G266600	Phvul.001G266600	PF00464 PTHR11680,P <sup>-</sup>	0
36	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764
37					
38	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764
39	1	Phvul.003G037500	Phvul.003G037500	PF00454 PTHR15245,P <sup>-</sup>	KOG2381
40					
41	1	Phvul.009G007300	Phvul.009G007300	0 PTHR35993	0
42					
43	1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>	0
44	1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>	0
45	1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>	0
46					
47	1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>	0
48	1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>	0
49	1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>	0
50					
51	1	Phvul.007G156200	Phvul.007G156200	PF00010 PTHR12565,P <sup>-</sup>	0
52	1	Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P <sup>-</sup>	KOG4172
53	1	Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P <sup>-</sup>	KOG4172
54					
55	2	Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P <sup>-</sup>	0
56	1	Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P <sup>-</sup>	KOG4172
57	1	Phvul.008G243700	Phvul.008G243700	PF01764 PTHR21493,P <sup>-</sup>	0
58	1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P <sup>-</sup>	KOG0773
59					
60	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0

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2	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
3	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
4	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P <sup>-</sup>	0
5	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
6	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
7	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
8	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P <sup>-</sup>	0
9	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
10	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
11	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
12	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P <sup>-</sup>	0
13	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
14	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
15	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
16	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P <sup>-</sup>	0
17	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup>	KOG4551
18	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P <sup>-</sup>	0
19	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
20	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
21	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
22	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
23	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
24	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
25	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
26	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
27	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
28	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
29	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
30	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
31	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
32	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
33	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
34	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
35	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
36	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
37	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P <sup>-</sup>	0
38	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
39	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
40	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
41	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
42	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
43	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
44	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
45	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
46	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
47	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
48	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
49	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
50	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
51	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup>	KOG1764
52	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup>	KOG1764
53	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup>	KOG1764
54	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>-</sup>	KOG2381
55	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
56	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
57	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
58	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
59	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P <sup>-</sup>	0
60	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P <sup>-</sup>	0
	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P <sup>-</sup>	0



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2	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
3	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
4	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
5	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
6	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
7	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
8	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
9	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
10	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P		KOG0773
11	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
12	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
13	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
14	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
15	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
16	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
17	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
18	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
19	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
20	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
21	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
22	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
23	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
24	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
25	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
26	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
27	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
28	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
29	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
30	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
31	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P		0
32	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P	0
33	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
34	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
35	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
36	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
37	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
38	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
39	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
40	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
41	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
42	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
43	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
44	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P		0
45	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P		0
46	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
47	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
48	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
49	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
50	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
51	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
52	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
53	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0



1					
2	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
3	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
4	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
5					
6	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
7	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
8	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
9					
10	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
11	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
12	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
13					
14	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
15	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
16	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
17					
18	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
19	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
20	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
21					
22	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
23	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
24	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
25					
26	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
27	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
28	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
29	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
30					
31	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
32	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
33	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
34					
35	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
36	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
37	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
38					
39	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
40	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
41	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
42					
43	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
44	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
45	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P		0
46					
47	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P	0
48	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
49	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
50	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
51					
52	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
53	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
54					
55	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
56	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
57	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
58	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
59	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
60	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0

1					
2	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P		0
3	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P		0
4	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
5					
6	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
7	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
8	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
9					
10	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
11	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
12	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
13					
14	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
15	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
16	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
17	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
18	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
19					
20	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
21					
22	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
23	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
24	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
25					
26	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
27	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
28	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
29					
30	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
31	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
32	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
33					
34	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
35	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
36	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
37	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
38					
39	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
40	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
41					
42	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
43	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
44	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
45	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
46					
47	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
48	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
49	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
50					
51	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
52	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
53	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
54					
55	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
56	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
57	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
58	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P		0
59	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P	0
60	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0

1					
2	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>+</sup> KOG4658	
3	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>+</sup> KOG4658	
4	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>+</sup>	0
5					
6	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>+</sup>	0
7	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>+</sup>	0
8	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>+</sup>		0
9					
10	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>+</sup>		0
11	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>+</sup>		0
12	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>+</sup>		0
13					
14	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>+</sup>	0
15	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P <sup>+</sup>		0
16	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P <sup>+</sup>		0
17					
18	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>+</sup>	0
19	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>+</sup>	0
20	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>+</sup>	0
21					
22	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>+</sup>	0
23	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>+</sup>	0
24	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>+</sup>	0
25					
26	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>+</sup>	0
27	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>+</sup>	0
28	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>+</sup>	0
29					
30	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>+</sup> KOG1764		
31	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>+</sup> KOG1764		
32	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>+</sup> KOG2381	
33					
34	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
35	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>+</sup>		0
36	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>+</sup>		0
37	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>+</sup>		0
38					
39	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>+</sup>		0
40	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>+</sup>		0
41	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>+</sup>		0
42					
43	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P <sup>+</sup>	0
44	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>+</sup> KOG4172	
45	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>+</sup> KOG4172	
46					
47	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>+</sup>	0
48	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>+</sup> KOG4172	
49	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>+</sup>	0
50					
51	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P <sup>+</sup> KOG0773		
52	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>+</sup>	0
53	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>+</sup>	0
54					
55	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>+</sup>	0
56	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>+</sup>	0
57	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P <sup>+</sup>	0
58					
59	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>+</sup>	0
60	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>+</sup>	0
	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P <sup>+</sup>	0

1					
2	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
3	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
4	1	Phvul.005G059700	Phvul.005G059700	PF00141 PTHR31235,P <sup>-</sup>	0
5	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
6	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
7	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P <sup>-</sup>	0
8	1	Phvul.005G059500	Phvul.005G059500	PF00141 PTHR31235,P <sup>-</sup>	0
9	1	Phvul.002G116800	Phvul.002G116800	PF10181 PTHR15231,P <sup>-</sup>	KOG4551
10	1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P <sup>-</sup>	0
11	1	Phvul.008G075300	Phvul.008G075300	0 PTHR33601,P <sup>-</sup>	0
12	1	Phvul.003G262800	Phvul.003G262800	PF02519 PTHR31374,P <sup>-</sup>	0
13	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P <sup>-</sup>	KOG4658
14	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P <sup>-</sup>	KOG4658
15	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
16	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
17	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
18	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>	0
19	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>	0
20	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>	0
21	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>	0
22	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P <sup>-</sup>	0
23	1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P <sup>-</sup>	0
24	1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P <sup>-</sup>	0
25	1	Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P <sup>-</sup>	0
26	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P <sup>-</sup>	0
27	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P <sup>-</sup>	0
28	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P <sup>-</sup>	0
29	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P <sup>-</sup>	0
30	1	Phvul.006G075600	Phvul.006G075600	PF00141 PTHR31388,P <sup>-</sup>	0
31	1	Phvul.008G284900	Phvul.008G284900	PF08801 PTHR13405,P <sup>-</sup>	0
32	1	Phvul.007G163400	Phvul.007G163400	PF00632 PTHR11254,P <sup>-</sup>	0
33	1	Phvul.001G266600	Phvul.001G266600	PF00464 PTHR11680,P <sup>-</sup>	0
34	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764
35	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764
36	1	Phvul.003G037500	Phvul.003G037500	PF00454 PTHR15245,P <sup>-</sup>	KOG2381
37	1	Phvul.009G007300	Phvul.009G007300	0 PTHR35993	0
38	1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>	0
39	1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>	0
40	1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>	0
41	1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>	0
42	1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>	0
43	1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>	0
44	1	Phvul.007G156200	Phvul.007G156200	PF00010 PTHR12565,P <sup>-</sup>	0
45	1	Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P <sup>-</sup>	KOG4172
46	1	Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P <sup>-</sup>	KOG4172
47	2	Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P <sup>-</sup>	0
48	1	Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P <sup>-</sup>	KOG4172

1					
2	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>-</sup>	0
3	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P <sup>-</sup>	KOG0773	
4	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
5					
6	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
7	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
8	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
9					
10	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P <sup>-</sup>	0
11	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
12	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
13					
14	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P <sup>-</sup>	0
15	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
16	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
17					
18	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P <sup>-</sup>	0
19	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
20	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P <sup>-</sup>	0
21					
22	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P <sup>-</sup>	0
23	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup>	KOG4551
24	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P <sup>-</sup>		0
25					
26	1 Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P <sup>-</sup>	0
27	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
28	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
29	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
30					
31	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P <sup>-</sup>	0
32	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P <sup>-</sup>	0
33	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P <sup>-</sup>	0
34					
35	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>		0
36	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>		0
37	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>		0
38					
39	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>		0
40	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P <sup>-</sup>	0
41	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P <sup>-</sup>		0
42					
43	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P <sup>-</sup>		0
44	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
45	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
46	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
47					
48	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
49	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
50					
51	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
52	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
53	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
54					
55	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
56	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764	
57	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764	
58					
59	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>-</sup>	KOG2381
60	1 Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>		0



1					
2	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
3	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
4	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
5	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
6	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
7	1 Phvul.007G156200	Phvul.007G156200	PF00010 PTHR12565,P		0
8	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P KOG4172		
9	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P KOG4172		
10	2 Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P		0
11	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P KOG4172		
12	1 Phvul.008G243700	Phvul.008G243700	PF01764 PTHR21493,P		0
13	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
14	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
15	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
16	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
17	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
18	1 Phvul.003G181600	Phvul.003G181600	PF13639 PTHR22763,P		0
19	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
20	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
21	1 Phvul.006G164800	Phvul.006G164800	PF04765 PTHR12956,P		0
22	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
23	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
24	1 Phvul.005G059700	Phvul.005G059700	PF00141 PTHR31235,P		0
25	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
26	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
27	1 Phvul.005G059500	Phvul.005G059500	PF00141 PTHR31235,P		0
28	1 Phvul.002G116800	Phvul.002G116800	PF10181 PTHR15231,P	KOG4551	
29	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P		0
30	1 Phvul.008G075300	Phvul.008G075300	0 PTHR33601,P		0
31	1 Phvul.003G262800	Phvul.003G262800	PF02519 PTHR31374,P		0
32	1 Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658	
33	1 Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658	
34	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
35	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
36	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
37	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
38	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
39	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
40	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
41	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
42	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P		0
43	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P		0
44	1 Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P		0
45	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
46	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
47	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0



1					
2	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
3	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
4	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
5					
6	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
7	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
8					
9	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
10	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
11	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
12	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
13					
14	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
15	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
16	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
17					
18	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
19	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
20	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
21					
22	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
23	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
24	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
25					
26	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
27	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
28	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
29					
30	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
31	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
32	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
33					
34	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
35	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
36	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
37	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
38					
39	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
40	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
41	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
42					
43	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
44	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
45	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
46					
47	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
48	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
49	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
50					
51	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P		0
52	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P	0
53	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
54					
55	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
56	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
57	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
58					
59	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
60	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0

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2	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
3	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
4	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
5					
6	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
7	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P		0
8	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P		0
9					
10	1 Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P		0
11	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
12	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
13					
14	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0
15	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0
16	1 Phvul.006G075600	Phvul.006G075600	PF00141 PTHR31388,P		0
17					
18	1 Phvul.008G284900	Phvul.008G284900	PF08801 PTHR13405,P		0
19	1 Phvul.007G163400	Phvul.007G163400	PF00632 PTHR11254,P		0
20	1 Phvul.001G266600	Phvul.001G266600	PF00464 PTHR11680,P		0
21					
22	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
23	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
24	1 Phvul.003G037500	Phvul.003G037500	PF00454 PTHR15245,P	KOG2381	
25					
26	1 Phvul.009G007300	Phvul.009G007300	0 PTHR35993		0
27	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
28	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
29					
30	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
31	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
32	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
33	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
34					
35	1 Phvul.007G156200	Phvul.007G156200	PF00010 PTHR12565,P		0
36	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
37	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
38					
39	2 Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P		0
40	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
41					
42	1 Phvul.008G243700	Phvul.008G243700	PF01764 PTHR21493,P		0
43	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
44	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
45	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
46					
47	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
48	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
49	1 Phvul.003G181600	Phvul.003G181600	PF13639 PTHR22763,P		0
50					
51	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
52	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
53					
54	1 Phvul.006G164800	Phvul.006G164800	PF04765 PTHR12956,P		0
55	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
56	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
57	1 Phvul.005G059700	Phvul.005G059700	PF00141 PTHR31235,P		0
58					
59	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
60	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
	1 Phvul.005G059500	Phvul.005G059500	PF00141 PTHR31235,P		0

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2	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup> KOG4551	
3	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P <sup>-</sup>	0
4	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
5					
6	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
7	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup> KOG4658	
8	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup> KOG4658	
9					
10	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
11	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
12					
13	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
14	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
15	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
16	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
17					
18	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
19	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
20	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P <sup>-</sup>	0
21					
22	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
23	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
24	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
25					
26	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
27	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
28	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
29					
30	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
31	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
32	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
33					
34	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
35	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup> KOG1764	
36	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup> KOG1764	
37					
38	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>-</sup> KOG2381	
39	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
40	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
41	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
42					
43	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P <sup>-</sup>	0
44	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P <sup>-</sup>	0
45					
46	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P <sup>-</sup>	0
47	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P <sup>-</sup>	0
48	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P <sup>-</sup>	0
49	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
50	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
51					
52	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
53	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
54					
55	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>-</sup>	0
56	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P <sup>-</sup> KOG0773	
57	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
58	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
59	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
60	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0

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2	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
3	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
4	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
5					
6	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
7	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
8	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
9					
10	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
11	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
12	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P	0
13					
14	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
15	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P KOG4551	
16	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
17					
18	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P	0
19	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
20	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P KOG4658	
21					
22	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P KOG4658	
23	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
24	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
25					
26	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
27	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
28	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
29					
30	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
31	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
32	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P	0
33					
34	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
35	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
36	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
37	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
38					
39	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
40	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
41	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
42					
43	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
44	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
45	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
46					
47	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
48	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P KOG1764	
49	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P KOG1764	
50					
51	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P KOG2381	
52	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
53	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
54					
55	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
56	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
57	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
58					
59	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
60	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0

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2	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
3	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
4	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
5					
6	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
7	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>-</sup>	0
8					
9	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P <sup>-</sup> KOG0773	
10	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
11	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
12	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
13					
14	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
15	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P <sup>-</sup>	0
16	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
17					
18	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
19	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P <sup>-</sup>	0
20	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
21					
22	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
23	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P <sup>-</sup>	0
24	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
25					
26	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
27	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P <sup>-</sup>	0
28	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup> KOG4551	
29					
30	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P <sup>-</sup>	0
31	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
32	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
33					
34	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup> KOG4658	
35	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup> KOG4658	
36	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
37	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
38					
39	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
40	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
41	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
42					
43	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
44	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
45	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
46					
47	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P <sup>-</sup>	0
48	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
49	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
50					
51	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
52	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
53					
54	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
55	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
56	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
57	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
58					
59	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
60	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup> KOG1764	



1				
2	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764
3	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P KOG2381
4	1 Phvul.009G007300	Phvul.009G007300	0	PTHR35993 0
5				
6	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P	0
7	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P	0
8	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P	0
9				
10	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P	0
11	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P	0
12	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P	0
13				
14	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P 0
15	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P KOG4172
16	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P KOG4172
17				
18	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P 0
19	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P KOG4172
20	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P 0
21				
22	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773
23	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
24	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
25				
26	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
27	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
28	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P 0
29	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
30				
31	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
32	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P 0
33	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
34				
35	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
36	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P 0
37	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
38				
39	2 Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P 0
40	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P 0
41	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P KOG4551
42				
43	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P	0
44	1 Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P 0
45	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P 0
46				
47	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P KOG4658
48	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P KOG4658
49	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P 0
50				
51	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P 0
52	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P 0
53	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P	0
54				
55	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P	0
56	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P	0
57	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P	0
58				
59	1 Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P 0
60	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P	0
	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P	0



1					
2	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
3	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
4	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
5					
6	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
7	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
8	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
9					
10	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
11	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
12	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
13					
14	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764	
15	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P <sup>-</sup>	KOG1764	
16	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>-</sup>	KOG2381
17					
18	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
19	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>		0
20	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P <sup>-</sup>		0
21					
22	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>		0
23	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P <sup>-</sup>		0
24	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>		0
25					
26	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P <sup>-</sup>		0
27	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P <sup>-</sup>	0
28	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup>	KOG4172
29	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup>	KOG4172
30					
31	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
32	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup>	KOG4172
33					
34	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>-</sup>	0
35	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P <sup>-</sup>	KOG0773	
36	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
37	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
38					
39	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
40	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
41					
42	1 Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P <sup>-</sup>	0
43	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
44	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
45					
46	1 Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P <sup>-</sup>	0
47	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
48	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
49					
50	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P <sup>-</sup>	0
51	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
52	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
53					
54	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P <sup>-</sup>	0
55	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup>	KOG4551
56	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14PTHR31314,P <sup>-</sup>		0
57	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
58					
59	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
60	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658
	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup>	KOG4658

1					
2	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
3	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
4	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
5					
6	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
7	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
8	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P		0
9					
10	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P		0
11	1 Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P		0
12	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01PTHR31707,P		0
13					
14	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04PTHR21450,P		0
15	1 Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P		0
16	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
17					
18	1 Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P		0
19	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0
20	1 Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P		0
21					
22	1 Phvul.006G075600	Phvul.006G075600	PF00141 PTHR31388,P		0
23	1 Phvul.008G284900	Phvul.008G284900	PF08801 PTHR13405,P		0
24	1 Phvul.007G163400	Phvul.007G163400	PF00632 PTHR11254,P		0
25					
26	1 Phvul.001G266600	Phvul.001G266600	PF00464 PTHR11680,P		0
27	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
28	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16PTHR13780,P	KOG1764	
29					
30	1 Phvul.003G037500	Phvul.003G037500	PF00454 PTHR15245,P	KOG2381	
31	1 Phvul.009G007300	Phvul.009G007300	0 PTHR35993		0
32	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
33					
34	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00PTHR10799,P		0
35	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
36	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00PTHR23315,P		0
37					
38	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
39	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05PTHR11096,P		0
40	1 Phvul.007G156200	Phvul.007G156200	PF00010 PTHR12565,P		0
41					
42	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
43	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
44	2 Phvul.005G001000	Phvul.005G001000	PF03552 PTHR13301,P		0
45	1 Phvul.002G006400	Phvul.002G006400	PF13920 PTHR10044,P	KOG4172	
46					
47	1 Phvul.008G243700	Phvul.008G243700	PF01764 PTHR21493,P		0
48	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05PTHR11850,P	KOG0773	
49	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
50					
51	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
52	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
53	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
54					
55	1 Phvul.003G181600	Phvul.003G181600	PF13639 PTHR22763,P		0
56	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
57	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
58					
59	1 Phvul.006G164800	Phvul.006G164800	PF04765 PTHR12956,P		0
60	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0
	2 Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P		0

1					
2	1 Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P <sup>-</sup>	0
3	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
4	2 Phvul.007G157500	Phvul.007G157500		0 PTHR24320,P <sup>-</sup>	0
5					
6	1 Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P <sup>-</sup>	0
7	1 Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P <sup>-</sup> KOG4551	
8	1 Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P <sup>-</sup>	0
9					
10	1 Phvul.008G075300	Phvul.008G075300		0 PTHR33601,P <sup>-</sup>	0
11	1 Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P <sup>-</sup>	0
12	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup> KOG4658	
13					
14	1 Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P <sup>-</sup> KOG4658	
15	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
16	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
17					
18	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
19	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
20	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
21					
22	1 Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P <sup>-</sup>	0
23	1 Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P <sup>-</sup>	0
24	1 Phvul.004G088300	Phvul.004G088300		0 PTHR36319,P <sup>-</sup>	0
25					
26	1 Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P <sup>-</sup>	0
27	1 Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P <sup>-</sup>	0
28	1 Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P <sup>-</sup>	0
29	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
30					
31	1 Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P <sup>-</sup>	0
32	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
33	1 Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P <sup>-</sup>	0
34					
35	1 Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P <sup>-</sup>	0
36	1 Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P <sup>-</sup>	0
37	1 Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P <sup>-</sup>	0
38					
39	1 Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P <sup>-</sup>	0
40	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup> KOG1764	
41	1 Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P <sup>-</sup> KOG1764	
42					
43	1 Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P <sup>-</sup> KOG2381	
44	1 Phvul.009G007300	Phvul.009G007300		0 PTHR35993	0
45	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
46					
47	1 Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P <sup>-</sup>	0
48	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P <sup>-</sup>	0
49	1 Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P <sup>-</sup>	0
50					
51	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P <sup>-</sup>	0
52	1 Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P <sup>-</sup>	0
53	1 Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P <sup>-</sup>	0
54					
55	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
56	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
57					
58	2 Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P <sup>-</sup>	0
59	1 Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P <sup>-</sup> KOG4172	
60	1 Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P <sup>-</sup>	0
	1 Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P <sup>-</sup> KOG0773	

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2	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
3	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
4	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
5	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
6	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
7	1	Phvul.003G181600	Phvul.003G181600	PF13639 PTHR22763,P	0
8	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
9	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
10	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
11	1	Phvul.006G164800	Phvul.006G164800	PF04765 PTHR12956,P	0
12	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
13	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
14	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
15	1	Phvul.005G059700	Phvul.005G059700	PF00141 PTHR31235,P	0
16	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
17	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
18	2	Phvul.007G157500	Phvul.007G157500	0 PTHR24320,P	0
19	1	Phvul.005G059500	Phvul.005G059500	PF00141 PTHR31235,P	0
20	1	Phvul.002G116800	Phvul.002G116800	PF10181 PTHR15231,P	KOG4551
21	1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P
22	1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P
23	1	Phvul.008G075300	Phvul.008G075300	0 PTHR33601,P	0
24	1	Phvul.003G262800	Phvul.003G262800	PF02519 PTHR31374,P	0
25	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658
26	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658
27	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658
28	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P	0
29	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P	0
30	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P	0
31	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P	0
32	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P
33	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P
34	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P
35	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P
36	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P
37	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P
38	1	Phvul.004G088300	Phvul.004G088300	0 PTHR36319,P	0
39	1	Phvul.006G075600	Phvul.006G075600	PF00141 PTHR31388,P	0
40	1	Phvul.008G284900	Phvul.008G284900	PF08801 PTHR13405,P	0
41	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P
42	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P
43	1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P
44	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P
45	1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P
46	1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P
47	1	Phvul.005G099500	Phvul.005G099500	PF02469 PTHR32077,P	0
48	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P	0
49	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P	0
50	1	Phvul.003G181900	Phvul.003G181900	PF00010 PTHR12565,P	0
51	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P	0
52	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P	0
53	1	Phvul.003G121200	Phvul.003G121200	PF03151 PTHR11132,P	0
54	1	Phvul.005G059700	Phvul.005G059700	PF00141 PTHR31235,P	0
55	1	Phvul.005G059500	Phvul.005G059500	PF00141 PTHR31235,P	0
56	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658
57	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658
58	1	Phvul.008G072300	Phvul.008G072300	PF00931 PTHR23155,P	KOG4658
59	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P
60	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P
	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P

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2	1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12PTHR24092,P <sup>-</sup>	0
3	1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02PTHR32002,P <sup>-</sup>	0
4	1	Phvul.009G114400	Phvul.009G114400	PF00069 PTHR27000,P <sup>-</sup>	KOG1187
5					
6	1	Phvul.003G240100	Phvul.003G240100	PF12710,PF00PTHR24093,P <sup>-</sup>	0
7	1	Phvul.002G283000	Phvul.002G283000	PF12627,PF01PTHR13734,P <sup>-</sup>	0
8	1	Phvul.002G283000	Phvul.002G283000	PF12627,PF01PTHR13734,P <sup>-</sup>	0
9					
10	1	Phvul.002G283000	Phvul.002G283000	PF12627,PF01PTHR13734,P <sup>-</sup>	0
11	1	Phvul.003G170100	Phvul.003G170100	PF00862,PF05PTHR12526,P <sup>-</sup>	KOG0853
12	1	Phvul.011G173600	Phvul.011G173600	PF01535,PF13PTHR24015,P <sup>-</sup>	0
13					
14	1	Phvul.003G283500	Phvul.003G283500	PF07297 PTHR15039,P <sup>-</sup>	KOG3488
15	1	Phvul.007G163400	Phvul.007G163400	PF00632 PTHR11254,P <sup>-</sup>	0
16	1	Phvul.003G037500	Phvul.003G037500	PF00454 PTHR15245,P <sup>-</sup>	KOG2381
17					
18	1	Phvul.001G266600	Phvul.001G266600	PF00464 PTHR11680,P <sup>-</sup>	0
19	1	Phvul.001G243500	Phvul.001G243500	PF00069 PTHR27003,P <sup>-</sup>	KOG1187
20	2	Phvul.006G067900	Phvul.006G067900	PF01699 PTHR31503,P <sup>-</sup>	KOG1397
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22	1	Phvul.008G140600	Phvul.008G140600	PF00201 PTHR11926,P <sup>-</sup>	0
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6	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
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9					
10		0	0	0 AT2G37100.1	0
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14	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
15		0 K00588		GO:0008171 AT4G26220.1	0
16	3.1.1.3			0 GO:0016788 AT1G29670.1	0
17					
18		0	0	0 AT2G37100.1	0
19	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
20	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
21					
22	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
23		0 K00588		GO:0008171 AT4G26220.1	0
24	3.1.1.3			0 GO:0016788 AT1G29670.1	0
25					
26		0	0	0 AT2G37100.1	0
27	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
28	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
29					
30	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
31		0 K00588		GO:0008171 AT4G26220.1	0
32	3.1.1.3			0 GO:0016788 AT1G29670.1	0
33					
34		0	0	0 AT2G37100.1	0
35	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
36	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
37					
38	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
39		0 K00588		GO:0008171 AT4G26220.1	0
40	3.1.1.3			0 GO:0016788 AT1G29670.1	0
41					
42		0	0	0 AT2G37100.1	0
43	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
44	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
45					
46	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
47		0 K00588		GO:0008171 AT4G26220.1	0
48	3.1.1.3			0 GO:0016788 AT1G29670.1	0
49					
50		0	0	0 AT2G37100.1	0
51	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
52	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
53					
54	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
55		0 K00588		GO:0008171 AT4G26220.1	0
56	3.1.1.3			0 GO:0016788 AT1G29670.1	0
57					
58		0	0	0 AT2G37100.1	0
59	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
60	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	
	4.1.1.35	K08678		GO:0055114,(AT2G28760.3 UXS6	

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2		0 K00588	GO:0008171 AT4G26220.1		0
3	3.1.1.3		0 GO:0016788 AT1G29670.1		0
4		0	0 0 AT2G37100.1		0
5					
6	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
7	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
8	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
9					
10		0 K00588	GO:0008171 AT4G26220.1		0
11	3.1.1.3		0 GO:0016788 AT1G29670.1		0
12		0	0 0 AT2G37100.1		0
13					
14	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
15	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
16	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
17					
18		0 K00588	GO:0008171 AT4G26220.1		0
19	3.1.1.3		0 GO:0016788 AT1G29670.1		0
20		0	0 0 AT2G37100.1		0
21					
22	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
23	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
24	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
25					
26		0 K00588	GO:0008171 AT4G26220.1		0
27	3.1.1.3		0 GO:0016788 AT1G29670.1		0
28		0	0 0 AT2G37100.1		0
29					
30	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
31	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
32	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
33					
34		0 K00588	GO:0008171 AT4G26220.1		0
35	3.1.1.3		0 GO:0016788 AT1G29670.1		0
36		0	0 0 AT2G37100.1		0
37					
38	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
39	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
40	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
41					
42		0 K00588	GO:0008171 AT4G26220.1		0
43	3.1.1.3		0 GO:0016788 AT1G29670.1		0
44		0	0 0 AT2G37100.1		0
45					
46	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
47	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
48	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
49					
50		0 K00588	GO:0008171 AT4G26220.1		0
51	3.1.1.3		0 GO:0016788 AT1G29670.1		0
52		0	0 0 AT2G37100.1		0
53					
54	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
55	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
56	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		
57					
58		0 K00588	GO:0008171 AT4G26220.1		0
59	3.1.1.3		0 GO:0016788 AT1G29670.1		0
60		0	0 0 AT2G37100.1		0
	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6		

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2	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
3	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
4		0 K00588	GO:0008171 AT4G26220.1	0
5				
6	3.1.1.3		0 GO:0016788 AT1G29670.1	0
7		0	0 AT2G37100.1	0
8	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
9	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
10	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
11	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
12		0 K00588	GO:0008171 AT4G26220.1	0
13				
14	3.1.1.3		0 GO:0016788 AT1G29670.1	0
15		0	0 AT2G37100.1	0
16	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
17	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
18	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
19	4.1.1.35	K08678	GO:0055114,(CAT2G28760.3 UXS6	
20		0 K00588	GO:0008171 AT4G26220.1	0
21		0	0 AT2G45680.1	0
22				
23	2.4.1.227	K02563	GO:0030259,(CAT1G73740.1	0
24		0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
25	3.1.1.3		0 GO:0016788 AT1G33811.1	0
26		0	0 AT5G40600.1	0
27		0	0 AT5G40600.1	0
28		0	0 AT5G40600.1	0
29		0	0 AT5G40600.1	0
30		0	0	0
31		0	0	0
32		0 K13754	GO:0055085,(CAT1G54115.1 ATCCX4,CCX4	
33		0	0 AT2G45680.1	0
34				
35	2.4.1.227	K02563	GO:0030259,(CAT1G73740.1	0
36		0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
37	3.1.1.3		0 GO:0016788 AT1G33811.1	0
38		0	0 AT5G40600.1	0
39		0	0 AT5G40600.1	0
40		0	0 AT5G40600.1	0
41		0	0 AT5G40600.1	0
42		0	0	0
43		0	0	0
44		0 K13754	GO:0055085,(CAT1G54115.1 ATCCX4,CCX4	
45		0	0 AT2G45680.1	0
46				
47	2.4.1.227	K02563	GO:0030259,(CAT1G73740.1	0
48		0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
49	3.1.1.3		0 GO:0016788 AT1G33811.1	0
50		0	0 AT5G40600.1	0
51		0	0 AT5G40600.1	0
52		0	0 AT5G40600.1	0
53		0	0 AT5G40600.1	0
54		0	0	0
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56		0 K13754	GO:0055085,(CAT1G54115.1 ATCCX4,CCX4	
57		0	0 AT2G45680.1	0
58				
59	2.4.1.227	K02563	GO:0030259,(CAT1G73740.1	0
60		0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
	3.1.1.3		0 GO:0016788 AT1G33811.1	0

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2		0	0	0 AT5G40600.1
3		0	0	0 AT5G40600.1
4		0	0	0 AT5G40600.1
5		0	0	0
6		0	0	0
7		0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
8		0	0	0 AT2G45680.1
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10	2.4.1.227	K02563	GO:0030259,(AT1G73740.1	0
11		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6
12	3.1.1.3		0 GO:0016788 AT1G33811.1	0
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14		0	0	0 AT5G40600.1
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17		0	0	0
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19		0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
20		0	0	0 AT2G45680.1
21				
22	2.4.1.227	K02563	GO:0030259,(AT1G73740.1	0
23		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6
24	3.1.1.3		0 GO:0016788 AT1G33811.1	0
25				
26		0	0	0 AT5G40600.1
27		0	0	0 AT5G40600.1
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29		0	0	0
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31		0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
32		0	0	0 AT2G45680.1
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34	2.4.1.227	K02563	GO:0030259,(AT1G73740.1	0
35		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6
36	3.1.1.3		0 GO:0016788 AT1G33811.1	0
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38		0	0	0 AT5G40600.1
39		0	0	0 AT5G40600.1
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41		0	0	0
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43		0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
44		0	0	0 AT2G45680.1
45				
46	2.4.1.227	K02563	GO:0030259,(AT1G73740.1	0
47		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6
48	3.1.1.3		0 GO:0016788 AT1G33811.1	0
49				
50		0	0	0 AT5G40600.1
51		0	0	0 AT5G40600.1
52		0	0	0 AT5G40600.1
53		0	0	0
54		0	0	0
55		0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
56		0	0	0 AT2G45680.1
57				
58	2.4.1.227	K02563	GO:0030259,(AT1G73740.1	0
59		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6
60	3.1.1.3		0 GO:0016788 AT1G33811.1	0
		0	0	0 AT5G40600.1

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	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 0	0
	0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4		
	0	0	0 AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(AT1G73740.1		0
	0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0 GO:0016788 AT1G33811.1		0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 0	0
	0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4		
	0	0	0 AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(AT1G73740.1		0
	0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0 GO:0016788 AT1G33811.1		0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 0	0
	0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4		
	0	0	0 AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(AT1G73740.1		0
	0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0 GO:0016788 AT1G33811.1		0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 0	0
	0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4		
	0	0	0 AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(AT1G73740.1		0
	0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0 GO:0016788 AT1G33811.1		0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 0	0
	0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4		
	0	0	0 AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(AT1G73740.1		0
	0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0 GO:0016788 AT1G33811.1		0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0
	0	0	0 0	0
	0 K13754	GO:0055085,(AT1G54115.1 ATCCX4,CCX4		
	0	0	0 AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(AT1G73740.1		0
	0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0 GO:0016788 AT1G33811.1		0
	0	0	0 AT5G40600.1	0
	0	0	0 AT5G40600.1	0



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2		0	0	0 AT5G40600.1	0
3		0	0	0	0
4		0 K13754		GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
5		0	0	0 AT2G45680.1	0
6		0	0	0 AT2G45680.1	0
7	2.4.1.227	K02563		GO:0030259,(AT1G73740.1	0
8		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
9		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
10	3.1.1.3			0 GO:0016788 AT1G33811.1	0
11		0	0	0 AT5G40600.1	0
12		0	0	0 AT5G40600.1	0
13		0	0	0 AT5G40600.1	0
14		0	0	0 AT5G40600.1	0
15		0	0	0	0
16		0 K13754		GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
17		0	0	0 AT2G45680.1	0
18		0	0	0 AT2G45680.1	0
19	2.4.1.227	K02563		GO:0030259,(AT1G73740.1	0
20		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
21		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
22	3.1.1.3			0 GO:0016788 AT1G33811.1	0
23		0	0	0 AT5G40600.1	0
24		0	0	0 AT5G40600.1	0
25		0	0	0 AT5G40600.1	0
26		0	0	0 AT5G40600.1	0
27		0	0	0	0
28		0 K13754		GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
29		0	0	0 AT2G45680.1	0
30		0	0	0 AT2G45680.1	0
31	2.4.1.227	K02563		GO:0030259,(AT1G73740.1	0
32		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
33		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
34	3.1.1.3			0 GO:0016788 AT1G33811.1	0
35		0	0	0 AT5G40600.1	0
36		0	0	0 AT5G40600.1	0
37		0	0	0 AT5G40600.1	0
38		0	0	0 AT5G40600.1	0
39		0	0	0	0
40		0 K13754		GO:0055085,(AT1G54115.1 ATCCX4,CCX4	
41		0	0	0 AT2G45680.1	0
42		0	0	0 AT2G45680.1	0
43	2.4.1.227	K02563		GO:0030259,(AT1G73740.1	0
44		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
45		0	0	0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6	
46	3.1.1.3			0 GO:0016788 AT1G33811.1	0
47		0	0	0 AT5G40600.1	0
48		0	0	0 AT5G40600.1	0
49		0	0	0 AT5G40600.1	0
50		0	0	0 AT5G40600.1	0
51		0 K12124		0 AT1G22770.1 FB,GI	
52		0 K12124		0 AT1G22770.1 FB,GI	
53		0 K09338		GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
54		0	0	0 AT5G60690.1 IFL,IFL1,REV	
55	2.7.11.1			0 GO:0006468,(AT4G05200.1 CRK25	
56		0	0	0 AT4G28100.1	0
57		0	0	0 AT4G05200.1 CRK25	
58		0	0	0 AT4G05200.1 CRK25	
59		0	0	0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF	
60	2.3.1.30	K00640		GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
		0	0	0	0

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2		0 K13354	0 AT2G39970.1		0
3	3.6.4.12	K11647	GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2		
4	5.2.1.8	K05864	GO:0005515,(AT2G15790.1 CYP40,SQN		
5					
6		0	0 GO:0008168 AT5G64030.1		0
7		0	0 0 0		0
8					
9		0 K09264	GO:0006355,(AT5G20240.1 PI		
10		0	0 GO:0008168,(AT2G16030.1		0
11		0	0 GO:0005524,(AT1G05910.1		0
12		0 K12124	0 AT1G22770.1 FB,GI		
13		0 K12124	0 AT1G22770.1 FB,GI		
14					
15		0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV		
16	2.7.11.1		0 GO:0006468,(AT4G05200.1 CRK25		
17					
18		0	0 0 AT4G28100.1		0
19		0	0 0 AT4G05200.1 CRK25		
20					
21		0	0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF		
22	2.3.1.30	K00640	GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
23		0	0 0 0		0
24		0 K13354	0 AT2G39970.1		0
25					
26	3.6.4.12	K11647	GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2		
27	5.2.1.8	K05864	GO:0005515,(AT2G15790.1 CYP40,SQN		
28					
29		0	0 GO:0008168 AT5G64030.1		0
30		0	0 0 0		0
31					
32		0 K09264	GO:0006355,(AT5G20240.1 PI		
33		0	0 GO:0008168,(AT2G16030.1		0
34		0	0 GO:0005524,(AT1G05910.1		0
35		0 K12124	0 AT1G22770.1 FB,GI		
36		0 K12124	0 AT1G22770.1 FB,GI		
37					
38		0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV		
39	2.7.11.1		0 GO:0006468,(AT4G05200.1 CRK25		
40					
41		0	0 0 AT4G28100.1		0
42		0	0 0 AT4G05200.1 CRK25		
43					
44		0	0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF		
45	2.3.1.30	K00640	GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
46		0	0 0 0		0
47		0 K13354	0 AT2G39970.1		0
48					
49	3.6.4.12	K11647	GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2		
50	5.2.1.8	K05864	GO:0005515,(AT2G15790.1 CYP40,SQN		
51					
52		0	0 GO:0008168 AT5G64030.1		0
53		0	0 0 0		0
54					
55		0 K09264	GO:0006355,(AT5G20240.1 PI		
56		0	0 GO:0008168,(AT2G16030.1		0
57		0	0 GO:0005524,(AT1G05910.1		0
58		0 K12124	0 AT1G22770.1 FB,GI		
59		0 K12124	0 AT1G22770.1 FB,GI		
60					
		0 K09338	GO:0003677,(AT5G60690.1 IFL,IFL1,REV		
	2.7.11.1		0 GO:0006468,(AT4G05200.1 CRK25		

1					
2		0	0	0 AT4G28100.1	0
3		0	0	0 AT4G05200.1 CRK25	
4		0			
5		0		0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
6	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
7		0	0	0 0	0
8		0 K13354		0 AT2G39970.1	0
9					
10	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
11	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
12		0	0	0 GO:0008168 AT5G64030.1	0
13		0	0	0 0	0
14		0 K09264		GO:0006355,(CAT5G20240.1 PI	
15		0	0	0 GO:0008168,(CAT2G16030.1	0
16		0	0	0 GO:0005524,(CAT1G05910.1	0
17		0 K12124		0 AT1G22770.1 FB,GI	
18		0 K12124		0 AT1G22770.1 FB,GI	
19		0 K09338		GO:0003677,(CAT5G60690.1 IFL,IFL1,REV	
20					
21	2.7.11.1			0 GO:0006468,(CAT4G05200.1 CRK25	
22		0	0	0 AT4G28100.1	0
23		0	0	0 AT4G05200.1 CRK25	
24		0	0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
25	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
26		0	0	0 0	0
27		0 K13354		0 AT2G39970.1	0
28	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
29	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
30		0	0	0 GO:0008168 AT5G64030.1	0
31		0	0	0 0	0
32		0 K09264		GO:0006355,(CAT5G20240.1 PI	
33		0	0	0 GO:0008168,(CAT2G16030.1	0
34		0	0	0 GO:0005524,(CAT1G05910.1	0
35		0 K12124		0 AT1G22770.1 FB,GI	
36		0 K12124		0 AT1G22770.1 FB,GI	
37		0 K09338		GO:0003677,(CAT5G60690.1 IFL,IFL1,REV	
38					
39	2.7.11.1			0 GO:0006468,(CAT4G05200.1 CRK25	
40		0	0	0 AT4G28100.1	0
41		0	0	0 AT4G05200.1 CRK25	
42		0	0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
43	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
44		0	0	0 0	0
45		0 K13354		0 AT2G39970.1	0
46	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
47	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
48		0	0	0 GO:0008168 AT5G64030.1	0
49		0	0	0 0	0
50		0 K09264		GO:0006355,(CAT5G20240.1 PI	
51		0	0	0 GO:0008168,(CAT2G16030.1	0
52		0	0	0 GO:0005524,(CAT1G05910.1	0
53		0 K12124		0 AT1G22770.1 FB,GI	
54		0 K12124		0 AT1G22770.1 FB,GI	
55		0 K09338		GO:0003677,(CAT5G60690.1 IFL,IFL1,REV	
56					
57	2.7.11.1			0 GO:0006468,(CAT4G05200.1 CRK25	
58		0	0	0 AT4G28100.1	0
59		0	0	0 AT4G05200.1 CRK25	
60		0	0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
61	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
62		0	0	0 0	0
63		0 K13354		0 AT2G39970.1	0
64	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
65	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
66		0	0	0 GO:0008168 AT5G64030.1	0
67		0	0	0 0	0
68		0 K09264		GO:0006355,(CAT5G20240.1 PI	
69		0	0	0 GO:0008168,(CAT2G16030.1	0

1					
2		0	0 GO:0005524,(CAT1G05910.1		0
3		0 K12124	0 AT1G22770.1 FB,GI		
4		0 K12124	0 AT1G22770.1 FB,GI		
5		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
6					
7	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
8		0	0 0 AT4G28100.1		0
9					
10		0	0 AT4G05200.1 CRK25		
11		0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF		
12	2.3.1.30	K00640	GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
13					
14		0	0 0 0		0
15		0 K13354	0 AT2G39970.1		0
16	3.6.4.12	K11647	GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2		
17	5.2.1.8	K05864	GO:0005515,(CAT2G15790.1 CYP40,SQN		
18					
19		0	0 GO:0008168 AT5G64030.1		0
20		0	0 0 0		0
21					
22		0 K09264	GO:0006355,(CAT5G20240.1 PI		
23		0	0 GO:0008168,(CAT2G16030.1		0
24		0	0 GO:0005524,(CAT1G05910.1		0
25					
26		0 K12124	0 AT1G22770.1 FB,GI		
27		0 K12124	0 AT1G22770.1 FB,GI		
28		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
29					
30	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
31		0	0 0 AT4G28100.1		0
32		0	0 AT4G05200.1 CRK25		
33					
34		0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF		
35	2.3.1.30	K00640	GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
36		0	0 0 0		0
37		0 K13354	0 AT2G39970.1		0
38					
39	3.6.4.12	K11647	GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2		
40	5.2.1.8	K05864	GO:0005515,(CAT2G15790.1 CYP40,SQN		
41					
42		0	0 GO:0008168 AT5G64030.1		0
43		0	0 0 0		0
44		0 K09264	GO:0006355,(CAT5G20240.1 PI		
45		0	0 GO:0008168,(CAT2G16030.1		0
46					
47		0	0 GO:0005524,(CAT1G05910.1		0
48		0 K12124	0 AT1G22770.1 FB,GI		
49		0 K12124	0 AT1G22770.1 FB,GI		
50					
51		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
52	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
53		0	0 0 AT4G28100.1		0
54					
55		0	0 AT4G05200.1 CRK25		
56		0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF		
57	2.3.1.30	K00640	GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
58					
59		0	0 0 0		0
60		0 K13354	0 AT2G39970.1		0
	3.6.4.12	K11647	GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2		

1					
2	5.2.1.8	K05864	GO:0005515,(CAT2G15790.1 CYP40,SQN		
3		0	0 GO:0008168 AT5G64030.1		0
4		0	0 0 0		0
5		0			
6		0 K09264	GO:0006355,(CAT5G20240.1 PI		
7		0	0 GO:0008168,(CAT2G16030.1		0
8		0	0 GO:0005524,(CAT1G05910.1		0
9		0			
10		0 K12124	0 AT1G22770.1 FB,GI		
11		0 K12124	0 AT1G22770.1 FB,GI		
12		0			
13		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
14	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
15		0	0 0 AT4G28100.1		0
16		0	0 0 AT4G05200.1 CRK25		
17		0			
18		0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF		
19	2.3.1.30	K00640	GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
20		0	0 0 0		0
21		0			
22		0 K13354	0 AT2G39970.1		0
23	3.6.4.12	K11647	GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2		
24	5.2.1.8	K05864	GO:0005515,(CAT2G15790.1 CYP40,SQN		
25		0	0 GO:0008168 AT5G64030.1		0
26		0	0 0 0		0
27		0			
28		0 K09264	GO:0006355,(CAT5G20240.1 PI		
29		0	0 GO:0008168,(CAT2G16030.1		0
30		0	0 GO:0005524,(CAT1G05910.1		0
31		0			
32		0 K12124	0 AT1G22770.1 FB,GI		
33		0 K12124	0 AT1G22770.1 FB,GI		
34		0			
35		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
36	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
37		0	0 0 AT4G28100.1		0
38		0	0 0 AT4G05200.1 CRK25		
39		0			
40		0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF		
41	2.3.1.30	K00640	GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
42		0	0 0 0		0
43		0			
44		0 K13354	0 AT2G39970.1		0
45	3.6.4.12	K11647	GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2		
46	5.2.1.8	K05864	GO:0005515,(CAT2G15790.1 CYP40,SQN		
47		0	0 GO:0008168 AT5G64030.1		0
48		0	0 0 0		0
49		0			
50		0 K09264	GO:0006355,(CAT5G20240.1 PI		
51		0	0 GO:0008168,(CAT2G16030.1		0
52		0	0 GO:0005524,(CAT1G05910.1		0
53		0			
54		0 K12124	0 AT1G22770.1 FB,GI		
55		0 K12124	0 AT1G22770.1 FB,GI		
56		0			
57		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
58	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
59		0	0 0 AT4G28100.1		0
60		0	0 0 AT4G05200.1 CRK25		

1					
2		0	0	GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF	
3	2.3.1.30	K00640		GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
4		0	0	0	0
5		0			
6		0 K13354		0 AT2G39970.1	0
7	3.6.4.12	K11647		GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2	
8	5.2.1.8	K05864		GO:0005515,(AT2G15790.1 CYP40,SQN	
9		0			
10		0	0	GO:0008168 AT5G64030.1	0
11		0	0	0	0
12		0			
13		0 K09264		GO:0006355,(AT5G20240.1 PI	
14		0		0 GO:0008168,(AT2G16030.1	0
15		0		0 GO:0005524,(AT1G05910.1	0
16		0 K12124		0 AT1G22770.1 FB,GI	
17		0 K12124		0 AT1G22770.1 FB,GI	
18		0 K09338		GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
19		0			
20	2.7.11.1			0 GO:0006468,(AT4G05200.1 CRK25	
21		0			
22		0	0	0 AT4G28100.1	0
23		0		0 AT4G05200.1 CRK25	
24		0			
25		0		0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF	
26	2.3.1.30	K00640		GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
27		0	0	0	0
28		0 K13354		0 AT2G39970.1	0
29	3.6.4.12	K11647		GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2	
30	5.2.1.8	K05864		GO:0005515,(AT2G15790.1 CYP40,SQN	
31		0			
32		0	0	GO:0008168 AT5G64030.1	0
33		0	0	0	0
34		0			
35		0 K09264		GO:0006355,(AT5G20240.1 PI	
36		0		0 GO:0008168,(AT2G16030.1	0
37		0		0 GO:0005524,(AT1G05910.1	0
38		0			
39		0 K12124		0 AT1G22770.1 FB,GI	
40		0 K12124		0 AT1G22770.1 FB,GI	
41		0 K09338		GO:0003677,(AT5G60690.1 IFL,IFL1,REV	
42		0			
43	2.7.11.1			0 GO:0006468,(AT4G05200.1 CRK25	
44		0			
45		0	0	0 AT4G28100.1	0
46		0		0 AT4G05200.1 CRK25	
47		0			
48		0		0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF	
49	2.3.1.30	K00640		GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
50		0	0	0	0
51		0 K13354		0 AT2G39970.1	0
52	3.6.4.12	K11647		GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2	
53	5.2.1.8	K05864		GO:0005515,(AT2G15790.1 CYP40,SQN	
54		0			
55		0	0	GO:0008168 AT5G64030.1	0
56		0	0	0	0
57		0			
58		0 K09264		GO:0006355,(AT5G20240.1 PI	
59		0		0 GO:0008168,(AT2G16030.1	0
60		0		0 GO:0005524,(AT1G05910.1	0
		0 K12124		0 AT1G22770.1 FB,GI	



1					
2		0 K12124		0 AT1G22770.1 FB,GI	
3		0 K09338		GO:0003677,(CAT5G60690.1 IFL,IFL1,REV	
4	2.7.11.1			0 GO:0006468,(CAT4G05200.1 CRK25	
5					
6		0	0	0 AT4G28100.1	0
7		0	0	0 AT4G05200.1 CRK25	
8		0			
9				0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
10	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
11		0	0	0 0	0
12		0 K13354		0 AT2G39970.1	0
13					
14	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
15	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
16		0		0 GO:0008168 AT5G64030.1	0
17		0	0	0 0	0
18		0			
19		0 K09264		GO:0006355,(CAT5G20240.1 PI	
20		0		0 GO:0008168,(CAT2G16030.1	0
21		0			
22		0		0 GO:0005524,(CAT1G05910.1	0
23		0 K12124		0 AT1G22770.1 FB,GI	
24		0 K12124		0 AT1G22770.1 FB,GI	
25		0 K09338		GO:0003677,(CAT5G60690.1 IFL,IFL1,REV	
26					
27	2.7.11.1			0 GO:0006468,(CAT4G05200.1 CRK25	
28		0	0	0 AT4G28100.1	0
29		0	0	0 AT4G05200.1 CRK25	
30		0			
31		0		0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
32	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
33		0	0	0 0	0
34		0 K13354		0 AT2G39970.1	0
35					
36	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
37	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
38		0		0 GO:0008168 AT5G64030.1	0
39		0	0	0 0	0
40		0			
41		0 K09264		GO:0006355,(CAT5G20240.1 PI	
42		0		0 GO:0008168,(CAT2G16030.1	0
43		0		0 GO:0005524,(CAT1G05910.1	0
44		0			
45		0 K12124		0 AT1G22770.1 FB,GI	
46		0 K12124		0 AT1G22770.1 FB,GI	
47		0 K09338		GO:0003677,(CAT5G60690.1 IFL,IFL1,REV	
48					
49	2.7.11.1			0 GO:0006468,(CAT4G05200.1 CRK25	
50		0	0	0 AT4G28100.1	0
51		0	0	0 AT4G05200.1 CRK25	
52		0			
53		0		0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF	
54					
55	2.3.1.30	K00640		GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M	
56		0	0	0 0	0
57		0 K13354		0 AT2G39970.1	0
58					
59	3.6.4.12	K11647		GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2	
60	5.2.1.8	K05864		GO:0005515,(CAT2G15790.1 CYP40,SQN	
		0		0 GO:0008168 AT5G64030.1	0

1					
2		0	0	0	0
3		0 K09264	GO:0006355,(CAT5G20240.1 PI		
4		0	0 GO:0008168,(CAT2G16030.1		0
5		0	0 GO:0005524,(CAT1G05910.1		0
6		0	0 GO:0005524,(CAT1G05910.1		0
7		0 K12124	0 AT1G22770.1 FB,GI		
8		0 K12124	0 AT1G22770.1 FB,GI		
9		0 K09338	GO:0003677,(CAT5G60690.1 IFL,IFL1,REV		
10		0	0 GO:0005524,(CAT1G05910.1		0
11		0	0 GO:0005524,(CAT1G05910.1		0
12	2.7.11.1		0 GO:0006468,(CAT4G05200.1 CRK25		
13					
14		0	0 0 AT4G28100.1		0
15		0	0 0 AT4G05200.1 CRK25		
16		0	0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF		
17		0	0 GO:0016021,(CAT5G40240.1		0
18		0	0 GO:0016021,(CAT5G40240.1		0
19		0	0 GO:0016021,(CAT5G40240.1		0
20		0	0 GO:0016021,(CAT5G40240.1		0
21		0	0 GO:0016021,(CAT5G40240.1		0
22	2.3.1.30	K00640	GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M		
23		0	0 0 0 0		0
24		0 K13354	0 AT2G39970.1		0
25					
26	3.6.4.12	K11647	GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2		
27	5.2.1.8	K05864	GO:0005515,(CAT2G15790.1 CYP40,SQN		
28		0	0 GO:0008168 AT5G64030.1		0
29					
30	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7		
31		0	0 0 AT1G63470.1		0
32					
33	2.4.2.24		0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L		
34		0	0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5		
35	3.1.1.3		0 GO:0016788 AT4G26790.1		0
36	3.4.23.12		0 GO:0006508,(CAT1G03220.1		0
37					
38		0	0 0 AT3G63180.1 ATTKL,TKL		
39		0 K02985	GO:0003723 AT5G35530.1		0
40	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2		
41					
42	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2		
43		0	0 0 AT2G37570.1 SLT1		
44		0	0 0 AT2G37570.1 SLT1		
45	2.7.4.22	K09903	0 AT3G10030.1		0
46					
47		0	0 0 AT3G02250.1		0
48		0	0 GO:0003723 AT3G21740.1 APO4		
49		0	0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1		
50					
51	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1		0
52	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1		0
53					
54		0 K09874	GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8		
55		0	0 0 AT2G16800.1		0
56		0	0 0 AT3G04630.1 WDL1		
57		0	0 0 AT3G04630.1 WDL1		
58		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1		
59		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1		
60		0	0 0 0 0		0

1				
2		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I
3	3.4.23.12		0 GO:0006508,(AT2G17760.1	0
4		0	0 GO:0007165 AT3G29575.3 AFP3	
5				
6	2.7.11.1		0 GO:0005515,(AT4G20140.1 GSO1	
7	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
8		0	0	0 AT1G63470.1
9				
10	2.4.2.24		0 GO:0016020,(AT1G27600.2 I9H,IRX9-L	
11		0	0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
12	3.1.1.3		0 GO:0016788 AT4G26790.1	0
13				
14	3.4.23.12		0 GO:0006508,(AT1G03220.1	0
15		0	0	0 AT3G63180.1 ATTKL,TKL
16		0 K02985	GO:0003723 AT5G35530.1	0
17				
18	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
19	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
20		0	0	0 AT2G37570.1 SLT1
21		0	0	0 AT2G37570.1 SLT1
22				
23	2.7.4.22	K09903	0 AT3G10030.1	0
24		0	0	0 AT3G02250.1
25				
26		0	0 GO:0003723 AT3G21740.1 APO4	
27		0	0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
28	2.1.1.216	K00555	GO:0008033,(AT5G15810.1	0
29	2.1.1.216	K00555	GO:0008033,(AT5G15810.1	0
30				
31		0 K09874	GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
32		0	0	0 AT2G16800.1
33		0	0	0 AT3G04630.1 WDL1
34				
35		0	0	0 AT3G04630.1 WDL1
36		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
37		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
38				
39		0	0	0 0
40		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I
41	3.4.23.12		0 GO:0006508,(AT2G17760.1	0
42		0	0 GO:0007165 AT3G29575.3 AFP3	
43				
44	2.7.11.1		0 GO:0005515,(AT4G20140.1 GSO1	
45	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
46		0	0	0 AT1G63470.1
47				
48	2.4.2.24		0 GO:0016020,(AT1G27600.2 I9H,IRX9-L	
49		0	0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
50				
51	3.1.1.3		0 GO:0016788 AT4G26790.1	0
52	3.4.23.12		0 GO:0006508,(AT1G03220.1	0
53		0	0	0 AT3G63180.1 ATTKL,TKL
54		0 K02985	GO:0003723 AT5G35530.1	0
55				
56	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
57	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
58				
59		0	0	0 AT2G37570.1 SLT1
60		0	0	0 AT2G37570.1 SLT1
	2.7.4.22	K09903	0 AT3G10030.1	0

1					
2		0	0	0 AT3G02250.1	0
3		0	0	0 GO:0003723 AT3G21740.1 APO4	
4		0	0	0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
5					
6	2.1.1.216	K00555		GO:0008033,(AT5G15810.1	0
7	2.1.1.216	K00555		GO:0008033,(AT5G15810.1	0
8					
9		0 K09874		GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
10		0	0	0 AT2G16800.1	0
11		0	0	0 AT3G04630.1 WDL1	
12		0	0	0 AT3G04630.1 WDL1	
13					
14		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
15		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
16		0	0	0 0	0
17		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
18					
19	3.4.23.12			0 GO:0006508,(AT2G17760.1	0
20		0	0	0 GO:0007165 AT3G29575.3 AFP3	
21					
22	2.7.11.1			0 GO:0005515,(AT4G20140.1 GSO1	
23	2.7.11.1			0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
24		0	0	0 AT1G63470.1	0
25					
26	2.4.2.24			0 GO:0016020,(AT1G27600.2 I9H,IRX9-L	
27		0	0	0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
28	3.1.1.3			0 GO:0016788 AT4G26790.1	0
29	3.4.23.12			0 GO:0006508,(AT1G03220.1	0
30					
31		0	0	0 AT3G63180.1 ATTKL,TKL	
32		0 K02985		GO:0003723 AT5G35530.1	0
33					
34	2.7.11.1			0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
35	2.7.11.1			0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
36		0	0	0 AT2G37570.1 SLT1	
37		0	0	0 AT2G37570.1 SLT1	
38					
39	2.7.4.22	K09903		0 AT3G10030.1	0
40		0	0	0 AT3G02250.1	0
41					
42		0	0	0 GO:0003723 AT3G21740.1 APO4	
43		0	0	0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
44	2.1.1.216	K00555		GO:0008033,(AT5G15810.1	0
45	2.1.1.216	K00555		GO:0008033,(AT5G15810.1	0
46					
47		0 K09874		GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
48		0	0	0 AT2G16800.1	0
49		0	0	0 AT3G04630.1 WDL1	
50		0	0	0 AT3G04630.1 WDL1	
51					
52		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
53		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
54					
55		0	0	0 0	0
56		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
57	3.4.23.12			0 GO:0006508,(AT2G17760.1	0
58		0	0	0 GO:0007165 AT3G29575.3 AFP3	
59					
60	2.7.11.1			0 GO:0005515,(AT4G20140.1 GSO1	
	2.7.11.1			0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	

1					
2		0	0	0 AT1G63470.1	0
3	2.4.2.24			0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L	
4		0		0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5	
5					
6	3.1.1.3			0 GO:0016788 AT4G26790.1	0
7	3.4.23.12			0 GO:0006508,(CAT1G03220.1	0
8		0	0	0 AT3G63180.1 ATTKL,TKL	
9					
10		0 K02985		GO:0003723 AT5G35530.1	0
11	2.7.11.1			0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
12	2.7.11.1			0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
13					
14		0	0	0 AT2G37570.1 SLT1	
15		0	0	0 AT2G37570.1 SLT1	
16	2.7.4.22	K09903		0 AT3G10030.1	0
17					
18		0	0	0 AT3G02250.1	0
19					
20		0		0 GO:0003723 AT3G21740.1 APO4	
21					
22	2.1.1.216	K00555		GO:0008033,(CAT5G15810.1	0
23	2.1.1.216	K00555		GO:0008033,(CAT5G15810.1	0
24					
25		0 K09874		GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8	
26		0	0	0 AT2G16800.1	0
27					
28		0	0	0 AT3G04630.1 WDL1	
29					
30		0		0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
31					
32		0	0	0 0	0
33					
34		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
35	3.4.23.12			0 GO:0006508,(CAT2G17760.1	0
36		0		0 GO:0007165 AT3G29575.3 AFP3	
37					
38	2.7.11.1			0 GO:0005515,(CAT4G20140.1 GSO1	
39	2.7.11.1			0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
40		0	0	0 AT1G63470.1	0
41	2.4.2.24			0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L	
42					
43		0		0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5	
44	3.1.1.3			0 GO:0016788 AT4G26790.1	0
45	3.4.23.12			0 GO:0006508,(CAT1G03220.1	0
46					
47		0	0	0 AT3G63180.1 ATTKL,TKL	
48		0 K02985		GO:0003723 AT5G35530.1	0
49	2.7.11.1			0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
50					
51	2.7.11.1			0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
52		0	0	0 AT2G37570.1 SLT1	
53		0	0	0 AT2G37570.1 SLT1	
54					
55	2.7.4.22	K09903		0 AT3G10030.1	0
56		0	0	0 AT3G02250.1	0
57					
58		0		0 GO:0003723 AT3G21740.1 APO4	
59					
60		0		0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1	
	2.1.1.216	K00555		GO:0008033,(CAT5G15810.1	0
	2.1.1.216	K00555		GO:0008033,(CAT5G15810.1	0

1				
2		0 K09874	GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
3		0	0 AT2G16800.1	0
4		0	0 AT3G04630.1 WDL1	
5		0	0 AT3G04630.1 WDL1	
6		0	0 AT3G04630.1 WDL1	
7		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
8		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
9		0	0 0 0	0
10		0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
11		0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
12	3.4.23.12		0 GO:0006508,(AT2G17760.1	0
13				
14		0	0 GO:0007165 AT3G29575.3 AFP3	
15	2.7.11.1		0 GO:0005515,(AT4G20140.1 GSO1	
16	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
17				
18		0	0 AT1G63470.1	0
19	2.4.2.24		0 GO:0016020,(AT1G27600.2 I9H,IRX9-L	
20				
21		0	0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
22	3.1.1.3		0 GO:0016788 AT4G26790.1	0
23	3.4.23.12		0 GO:0006508,(AT1G03220.1	0
24				
25		0	0 AT3G63180.1 ATTKL,TKL	
26		0 K02985	GO:0003723 AT5G35530.1	0
27	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
28	2.7.11.1		0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
29				
30		0	0 AT2G37570.1 SLT1	
31		0	0 AT2G37570.1 SLT1	
32	2.7.4.22	K09903	0 AT3G10030.1	0
33				
34		0	0 AT3G02250.1	0
35				
36		0	0 GO:0003723 AT3G21740.1 APO4	
37				
38	2.1.1.216	K00555	GO:0008033,(AT5G15810.1	0
39	2.1.1.216	K00555	GO:0008033,(AT5G15810.1	0
40				
41		0 K09874	GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
42		0	0 AT2G16800.1	0
43		0	0 AT3G04630.1 WDL1	
44		0	0 AT3G04630.1 WDL1	
45		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
46		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
47		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
48		0	0 0 0	0
49		0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
50				
51	3.4.23.12		0 GO:0006508,(AT2G17760.1	0
52				
53		0	0 GO:0007165 AT3G29575.3 AFP3	
54	2.7.11.1		0 GO:0005515,(AT4G20140.1 GSO1	
55	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
56				
57		0	0 AT1G63470.1	0
58	2.4.2.24		0 GO:0016020,(AT1G27600.2 I9H,IRX9-L	
59				
60		0	0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
	3.1.1.3		0 GO:0016788 AT4G26790.1	0
	3.4.23.12		0 GO:0006508,(AT1G03220.1	0



1				
2		0	0	0 AT3G63180.1 ATTKL,TKL
3		0 K02985	GO:0003723	AT5G35530.1 0
4	2.7.11.1		0 GO:0005515,(	AT3G02130.1 RPK2,TOAD2
5				
6	2.7.11.1		0 GO:0005515,(	AT3G02130.1 RPK2,TOAD2
7		0	0	0 AT2G37570.1 SLT1
8		0	0	0 AT2G37570.1 SLT1
9				
10	2.7.4.22	K09903		0 AT3G10030.1 0
11		0	0	0 AT3G02250.1 0
12				
13		0	0 GO:0003723	AT3G21740.1 APO4
14		0	0 GO:0006355,(	AT2G22840.1 AtGRF1,GRF1
15	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1 0
16	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1 0
17				
18		0 K09874	GO:0016020,(	AT4G10380.1 NIP5;1,NLM6,NLM8
19		0	0	0 AT2G16800.1 0
20		0	0	0 AT3G04630.1 WDL1
21				
22		0	0	0 AT3G04630.1 WDL1
23		0	0 GO:0007275	AT2G45190.1 AFO,FIL,YAB1
24		0	0 GO:0007275	AT2G45190.1 AFO,FIL,YAB1
25				
26		0	0	0 0 0
27		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I
28	3.4.23.12		0 GO:0006508,(	AT2G17760.1 0
29		0	0 GO:0007165	AT3G29575.3 AFP3
30				
31	2.7.11.1		0 GO:0005515,(	AT4G20140.1 GSO1
32	2.7.11.1		0 GO:0005515	AT1G47890.1 AtRLP7,RLP7
33				
34		0	0	0 AT1G63470.1 0
35	2.4.2.24		0 GO:0016020,(	AT1G27600.2 I9H,IRX9-L
36		0	0 GO:0055085,(	AT3G18830.1 ATPLT5,ATPMT5,PMT5
37				
38	3.1.1.3		0 GO:0016788	AT4G26790.1 0
39	3.4.23.12		0 GO:0006508,(	AT1G03220.1 0
40		0	0	0 AT3G63180.1 ATTKL,TKL
41		0 K02985	GO:0003723	AT5G35530.1 0
42				
43	2.7.11.1		0 GO:0005515,(	AT3G02130.1 RPK2,TOAD2
44	2.7.11.1		0 GO:0005515,(	AT3G02130.1 RPK2,TOAD2
45		0	0	0 AT2G37570.1 SLT1
46		0	0	0 AT2G37570.1 SLT1
47				
48	2.7.4.22	K09903		0 AT3G10030.1 0
49		0	0	0 AT3G02250.1 0
50				
51		0	0 GO:0003723	AT3G21740.1 APO4
52		0	0 GO:0006355,(	AT2G22840.1 AtGRF1,GRF1
53	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1 0
54	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1 0
55				
56		0 K09874	GO:0016020,(	AT4G10380.1 NIP5;1,NLM6,NLM8
57		0	0	0 AT2G16800.1 0
58		0	0	0 AT3G04630.1 WDL1
59		0	0	0 AT3G04630.1 WDL1
60		0	0 GO:0007275	AT2G45190.1 AFO,FIL,YAB1

1					
2		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
3		0	0	0	0
4		0	0	0	0
5		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
6	3.4.23.12		0	GO:0006508,(AT2G17760.1	0
7		0	0	GO:0007165 AT3G29575.3 AFP3	
8	2.7.11.1		0	GO:0005515,(AT4G20140.1 GSO1	
9					
10	2.7.11.1		0	GO:0005515 AT1G47890.1 AtRLP7,RLP7	
11		0	0	0 AT1G63470.1	0
12	2.4.2.24		0	GO:0016020,(AT1G27600.2 I9H,IRX9-L	
13					
14		0	0	GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
15	3.1.1.3		0	GO:0016788 AT4G26790.1	0
16	3.4.23.12		0	GO:0006508,(AT1G03220.1	0
17					
18		0	0	0 AT3G63180.1 ATTKL,TKL	
19		0 K02985	0	GO:0003723 AT5G35530.1	0
20	2.7.11.1		0	GO:0005515,(AT3G02130.1 RPK2,TOAD2	
21					
22	2.7.11.1		0	GO:0005515,(AT3G02130.1 RPK2,TOAD2	
23		0	0	0 AT2G37570.1 SLT1	
24		0	0	0 AT2G37570.1 SLT1	
25					
26	2.7.4.22	K09903	0	AT3G10030.1	0
27		0	0	0 AT3G02250.1	0
28		0	0	GO:0003723 AT3G21740.1 APO4	
29		0	0	GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
30					
31	2.1.1.216	K00555	0	GO:0008033,(AT5G15810.1	0
32	2.1.1.216	K00555	0	GO:0008033,(AT5G15810.1	0
33					
34		0 K09874	0	GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
35		0	0	0 AT2G16800.1	0
36		0	0	0 AT3G04630.1 WDL1	
37		0	0	0 AT3G04630.1 WDL1	
38					
39		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
40		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
41		0	0	0	0
42		0	0	0	0
43		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
44	3.4.23.12		0	GO:0006508,(AT2G17760.1	0
45		0	0	GO:0007165 AT3G29575.3 AFP3	
46					
47	2.7.11.1		0	GO:0005515,(AT4G20140.1 GSO1	
48	2.7.11.1		0	GO:0005515 AT1G47890.1 AtRLP7,RLP7	
49		0	0	0 AT1G63470.1	0
50					
51	2.4.2.24		0	GO:0016020,(AT1G27600.2 I9H,IRX9-L	
52		0	0	GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
53	3.1.1.3		0	GO:0016788 AT4G26790.1	0
54	3.4.23.12		0	GO:0006508,(AT1G03220.1	0
55					
56		0	0	0 AT3G63180.1 ATTKL,TKL	
57		0 K02985	0	GO:0003723 AT5G35530.1	0
58					
59	2.7.11.1		0	GO:0005515,(AT3G02130.1 RPK2,TOAD2	
60	2.7.11.1		0	GO:0005515,(AT3G02130.1 RPK2,TOAD2	
		0	0	0 AT2G37570.1 SLT1	

1					
2		0	0	0 AT2G37570.1 SLT1	
3	2.7.4.22	K09903		0 AT3G10030.1	0
4		0	0	0 AT3G02250.1	0
5		0	0	0 GO:0003723 AT3G21740.1 APO4	
6		0	0	0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
7		0	0	0 GO:0008033,(AT5G15810.1	0
8	2.1.1.216	K00555		0 GO:0008033,(AT5G15810.1	0
9	2.1.1.216	K00555		0 GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
10		0 K09874		0 AT2G16800.1	0
11		0	0	0 AT3G04630.1 WDL1	
12		0	0	0 AT3G04630.1 WDL1	
13		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
14		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
15		0	0	0 0 0	0
16		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
17	3.4.23.12			0 GO:0006508,(AT2G17760.1	0
18		0	0	0 GO:0007165 AT3G29575.3 AFP3	
19	2.7.11.1			0 GO:0005515,(AT4G20140.1 GSO1	
20	2.7.11.1			0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
21		0	0	0 AT1G63470.1	0
22	2.4.2.24			0 GO:0016020,(AT1G27600.2 I9H,IRX9-L	
23		0	0	0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
24	3.1.1.3			0 GO:0016788 AT4G26790.1	0
25	3.4.23.12			0 GO:0006508,(AT1G03220.1	0
26		0	0	0 AT3G63180.1 ATTKL,TKL	
27		0 K02985		0 GO:0003723 AT5G35530.1	0
28	2.7.11.1			0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
29	2.7.11.1			0 GO:0005515,(AT3G02130.1 RPK2,TOAD2	
30		0	0	0 AT2G37570.1 SLT1	
31		0	0	0 AT2G37570.1 SLT1	
32	2.7.4.22	K09903		0 AT3G10030.1	0
33		0	0	0 AT3G02250.1	0
34		0	0	0 GO:0003723 AT3G21740.1 APO4	
35		0	0	0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
36	2.1.1.216	K00555		0 GO:0008033,(AT5G15810.1	0
37	2.1.1.216	K00555		0 GO:0008033,(AT5G15810.1	0
38		0 K09874		0 GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
39		0	0	0 AT2G16800.1	0
40		0	0	0 AT3G04630.1 WDL1	
41		0	0	0 AT3G04630.1 WDL1	
42		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
43		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
44		0	0	0 0 0	0
45		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
46	3.4.23.12			0 GO:0006508,(AT2G17760.1	0
47		0	0	0 GO:0007165 AT3G29575.3 AFP3	

1				
2	2.7.11.1		0 GO:0005515,(CAT4G20140.1 GSO1	
3	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
4				
5		0	0 AT1G63470.1	0
6	2.4.2.24		0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L	
7		0	0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5	
8	3.1.1.3		0 GO:0016788 AT4G26790.1	0
9	3.4.23.12		0 GO:0006508,(CAT1G03220.1	0
10				
11		0	0 AT3G63180.1 ATTKL,TKL	
12		0 K02985	GO:0003723 AT5G35530.1	0
13				
14	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
15	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
16		0	0 AT2G37570.1 SLT1	
17		0	0 AT2G37570.1 SLT1	
18				
19	2.7.4.22	K09903	0 AT3G10030.1	0
20		0	0 AT3G02250.1	0
21				
22		0	0 GO:0003723 AT3G21740.1 APO4	
23		0	0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1	
24	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1	0
25	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1	0
26				
27		0 K09874	GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8	
28		0	0 AT2G16800.1	0
29				
30		0	0 AT3G04630.1 WDL1	
31		0	0 AT3G04630.1 WDL1	
32		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
33		0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
34				
35		0	0 0 0	0
36		0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
37	3.4.23.12		0 GO:0006508,(CAT2G17760.1	0
38				
39		0	0 GO:0007165 AT3G29575.3 AFP3	
40	2.7.11.1		0 GO:0005515,(CAT4G20140.1 GSO1	
41	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7	
42				
43		0	0 AT1G63470.1	0
44	2.4.2.24		0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L	
45		0	0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5	
46				
47	3.1.1.3		0 GO:0016788 AT4G26790.1	0
48	3.4.23.12		0 GO:0006508,(CAT1G03220.1	0
49		0	0 AT3G63180.1 ATTKL,TKL	
50		0 K02985	GO:0003723 AT5G35530.1	0
51				
52	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
53	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2	
54				
55		0	0 AT2G37570.1 SLT1	
56		0	0 AT2G37570.1 SLT1	
57	2.7.4.22	K09903	0 AT3G10030.1	0
58		0	0 AT3G02250.1	0
59		0	0 GO:0003723 AT3G21740.1 APO4	
60		0	0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1	

1					
2	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1		0
3	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1		0
4		0 K09874	GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8		
5		0	0	0 AT2G16800.1	0
6		0	0	0 AT3G04630.1 WDL1	
7		0	0	0 AT3G04630.1 WDL1	
8		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
9		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
10		0	0	0	0
11		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
12	3.4.23.12		0 GO:0006508,(CAT2G17760.1		0
13		0	0 GO:0007165 AT3G29575.3 AFP3		
14	2.7.11.1		0 GO:0005515,(CAT4G20140.1 GSO1		
15	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7		
16		0	0	0 AT1G63470.1	0
17	2.4.2.24		0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L		
18		0	0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5		
19	3.1.1.3		0 GO:0016788 AT4G26790.1		0
20	3.4.23.12		0 GO:0006508,(CAT1G03220.1		0
21		0	0	0 AT3G63180.1 ATTKL,TKL	
22		0 K02985	GO:0003723 AT5G35530.1		0
23	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2		
24	2.7.11.1		0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2		
25		0	0	0 AT2G37570.1 SLT1	
26		0	0	0 AT2G37570.1 SLT1	
27	2.7.4.22	K09903	0 AT3G10030.1		0
28		0	0	0 AT3G02250.1	0
29		0	0 GO:0003723 AT3G21740.1 APO4		
30		0	0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1		
31	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1		0
32	2.1.1.216	K00555	GO:0008033,(CAT5G15810.1		0
33		0 K09874	GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8		
34		0	0	0 AT2G16800.1	0
35		0	0	0 AT3G04630.1 WDL1	
36		0	0	0 AT3G04630.1 WDL1	
37		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
38		0	0	0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
39		0	0	0	0
40		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
41	3.4.23.12		0 GO:0006508,(CAT2G17760.1		0
42		0	0 GO:0007165 AT3G29575.3 AFP3		
43	2.7.11.1		0 GO:0005515,(CAT4G20140.1 GSO1		
44	2.7.11.1		0 GO:0005515 AT1G47890.1 AtRLP7,RLP7		
45		0	0	0 AT1G63470.1	0
46	2.4.2.24		0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L		
47		0	0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5		

1					
2	3.1.1.3		0 GO:0016788	AT4G26790.1	0
3	3.4.23.12		0 GO:0006508,(	AT1G03220.1	0
4			0	0 AT3G63180.1	ATTKL,TKL
5		0	0	0 AT3G63180.1	ATTKL,TKL
6		0 K02985	GO:0003723	AT5G35530.1	0
7	2.7.11.1		0 GO:0005515,(	AT3G02130.1	RPK2,TOAD2
8	2.7.11.1		0 GO:0005515,(	AT3G02130.1	RPK2,TOAD2
9					
10		0	0	0 AT2G37570.1	SLT1
11		0	0	0 AT2G37570.1	SLT1
12	2.7.4.22	K09903		0 AT3G10030.1	
13					0
14		0	0	0 AT3G02250.1	
15		0	0 GO:0003723	AT3G21740.1	APO4
16		0	0 GO:0006355,(	AT2G22840.1	AtGRF1,GRF1
17					
18	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	
19	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	
20		0 K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8
21					
22		0	0	0 AT2G16800.1	
23		0	0	0 AT3G04630.1	WDL1
24		0	0	0 AT3G04630.1	WDL1
25		0	0 GO:0007275	AT2G45190.1	AFO,FIL,YAB1
26		0	0 GO:0007275	AT2G45190.1	AFO,FIL,YAB1
27		0	0	0	0
28		0	0	0	0
29		0	0	0 AT4G33200.1	ATXI-I,XI-15,XI-I
30					
31	3.4.23.12		0 GO:0006508,(	AT2G17760.1	
32		0	0 GO:0007165	AT3G29575.3	AFP3
33					
34	2.7.11.1		0 GO:0005515,(	AT4G20140.1	GSO1
35	2.7.11.1		0 GO:0005515	AT1G47890.1	AtRLP7,RLP7
36		0	0	0 AT1G63470.1	
37					0
38	2.4.2.24		0 GO:0016020,(	AT1G27600.2	I9H,IRX9-L
39		0	0 GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5
40	3.1.1.3		0 GO:0016788	AT4G26790.1	
41	3.4.23.12		0 GO:0006508,(	AT1G03220.1	
42					0
43		0	0	0 AT3G63180.1	ATTKL,TKL
44		0 K02985	GO:0003723	AT5G35530.1	
45					0
46	2.7.11.1		0 GO:0005515,(	AT3G02130.1	RPK2,TOAD2
47	2.7.11.1		0 GO:0005515,(	AT3G02130.1	RPK2,TOAD2
48		0	0	0 AT2G37570.1	SLT1
49		0	0	0 AT2G37570.1	SLT1
50					
51	2.7.4.22	K09903		0 AT3G10030.1	
52		0	0	0 AT3G02250.1	
53		0	0 GO:0003723	AT3G21740.1	APO4
54		0	0 GO:0006355,(	AT2G22840.1	AtGRF1,GRF1
55					
56	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	
57	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	
58		0 K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8
59					
60		0	0	0 AT2G16800.1	
		0	0	0 AT3G04630.1	WDL1



1					
2		0	0	0 AT3G04630.1 WDL1	
3		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
4		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
5		0	0	0	0
6		0	0	0	0
7		0	0	0 AT4G33200.1 ATXI-I,XI-15,XI-I	
8	3.4.23.12		0	GO:0006508,(AT2G17760.1	0
9		0	0	GO:0007165 AT3G29575.3 AFP3	
10		0	0	GO:0005515,(AT4G20140.1 GSO1	
11	2.7.11.1		0	GO:0005515,(AT4G20140.1 GSO1	
12	2.7.4.22	K09903	0	AT3G10030.1	0
13		0	0	GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5	
14		0	0	0 AT3G04630.1 WDL1	
15		0	0	0 AT3G04630.1 WDL1	
16		0	0	0 AT3G04630.1 WDL1	
17	3.1.1.3		0	GO:0016788 AT4G26790.1	0
18	2.7.11.1		0	GO:0005515 AT1G47890.1 AtRLP7,RLP7	
19		0	0	0 AT1G63470.1	0
20		0	0	0 AT1G63470.1	0
21	2.4.2.24		0	GO:0016020,(AT1G27600.2 I9H,IRX9-L	
22	3.4.23.12		0	GO:0006508,(AT1G03220.1	0
23		0	0	0 AT3G63180.1 ATTKL,TKL	
24		0	0	0 AT3G63180.1 ATTKL,TKL	
25	2.7.11.1		0	GO:0005515,(AT4G20140.1 GSO1	
26	2.7.1.68	K00889	GO:0046488,(AT1G77740.1 PIP5K2		
27	2.7.1.68	K00889	GO:0046488,(AT1G77740.1 PIP5K2		
28		0	0	0 AT2G37570.1 SLT1	
29		0	0	0 AT2G37570.1 SLT1	
30		0	0	0 AT2G37570.1 SLT1	
31		0	0	0 AT3G02250.1	0
32		0	0	0 AT3G02250.1	0
33		0	0	0 AT3G02250.1	0
34		0	0	0 AT3G02250.1	0
35	2.7.11.1		0	GO:0003723 AT5G35530.1	0
36	2.7.11.1		0	GO:0005515,(AT3G02130.1 RPK2,TOAD2	
37	2.7.11.1		0	GO:0005515,(AT3G02130.1 RPK2,TOAD2	
38		0	0	GO:0003723 AT3G21740.1 APO4	
39		0	0	GO:0006355,(AT2G22840.1 AtGRF1,GRF1	
40	2.1.1.216	K00555	GO:0008033,(AT5G15810.1	0	
41	2.1.1.216	K00555	GO:0008033,(AT5G15810.1	0	
42		0	0	0 AT2G37570.1 SLT1	
43	3.4.23.12		0	GO:0006508,(AT2G17760.1	0
44		0	0	GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8	
45		0	0	0 AT2G16800.1	0
46		0	0	0 AT2G16800.1	0
47		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
48		0	0	GO:0007275 AT2G45190.1 AFO,FIL,YAB1	
49		0	0	0	0
50		0	0	0	0
51	2.7.11.1		0	GO:0005515,(AT1G68400.1	0
52		0	0	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
53		0	0	0 AT2G34670.2	0
54		0	0	0 AT2G34670.2	0
55		0	0	GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
56		0	0	0 AT4G33100.1	0
57		0	0	0 AT4G33100.1	0
58		0	0	0 AT5G06240.1 emb2735	
59		0	0	0 AT5G06240.1 emb2735	
60		0	0	0 AT4G30700.1	0
	2.1.1.163		0	GO:0008168,(AT1G78140.1	0

1				
2	1.11.1.15	0	GO:0055114,(CAT1G65980.1 TPX1	
3		0	0 AT5G17270.1	0
4		0	0 AT5G13210.1	0
5				
6	2.3.2.2,2.6.1.4K14272		GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
7	2.8.1.7,4.4.1.1	0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
8		0 K10956	GO:0016020,(CAT2G34250.1	0
9		0	0 AT1G64770.1 NDF2,NDH45	
10		0	0 AT5G17170.1 ENH1	
11				
12	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
13				
14	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
15		0 K02639	GO:0051536,(CAT2G27510.1 ATFD3,FD3	
16		0	0 GO:0005515 AT2G46560.1	0
17		0	0 GO:0005515 AT2G46560.1	0
18		0	0 AT3G23590.1 MED33A,RFR1	
19				
20	2.4.1.18	K00700	GO:0005975,(CAT3G20440.2 BE1,EMB2729	
21				
22	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
23		0	0 AT4G18470.1 SNI1	
24		0	0 AT4G18470.1 SNI1	
25				
26	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
27	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
28		0	0 AT4G18470.1 SNI1	
29				
30	1.14.13.152		0 GO:0055114,(CAT2G45550.1 CYP76C4	
31		0	0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
32		0	0 AT2G33390.1	0
33		0	0 AT2G33390.1	0
34		0	0 AT2G01770.1 ATVIT1,VIT1	
35		0	0 AT2G01770.1 ATVIT1,VIT1	
36		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
37		0	0 AT2G34670.2	0
38		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
39		0	0 AT4G33100.1	0
40		0 K17968	0 AT4G33100.1	0
41		0	0 AT5G06240.1 emb2735	
42		0	0 AT5G06240.1 emb2735	
43		0	0 AT4G30700.1	0
44		0	0 AT4G30700.1	0
45				
46	2.1.1.163		0 GO:0008168,(CAT1G78140.1	0
47	1.11.1.15		0 GO:0055114,(CAT1G65980.1 TPX1	
48		0	0 AT5G17270.1	0
49		0	0 AT5G13210.1	0
50				
51	2.3.2.2,2.6.1.4K14272		GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
52	2.8.1.7,4.4.1.1	0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
53		0 K10956	GO:0016020,(CAT2G34250.1	0
54		0	0 AT1G64770.1 NDF2,NDH45	
55		0	0 AT5G17170.1 ENH1	
56				
57	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
58				
59	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
60		0 K02639	GO:0051536,(CAT2G27510.1 ATFD3,FD3	
		0	0 GO:0005515 AT2G46560.1	0

1				
2		0	0 GO:0005515 AT2G46560.1	0
3		0	0 0 AT3G23590.1 MED33A,RFR1	
4	2.4.1.18	K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729	
5				
6	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
7		0	0 0 AT4G18470.1 SNI1	
8		0	0 0 AT4G18470.1 SNI1	
9				
10	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
11	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
12		0	0 0 AT4G18470.1 SNI1	
13				
14	1.14.13.152		0 GO:0055114,(AT2G45550.1 CYP76C4	
15		0	0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1	
16		0	0 0 AT2G33390.1	0
17		0	0 0 AT2G33390.1	0
18		0	0 0 AT2G01770.1 ATVIT1,VIT1	
19		0	0 0 AT2G01770.1 ATVIT1,VIT1	
20		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
21		0	0 0 AT2G34670.2	0
22		0	0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
23		0	0 0 AT4G33100.1	0
24		0 K17968	0 AT5G06240.1 emb2735	
25		0	0 0 AT5G06240.1 emb2735	
26		0	0 0 AT4G30700.1	0
27		0	0 0 AT4G30700.1	0
28		0	0 0 AT4G30700.1	0
29		0	0 0 AT4G30700.1	0
30	2.1.1.163		0 GO:0008168,(AT1G78140.1	0
31	1.11.1.15		0 GO:0055114,(AT1G65980.1 TPX1	
32		0	0 0 AT5G17270.1	0
33		0	0 0 AT5G17270.1	0
34		0	0 0 AT5G13210.1	0
35	2.3.2.2,2.6.1.4K14272		GO:0030170,(AT1G70580.2 AOAT2,GGT2	
36	2.8.1.7,4.4.1.1		0 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
37		0 K10956	GO:0016020,(AT2G34250.1	0
38		0	0 0 AT1G64770.1 NDF2,NDH45	
39		0	0 0 AT1G64770.1 NDF2,NDH45	
40		0	0 0 AT5G17170.1 ENH1	
41	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
42				
43	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
44		0 K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3	
45		0	0 GO:0005515 AT2G46560.1	0
46		0	0 GO:0005515 AT2G46560.1	0
47		0	0 GO:0005515 AT2G46560.1	0
48		0	0 0 AT3G23590.1 MED33A,RFR1	
49	2.4.1.18	K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729	
50				
51	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
52		0	0 0 AT4G18470.1 SNI1	
53		0	0 0 AT4G18470.1 SNI1	
54				
55	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
56	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
57		0	0 0 AT4G18470.1 SNI1	
58				
59	1.14.13.152		0 GO:0055114,(AT2G45550.1 CYP76C4	
60		0	0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1	
		0	0 0 AT2G33390.1	0

1				
2		0	0	0 AT2G33390.1
3		0	0	0 AT2G01770.1 ATVIT1,VIT1
4		0 K00507	GO:0006629	AT3G15850.1 ADS3,FAD5,FADB,JB67
5		0	0	0 AT2G34670.2
6		0	0	0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1
7		0 K17968		0 AT4G33100.1
8		0	0	0 AT5G06240.1 emb2735
9		0	0	0 AT5G06240.1 emb2735
10		0	0	0 AT4G30700.1
11	2.1.1.163		0	GO:0008168,(AT1G78140.1
12	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1
13		0	0	0 AT5G17270.1
14		0	0	0 AT5G13210.1
15	2.3.2.2,2.6.1.4K14272		GO:0030170,(AT1G70580.2 AOAT2,GGT2	
16	2.8.1.7,4.4.1.1	0	0	AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF
17		0 K10956	GO:0016020,(AT2G34250.1	
18		0	0	0 AT1G64770.1 NDF2,NDH45
19		0	0	0 AT5G17170.1 ENH1
20	2.7.11.1		0	GO:0006468,(AT4G02630.1
21	2.7.11.1		0	GO:0006468,(AT4G02630.1
22		0 K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3	
23		0	0	0 GO:0005515 AT2G46560.1
24		0	0	0 GO:0005515 AT2G46560.1
25		0	0	0 AT3G23590.1 MED33A,RFR1
26	2.4.1.18	K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729	
27	2.4.1.12		0	GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1
28		0	0	0 AT4G18470.1 SNI1
29		0	0	0 AT4G18470.1 SNI1
30	4.1.2.27		0	GO:0030170,(AT1G27980.1 ATDPL1,DPL1
31	4.1.2.27		0	GO:0030170,(AT1G27980.1 ATDPL1,DPL1
32		0	0	0 AT4G18470.1 SNI1
33	1.14.13.152		0	GO:0055114,(AT2G45550.1 CYP76C4
34		0	0	0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1
35		0	0	0 AT2G33390.1
36		0	0	0 AT2G33390.1
37		0	0	0 AT2G01770.1 ATVIT1,VIT1
38		0 K00507	GO:0006629	AT3G15850.1 ADS3,FAD5,FADB,JB67
39		0	0	0 AT2G34670.2
40		0	0	0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1
41		0 K17968		0 AT4G33100.1
42		0	0	0 AT5G06240.1 emb2735
43		0	0	0 AT5G06240.1 emb2735
44		0	0	0 AT4G30700.1
45	2.1.1.163		0	GO:0008168,(AT1G78140.1
46	1.11.1.15		0	GO:0055114,(AT1G65980.1 TPX1
47		0	0	0 AT5G17270.1

1				
2		0	0	0 AT5G13210.1
3	2.3.2.2,2.6.1.4K14272			GO:0030170,(CAT1G70580.2 AOAT2,GGT2
4	2.8.1.7,4.4.1.1		0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF
5		0 K10956		GO:0016020,(CAT2G34250.1
6		0		0 AT1G64770.1 NDF2,NDH45
7		0		0 AT5G17170.1 ENH1
8				
9	2.7.11.1		0	GO:0006468,(CAT4G02630.1
10	2.7.11.1		0	GO:0006468,(CAT4G02630.1
11		0 K02639		GO:0051536,(CAT2G27510.1 ATFD3,FD3
12		0		0 GO:0005515 AT2G46560.1
13		0		0 GO:0005515 AT2G46560.1
14		0		0 AT3G23590.1 MED33A,RFR1
15	2.4.1.18	K00700		GO:0005975,(CAT3G20440.2 BE1,EMB2729
16	2.4.1.12		0	GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1
17		0		0 AT4G18470.1 SNI1
18		0		0 AT4G18470.1 SNI1
19	4.1.2.27		0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1
20	4.1.2.27		0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1
21		0		0 AT4G18470.1 SNI1
22	1.14.13.152		0	GO:0055114,(CAT2G45550.1 CYP76C4
23		0		0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1
24		0		0 AT2G33390.1
25		0		0 AT2G33390.1
26		0		0 AT2G01770.1 ATVIT1,VIT1
27		0 K00507		GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67
28		0		0 AT2G34670.2
29		0		0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1
30		0 K17968		0 AT4G33100.1
31		0		0 AT5G06240.1 emb2735
32		0		0 AT5G06240.1 emb2735
33		0		0 AT4G30700.1
34	2.1.1.163		0	GO:0008168,(CAT1G78140.1
35	1.11.1.15		0	GO:0055114,(CAT1G65980.1 TPX1
36		0		0 AT5G17270.1
37		0		0 AT5G13210.1
38	2.3.2.2,2.6.1.4K14272			GO:0030170,(CAT1G70580.2 AOAT2,GGT2
39	2.8.1.7,4.4.1.1		0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF
40		0 K10956		GO:0016020,(CAT2G34250.1
41		0		0 AT1G64770.1 NDF2,NDH45
42		0		0 AT5G17170.1 ENH1
43	2.7.11.1		0	GO:0006468,(CAT4G02630.1
44	2.7.11.1		0	GO:0006468,(CAT4G02630.1
45		0 K02639		GO:0051536,(CAT2G27510.1 ATFD3,FD3
46		0		0 GO:0005515 AT2G46560.1
47		0		0 GO:0005515 AT2G46560.1
48		0		0 AT3G23590.1 MED33A,RFR1

1				
2	2.4.1.18	K00700	GO:0005975,(CAT3G20440.2 BE1,EMB2729	
3	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
4		0	0 AT4G18470.1 SNI1	
5		0	0 AT4G18470.1 SNI1	
6		0	0 AT4G18470.1 SNI1	
7	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
8	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
9		0	0 AT4G18470.1 SNI1	
10		0	0 AT4G18470.1 SNI1	
11	1.14.13.152		0 GO:0055114,(CAT2G45550.1 CYP76C4	
12		0	0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
13		0	0 AT2G33390.1	0
14		0	0 AT2G33390.1	0
15		0	0 AT2G33390.1	0
16		0	0 AT2G01770.1 ATVIT1,VIT1	
17		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
18		0	0 AT2G34670.2	0
19		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
20		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
21		0 K17968	0 AT4G33100.1	0
22		0	0 AT4G33100.1	0
23		0	0 AT5G06240.1 emb2735	
24		0	0 AT5G06240.1 emb2735	
25		0	0 AT5G06240.1 emb2735	
26		0	0 AT4G30700.1	0
27	2.1.1.163		0 GO:0008168,(CAT1G78140.1	0
28	1.11.1.15		0 GO:0055114,(CAT1G65980.1 TPX1	
29		0	0 AT5G17270.1	0
30		0	0 AT5G17270.1	0
31		0	0 AT5G13210.1	0
32	2.3.2.2,2.6.1.4K14272		GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
33	2.8.1.7,4.4.1.1		0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
34		0 K10956	GO:0016020,(CAT2G34250.1	0
35		0	0 AT1G64770.1 NDF2,NDH45	
36		0	0 AT1G64770.1 NDF2,NDH45	
37		0	0 AT5G17170.1 ENH1	
38		0	0 AT5G17170.1 ENH1	
39	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
40	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
41		0 K02639	GO:0051536,(CAT2G27510.1 ATFD3,FD3	
42		0	0 GO:0051536,(CAT2G27510.1 ATFD3,FD3	
43		0	0 GO:0005515 AT2G46560.1	0
44		0	0 GO:0005515 AT2G46560.1	0
45		0	0 AT3G23590.1 MED33A,RFR1	
46		0	0 AT3G23590.1 MED33A,RFR1	
47	2.4.1.18	K00700	GO:0005975,(CAT3G20440.2 BE1,EMB2729	
48	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
49		0	0 AT4G18470.1 SNI1	
50		0	0 AT4G18470.1 SNI1	
51		0	0 AT4G18470.1 SNI1	
52	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
53	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
54		0	0 AT4G18470.1 SNI1	
55		0	0 AT4G18470.1 SNI1	
56	1.14.13.152		0 GO:0055114,(CAT2G45550.1 CYP76C4	
57		0	0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
58		0	0 AT2G33390.1	0
59		0	0 AT2G33390.1	0
60		0	0 AT2G33390.1	0
		0	0 AT2G01770.1 ATVIT1,VIT1	



1				
2		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
3		0	0 AT2G34670.2	0
4		0	0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
5		0 K17968	0 AT4G33100.1	0
6		0	0 AT5G06240.1 emb2735	
7		0	0 AT5G06240.1 emb2735	
8		0	0 AT4G30700.1	0
9		0	0 AT4G30700.1	0
10		0	0 AT4G30700.1	0
11	2.1.1.163		0 GO:0008168,(AT1G78140.1	0
12	1.11.1.15		0 GO:0055114,(AT1G65980.1 TPX1	
13		0	0 AT5G17270.1	0
14		0	0 AT5G13210.1	0
15		0	0 AT5G13210.1	0
16	2.3.2.2,2.6.1.4K14272		GO:0030170,(AT1G70580.2 AOAT2,GGT2	
17	2.8.1.7,4.4.1.1		0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
18		0 K10956	GO:0016020,(AT2G34250.1	0
19		0	0 AT1G64770.1 NDF2,NDH45	
20		0	0 AT5G17170.1 ENH1	
21		0	0 AT5G17170.1 ENH1	
22		0	0 AT5G17170.1 ENH1	
23	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
24	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
25		0 K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3	
26		0	0 GO:0005515 AT2G46560.1	0
27		0	0 GO:0005515 AT2G46560.1	0
28		0	0 GO:0005515 AT2G46560.1	0
29		0	0 AT3G23590.1 MED33A,RFR1	
30		0	0 AT3G23590.1 MED33A,RFR1	
31	2.4.1.18	K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729	
32	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
33		0	0 AT4G18470.1 SNI1	
34		0	0 AT4G18470.1 SNI1	
35		0	0 AT4G18470.1 SNI1	
36	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
37	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
38		0	0 AT4G18470.1 SNI1	
39		0	0 AT4G18470.1 SNI1	
40	1.14.13.152		0 GO:0055114,(AT2G45550.1 CYP76C4	
41		0	0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1	
42		0	0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1	
43		0	0 AT2G33390.1	0
44		0	0 AT2G33390.1	0
45		0	0 AT2G01770.1 ATVIT1,VIT1	
46		0	0 AT2G01770.1 ATVIT1,VIT1	
47		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
48		0	0 AT2G34670.2	0
49		0	0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
50		0 K17968	0 AT4G33100.1	0
51		0	0 AT4G33100.1	0
52		0	0 AT5G06240.1 emb2735	
53		0	0 AT5G06240.1 emb2735	
54		0	0 AT5G06240.1 emb2735	
55		0	0 AT4G30700.1	0
56	2.1.1.163		0 GO:0008168,(AT1G78140.1	0
57	1.11.1.15		0 GO:0055114,(AT1G65980.1 TPX1	
58		0	0 AT5G17270.1	0
59		0	0 AT5G17270.1	0
60		0	0 AT5G13210.1	0
	2.3.2.2,2.6.1.4K14272		GO:0030170,(AT1G70580.2 AOAT2,GGT2	

1				
2	2.8.1.7,4.4.1.1	0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
3		0 K10956	GO:0016020,(AT2G34250.1	0
4		0	0 AT1G64770.1 NDF2,NDH45	
5		0	0 AT5G17170.1 ENH1	
6		0	0 AT5G17170.1 ENH1	
7	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
8	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
9				
10		0 K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3	
11		0	0 GO:0005515 AT2G46560.1	0
12		0	0 GO:0005515 AT2G46560.1	0
13		0	0 GO:0005515 AT2G46560.1	0
14		0	0 AT3G23590.1 MED33A,RFR1	
15	2.4.1.18	K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729	
16	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
17				
18		0	0 AT4G18470.1 SNI1	
19		0	0 AT4G18470.1 SNI1	
20	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
21				
22	4.1.2.27		0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1	
23		0	0 AT4G18470.1 SNI1	
24	1.14.13.152		0 GO:0055114,(AT2G45550.1 CYP76C4	
25				
26		0	0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1	
27		0	0 AT2G33390.1	0
28		0	0 AT2G33390.1	0
29		0	0 AT2G01770.1 ATVIT1,VIT1	
30		0	0 AT2G01770.1 ATVIT1,VIT1	
31		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
32		0	0 AT2G34670.2	0
33		0	0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
34				
35		0 K17968	0 AT4G33100.1	0
36		0	0 AT5G06240.1 emb2735	
37		0	0 AT5G06240.1 emb2735	
38		0	0 AT5G06240.1 emb2735	
39		0	0 AT4G30700.1	0
40	2.1.1.163		0 GO:0008168,(AT1G78140.1	0
41	1.11.1.15		0 GO:0055114,(AT1G65980.1 TPX1	
42				
43		0	0 AT5G17270.1	0
44		0	0 AT5G13210.1	0
45	2.3.2.2,2.6.1.4K14272		GO:0030170,(AT1G70580.2 AOAT2,GGT2	
46				
47	2.8.1.7,4.4.1.1	0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
48		0 K10956	GO:0016020,(AT2G34250.1	0
49		0	0 AT1G64770.1 NDF2,NDH45	
50		0	0 AT5G17170.1 ENH1	
51		0	0 AT5G17170.1 ENH1	
52	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
53	2.7.11.1		0 GO:0006468,(AT4G02630.1	0
54				
55		0 K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3	
56		0	0 GO:0005515 AT2G46560.1	0
57		0	0 GO:0005515 AT2G46560.1	0
58		0	0 GO:0005515 AT2G46560.1	0
59		0	0 AT3G23590.1 MED33A,RFR1	
60	2.4.1.18	K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729	
	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	

1					
2		0	0	0 AT4G18470.1 SNI1	
3		0	0	0 AT4G18470.1 SNI1	
4	4.1.2.27			0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
5					
6	4.1.2.27			0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
7		0	0	0 AT4G18470.1 SNI1	
8	1.14.13.152			0 GO:0055114,(CAT2G45550.1 CYP76C4	
9					
10		0		0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
11		0	0	0 AT2G33390.1	0
12		0	0	0 AT2G33390.1	0
13		0	0	0 AT2G01770.1 ATVIT1,VIT1	
14		0	0	0 AT2G01770.1 ATVIT1,VIT1	
15		0 K00507		GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
16		0	0	0 AT2G34670.2	0
17		0			
18		0		0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
19		0 K17968		0 AT4G33100.1	0
20		0	0	0 AT5G06240.1 emb2735	
21		0	0	0 AT5G06240.1 emb2735	
22		0	0	0 AT5G06240.1 emb2735	
23		0	0	0 AT4G30700.1	0
24	2.1.1.163			0 GO:0008168,(CAT1G78140.1	0
25					
26	1.11.1.15			0 GO:0055114,(CAT1G65980.1 TPX1	
27		0	0	0 AT5G17270.1	0
28		0	0	0 AT5G13210.1	0
29					
30	2.3.2.2,2.6.1.4	K14272		GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
31	2.8.1.7,4.4.1.1		0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
32		0 K10956		GO:0016020,(CAT2G34250.1	0
33		0	0	0 AT1G64770.1 NDF2,NDH45	
34		0	0	0 AT1G64770.1 NDF2,NDH45	
35		0	0	0 AT5G17170.1 ENH1	
36	2.7.11.1			0 GO:0006468,(CAT4G02630.1	0
37					
38	2.7.11.1			0 GO:0006468,(CAT4G02630.1	0
39		0 K02639		GO:0051536,(CAT2G27510.1 ATFD3,FD3	
40		0		0 GO:0005515 AT2G46560.1	0
41		0		0 GO:0005515 AT2G46560.1	0
42		0		0 GO:0005515 AT2G46560.1	0
43		0	0	0 AT3G23590.1 MED33A,RFR1	
44	2.4.1.18	K00700		GO:0005975,(CAT3G20440.2 BE1,EMB2729	
45	2.4.1.12			0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
46					
47		0	0	0 AT4G18470.1 SNI1	
48		0	0	0 AT4G18470.1 SNI1	
49	4.1.2.27			0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
50					
51	4.1.2.27			0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
52		0	0	0 AT4G18470.1 SNI1	
53	1.14.13.152			0 GO:0055114,(CAT2G45550.1 CYP76C4	
54					
55		0		0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
56		0	0	0 AT2G33390.1	0
57		0	0	0 AT2G33390.1	0
58		0	0	0 AT2G01770.1 ATVIT1,VIT1	
59		0	0	0 AT2G01770.1 ATVIT1,VIT1	
60		0 K00507		GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
		0	0	0 AT2G34670.2	0

1				
2		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
3		0 K17968	0 AT4G33100.1	0
4		0	0 AT5G06240.1 emb2735	
5		0	0 AT5G06240.1 emb2735	
6		0	0 AT4G30700.1	0
7		0	0 AT4G30700.1	0
8	2.1.1.163		0 GO:0008168,(CAT1G78140.1	0
9				
10	1.11.1.15		0 GO:0055114,(CAT1G65980.1 TPX1	
11		0	0 AT5G17270.1	0
12		0	0 AT5G13210.1	0
13				
14	2.3.2.2,2.6.1.4K14272		GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
15	2.8.1.7,4.4.1.1		0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
16		0 K10956	GO:0016020,(CAT2G34250.1	0
17		0	0 AT1G64770.1 NDF2,NDH45	
18		0	0 AT5G17170.1 ENH1	
19		0	0 AT5G17170.1 ENH1	
20	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
21				
22	2.7.11.1		0 GO:0006468,(CAT4G02630.1	0
23		0 K02639	GO:0051536,(CAT2G27510.1 ATFD3,FD3	
24		0	0 GO:0005515 AT2G46560.1	0
25		0	0 GO:0005515 AT2G46560.1	0
26		0	0 GO:0005515 AT2G46560.1	0
27		0	0 AT3G23590.1 MED33A,RFR1	
28	2.4.1.18	K00700	GO:0005975,(CAT3G20440.2 BE1,EMB2729	
29				
30	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
31		0	0 AT4G18470.1 SNI1	
32		0	0 AT4G18470.1 SNI1	
33				
34	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
35	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
36		0	0 AT4G18470.1 SNI1	
37				
38	1.14.13.152		0 GO:0055114,(CAT2G45550.1 CYP76C4	
39		0	0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
40		0	0 AT2G33390.1	0
41		0	0 AT2G33390.1	0
42		0	0 AT2G33390.1	0
43		0	0 AT2G01770.1 ATVIT1,VIT1	
44		0 K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
45		0	0 AT2G34670.2	0
46		0	0 AT2G34670.2	0
47		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
48		0 K17968	0 AT4G33100.1	0
49		0	0 AT5G06240.1 emb2735	
50		0	0 AT5G06240.1 emb2735	
51		0	0 AT5G06240.1 emb2735	
52		0	0 AT4G30700.1	0
53				
53	2.1.1.163		0 GO:0008168,(CAT1G78140.1	0
54				
55	1.11.1.15		0 GO:0055114,(CAT1G65980.1 TPX1	
56		0	0 AT5G17270.1	0
57		0	0 AT5G13210.1	0
58				
59	2.3.2.2,2.6.1.4K14272		GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
60	2.8.1.7,4.4.1.1		0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
		0 K10956	GO:0016020,(CAT2G34250.1	0

1				
2		0	0	0 AT1G64770.1 NDF2,NDH45
3		0	0	0 AT5G17170.1 ENH1
4	2.7.11.1		0	GO:0006468,(AT4G02630.1
5				0
6	2.7.11.1		0	GO:0006468,(AT4G02630.1
7		0	K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3
8		0		0 GO:0005515 AT2G46560.1
9				0
10		0		0 GO:0005515 AT2G46560.1
11				0
12	2.4.1.18		K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729
13				
14	2.4.1.12			0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1
15		0		0 AT4G18470.1 SNI1
16		0		0 AT4G18470.1 SNI1
17				
18	4.1.2.27			0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1
19	4.1.2.27			0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1
20		0		0 AT4G18470.1 SNI1
21				
22	1.14.13.152			0 GO:0055114,(AT2G45550.1 CYP76C4
23		0		0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1
24		0		0 AT2G33390.1
25				0
26		0		0 AT2G33390.1
27		0		0 AT2G01770.1 ATVIT1,VIT1
28		0	K00507	GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67
29		0		0 AT2G34670.2
30				0
31		0		0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1
32		0	K17968	0 AT4G33100.1
33				0
34		0		0 AT5G06240.1 emb2735
35		0		0 AT5G06240.1 emb2735
36		0		0 AT4G30700.1
37				0
38	2.1.1.163			0 GO:0008168,(AT1G78140.1
39	1.11.1.15			0 GO:0055114,(AT1G65980.1 TPX1
40		0		0 AT5G17270.1
41		0		0 AT5G13210.1
42				0
43	2.3.2.2,2.6.1.4		K14272	GO:0030170,(AT1G70580.2 AOAT2,GGT2
44	2.8.1.7,4.4.1.1			0 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF
45		0	K10956	GO:0016020,(AT2G34250.1
46				0
47		0		0 AT1G64770.1 NDF2,NDH45
48		0		0 AT5G17170.1 ENH1
49	2.7.11.1			0 GO:0006468,(AT4G02630.1
50				0
51	2.7.11.1			0 GO:0006468,(AT4G02630.1
52		0	K02639	GO:0051536,(AT2G27510.1 ATFD3,FD3
53		0		0 GO:0005515 AT2G46560.1
54				0
55		0		0 GO:0005515 AT2G46560.1
56		0		0 AT3G23590.1 MED33A,RFR1
57	2.4.1.18		K00700	GO:0005975,(AT3G20440.2 BE1,EMB2729
58				
59	2.4.1.12			0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1
60		0		0 AT4G18470.1 SNI1
		0		0 AT4G18470.1 SNI1

1				
2	4.1.2.27	0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
3	4.1.2.27	0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
4		0	0 AT4G18470.1 SNI1	
5		0	0 AT4G18470.1 SNI1	
6	1.14.13.152	0	GO:0055114,(CAT2G45550.1 CYP76C4	
7		0	GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
8		0	0 AT2G33390.1	0
9		0	0 AT2G33390.1	0
10		0	0 AT2G33390.1	0
11		0	0 AT2G01770.1 ATVIT1,VIT1	
12		0	0 AT2G01770.1 ATVIT1,VIT1	
13	0 K00507	GO:0006629	AT3G15850.1 ADS3,FAD5,FADB,JB67	
14		0	0 AT2G34670.2	0
15		0	GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
16	0 K17968		0 AT4G33100.1	0
17		0	0 AT4G33100.1	0
18		0	0 AT5G06240.1 emb2735	
19		0	0 AT5G06240.1 emb2735	
20		0	0 AT5G06240.1 emb2735	
21		0	0 AT4G30700.1	0
22	2.1.1.163	0	GO:0008168,(CAT1G78140.1	0
23	1.11.1.15	0	GO:0055114,(CAT1G65980.1 TPX1	
24		0	0 AT5G17270.1	0
25		0	0 AT5G17270.1	0
26		0	0 AT5G13210.1	0
27	2.3.2.2,2.6.1.4K14272	GO:0030170,(CAT1G70580.2 AOAT2,GGT2		
28	2.8.1.7,4.4.1.1	0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
29		0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
30	0 K10956	GO:0016020,(CAT2G34250.1		0
31		0	0 AT1G64770.1 NDF2,NDH45	
32		0	0 AT1G64770.1 NDF2,NDH45	
33		0	0 AT5G17170.1 ENH1	
34	2.7.11.1	0	GO:0006468,(CAT4G02630.1	0
35	2.7.11.1	0	GO:0006468,(CAT4G02630.1	0
36		0	0 K02639 GO:0051536,(CAT2G27510.1 ATFD3,FD3	
37		0	0 GO:0005515 AT2G46560.1	0
38		0	0 GO:0005515 AT2G46560.1	0
39		0	0 GO:0005515 AT2G46560.1	0
40		0	0 AT3G23590.1 MED33A,RFR1	
41	2.4.1.18	K00700	GO:0005975,(CAT3G20440.2 BE1,EMB2729	
42		0	0 K00700 GO:0005975,(CAT3G20440.2 BE1,EMB2729	
43	2.4.1.12	0	GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
44		0	0 AT4G18470.1 SNI1	
45		0	0 AT4G18470.1 SNI1	
46		0	0 AT4G18470.1 SNI1	
47	4.1.2.27	0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
48	4.1.2.27	0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
49		0	0 AT4G18470.1 SNI1	
50		0	0 AT4G18470.1 SNI1	
51	1.14.13.152	0	GO:0055114,(CAT2G45550.1 CYP76C4	
52		0	GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
53		0	0 AT2G33390.1	0
54		0	0 AT2G33390.1	0
55		0	0 AT2G33390.1	0
56		0	0 AT2G01770.1 ATVIT1,VIT1	
57	0 K00507	GO:0006629	AT3G15850.1 ADS3,FAD5,FADB,JB67	
58		0	0 AT2G34670.2	0
59		0	GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
60		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
	0 K17968		0 AT4G33100.1	0



1				
2		0	0	0 AT5G06240.1 emb2735
3		0	0	0 AT5G06240.1 emb2735
4		0	0	0 AT4G30700.1
5		0	0	0 AT4G30700.1
6	2.1.1.163		0	GO:0008168,(CAT1G78140.1
7	1.11.1.15		0	GO:0055114,(CAT1G65980.1 TPX1
8		0	0	0 AT5G17270.1
9		0	0	0 AT5G13210.1
10		0	0	0 AT5G13210.1
11	2.3.2.2,2.6.1.4K14272		0	GO:0030170,(CAT1G70580.2 AOAT2,GGT2
12	2.8.1.7,4.4.1.1		0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF
13		0 K10956		GO:0016020,(CAT2G34250.1
14		0	0	0 AT1G64770.1 NDF2,NDH45
15		0	0	0 AT5G17170.1 ENH1
16		0	0	0 AT5G17170.1 ENH1
17	2.7.11.1		0	GO:0006468,(CAT4G02630.1
18	2.7.11.1		0	GO:0006468,(CAT4G02630.1
19		0 K02639		GO:0051536,(CAT2G27510.1 ATFD3,FD3
20		0	0	GO:0005515 AT2G46560.1
21		0	0	GO:0005515 AT2G46560.1
22		0	0	0 AT3G23590.1 MED33A,RFR1
23	2.4.1.18	K00700		GO:0005975,(CAT3G20440.2 BE1,EMB2729
24	2.4.1.12		0	GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1
25		0	0	0 AT4G18470.1 SNI1
26		0	0	0 AT4G18470.1 SNI1
27	4.1.2.27		0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1
28	4.1.2.27		0	GO:0030170,(CAT1G27980.1 ATDPL1,DPL1
29		0	0	0 AT4G18470.1 SNI1
30	1.14.13.152		0	GO:0055114,(CAT2G45550.1 CYP76C4
31		0	0	GO:0016021,(CAT1G28230.1 ATPUP1,PUP1
32		0	0	0 AT2G33390.1
33		0	0	0 AT2G33390.1
34		0	0	0 AT2G01770.1 ATVIT1,VIT1
35		0 K00507		GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67
36		0	0	0 AT2G34670.2
37		0	0	GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1
38		0 K17968		0 AT4G33100.1
39		0	0	0 AT5G06240.1 emb2735
40		0	0	0 AT5G06240.1 emb2735
41		0	0	0 AT4G30700.1
42	2.1.1.163		0	GO:0008168,(CAT1G78140.1
43	1.11.1.15		0	GO:0055114,(CAT1G65980.1 TPX1
44		0	0	0 AT5G17270.1
45		0	0	0 AT5G13210.1
46	2.3.2.2,2.6.1.4K14272		0	GO:0030170,(CAT1G70580.2 AOAT2,GGT2
47	2.8.1.7,4.4.1.1		0	0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF
48		0 K10956		GO:0016020,(CAT2G34250.1
49		0	0	0 AT1G64770.1 NDF2,NDH45
50		0	0	0 AT5G17170.1 ENH1

1				
2	2.7.11.1	0	GO:0006468,(CAT4G02630.1	0
3	2.7.11.1	0	GO:0006468,(CAT4G02630.1	0
4		0	K02639 GO:0051536,(AT2G27510.1 ATFD3,FD3	
5		0		
6		0	GO:0005515 AT2G46560.1	0
7		0	GO:0005515 AT2G46560.1	0
8		0		
9		0	0 AT3G23590.1 MED33A,RFR1	
10	2.4.1.18	K00700	GO:0005975,(CAT3G20440.2 BE1,EMB2729	
11	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
12		0	0 AT4G18470.1 SNI1	
13		0	0 AT4G18470.1 SNI1	
14		0	0 AT4G18470.1 SNI1	
15	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
16	4.1.2.27		0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1	
17		0	0 AT4G18470.1 SNI1	
18		0	0 AT4G18470.1 SNI1	
19	1.14.13.152		0 GO:0055114,(CAT2G45550.1 CYP76C4	
20		0	0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1	
21		0	0 AT2G33390.1	0
22		0	0 AT2G33390.1	0
23		0	0 AT2G01770.1 ATVIT1,VIT1	
24		0	0 AT2G01770.1 ATVIT1,VIT1	
25		0	0 AT2G01770.1 ATVIT1,VIT1	
26		0	K00507 GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67	
27		0	0 AT5G17270.1	0
28		0	0 AT2G34670.2	0
29		0	0 K02639 GO:0051536,(CAT2G27510.1 ATFD3,FD3	
30		0	0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1	
31		0	0 K17968 0 AT4G33100.1	0
32		0	0 AT5G06240.1 emb2735	
33		0	0 AT5G06240.1 emb2735	
34		0	0 AT5G06240.1 emb2735	
35		0	0 AT5G06240.1 emb2735	
36		0	0 GO:0008152,(CAT5G63380.1	0
37		0	0 AT4G30700.1	0
38		0	0 AT4G30700.1	0
39		0	0 AT1G14780.1	0
40		0	0 AT1G14780.1	0
41		0	0 AT1G14780.1	0
42	2.1.1.163		0 GO:0008168,(CAT1G78140.1	0
43	1.11.1.15		0 GO:0055114,(CAT1G65980.1 TPX1	
44		0	0 AT5G13210.1	0
45	2.3.2.2,2.6.1.4	K14272	GO:0030170,(CAT1G70580.2 AOAT2,GGT2	
46	2.8.1.7,4.4.1.1		0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
47		0	0 K10956 GO:0016020,(CAT2G34250.1	0
48		0	0 K07300 GO:0055085,(CAT2G38170.3 ATCAX1,CAX1,RCI4	
49		0	0 AT1G64770.1 NDF2,NDH45	
50		0	0 AT1G64770.1 NDF2,NDH45	
51		0	0 AT5G17170.1 ENH1	
52		0	0 AT5G17170.1 ENH1	
53		0	0 GO:0005515 AT2G46560.1	0
54		0	0 GO:0005515 AT2G46560.1	0
55		0	0 GO:0005515 AT2G46560.1	0
56		0	0 GO:0005515 AT4G11610.1	0
57	3.1.1.11	K01051	GO:0004857,(CAT4G33230.1	0
58		0	0 AT3G51290.2	0
59		0	0 AT1G03870.1 FLA9	
60		0	0 GO:0046983 AT5G08130.5 BIM1	

1				
2		0	0 GO:0046983 AT5G08130.5 BIM1	
3		0	0 0 AT3G17430.1	0
4		0	0 0 AT3G17430.1	0
5		0	0 0 AT3G17430.1	0
6	1.11.1.7	K00430	GO:0055114,(AT5G05340.1	0
7		0 K14300	0 AT2G05120.1	0
8	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4	
9	2.1.2.1	K00600	GO:0016740 AT4G13930.1 SHM4	
10		0	0 0 AT1G09020.1 ATSNF4,SNF4	
11		0	0 0 AT1G09020.1 ATSNF4,SNF4	
12		0	0 0 AT1G09020.1 ATSNF4,SNF4	
13	2.7.1.67		0 GO:0016773 AT1G26270.1	0
14		0	0 0 AT1G76405.2	0
15		0	0 0 AT1G76405.2	0
16	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	
17	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	
18		0	0 GO:0005515 AT2G22125.1 CSI1	
19		0	0 GO:0005515 AT2G22125.1 CSI1	
20	6.5.1.4		0 GO:0006396 AT5G22100.1	0
21	6.5.1.4		0 GO:0006396 AT5G22100.1	0
22		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5	
23		0	0 0 AT2G35330.1	0
24		0	0 0 AT2G35330.1	0
25		0	0 0 AT2G35330.1	0
26	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
27		0	0 0 AT2G35330.1	0
28		0	0 GO:0006629 AT4G16070.1	0
29		0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
30	1.1.1.330		0 0 AT5G02540.1	0
31	1.1.1.330		0 0 AT5G02540.1	0
32	1.1.1.330		0 0 AT5G02540.1	0
33	1.1.1.330		0 0 AT5G02540.1	0
34	6.3.2.19		0 GO:0008270,(AT5G60820.1	0
35	1.1.1.330		0 0 AT5G02540.1	0
36	1.1.1.330		0 0 AT5G02540.1	0
37	1.1.1.330		0 0 AT5G02540.1	0
38	1.1.1.330		0 0 AT5G02540.1	0
39		0	0 0 AT5G46220.1	0
40	1.1.1.330		0 0 AT5G02540.1	0
41	1.1.1.330		0 0 AT5G02540.1	0
42		0	0 0 AT5G46220.1	0
43	1.1.1.330		0 0 AT5G02540.1	0
44	1.1.1.330		0 0 AT5G02540.1	0
45	1.1.1.330		0 0 AT5G02540.1	0
46	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
47	1.1.1.330		0 0 AT5G02540.1	0
48	1.1.1.330		0 0 AT5G02540.1	0
49	1.1.1.330		0 0 AT5G02540.1	0
50	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
51	2.4.1.198	K03858	GO:0017176 AT4G35530.1	0
52		0	0 0 AT2G01060.1	0
53		0	0 0 AT3G60890.2 ZPR2	
54		0 K14488	GO:0009733 AT4G34760.1	0
55		0	0 GO:0043531 AT1G63350.1	0
56		0	0 GO:0043531 AT1G63350.1	0
57		0	0 0 AT1G22770.1 FB,GI	
58		0	0 0 AT1G22770.1 FB,GI	
59		0	0 0 AT1G22770.1 FB,GI	
60		0	0 0 AT1G22770.1 FB,GI	

1					
2		0	0	0 AT1G22770.1 FB,GI	
3	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
4		0	0	GO:0005515 AT2G43500.1	0
5		0	0	GO:0005515 AT2G43500.1	0
6		0	0	GO:0005515 AT2G43500.1	0
7	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
8		0	0	0 AT1G22770.1 FB,GI	
9					
10	3.1.1.11	K01051		GO:0004857,(AT4G33230.1	0
11		0	0	0 AT3G51290.2	0
12		0	0	0 AT1G03870.1 FLA9	
13		0	0	GO:0046983 AT5G08130.5 BIM1	
14		0	0	GO:0046983 AT5G08130.5 BIM1	
15		0	0	0 AT3G17430.1	0
16		0	0	0 AT3G17430.1	0
17		0	0	0 AT3G17430.1	0
18		0	0	0 AT3G17430.1	0
19	1.11.1.7	K00430		GO:0055114,(AT5G05340.1	0
20		0 K14300		0 AT2G05120.1	0
21					
22	6.3.2.19	K10590		GO:0004842 AT5G02880.1 UPL4	
23	2.1.2.1	K00600		GO:0016740 AT4G13930.1 SHM4	
24		0	0	0 AT1G09020.1 ATSNF4,SNF4	
25		0	0	0 AT1G09020.1 ATSNF4,SNF4	
26		0	0	0 AT1G09020.1 ATSNF4,SNF4	
27	2.7.1.67			0 GO:0016773 AT1G26270.1	0
28		0	0	0 AT1G76405.2	0
29					
30	3.6.4.12			0 GO:0016787,(AT2G28290.1 CHR3,SYD	
31	3.6.4.12			0 GO:0016787,(AT2G28290.1 CHR3,SYD	
32		0	0	0 GO:0005515 AT2G22125.1 CSI1	
33		0	0	0 GO:0005515 AT2G22125.1 CSI1	
34					
35	6.5.1.4			0 GO:0006396 AT5G22100.1	0
36	6.5.1.4			0 GO:0006396 AT5G22100.1	0
37					
38		0	0	0 GO:0046983 AT2G20180.2 PIF1,PIL5	
39		0	0	0 AT2G35330.1	0
40		0	0	0 AT2G35330.1	0
41					
42	2.4.1.12			0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
43		0	0	0 AT2G35330.1	0
44		0	0	0 GO:0006629 AT4G16070.1	0
45		0	0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
46					
47	1.1.1.330		0	0 AT5G02540.1	0
48	1.1.1.330		0	0 AT5G02540.1	0
49	1.1.1.330		0	0 AT5G02540.1	0
50	1.1.1.330		0	0 AT5G02540.1	0
51	1.1.1.330		0	0 AT5G02540.1	0
52	6.3.2.19			0 GO:0008270,(AT5G60820.1	0
53	1.1.1.330		0	0 AT5G02540.1	0
54	1.1.1.330		0	0 AT5G02540.1	0
55	1.1.1.330		0	0 AT5G02540.1	0
56		0	0	0 AT5G46220.1	0
57	1.1.1.330		0	0 AT5G02540.1	0
58	1.1.1.330		0	0 AT5G02540.1	0
59	1.1.1.330		0	0 AT5G02540.1	0
60	1.11.1.7	K00430		GO:0055114,(AT4G33870.1	0
	1.1.1.330		0	0 AT5G02540.1	0

1					
2	1.1.1.330		0	0 AT5G02540.1	0
3	1.11.1.7	K00430		GO:0055114,(AT4G33870.1	0
4	2.4.1.198	K03858		GO:0017176 AT4G35530.1	0
5					
6		0	0	0 AT2G01060.1	0
7		0	0	0 AT3G60890.2 ZPR2	
8		0 K14488		GO:0009733 AT4G34760.1	0
9					
10		0	0	GO:0043531 AT1G63350.1	0
11		0	0	GO:0043531 AT1G63350.1	0
12		0	0	0 AT1G22770.1 FB,GI	
13		0	0	0 AT1G22770.1 FB,GI	
14		0	0	0 AT1G22770.1 FB,GI	
15		0	0	0 AT1G22770.1 FB,GI	
16	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
17					
18		0	0	GO:0005515 AT2G43500.1	0
19		0	0	GO:0005515 AT2G43500.1	0
20	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
21					
22		0	0	0 AT1G22770.1 FB,GI	
23	3.1.1.11	K01051		GO:0004857,(AT4G33230.1	0
24		0	0	0 AT3G51290.2	0
25		0	0	0 AT1G03870.1 FLA9	
26		0	0	GO:0046983 AT5G08130.5 BIM1	
27		0	0	GO:0046983 AT5G08130.5 BIM1	
28		0	0	0 AT3G17430.1	0
29		0	0	0 AT3G17430.1	0
30		0	0	0 AT3G17430.1	0
31		0	0	0 AT3G17430.1	0
32	1.11.1.7	K00430		GO:0055114,(AT5G05340.1	0
33		0 K14300		0 AT2G05120.1	0
34					
35	6.3.2.19	K10590		GO:0004842 AT5G02880.1 UPL4	
36	2.1.2.1	K00600		GO:0016740 AT4G13930.1 SHM4	
37		0	0	0 AT1G09020.1 ATSNF4,SNF4	
38		0	0	0 AT1G09020.1 ATSNF4,SNF4	
39		0	0	0 AT1G09020.1 ATSNF4,SNF4	
40	2.7.1.67		0	GO:0016773 AT1G26270.1	0
41		0	0	0 AT1G76405.2	0
42					
43	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
44	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
45		0	0	GO:0005515 AT2G22125.1 CSI1	
46		0	0	GO:0005515 AT2G22125.1 CSI1	
47		0	0	GO:0005515 AT2G22125.1 CSI1	
48	6.5.1.4		0	GO:0006396 AT5G22100.1	0
49	6.5.1.4		0	GO:0006396 AT5G22100.1	0
50		0	0	GO:0046983 AT2G20180.2 PIF1,PIL5	
51		0	0	0 AT2G35330.1	0
52		0	0	0 AT2G35330.1	0
53		0	0	0 AT2G35330.1	0
54		0	0	0 AT2G35330.1	0
55	2.4.1.12		0	GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
56		0	0	0 AT2G35330.1	0
57		0	0	GO:0006629 AT4G16070.1	0
58		0	0	GO:0003677,(AT1G70510.1 ATK1,KNAT2	
59		0	0	0 AT5G02540.1	0
60	1.1.1.330		0	0 AT5G02540.1	0
	1.1.1.330		0	0 AT5G02540.1	0

1						
2	1.1.1.330	0	0	AT5G02540.1	0	
3	1.1.1.330	0	0	AT5G02540.1	0	
4	6.3.2.19	0	GO:0008270,(	AT5G60820.1	0	
5						
6	1.1.1.330	0	0	AT5G02540.1	0	
7	1.1.1.330	0	0	AT5G02540.1	0	
8						
9	0	0	0	AT5G46220.1	0	
10	1.1.1.330	0	0	AT5G02540.1	0	
11	1.1.1.330	0	0	AT5G02540.1	0	
12	1.11.1.7	K00430	GO:0055114,(	AT4G33870.1	0	
13						
14	1.1.1.330	0	0	AT5G02540.1	0	
15	1.1.1.330	0	0	AT5G02540.1	0	
16	1.11.1.7	K00430	GO:0055114,(	AT4G33870.1	0	
17						
18	2.4.1.198	K03858	GO:0017176	AT4G35530.1	0	
19		0	0	AT2G01060.1	0	
20		0	0	AT3G60890.2 ZPR2		
21						
22	0	K14488	GO:0009733	AT4G34760.1	0	
23		0	0	GO:0043531	AT1G63350.1	0
24		0	0	GO:0043531	AT1G63350.1	0
25						
26		0	0	AT1G22770.1	FB,GI	
27		0	0	AT1G22770.1	FB,GI	
28		0	0	AT1G22770.1	FB,GI	
29						
30	3.6.3.1		0	GO:0046872,(	AT1G68710.1	0
31		0	0	GO:0005515	AT2G43500.1	0
32		0	0	GO:0005515	AT2G43500.1	0
33						
34	3.6.3.1		0	GO:0046872,(	AT1G68710.1	0
35		0	0	AT1G22770.1	FB,GI	
36	3.1.1.11	K01051	GO:0004857,(	AT4G33230.1	0	
37		0	0	AT3G51290.2	0	
38						
39		0	0	AT1G03870.1	FLA9	
40		0	0	GO:0046983	AT5G08130.5	BIM1
41		0	0	GO:0046983	AT5G08130.5	BIM1
42						
43		0	0	AT3G17430.1	0	
44		0	0	AT3G17430.1	0	
45						
46	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0	
47		0	K14300	AT2G05120.1	0	
48	6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
49	2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
50						
51		0	0	AT1G09020.1	ATSNF4,SNF4	
52		0	0	AT1G09020.1	ATSNF4,SNF4	
53						
54	2.7.1.67		0	GO:0016773	AT1G26270.1	0
55		0	0	AT1G76405.2	0	
56	3.6.4.12		0	GO:0016787,(	AT2G28290.1	CHR3,SYD
57	3.6.4.12		0	GO:0016787,(	AT2G28290.1	CHR3,SYD
58						
59		0	0	GO:0005515	AT2G22125.1	CSI1
60		0	0	GO:0005515	AT2G22125.1	CSI1
	6.5.1.4		0	GO:0006396	AT5G22100.1	0



1				
2	6.5.1.4		0 GO:0006396 AT5G22100.1	0
3		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5	
4		0	0 AT2G35330.1	0
5		0	0 AT2G35330.1	0
6		0	0 AT2G35330.1	0
7	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
8		0	0 AT2G35330.1	0
9		0	0 GO:0006629 AT4G16070.1	0
10		0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
11		0	0 AT5G02540.1	0
12	1.1.1.330		0 AT5G02540.1	0
13	1.1.1.330		0 AT5G02540.1	0
14	1.1.1.330		0 AT5G02540.1	0
15	1.1.1.330		0 AT5G02540.1	0
16	1.1.1.330		0 AT5G02540.1	0
17	6.3.2.19		0 GO:0008270,(AT5G60820.1	0
18	1.1.1.330		0 AT5G02540.1	0
19	1.1.1.330		0 AT5G02540.1	0
20	1.1.1.330		0 AT5G02540.1	0
21		0	0 AT5G46220.1	0
22	1.1.1.330		0 AT5G02540.1	0
23	1.1.1.330		0 AT5G02540.1	0
24	1.1.1.330		0 AT5G02540.1	0
25	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
26	1.1.1.330		0 AT5G02540.1	0
27	1.1.1.330		0 AT5G02540.1	0
28	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
29	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
30	2.4.1.198	K03858	GO:0017176 AT4G35530.1	0
31		0	0 AT2G01060.1	0
32		0	0 AT3G60890.2 ZPR2	
33		0 K14488	GO:0009733 AT4G34760.1	0
34		0	0 GO:0043531 AT1G63350.1	0
35		0	0 GO:0043531 AT1G63350.1	0
36		0	0 AT1G22770.1 FB,GI	
37		0	0 AT1G22770.1 FB,GI	
38		0	0 AT1G22770.1 FB,GI	
39	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
40		0	0 GO:0005515 AT2G43500.1	0
41		0	0 GO:0005515 AT2G43500.1	0
42	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
43		0	0 AT1G22770.1 FB,GI	
44	3.1.1.11	K01051	GO:0004857,(AT4G33230.1	0
45		0	0 AT3G51290.2	0
46		0	0 AT1G03870.1 FLA9	
47		0	0 GO:0046983 AT5G08130.5 BIM1	
48		0	0 GO:0046983 AT5G08130.5 BIM1	
49		0	0 AT3G17430.1	0
50		0	0 AT3G17430.1	0
51	1.11.1.7	K00430	GO:0055114,(AT5G05340.1	0
52		0 K14300	0 AT2G05120.1	0
53	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4	

1					
2	2.1.2.1	K00600	GO:0016740	AT4G13930.1 SHM4	
3		0	0	0 AT1G09020.1 ATSNF4,SNF4	
4		0	0	0 AT1G09020.1 ATSNF4,SNF4	
5					
6	2.7.1.67		0 GO:0016773	AT1G26270.1	0
7		0	0	0 AT1G76405.2	0
8	3.6.4.12		0 GO:0016787,(CAT2G28290.1	CHR3,SYD	
9	3.6.4.12		0 GO:0016787,(CAT2G28290.1	CHR3,SYD	
10					
11		0	0 GO:0005515	AT2G22125.1 CSI1	
12		0	0 GO:0005515	AT2G22125.1 CSI1	
13					
14	6.5.1.4		0 GO:0006396	AT5G22100.1	0
15	6.5.1.4		0 GO:0006396	AT5G22100.1	0
16		0	0 GO:0046983	AT2G20180.2 PIF1,PIL5	
17		0	0	0 AT2G35330.1	0
18		0	0	0 AT2G35330.1	0
19		0	0	0 AT2G35330.1	0
20	2.4.1.12		0 GO:0030244,(CAT4G24010.1	ATCSLG1,CSLG1	
21		0	0	0 AT2G35330.1	0
22		0	0 GO:0006629	AT4G16070.1	0
23		0	0 GO:0003677,(CAT1G70510.1	ATK1,KNAT2	
24		0	0	0 AT5G02540.1	0
25	1.1.1.330		0	0 AT5G02540.1	0
26	1.1.1.330		0	0 AT5G02540.1	0
27	1.1.1.330		0	0 AT5G02540.1	0
28	1.1.1.330		0	0 AT5G02540.1	0
29	1.1.1.330		0	0 AT5G02540.1	0
30	6.3.2.19		0 GO:0008270,(CAT5G60820.1		0
31	1.1.1.330		0	0 AT5G02540.1	0
32	1.1.1.330		0	0 AT5G02540.1	0
33	1.1.1.330		0	0 AT5G46220.1	0
34		0	0	0 AT5G46220.1	0
35	1.1.1.330		0	0 AT5G02540.1	0
36	1.1.1.330		0	0 AT5G02540.1	0
37	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1		0
38	1.1.1.330		0	0 AT5G02540.1	0
39	1.1.1.330		0	0 AT5G02540.1	0
40	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1		0
41	2.4.1.198	K03858	GO:0017176	AT4G35530.1	0
42		0	0	0 AT2G01060.1	0
43		0	0	0 AT3G60890.2 ZPR2	
44		0 K14488	GO:0009733	AT4G34760.1	0
45		0	0 GO:0043531	AT1G63350.1	0
46		0	0 GO:0043531	AT1G63350.1	0
47		0	0	0 AT1G22770.1 FB,GI	
48		0	0	0 AT1G22770.1 FB,GI	
49		0	0	0 AT1G22770.1 FB,GI	
50	3.6.3.1		0 GO:0046872,(CAT1G68710.1		0
51		0	0 GO:0005515	AT2G43500.1	0
52		0	0 GO:0005515	AT2G43500.1	0
53	3.6.3.1		0 GO:0046872,(CAT1G68710.1		0
54		0	0	0 AT1G22770.1 FB,GI	
55					
56					
57					
58					
59					
60					

1					
2	3.1.1.11	K01051	GO:0004857,(CAT4G33230.1		0
3		0	0	0 AT3G51290.2	0
4		0	0	0 AT1G03870.1 FLA9	
5		0	0	GO:0046983 AT5G08130.5 BIM1	
6		0	0	GO:0046983 AT5G08130.5 BIM1	
7		0	0	0 AT3G17430.1	0
8		0	0	0 AT3G17430.1	0
9		0	0	0 AT3G17430.1	0
10		0	0	0 AT3G17430.1	0
11	1.11.1.7	K00430	GO:0055114,(CAT5G05340.1		0
12		0 K14300	0 AT2G05120.1		0
13	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4		
14	2.1.2.1	K00600	GO:0016740 AT4G13930.1 SHM4		
15		0	0	0 AT1G09020.1 ATSNF4,SNF4	
16		0	0	0 AT1G09020.1 ATSNF4,SNF4	
17	2.7.1.67		0 GO:0016773 AT1G26270.1		0
18		0	0	0 AT1G76405.2	0
19	3.6.4.12		0 GO:0016787,(CAT2G28290.1 CHR3,SYD		
20	3.6.4.12		0 GO:0016787,(CAT2G28290.1 CHR3,SYD		
21		0	0 GO:0005515 AT2G22125.1 CSI1		
22		0	0 GO:0005515 AT2G22125.1 CSI1		
23	6.5.1.4		0 GO:0006396 AT5G22100.1		0
24	6.5.1.4		0 GO:0006396 AT5G22100.1		0
25		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5		
26		0	0	0 AT2G35330.1	0
27		0	0	0 AT2G35330.1	0
28	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1		
29		0	0	0 AT2G35330.1	0
30		0	0	0 GO:0006629 AT4G16070.1	0
31		0	0	0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2	
32	1.1.1.330		0	0 AT5G02540.1	0
33	1.1.1.330		0	0 AT5G02540.1	0
34	1.1.1.330		0	0 AT5G02540.1	0
35	1.1.1.330		0	0 AT5G02540.1	0
36	6.3.2.19		0 GO:0008270,(CAT5G60820.1		0
37	1.1.1.330		0	0 AT5G02540.1	0
38	1.1.1.330		0	0 AT5G02540.1	0
39		0	0	0 AT5G46220.1	0
40	1.1.1.330		0	0 AT5G02540.1	0
41	1.1.1.330		0	0 AT5G02540.1	0
42	1.1.1.330		0	0 AT5G02540.1	0
43	1.1.1.330		0	0 AT5G02540.1	0
44	1.1.1.330		0	0 AT5G02540.1	0
45	1.1.1.330		0	0 AT5G02540.1	0
46	1.1.1.330		0	0 AT5G02540.1	0
47	1.1.1.330		0	0 AT5G02540.1	0
48	1.1.1.330		0	0 AT5G02540.1	0
49	1.1.1.330		0	0 AT5G02540.1	0
50	1.1.1.330		0	0 AT5G02540.1	0
51	1.1.1.330		0	0 AT5G02540.1	0
52	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1		0
53	1.1.1.330		0	0 AT5G02540.1	0
54	1.1.1.330		0	0 AT5G02540.1	0
55	1.1.1.330		0	0 AT5G02540.1	0
56	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1		0
57	2.4.1.198	K03858	GO:0017176 AT4G35530.1		0
58		0	0	0 AT2G01060.1	0
59		0	0	0 AT3G60890.2 ZPR2	0
60		0 K14488	GO:0009733 AT4G34760.1		0

1				
2		0	0 GO:0043531 AT1G63350.1	0
3		0	0 GO:0043531 AT1G63350.1	0
4		0	0 AT1G22770.1 FB,GI	
5		0	0 AT1G22770.1 FB,GI	
6		0	0 AT1G22770.1 FB,GI	
7		0	0 AT1G22770.1 FB,GI	
8	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
9		0	0 GO:0005515 AT2G43500.1	0
10		0	0 GO:0005515 AT2G43500.1	0
11		0	0 GO:0005515 AT2G43500.1	0
12	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
13		0	0 AT1G22770.1 FB,GI	
14		0	0 AT1G22770.1 FB,GI	
15	3.1.1.11	K01051	GO:0004857,(AT4G33230.1	0
16		0	0 AT3G51290.2	0
17		0	0 AT1G03870.1 FLA9	
18		0	0 GO:0046983 AT5G08130.5 BIM1	
19		0	0 GO:0046983 AT5G08130.5 BIM1	
20		0	0 GO:0046983 AT5G08130.5 BIM1	
21		0	0 AT3G17430.1	0
22		0	0 AT3G17430.1	0
23		0	0 AT3G17430.1	0
24	1.11.1.7	K00430	GO:0055114,(AT5G05340.1	0
25		0 K14300	0 AT2G05120.1	0
26		0 K14300	0 AT2G05120.1	0
27	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4	
28	2.1.2.1	K00600	GO:0016740 AT4G13930.1 SHM4	
29		0	0 AT1G09020.1 ATSNF4,SNF4	
30		0	0 AT1G09020.1 ATSNF4,SNF4	
31		0	0 AT1G09020.1 ATSNF4,SNF4	
32	2.7.1.67		0 GO:0016773 AT1G26270.1	0
33		0	0 AT1G76405.2	0
34		0	0 AT1G76405.2	0
35	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	
36	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	
37		0	0 GO:0005515 AT2G22125.1 CSI1	
38		0	0 GO:0005515 AT2G22125.1 CSI1	
39		0	0 GO:0005515 AT2G22125.1 CSI1	
40	6.5.1.4		0 GO:0006396 AT5G22100.1	0
41	6.5.1.4		0 GO:0006396 AT5G22100.1	0
42		0	0 GO:0006396 AT5G22100.1	0
43		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5	
44		0	0 AT2G35330.1	0
45		0	0 AT2G35330.1	0
46		0	0 AT2G35330.1	0
47	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
48		0	0 AT2G35330.1	0
49		0	0 GO:0006629 AT4G16070.1	0
50		0	0 GO:0006629 AT4G16070.1	0
51		0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
52	1.1.1.330		0 AT5G02540.1	0
53	1.1.1.330		0 AT5G02540.1	0
54	1.1.1.330		0 AT5G02540.1	0
55	1.1.1.330		0 AT5G02540.1	0
56	1.1.1.330		0 AT5G02540.1	0
57	6.3.2.19		0 GO:0008270,(AT5G60820.1	0
58	1.1.1.330		0 AT5G02540.1	0
59	1.1.1.330		0 AT5G02540.1	0
60	1.1.1.330		0 AT5G02540.1	0
		0	0 AT5G46220.1	0

1					
2	1.1.1.330		0	0 AT5G02540.1	0
3	1.1.1.330		0	0 AT5G02540.1	0
4	1.11.1.7	K00430		GO:0055114,(AT4G33870.1	0
5					
6	1.1.1.330		0	0 AT5G02540.1	0
7	1.1.1.330		0	0 AT5G02540.1	0
8	1.11.1.7	K00430		GO:0055114,(AT4G33870.1	0
9					
10	2.4.1.198	K03858		GO:0017176 AT4G35530.1	0
11		0	0	0 AT2G01060.1	0
12		0	0	0 AT3G60890.2 ZPR2	
13					
14		0 K14488		GO:0009733 AT4G34760.1	0
15		0	0	GO:0043531 AT1G63350.1	0
16		0	0	GO:0043531 AT1G63350.1	0
17		0	0	0 AT1G22770.1 FB,GI	
18		0	0	0 AT1G22770.1 FB,GI	
19		0	0	0 AT1G22770.1 FB,GI	
20		0	0	0 AT1G22770.1 FB,GI	
21					
22	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
23		0	0	GO:0005515 AT2G43500.1	0
24		0	0	GO:0005515 AT2G43500.1	0
25	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
26		0	0	0 AT1G22770.1 FB,GI	
27		0	0	0 AT1G22770.1 FB,GI	
28	3.1.1.11	K01051		GO:0004857,(AT4G33230.1	0
29		0	0	0 AT3G51290.2	0
30		0	0	0 AT1G03870.1 FLA9	
31		0	0	0 AT1G03870.1 FLA9	
32		0	0	GO:0046983 AT5G08130.5 BIM1	
33		0	0	GO:0046983 AT5G08130.5 BIM1	
34		0	0	0 AT3G17430.1	0
35		0	0	0 AT3G17430.1	0
36		0	0	0 AT3G17430.1	0
37	1.11.1.7	K00430		GO:0055114,(AT5G05340.1	0
38		0 K14300		0 AT2G05120.1	0
39					
40	6.3.2.19	K10590		GO:0004842 AT5G02880.1 UPL4	
41	2.1.2.1	K00600		GO:0016740 AT4G13930.1 SHM4	
42		0	0	0 AT1G09020.1 ATSNF4,SNF4	
43		0	0	0 AT1G09020.1 ATSNF4,SNF4	
44		0	0	0 AT1G09020.1 ATSNF4,SNF4	
45	2.7.1.67		0	GO:0016773 AT1G26270.1	0
46		0	0	0 AT1G76405.2	0
47					
48	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
49	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
50		0	0	GO:0005515 AT2G22125.1 CSI1	
51		0	0	GO:0005515 AT2G22125.1 CSI1	
52					
53	6.5.1.4		0	GO:0006396 AT5G22100.1	0
54	6.5.1.4		0	GO:0006396 AT5G22100.1	0
55		0	0	GO:0046983 AT2G20180.2 PIF1,PIL5	
56		0	0	0 AT2G35330.1	0
57		0	0	0 AT2G35330.1	0
58		0	0	0 AT2G35330.1	0
59		0	0	0 AT2G35330.1	0
60	2.4.1.12		0	GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
		0	0	0 AT2G35330.1	0

1				
2		0	0 GO:0006629 AT4G16070.1	0
3		0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
4	1.1.1.330		0 AT5G02540.1	0
5	1.1.1.330		0 AT5G02540.1	0
6	1.1.1.330		0 AT5G02540.1	0
7	1.1.1.330		0 AT5G02540.1	0
8	1.1.1.330		0 AT5G02540.1	0
9				
10	6.3.2.19		0 GO:0008270,(AT5G60820.1	0
11	1.1.1.330		0 AT5G02540.1	0
12	1.1.1.330		0 AT5G02540.1	0
13				
14		0	0 AT5G46220.1	0
15	1.1.1.330		0 AT5G02540.1	0
16	1.1.1.330		0 AT5G02540.1	0
17				
18	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
19	1.1.1.330		0 AT5G02540.1	0
20	1.1.1.330		0 AT5G02540.1	0
21				
22	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
23	2.4.1.198	K03858	GO:0017176 AT4G35530.1	0
24		0	0 AT2G01060.1	0
25		0	0 AT3G60890.2 ZPR2	
26				
27		0 K14488	GO:0009733 AT4G34760.1	0
28		0	0 GO:0043531 AT1G63350.1	0
29		0	0 GO:0043531 AT1G63350.1	0
30		0	0 AT1G22770.1 FB,GI	
31		0	0 AT1G22770.1 FB,GI	
32		0	0 AT1G22770.1 FB,GI	
33		0	0 AT1G22770.1 FB,GI	
34				
35	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
36		0	0 GO:0005515 AT2G43500.1	0
37		0	0 GO:0005515 AT2G43500.1	0
38				
39	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
40		0	0 AT1G22770.1 FB,GI	
41	3.1.1.11	K01051	GO:0004857,(AT4G33230.1	0
42		0	0 AT3G51290.2	0
43		0	0 AT1G03870.1 FLA9	
44		0	0 GO:0046983 AT5G08130.5 BIM1	
45		0	0 GO:0046983 AT5G08130.5 BIM1	
46		0	0 AT3G17430.1	0
47		0	0 AT3G17430.1	0
48				
49				
50				
51	1.11.1.7	K00430	GO:0055114,(AT5G05340.1	0
52		0 K14300	0 AT2G05120.1	0
53	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4	
54	2.1.2.1	K00600	GO:0016740 AT4G13930.1 SHM4	
55		0	0 AT1G09020.1 ATSNF4,SNF4	
56		0	0 AT1G09020.1 ATSNF4,SNF4	
57				
58	2.7.1.67		0 GO:0016773 AT1G26270.1	0
59		0	0 AT1G76405.2	0
60				
	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	



1				
2	3.6.4.12		0 GO:0016787,(CAT2G28290.1 CHR3,SYD	
3		0	0 GO:0005515 AT2G22125.1 CSI1	
4		0	0 GO:0005515 AT2G22125.1 CSI1	
5				
6	6.5.1.4		0 GO:0006396 AT5G22100.1	0
7	6.5.1.4		0 GO:0006396 AT5G22100.1	0
8		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5	
9				
10		0	0 AT2G35330.1	0
11		0	0 AT2G35330.1	0
12	2.4.1.12		0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1	
13				
14		0	0 AT2G35330.1	0
15		0	0 GO:0006629 AT4G16070.1	0
16		0	0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2	
17				
18	1.1.1.330		0 AT5G02540.1	0
19	1.1.1.330		0 AT5G02540.1	0
20	1.1.1.330		0 AT5G02540.1	0
21				
22	1.1.1.330		0 AT5G02540.1	0
23	6.3.2.19		0 GO:0008270,(CAT5G60820.1	0
24	1.1.1.330		0 AT5G02540.1	0
25				
26	1.1.1.330		0 AT5G02540.1	0
27		0	0 AT5G46220.1	0
28	1.1.1.330		0 AT5G02540.1	0
29				
30	1.1.1.330		0 AT5G02540.1	0
31	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1	0
32	1.1.1.330		0 AT5G02540.1	0
33	1.1.1.330		0 AT5G02540.1	0
34				
35	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1	0
36	2.4.1.198	K03858	GO:0017176 AT4G35530.1	0
37				
38		0	0 AT2G01060.1	0
39		0	0 AT3G60890.2 ZPR2	
40		0 K14488	GO:0009733 AT4G34760.1	0
41				
42		0	0 GO:0043531 AT1G63350.1	0
43		0	0 GO:0043531 AT1G63350.1	0
44		0	0 AT1G22770.1 FB,GI	
45		0	0 AT1G22770.1 FB,GI	
46		0	0 AT1G22770.1 FB,GI	
47		0	0 AT1G22770.1 FB,GI	
48	3.6.3.1		0 GO:0046872,(CAT1G68710.1	0
49		0	0 GO:0005515 AT2G43500.1	0
50				
51		0	0 GO:0005515 AT2G43500.1	0
52	3.6.3.1		0 GO:0046872,(CAT1G68710.1	0
53		0	0 AT1G22770.1 FB,GI	
54				
55	3.1.1.11	K01051	GO:0004857,(CAT4G33230.1	0
56		0	0 AT3G51290.2	0
57		0	0 AT1G03870.1 FLA9	
58				
59		0	0 GO:0046983 AT5G08130.5 BIM1	
60		0	0 GO:0046983 AT5G08130.5 BIM1	
		0	0 AT3G17430.1	0

1					
2		0	0	0 AT3G17430.1	0
3	1.11.1.7	K00430		GO:0055114,(AT5G05340.1	0
4		0 K14300		0 AT2G05120.1	0
5					
6	6.3.2.19	K10590		GO:0004842 AT5G02880.1 UPL4	
7	2.1.2.1	K00600		GO:0016740 AT4G13930.1 SHM4	
8		0	0	0 AT1G09020.1 ATSNF4,SNF4	
9		0	0	0 AT1G09020.1 ATSNF4,SNF4	
10					
11	2.7.1.67			0 GO:0016773 AT1G26270.1	0
12		0	0	0 AT1G76405.2	0
13					
14	3.6.4.12			0 GO:0016787,(AT2G28290.1 CHR3,SYD	
15	3.6.4.12			0 GO:0016787,(AT2G28290.1 CHR3,SYD	
16		0		0 GO:0005515 AT2G22125.1 CSI1	
17		0		0 GO:0005515 AT2G22125.1 CSI1	
18					
19	6.5.1.4			0 GO:0006396 AT5G22100.1	0
20	6.5.1.4			0 GO:0006396 AT5G22100.1	0
21					
22		0		0 GO:0046983 AT2G20180.2 PIF1,PIL5	
23		0	0	0 AT2G35330.1	0
24		0	0	0 AT2G35330.1	0
25					
26	2.4.1.12			0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
27		0	0	0 AT2G35330.1	0
28		0		0 GO:0006629 AT4G16070.1	0
29		0		0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
30					
31	1.1.1.330			0 AT5G02540.1	0
32	1.1.1.330			0 AT5G02540.1	0
33	1.1.1.330			0 AT5G02540.1	0
34	1.1.1.330			0 AT5G02540.1	0
35	1.1.1.330			0 AT5G02540.1	0
36	6.3.2.19			0 GO:0008270,(AT5G60820.1	0
37	1.1.1.330			0 AT5G02540.1	0
38	1.1.1.330			0 AT5G02540.1	0
39	1.1.1.330			0 AT5G02540.1	0
40		0		0 AT5G46220.1	0
41	1.1.1.330			0 AT5G02540.1	0
42	1.1.1.330			0 AT5G02540.1	0
43	1.1.1.330			0 AT5G02540.1	0
44	1.11.1.7	K00430		GO:0055114,(AT4G33870.1	0
45	1.1.1.330			0 AT5G02540.1	0
46	1.1.1.330			0 AT5G02540.1	0
47	1.1.1.330			0 AT5G02540.1	0
48	1.11.1.7	K00430		GO:0055114,(AT4G33870.1	0
49	2.4.1.198	K03858		GO:0017176 AT4G35530.1	0
50					
51		0	0	0 AT2G01060.1	0
52		0	0	0 AT3G60890.2 ZPR2	
53		0 K14488		GO:0009733 AT4G34760.1	0
54					
55		0		0 GO:0043531 AT1G63350.1	0
56		0		0 GO:0043531 AT1G63350.1	0
57		0	0	0 AT1G22770.1 FB,GI	
58		0	0	0 AT1G22770.1 FB,GI	
59		0	0	0 AT1G22770.1 FB,GI	
60		0	0	0 AT1G22770.1 FB,GI	
	3.6.3.1			0 GO:0046872,(AT1G68710.1	0

1				
2		0	0 GO:0005515 AT2G43500.1	0
3		0	0 GO:0005515 AT2G43500.1	0
4	3.6.3.1		0 GO:0046872,(AT1G68710.1	0
5				
6		0	0 AT1G22770.1 FB,GI	
7	3.1.1.11	K01051	GO:0004857,(AT4G33230.1	0
8		0	0 AT3G51290.2	0
9				
10		0	0 AT1G03870.1 FLA9	
11		0	0 GO:0046983 AT5G08130.5 BIM1	
12		0	0 GO:0046983 AT5G08130.5 BIM1	
13				
14		0	0 AT3G17430.1	0
15		0	0 AT3G17430.1	0
16	1.11.1.7	K00430	GO:0055114,(AT5G05340.1	0
17		0 K14300	0 AT2G05120.1	0
18				
19	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4	
20	2.1.2.1	K00600	GO:0016740 AT4G13930.1 SHM4	
21				
22		0	0 AT1G09020.1 ATSNF4,SNF4	
23		0	0 AT1G09020.1 ATSNF4,SNF4	
24	2.7.1.67		0 GO:0016773 AT1G26270.1	0
25		0	0 AT1G76405.2	0
26				
27	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	
28	3.6.4.12		0 GO:0016787,(AT2G28290.1 CHR3,SYD	
29				
30		0	0 GO:0005515 AT2G22125.1 CSI1	
31		0	0 GO:0005515 AT2G22125.1 CSI1	
32	6.5.1.4		0 GO:0006396 AT5G22100.1	0
33	6.5.1.4		0 GO:0006396 AT5G22100.1	0
34				
35		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5	
36		0	0 AT2G35330.1	0
37		0	0 AT2G35330.1	0
38				
39	2.4.1.12		0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
40		0	0 AT2G35330.1	0
41		0	0 GO:0006629 AT4G16070.1	0
42				
43		0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2	
44	1.1.1.330		0 AT5G02540.1	0
45	1.1.1.330		0 AT5G02540.1	0
46	1.1.1.330		0 AT5G02540.1	0
47	1.1.1.330		0 AT5G02540.1	0
48	1.1.1.330		0 AT5G02540.1	0
49	6.3.2.19		0 GO:0008270,(AT5G60820.1	0
50				
51	1.1.1.330		0 AT5G02540.1	0
52	1.1.1.330		0 AT5G02540.1	0
53		0	0 AT5G46220.1	0
54				
55	1.1.1.330		0 AT5G02540.1	0
56	1.1.1.330		0 AT5G02540.1	0
57	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0
58	1.1.1.330		0 AT5G02540.1	0
59	1.1.1.330		0 AT5G02540.1	0
60	1.1.1.330		0 AT5G02540.1	0
	1.11.1.7	K00430	GO:0055114,(AT4G33870.1	0

1					
2	2.4.1.198	K03858	GO:0017176	AT4G35530.1	0
3		0	0	0 AT2G01060.1	0
4		0	0	0 AT3G60890.2 ZPR2	
5					
6		0 K14488	GO:0009733	AT4G34760.1	0
7		0	0	GO:0043531 AT1G63350.1	0
8		0	0	GO:0043531 AT1G63350.1	0
9					
10		0	0	0 AT1G22770.1 FB,GI	
11		0	0	0 AT1G22770.1 FB,GI	
12		0	0	0 AT1G22770.1 FB,GI	
13					
14	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
15		0	0	GO:0005515 AT2G43500.1	0
16		0	0	GO:0005515 AT2G43500.1	0
17					
18	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
19		0	0	0 AT1G22770.1 FB,GI	
20	3.1.1.11	K01051	GO:0004857,(AT4G33230.1		0
21		0	0	0 AT3G51290.2	0
22		0	0	0 AT1G03870.1 FLA9	
23					
24		0	0	GO:0046983 AT5G08130.5 BIM1	
25		0	0	GO:0046983 AT5G08130.5 BIM1	
26					
27		0	0	0 AT3G17430.1	0
28		0	0	0 AT3G17430.1	0
29					
30	1.11.1.7	K00430	GO:0055114,(AT5G05340.1		0
31		0 K14300		0 AT2G05120.1	0
32	6.3.2.19	K10590	GO:0004842	AT5G02880.1 UPL4	
33	2.1.2.1	K00600	GO:0016740	AT4G13930.1 SHM4	
34					
35		0	0	0 AT1G09020.1 ATSNF4,SNF4	
36		0	0	0 AT1G09020.1 ATSNF4,SNF4	
37	2.7.1.67		0	GO:0016773 AT1G26270.1	0
38		0	0	0 AT1G76405.2	0
39					
40	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
41	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
42					
43		0	0	GO:0005515 AT2G22125.1 CSI1	
44		0	0	GO:0005515 AT2G22125.1 CSI1	
45	6.5.1.4		0	GO:0006396 AT5G22100.1	0
46	6.5.1.4		0	GO:0006396 AT5G22100.1	0
47					
48		0	0	GO:0046983 AT2G20180.2 PIF1,PIL5	
49		0	0	0 AT2G35330.1	0
50		0	0	0 AT2G35330.1	0
51					
52	2.4.1.12		0	GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
53		0	0	0 AT2G35330.1	0
54					
55		0	0	GO:0006629 AT4G16070.1	0
56		0	0	GO:0003677,(AT1G70510.1 ATK1,KNAT2	
57	1.1.1.330		0	0 AT5G02540.1	0
58	1.1.1.330		0	0 AT5G02540.1	0
59	1.1.1.330		0	0 AT5G02540.1	0
60	1.1.1.330		0	0 AT5G02540.1	0

1					
2	6.3.2.19		0 GO:0008270,(CAT5G60820.1		0
3	1.1.1.330		0 0 AT5G02540.1		0
4	1.1.1.330		0 0 AT5G02540.1		0
5					
6		0	0 0 AT5G46220.1		0
7	1.1.1.330		0 0 AT5G02540.1		0
8	1.1.1.330		0 0 AT5G02540.1		0
9					
10	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1		0
11	1.1.1.330		0 0 AT5G02540.1		0
12	1.1.1.330		0 0 AT5G02540.1		0
13					
14	1.11.1.7	K00430	GO:0055114,(CAT4G33870.1		0
15	2.4.1.198	K03858	GO:0017176 AT4G35530.1		0
16		0	0 0 AT2G01060.1		0
17		0	0 0 AT3G60890.2 ZPR2		
18		0	0 0 AT3G60890.2 ZPR2		
19		0 K14488	GO:0009733 AT4G34760.1		0
20		0	0 GO:0043531 AT1G63350.1		0
21		0	0 GO:0043531 AT1G63350.1		0
22		0	0 GO:0043531 AT1G63350.1		0
23		0	0 0 AT1G22770.1 FB,GI		
24		0	0 0 AT1G22770.1 FB,GI		
25		0	0 0 AT1G22770.1 FB,GI		
26		0	0 0 AT1G22770.1 FB,GI		
27	3.6.3.1		0 GO:0046872,(CAT1G68710.1		0
28		0	0 GO:0005515 AT2G43500.1		0
29		0	0 GO:0005515 AT2G43500.1		0
30		0	0 GO:0005515 AT2G43500.1		0
31	3.6.3.1		0 GO:0046872,(CAT1G68710.1		0
32		0	0 0 AT1G22770.1 FB,GI		
33	3.1.1.11	K01051	GO:0004857,(CAT4G33230.1		0
34		0	0 0 AT3G51290.2		0
35		0	0 0 AT3G51290.2		0
36		0	0 0 AT1G03870.1 FLA9		
37		0	0 0 AT1G03870.1 FLA9		
38		0	0 GO:0046983 AT5G08130.5 BIM1		
39		0	0 GO:0046983 AT5G08130.5 BIM1		
40		0	0 0 AT3G17430.1		0
41		0	0 0 AT3G17430.1		0
42		0	0 0 AT3G17430.1		0
43	1.11.1.7	K00430	GO:0055114,(CAT5G05340.1		0
44		0 K14300	0 AT2G05120.1		0
45	6.3.2.19	K10590	GO:0004842 AT5G02880.1 UPL4		
46	2.1.2.1	K00600	GO:0016740 AT4G13930.1 SHM4		
47		0	0 0 AT1G09020.1 ATSNF4,SNF4		
48		0	0 0 AT1G09020.1 ATSNF4,SNF4		
49		0	0 0 AT1G09020.1 ATSNF4,SNF4		
50		0	0 0 AT1G09020.1 ATSNF4,SNF4		
51	2.7.1.67		0 GO:0016773 AT1G26270.1		0
52		0	0 0 AT1G76405.2		0
53	3.6.4.12		0 GO:0016787,(CAT2G28290.1 CHR3,SYD		
54	3.6.4.12		0 GO:0016787,(CAT2G28290.1 CHR3,SYD		
55		0	0 GO:0005515 AT2G22125.1 CSI1		
56		0	0 GO:0005515 AT2G22125.1 CSI1		
57		0	0 GO:0005515 AT2G22125.1 CSI1		
58		0	0 GO:0005515 AT2G22125.1 CSI1		
59	6.5.1.4		0 GO:0006396 AT5G22100.1		0
60	6.5.1.4		0 GO:0006396 AT5G22100.1		0
		0	0 GO:0046983 AT2G20180.2 PIF1,PIL5		

1				
2		0	0	0 AT2G35330.1
3		0	0	0 AT2G35330.1
4	2.4.1.12			0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1
5				
6		0	0	0 AT2G35330.1
7		0	0	0 GO:0006629 AT4G16070.1
8		0	0	0 GO:0003677,(AT1G70510.1 ATK1,KNAT2
9				
10	1.1.1.330		0	0 AT5G02540.1
11	1.1.1.330		0	0 AT5G02540.1
12	1.1.1.330		0	0 AT5G02540.1
13	1.1.1.330		0	0 AT5G02540.1
14	1.1.1.330		0	0 AT5G02540.1
15	6.3.2.19		0	0 GO:0008270,(AT5G60820.1
16	1.1.1.330		0	0 AT5G02540.1
17	1.1.1.330		0	0 AT5G02540.1
18	1.1.1.330		0	0 AT5G02540.1
19		0	0	0 AT5G46220.1
20	1.1.1.330		0	0 AT5G02540.1
21	1.1.1.330		0	0 AT5G02540.1
22	1.1.1.330		0	0 AT5G02540.1
23	1.11.1.7	K00430		GO:0055114,(AT4G33870.1
24	1.1.1.330		0	0 AT5G02540.1
25	1.1.1.330		0	0 AT5G02540.1
26	1.1.1.330		0	0 AT5G02540.1
27	1.11.1.7	K00430		GO:0055114,(AT4G33870.1
28	2.4.1.198	K03858		GO:0017176 AT4G35530.1
29				
30		0	0	0 AT2G01060.1
31		0	0	0 AT3G60890.2 ZPR2
32		0 K14488		GO:0009733 AT4G34760.1
33		0	0	0 GO:0043531 AT1G63350.1
34		0	0	0 GO:0043531 AT1G63350.1
35		0	0	0 GO:0043531 AT1G63350.1
36		0	0	0 AT1G22770.1 FB,GI
37		0	0	0 AT1G22770.1 FB,GI
38		0	0	0 AT1G22770.1 FB,GI
39		0	0	0 AT1G22770.1 FB,GI
40	3.6.3.1			0 GO:0046872,(AT1G68710.1
41		0	0	0 GO:0005515 AT2G43500.1
42		0	0	0 GO:0005515 AT2G43500.1
43		0	0	0 GO:0005515 AT2G43500.1
44	3.6.3.1			0 GO:0046872,(AT1G68710.1
45		0	0	0 AT1G22770.1 FB,GI
46		0	0	0 AT1G22770.1 FB,GI
47	3.1.1.11	K01051		GO:0004857,(AT4G33230.1
48		0	0	0 AT3G51290.2
49		0	0	0 AT1G03870.1 FLA9
50		0	0	0 GO:0046983 AT5G08130.5 BIM1
51		0	0	0 GO:0046983 AT5G08130.5 BIM1
52		0	0	0 GO:0046983 AT5G08130.5 BIM1
53		0	0	0 AT3G17430.1
54		0	0	0 AT3G17430.1
55		0	0	0 AT3G17430.1
56	1.11.1.7	K00430		GO:0055114,(AT5G05340.1
57		0 K14300		0 AT2G05120.1
58				
59	6.3.2.19	K10590		GO:0004842 AT5G02880.1 UPL4
60	2.1.2.1	K00600		GO:0016740 AT4G13930.1 SHM4
		0	0	0 AT1G09020.1 ATSNF4,SNF4



1					
2		0	0	0 AT1G09020.1 ATSNF4,SNF4	
3	2.7.1.67		0	GO:0016773 AT1G26270.1	0
4		0	0	0 AT1G76405.2	0
5					
6	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
7	3.6.4.12		0	GO:0016787,(AT2G28290.1 CHR3,SYD	
8		0	0	GO:0005515 AT2G22125.1 CSI1	
9		0	0	GO:0005515 AT2G22125.1 CSI1	
10					
11	6.5.1.4		0	GO:0006396 AT5G22100.1	0
12	6.5.1.4		0	GO:0006396 AT5G22100.1	0
13					
14		0	0	GO:0046983 AT2G20180.2 PIF1,PIL5	
15		0	0	0 AT2G35330.1	0
16		0	0	0 AT2G35330.1	0
17					
18	2.4.1.12		0	GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1	
19		0	0	0 AT2G35330.1	0
20		0	0	GO:0006629 AT4G16070.1	0
21					
22		0	0	GO:0003677,(AT1G70510.1 ATK1,KNAT2	
23	1.1.1.330		0	0 AT5G02540.1	0
24	1.1.1.330		0	0 AT5G02540.1	0
25	1.1.1.330		0	0 AT5G02540.1	0
26	1.1.1.330		0	0 AT5G02540.1	0
27	1.1.1.330		0	0 AT5G02540.1	0
28	6.3.2.19		0	GO:0008270,(AT5G60820.1	0
29	1.1.1.330		0	0 AT5G02540.1	0
30	1.1.1.330		0	0 AT5G02540.1	0
31	1.1.1.330		0	0 AT5G02540.1	0
32		0	0	0 AT5G46220.1	0
33	1.1.1.330		0	0 AT5G02540.1	0
34	1.1.1.330		0	0 AT5G02540.1	0
35	1.1.1.330		0	0 AT5G02540.1	0
36	1.11.1.7	K00430	0	GO:0055114,(AT4G33870.1	0
37	1.1.1.330		0	0 AT5G02540.1	0
38	1.1.1.330		0	0 AT5G02540.1	0
39	1.1.1.330		0	0 AT5G02540.1	0
40	1.11.1.7	K00430	0	GO:0055114,(AT4G33870.1	0
41	2.4.1.198	K03858	0	GO:0017176 AT4G35530.1	0
42					
43		0	0	0 AT2G01060.1	0
44		0	0	0 AT3G60890.2 ZPR2	
45		0 K14488	0	GO:0009733 AT4G34760.1	0
46			0	GO:0043531 AT1G63350.1	0
47			0	GO:0043531 AT1G63350.1	0
48			0	0 AT1G22770.1 FB,GI	
49			0	0 AT1G22770.1 FB,GI	
50			0	0 AT1G22770.1 FB,GI	
51			0	0 AT1G22770.1 FB,GI	
52			0	0 AT1G22770.1 FB,GI	
53	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
54		0	0	GO:0005515 AT2G43500.1	0
55		0	0	GO:0005515 AT2G43500.1	0
56					
57	3.6.3.1		0	GO:0046872,(AT1G68710.1	0
58		0	0	0 AT1G22770.1 FB,GI	
59	3.1.1.11	K01051	0	GO:0004857,(AT4G33230.1	0
60		0	0	0 AT3G51290.2	0

1				
2		0	0	0 AT1G03870.1 FLA9
3		0	0	GO:0046983 AT5G08130.5 BIM1
4		0	0	GO:0046983 AT5G08130.5 BIM1
5		0	0	0 AT3G17430.1
6		0	0	0 AT3G17430.1
7		0	0	0 AT3G17430.1
8	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1
9		0 K14300	0	AT2G05120.1
10		0 K14300	0	AT2G05120.1
11	6.3.2.19	K10590	GO:0004842	AT5G02880.1 UPL4
12	2.1.2.1	K00600	GO:0016740	AT4G13930.1 SHM4
13		0	0	AT1G09020.1 ATSNF4,SNF4
14		0	0	AT1G09020.1 ATSNF4,SNF4
15		0	0	AT1G09020.1 ATSNF4,SNF4
16	2.7.1.67		0 GO:0016773	AT1G26270.1
17		0	0	AT1G76405.2
18		0	0	AT1G76405.2
19	3.6.4.12		0 GO:0016787,(	AT2G28290.1 CHR3,SYD
20	3.6.4.12		0 GO:0016787,(	AT2G28290.1 CHR3,SYD
21		0	0 GO:0005515	AT2G22125.1 CSI1
22		0	0 GO:0005515	AT2G22125.1 CSI1
23		0	0 GO:0005515	AT2G22125.1 CSI1
24	6.5.1.4		0 GO:0006396	AT5G22100.1
25	6.5.1.4		0 GO:0006396	AT5G22100.1
26		0	0 GO:0046983	AT2G20180.2 PIF1,PIL5
27		0	0	AT2G35330.1
28		0	0	AT2G35330.1
29		0	0	AT2G35330.1
30		0	0	AT2G35330.1
31	2.4.1.12		0 GO:0030244,(	AT4G24010.1 ATCSLG1,CSLG1
32		0	0	AT2G35330.1
33		0	0 GO:0006629	AT4G16070.1
34		0	0 GO:0003677,(	AT1G70510.1 ATK1,KNAT2
35		0	0 GO:0003677,(	AT1G70510.1 ATK1,KNAT2
36	1.1.1.330		0	AT5G02540.1
37	1.1.1.330		0	AT5G02540.1
38	1.1.1.330		0	AT5G02540.1
39	1.1.1.330		0	AT5G02540.1
40	1.1.1.330		0	AT5G02540.1
41	6.3.2.19		0 GO:0008270,(	AT5G60820.1
42		0	0	AT5G02540.1
43	1.1.1.330		0	AT5G02540.1
44	1.1.1.330		0	AT5G02540.1
45		0	0	AT5G46220.1
46		0	0	AT5G46220.1
47	1.1.1.330		0	AT5G02540.1
48	1.1.1.330		0	AT5G02540.1
49	1.11.1.7	K00430	GO:0055114,(	AT4G33870.1
50		0	0	AT5G02540.1
51	1.1.1.330		0	AT5G02540.1
52	1.1.1.330		0	AT5G02540.1
53	1.11.1.7	K00430	GO:0055114,(	AT4G33870.1
54		0	0	AT5G02540.1
55	2.4.1.198	K03858	GO:0017176	AT4G35530.1
56		0	0	AT2G01060.1
57		0	0	AT3G60890.2 ZPR2
58		0 K14488	GO:0009733	AT4G34760.1
59		0	0 GO:0043531	AT1G63350.1
60		0	0 GO:0043531	AT1G63350.1

1				
2		0	0	0 AT1G22770.1 FB,GI
3		0	0	0 AT1G22770.1 FB,GI
4		0	0	0 AT1G22770.1 FB,GI
5		0	0	0 AT1G22770.1 FB,GI
6	3.6.3.1		0 GO:0046872,(CAT1G68710.1	0
7		0	0 GO:0005515 AT2G43500.1	0
8		0	0 GO:0005515 AT2G43500.1	0
9		0	0 GO:0005515 AT2G43500.1	0
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1  
2 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SfPhvul.005G07  
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7	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvul.004G17
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46	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
47	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvul.004G17
48	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvul.006G16
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53	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
54	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
55	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvul.004G17
56	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvul.006G16
57		
58	protamine P1 family protein	Phvul.007G16PTHR33448:SfPhvul.007G16
59	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
60	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06

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2	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
3	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
4	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
5	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
6	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
7	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
8	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
9		
10	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
11	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
12	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
13	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
14	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
15	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
16	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
17		
18	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
19	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
20	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
21	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
22	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
23	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
24	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
25		
26	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
27	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
28	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
29	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
30	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
31	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
32	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
33		
34	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
35	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
36	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
37	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
38	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
39	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
40	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
41		
42	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
43	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
44	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
45	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
46	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
47	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
48	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
49		
50	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
51	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
52	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
53	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
54	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
55	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
56	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06
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58	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvu.004G17
59	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvu.006G16
60	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvu.007G16
	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvu.011G06



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2	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
3	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
4	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvul.004G17
5	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvul.006G16
6	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvul.007G16
7	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
8	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
9	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
10	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
11	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
12	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvul.004G17
13	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16PTHR22835//IPhvul.006G16
14	protamine P1 family protein	Phvul.007G16PTHR33448:SFPhvul.007G16
15	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
16	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
17	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
18	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
19	UDP-XYL synthase 6	Phvul.011G06PTHR10366//IPhvul.011G06
20	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.004G17PTHR10509//IPhvul.004G17
21	TCP family transcription factor	Phvul.010G08PTHR31072:SFPhvul.010G08
22	UDP-Glycosyltransferase superfamily protein	Phvul.002G322.4.1.227 - UnPhvul.002G32
23	paralog of ARC6	Phvul.004G13PTHR33925:SFPhvul.004G13
24	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00PTHR22835//IPhvul.005G00
25		0 Phvul.008G14PF17035 - BroPhvul.008G14
26		0 Phvul.008G14PF17035 - BroPhvul.008G14
27		0 Phvul.008G14PF17035 - BroPhvul.008G14
28		0 Phvul.008G14PF17035 - BroPhvul.008G14
29		0 Phvul.008G14PF17035 - BroPhvul.008G14
30		0 Phvul.008G14PF17035 - BroPhvul.008G14
31		0 0 0 Phvul.006G08
32	cation calcium exchanger 4	Phvul.010G12PTHR12266:SFPhvul.010G12
33	TCP family transcription factor	Phvul.010G08PTHR31072:SFPhvul.010G08
34	UDP-Glycosyltransferase superfamily protein	Phvul.002G322.4.1.227 - UnPhvul.002G32
35	paralog of ARC6	Phvul.004G13PTHR33925:SFPhvul.004G13
36	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00PTHR22835//IPhvul.005G00
37		0 Phvul.008G14PF17035 - BroPhvul.008G14
38		0 Phvul.008G14PF17035 - BroPhvul.008G14
39		0 Phvul.008G14PF17035 - BroPhvul.008G14
40		0 Phvul.008G14PF17035 - BroPhvul.008G14
41		0 Phvul.008G14PF17035 - BroPhvul.008G14
42		0 Phvul.008G14PF17035 - BroPhvul.008G14
43		0 0 0 Phvul.006G08
44	cation calcium exchanger 4	Phvul.010G12PTHR12266:SFPhvul.010G12
45	TCP family transcription factor	Phvul.010G08PTHR31072:SFPhvul.010G08
46	UDP-Glycosyltransferase superfamily protein	Phvul.002G322.4.1.227 - UnPhvul.002G32
47	paralog of ARC6	Phvul.004G13PTHR33925:SFPhvul.004G13
48	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00PTHR22835//IPhvul.005G00
49		0 Phvul.008G14PF17035 - BroPhvul.008G14
50		0 Phvul.008G14PF17035 - BroPhvul.008G14
51		0 Phvul.008G14PF17035 - BroPhvul.008G14
52		0 Phvul.008G14PF17035 - BroPhvul.008G14
53		0 Phvul.008G14PF17035 - BroPhvul.008G14
54		0 Phvul.008G14PF17035 - BroPhvul.008G14
55		0 0 0 Phvul.006G08
56	cation calcium exchanger 4	Phvul.010G12PTHR12266:SFPhvul.010G12
57	TCP family transcription factor	Phvul.010G08PTHR31072:SFPhvul.010G08
58	UDP-Glycosyltransferase superfamily protein	Phvul.002G322.4.1.227 - UnPhvul.002G32
59	paralog of ARC6	Phvul.004G13PTHR33925:SFPhvul.004G13
60	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00PTHR22835//IPhvul.005G00

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2		0	Phvul.008G14PF17035 - BroPhvul.008G14		
3		0	Phvul.008G14PF17035 - BroPhvul.008G14		
4		0	Phvul.008G14PF17035 - BroPhvul.008G14		
5					
6		0	0	0	Phvul.006G08
7	cation calcium exchanger 4		Phvul.010G12PTHR12266:Sf	Phvul.010G12	
8	TCP family transcription factor		Phvul.010G08PTHR31072:Sf	Phvul.010G08	
9	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - Un	Phvul.002G32	
10	paralog of ARC6		Phvul.004G13PTHR33925:Sf	Phvul.004G13	
11	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//I	Phvul.005G00	
12		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
13		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
14		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
15					
16		0	0	0	Phvul.006G08
17	cation calcium exchanger 4		Phvul.010G12PTHR12266:Sf	Phvul.010G12	
18	TCP family transcription factor		Phvul.010G08PTHR31072:Sf	Phvul.010G08	
19	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - Un	Phvul.002G32	
20	paralog of ARC6		Phvul.004G13PTHR33925:Sf	Phvul.004G13	
21	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//I	Phvul.005G00	
22		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
23		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
24		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
25					
26		0	0	0	Phvul.006G08
27	cation calcium exchanger 4		Phvul.010G12PTHR12266:Sf	Phvul.010G12	
28	TCP family transcription factor		Phvul.010G08PTHR31072:Sf	Phvul.010G08	
29	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - Un	Phvul.002G32	
30	paralog of ARC6		Phvul.004G13PTHR33925:Sf	Phvul.004G13	
31	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//I	Phvul.005G00	
32		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
33		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
34		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
35					
36		0	0	0	Phvul.006G08
37	cation calcium exchanger 4		Phvul.010G12PTHR12266:Sf	Phvul.010G12	
38	TCP family transcription factor		Phvul.010G08PTHR31072:Sf	Phvul.010G08	
39	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - Un	Phvul.002G32	
40	paralog of ARC6		Phvul.004G13PTHR33925:Sf	Phvul.004G13	
41	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//I	Phvul.005G00	
42		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
43		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
44		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
45					
46		0	0	0	Phvul.006G08
47	cation calcium exchanger 4		Phvul.010G12PTHR12266:Sf	Phvul.010G12	
48	TCP family transcription factor		Phvul.010G08PTHR31072:Sf	Phvul.010G08	
49	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - Un	Phvul.002G32	
50	paralog of ARC6		Phvul.004G13PTHR33925:Sf	Phvul.004G13	
51	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//I	Phvul.005G00	
52		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
53		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
54		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	
55					
56		0	0	0	Phvul.006G08
57	cation calcium exchanger 4		Phvul.010G12PTHR12266:Sf	Phvul.010G12	
58	TCP family transcription factor		Phvul.010G08PTHR31072:Sf	Phvul.010G08	
59	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - Un	Phvul.002G32	
60	paralog of ARC6		Phvul.004G13PTHR33925:Sf	Phvul.004G13	
61	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//I	Phvul.005G00	
62		0	Phvul.008G14PF17035 - Bro	Phvul.008G14	



1			
2		0	Phvul.008G14PF17035 - BroPhvul.008G14
3		0	Phvul.008G14PF17035 - BroPhvul.008G14
4		0	0
5		0	0 Phvul.006G08
6	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
7	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
8	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
9	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
10	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
11		0	Phvul.008G14PF17035 - BroPhvul.008G14
12		0	Phvul.008G14PF17035 - BroPhvul.008G14
13		0	Phvul.008G14PF17035 - BroPhvul.008G14
14		0	0
15		0	0 Phvul.006G08
16		0	0
17	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
18	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
19	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
20	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
21	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
22		0	Phvul.008G14PF17035 - BroPhvul.008G14
23		0	Phvul.008G14PF17035 - BroPhvul.008G14
24		0	Phvul.008G14PF17035 - BroPhvul.008G14
25		0	0
26		0	0 Phvul.006G08
27		0	0
28	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
29	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
30	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
31	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
32	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
33		0	Phvul.008G14PF17035 - BroPhvul.008G14
34		0	Phvul.008G14PF17035 - BroPhvul.008G14
35		0	Phvul.008G14PF17035 - BroPhvul.008G14
36		0	0
37		0	0 Phvul.006G08
38		0	0
39	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
40	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
41	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
42	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
43	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
44		0	Phvul.008G14PF17035 - BroPhvul.008G14
45		0	Phvul.008G14PF17035 - BroPhvul.008G14
46		0	Phvul.008G14PF17035 - BroPhvul.008G14
47		0	0
48		0	0 Phvul.006G08
49		0	0
50	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
51	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
52	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
53	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
54	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
55		0	Phvul.008G14PF17035 - BroPhvul.008G14
56		0	Phvul.008G14PF17035 - BroPhvul.008G14
57		0	Phvul.008G14PF17035 - BroPhvul.008G14
58		0	0
59		0	0 Phvul.006G08
60		0	0

1			
2		0	Phvul.008G14PF17035 - BroPhvul.008G14
3		0	0 0 Phvul.006G08
4	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
5	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
6	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
7	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
8	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
9			
10		0	Phvul.008G14PF17035 - BroPhvul.008G14
11		0	Phvul.008G14PF17035 - BroPhvul.008G14
12		0	Phvul.008G14PF17035 - BroPhvul.008G14
13		0	Phvul.008G14PF17035 - BroPhvul.008G14
14		0	0 0 Phvul.006G08
15	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
16	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
17	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
18	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
19	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
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22		0	Phvul.008G14PF17035 - BroPhvul.008G14
23		0	Phvul.008G14PF17035 - BroPhvul.008G14
24		0	Phvul.008G14PF17035 - BroPhvul.008G14
25		0	0 0 Phvul.006G08
26	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
27	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
28	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
29	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
30	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
31			
32		0	Phvul.008G14PF17035 - BroPhvul.008G14
33		0	Phvul.008G14PF17035 - BroPhvul.008G14
34		0	Phvul.008G14PF17035 - BroPhvul.008G14
35		0	0 0 Phvul.006G08
36	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
37	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
38	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
39	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
40	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
41			
42		0	Phvul.008G14PF17035 - BroPhvul.008G14
43		0	Phvul.008G14PF17035 - BroPhvul.008G14
44		0	Phvul.008G14PF17035 - BroPhvul.008G14
45		0	0 0 Phvul.006G08
46	cation calcium exchanger 4		Phvul.010G12PTHR12266:SfPhvul.010G12
47	TCP family transcription factor		Phvul.010G08PTHR31072:SfPhvul.010G08
48	UDP-Glycosyltransferase superfamily protein		Phvul.002G322.4.1.227 - UnPhvul.002G32
49	paralog of ARC6		Phvul.004G13PTHR33925:SfPhvul.004G13
50	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00PTHR22835//IPhvul.005G00
51			
52		0	Phvul.008G14PF17035 - BroPhvul.008G14
53		0	Phvul.008G14PF17035 - BroPhvul.008G14
54		0	Phvul.008G14PF17035 - BroPhvul.008G14
55	gigantea protein (GI)		Phvul.007G08K12124 - GIG/Phvul.007G08
56	gigantea protein (GI)		Phvul.007G08K12124 - GIG/Phvul.007G08
57	Homeobox-leucine zipper family protein / lipid-binding		Phvul.011G07PF08670 - ME Phvul.011G07
58	cysteine-rich RLK (RECEPTOR-like protein kinase) 25		Phvul.008G07PF01657//PF0Phvul.008G07
59		0	0 0 Phvul.011G11
60	cysteine-rich RLK (RECEPTOR-like protein kinase) 25		Phvul.008G07PTHR32099 - (Phvul.008G07
61	chloride channel F		Phvul.005G00PTHR11689:SfPhvul.005G00
62	serine acetyltransferase 2;2		Phvul.008G27PTHR23416:SfPhvul.008G27
63		0	0 0 Phvul.003G06

1			
2	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
3	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
4	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
5	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G13PTHR10108:SF	Phvul.009G13
6		0	0
7		0	0
8	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
9	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.011G10PTHR10108//I	Phvul.011G10
10	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
11	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
12	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
13	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
14	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
15		0	0
16		0	0
17	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 -	(Phvul.008G07
18	chloride channel F	Phvul.005G00PTHR11689:SF	Phvul.005G00
19	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:SF	Phvul.008G27
20		0	0
21		0	0
22	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
23	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
24	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
25	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G13PTHR10108:SF	Phvul.009G13
26		0	0
27		0	0
28	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
29	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.011G10PTHR10108//I	Phvul.011G10
30	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
31	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
32	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
33	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
34	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
35		0	0
36		0	0
37	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 -	(Phvul.008G07
38	chloride channel F	Phvul.005G00PTHR11689:SF	Phvul.005G00
39	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:SF	Phvul.008G27
40		0	0
41		0	0
42	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
43	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
44	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
45	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G13PTHR10108:SF	Phvul.009G13
46		0	0
47		0	0
48	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
49	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.011G10PTHR10108//I	Phvul.011G10
50	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
51	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
52	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
53	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
54	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
55		0	0
56		0	0
57	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 -	(Phvul.008G07
58	chloride channel F	Phvul.005G00PTHR11689:SF	Phvul.005G00
59	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:SF	Phvul.008G27
60		0	0
61		0	0
62	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
63	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
64	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
65	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G13PTHR10108:SF	Phvul.009G13
66		0	0
67		0	0
68	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
69	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.011G10PTHR10108//I	Phvul.011G10
70	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
71	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
72	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
73	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
74	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07

1		0	0	0	Phvul.011G11
2					
3	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099	-	(Phvul.008G07
4	chloride channel F	Phvul.005G00	PTHR11689	:Sf	Phvul.005G00
5					
6	serine acetyltransferase 2;2	Phvul.008G27	PTHR23416	:Sf	Phvul.008G27
7		0	0	0	Phvul.003G06
8	Mitochondrial substrate carrier family protein	Phvul.001G24	K13354	-	soluPhvul.001G24
9	transcription regulatory protein SNF2, putative	Phvul.008G06	K11647	-	SWI/Phvul.008G06
10	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24	K05864	-	peptPhvul.003G24
11	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108	:Sf	Phvul.009G13
12					
13		0	0	0	Phvul.005G08
14					
15	K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945	:Sf	Phvul.009G13
16	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108	//I	Phvul.011G10
17	cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069	-	Phvul.011G05
18	gigantea protein (GI)	Phvul.007G08	K12124	-	GIG/Phvul.007G08
19	gigantea protein (GI)	Phvul.007G08	K12124	-	GIG/Phvul.007G08
20					
21	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670	-	ME Phvul.011G07
22	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657	//PF0	Phvul.008G07
23					
24		0	0	0	Phvul.011G11
25					
26	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099	-	(Phvul.008G07
27	chloride channel F	Phvul.005G00	PTHR11689	:Sf	Phvul.005G00
28	serine acetyltransferase 2;2	Phvul.008G27	PTHR23416	:Sf	Phvul.008G27
29					
30		0	0	0	Phvul.003G06
31	Mitochondrial substrate carrier family protein	Phvul.001G24	K13354	-	soluPhvul.001G24
32	transcription regulatory protein SNF2, putative	Phvul.008G06	K11647	-	SWI/Phvul.008G06
33	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24	K05864	-	peptPhvul.003G24
34	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108	:Sf	Phvul.009G13
35					
36		0	0	0	Phvul.005G08
37					
38	K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945	:Sf	Phvul.009G13
39	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108	//I	Phvul.011G10
40	cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069	-	Phvul.011G05
41	gigantea protein (GI)	Phvul.007G08	K12124	-	GIG/Phvul.007G08
42	gigantea protein (GI)	Phvul.007G08	K12124	-	GIG/Phvul.007G08
43					
44	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670	-	ME Phvul.011G07
45	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657	//PF0	Phvul.008G07
46					
47		0	0	0	Phvul.011G11
48					
49	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099	-	(Phvul.008G07
50	chloride channel F	Phvul.005G00	PTHR11689	:Sf	Phvul.005G00
51	serine acetyltransferase 2;2	Phvul.008G27	PTHR23416	:Sf	Phvul.008G27
52					
53		0	0	0	Phvul.003G06
54	Mitochondrial substrate carrier family protein	Phvul.001G24	K13354	-	soluPhvul.001G24
55	transcription regulatory protein SNF2, putative	Phvul.008G06	K11647	-	SWI/Phvul.008G06
56	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24	K05864	-	peptPhvul.003G24
57	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108	:Sf	Phvul.009G13
58					
59		0	0	0	Phvul.005G08
60					
	K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945	:Sf	Phvul.009G13
	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108	//I	Phvul.011G10

1			
2	cell division cycle protein 48-related / CDC48-related	Phvul.011G05 PTHR23069 -	Phvul.011G05
3	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
4	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
5			
6	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07 PF08670 - ME	Phvul.011G07
7	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07 PF01657//PF0	Phvul.008G07
8		0	0 Phvul.011G11
9			
10	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07 PTHR32099 - (	Phvul.008G07
11	chloride channel F	Phvul.005G00 PTHR11689:Sf	Phvul.005G00
12	serine acetyltransferase 2;2	Phvul.008G27 PTHR23416:Sf	Phvul.008G27
13			
14		0	0 Phvul.003G06
15	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
16	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
17			
18	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
19	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13 PTHR10108:Sf	Phvul.009G13
20		0	0 Phvul.005G08
21			
22	K-box region and MADS-box transcription factor family	Phvul.009G13 PTHR11945:Sf	Phvul.009G13
23	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10 PTHR10108//I	Phvul.011G10
24	cell division cycle protein 48-related / CDC48-related	Phvul.011G05 PTHR23069 -	Phvul.011G05
25	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
26	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
27			
28	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07 PF08670 - ME	Phvul.011G07
29	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07 PF01657//PF0	Phvul.008G07
30		0	0 Phvul.011G11
31			
32	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07 PTHR32099 - (	Phvul.008G07
33	chloride channel F	Phvul.005G00 PTHR11689:Sf	Phvul.005G00
34	serine acetyltransferase 2;2	Phvul.008G27 PTHR23416:Sf	Phvul.008G27
35			
36		0	0 Phvul.003G06
37	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
38	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
39			
40	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
41	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13 PTHR10108:Sf	Phvul.009G13
42		0	0 Phvul.005G08
43			
44	K-box region and MADS-box transcription factor family	Phvul.009G13 PTHR11945:Sf	Phvul.009G13
45	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10 PTHR10108//I	Phvul.011G10
46	cell division cycle protein 48-related / CDC48-related	Phvul.011G05 PTHR23069 -	Phvul.011G05
47	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
48	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
49			
50	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07 PF08670 - ME	Phvul.011G07
51	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07 PF01657//PF0	Phvul.008G07
52		0	0 Phvul.011G11
53			
54	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07 PTHR32099 - (	Phvul.008G07
55	chloride channel F	Phvul.005G00 PTHR11689:Sf	Phvul.005G00
56	serine acetyltransferase 2;2	Phvul.008G27 PTHR23416:Sf	Phvul.008G27
57			
58		0	0 Phvul.003G06
59	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
60	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06



1 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYFPhvul.003G24K05864 - peptPhvul.003G24  
2 S-adenosyl-L-methionine-dependent methyltransferasePhvul.009G13PTHR10108:SFPhvul.009G13  
3  
4 0 0 0 Phvul.005G08  
5  
6 K-box region and MADS-box transcription factor family Phvul.009G13PTHR11945:SFPhvul.009G13  
7 S-adenosyl-L-methionine-dependent methyltransferasePhvul.011G10PTHR10108//IPhvul.011G10  
8 cell division cycle protein 48-related / CDC48-related Phvul.011G05PTHR23069 - Phvul.011G05  
9 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08  
10 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08  
11 Homeobox-leucine zipper family protein / lipid-binding Phvul.011G07PF08670 - ME Phvul.011G07  
12 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07PF01657//PF0Phvul.008G07  
13  
14 0 0 0 Phvul.011G11  
15  
16 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07PTHR32099 - (Phvul.008G07  
17 chloride channel F Phvul.005G00PTHR11689:SFPhvul.005G00  
18 serine acetyltransferase 2;2 Phvul.008G27PTHR23416:SFPhvul.008G27  
19  
20 0 0 0 Phvul.003G06  
21  
22 Mitochondrial substrate carrier family protein Phvul.001G24K13354 - solutPhvul.001G24  
23 transcription regulatory protein SNF2, putative Phvul.008G06K11647 - SWI/Phvul.008G06  
24 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYFPhvul.003G24K05864 - peptPhvul.003G24  
25 S-adenosyl-L-methionine-dependent methyltransferasePhvul.009G13PTHR10108:SFPhvul.009G13  
26  
27 0 0 0 Phvul.005G08  
28  
29 K-box region and MADS-box transcription factor family Phvul.009G13PTHR11945:SFPhvul.009G13  
30 S-adenosyl-L-methionine-dependent methyltransferasePhvul.011G10PTHR10108//IPhvul.011G10  
31 cell division cycle protein 48-related / CDC48-related Phvul.011G05PTHR23069 - Phvul.011G05  
32 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08  
33 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08  
34 Homeobox-leucine zipper family protein / lipid-binding Phvul.011G07PF08670 - ME Phvul.011G07  
35 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07PF01657//PF0Phvul.008G07  
36  
37 0 0 0 Phvul.011G11  
38  
39 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07PTHR32099 - (Phvul.008G07  
40 chloride channel F Phvul.005G00PTHR11689:SFPhvul.005G00  
41 serine acetyltransferase 2;2 Phvul.008G27PTHR23416:SFPhvul.008G27  
42  
43 0 0 0 Phvul.003G06  
44  
45 Mitochondrial substrate carrier family protein Phvul.001G24K13354 - solutPhvul.001G24  
46 transcription regulatory protein SNF2, putative Phvul.008G06K11647 - SWI/Phvul.008G06  
47 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYFPhvul.003G24K05864 - peptPhvul.003G24  
48 S-adenosyl-L-methionine-dependent methyltransferasePhvul.009G13PTHR10108:SFPhvul.009G13  
49  
50 0 0 0 Phvul.005G08  
51  
52 K-box region and MADS-box transcription factor family Phvul.009G13PTHR11945:SFPhvul.009G13  
53 S-adenosyl-L-methionine-dependent methyltransferasePhvul.011G10PTHR10108//IPhvul.011G10  
54 cell division cycle protein 48-related / CDC48-related Phvul.011G05PTHR23069 - Phvul.011G05  
55 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08  
56 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08  
57 Homeobox-leucine zipper family protein / lipid-binding Phvul.011G07PF08670 - ME Phvul.011G07  
58 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07PF01657//PF0Phvul.008G07  
59  
60 0 0 0 Phvul.011G11  
cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07PTHR32099 - (Phvul.008G07



1			
2	chloride channel F	Phvul.005G00PTHR11689:SF	Phvul.005G00
3	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:SF	Phvul.008G27
4		0	0
5		0	0 Phvul.003G06
6	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
7	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
8	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
9	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13PTHR10108:SF	Phvul.009G13
10		0	0
11		0	0 Phvul.005G08
12	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
13	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10PTHR10108//I	Phvul.011G10
14	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
15	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
16	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
17	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
18	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
19		0	0
20		0	0 Phvul.011G11
21	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 -	(Phvul.008G07
22	chloride channel F	Phvul.005G00PTHR11689:SF	Phvul.005G00
23	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:SF	Phvul.008G27
24		0	0
25		0	0 Phvul.003G06
26	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
27	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
28	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
29	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13PTHR10108:SF	Phvul.009G13
30		0	0
31		0	0 Phvul.005G08
32	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
33	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10PTHR10108//I	Phvul.011G10
34	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
35	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
36	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
37	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
38	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
39		0	0
40		0	0 Phvul.011G11
41	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 -	(Phvul.008G07
42	chloride channel F	Phvul.005G00PTHR11689:SF	Phvul.005G00
43	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:SF	Phvul.008G27
44		0	0
45		0	0 Phvul.003G06
46	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
47	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
48	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
49	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13PTHR10108:SF	Phvul.009G13
50		0	0
51		0	0 Phvul.005G08
52	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:SF	Phvul.009G13
53	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10PTHR10108//I	Phvul.011G10
54	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
55	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08

1			
2	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
3	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
4	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
5			
6		0	0 Phvul.011G11
7	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 - (	Phvul.008G07
8	chloride channel F	Phvul.005G00PTHR11689:Sf	Phvul.005G00
9			
10	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:Sf	Phvul.008G27
11		0	0 Phvul.003G06
12	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
13	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
14	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
15	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13PTHR10108:Sf	Phvul.009G13
16			
17		0	0 Phvul.005G08
18			
19	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:Sf	Phvul.009G13
20	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10PTHR10108//I	Phvul.011G10
21	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
22	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
23	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
24	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
26			
27		0	0 Phvul.011G11
28	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 - (	Phvul.008G07
29	chloride channel F	Phvul.005G00PTHR11689:Sf	Phvul.005G00
30			
31	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:Sf	Phvul.008G27
32		0	0 Phvul.003G06
33			
34	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
35	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
36	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
37	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13PTHR10108:Sf	Phvul.009G13
38			
39		0	0 Phvul.005G08
40			
41	K-box region and MADS-box transcription factor family	Phvul.009G13PTHR11945:Sf	Phvul.009G13
42	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10PTHR10108//I	Phvul.011G10
43	cell division cycle protein 48-related / CDC48-related	Phvul.011G05PTHR23069 -	Phvul.011G05
44	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
45	gigantea protein (GI)	Phvul.007G08K12124 - GIG/	Phvul.007G08
46	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07PF08670 - ME	Phvul.011G07
47	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PF01657//PF0	Phvul.008G07
48			
49		0	0 Phvul.011G11
50	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07PTHR32099 - (	Phvul.008G07
51	chloride channel F	Phvul.005G00PTHR11689:Sf	Phvul.005G00
52			
53	serine acetyltransferase 2;2	Phvul.008G27PTHR23416:Sf	Phvul.008G27
54		0	0 Phvul.003G06
55			
56	Mitochondrial substrate carrier family protein	Phvul.001G24K13354 - solut	Phvul.001G24
57	transcription regulatory protein SNF2, putative	Phvul.008G06K11647 - SWI/	Phvul.008G06
58	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24K05864 - pept	Phvul.003G24
59	S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13PTHR10108:Sf	Phvul.009G13
60			

1				
2		0	0	0 Phvul.005G08
3	K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:SF	Phvul.009G13
4	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.011G10	PTHR10108://I	Phvul.011G10
5	cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 - T	Phvul.011G05
6	gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
7	gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
8	Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
9	cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 - T	Phvul.011G05
10	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF0	Phvul.008G07
11		0	0	0 Phvul.011G11
12	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 - (	Phvul.008G07
13	chloride channel F	Phvul.005G00	PTHR11689:SF	Phvul.005G00
14	nodulin MtN21 /EamA-like transporter family protein	Phvul.002G07	KOG4510 - Pe	Phvul.002G07
15	nodulin MtN21 /EamA-like transporter family protein	Phvul.002G07	KOG4510 - Pe	Phvul.002G07
16	nodulin MtN21 /EamA-like transporter family protein	Phvul.002G07	KOG4510 - Pe	Phvul.002G07
17	serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:SF	Phvul.008G27
18		0	0	0 Phvul.003G06
19	Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solut	Phvul.001G24
20	transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI	Phvul.008G06
21	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF	Phvul.003G24	K05864 - pept	Phvul.003G24
22	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G13	PTHR10108:SF	Phvul.009G13
23	receptor like protein 7	Phvul.004G09	PF00560//PF0	Phvul.004G09
24	AT hook motif DNA-binding family protein	Phvul.002G15	PTHR31500:SF	Phvul.002G15
25	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14	PTHR10896:SF	Phvul.009G14
26	polyol/monosaccharide transporter 5	Phvul.011G04	PTHR23500:SF	Phvul.011G04
27	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02	PTHR22835://I	Phvul.006G02
28	Eukaryotic aspartyl protease family protein	Phvul.006G09	PTHR13683:SF	Phvul.006G09
29	TIC-like	Phvul.001G15	PTHR34798:SF	Phvul.001G15
30	Ribosomal protein S3 family protein	Phvul.007G23	K02985 - smal	Phvul.007G23
31	receptor-like protein kinase 2	Phvul.004G03	PTHR27000:SF	Phvul.004G03
32	receptor-like protein kinase 2	Phvul.004G03	PTHR27000:SF	Phvul.004G03
33	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SF	Phvul.007G15
34	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SF	Phvul.007G15
35	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10	PTHR21499://I	Phvul.007G10
36	O-fucosyltransferase family protein	Phvul.008G15	PF10250 - GD	Phvul.008G15
37	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11	PTHR10388:SF	Phvul.005G11
38	growth-regulating factor 1	Phvul.001G03	PTHR31602:SF	Phvul.001G03
39	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tR	Phvul.004G04
40	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tR	Phvul.004G04
41	NOD26-like intrinsic protein 5;1	Phvul.007G08	PTHR19139:SF	Phvul.007G08
42	high-affinity nickel-transport family protein	Phvul.009G11	PTHR33876:SF	Phvul.009G11
43	WVD2-like 1	Phvul.006G10	PTHR31358:SF	Phvul.006G10
44	WVD2-like 1	Phvul.006G10	PTHR31358:SF	Phvul.006G10
45	Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:SF	Phvul.010G07
46	Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:SF	Phvul.010G07
47		0	0	0 Phvul.008G12

1		
2	myosin, putative	Phvul.001G03 PTHR13140:SFPhvul.001G03
3	Eukaryotic aspartyl protease family protein	Phvul.002G10 PTHR13683:SFPhvul.002G10
4	ABI five binding protein 3	Phvul.008G03 PTHR31413:SFPhvul.008G03
5	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
6	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
7	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SFPhvul.002G15
8	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SFPhvul.009G14
9	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SFPhvul.011G04
10	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
11	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SFPhvul.006G09
12	TIC-like	Phvul.001G15 PTHR34798:SFPhvul.001G15
13	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
14	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
15	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
16	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
17	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
18	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
19	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
20	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SFPhvul.005G11
21	growth-regulating factor 1	Phvul.001G03 PTHR31602:SFPhvul.001G03
22	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
23	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
24	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SFPhvul.007G08
25	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SFPhvul.009G11
26	WVD2-like 1	Phvul.006G10 PTHR31358:SFPhvul.006G10
27	WVD2-like 1	Phvul.006G10 PTHR31358:SFPhvul.006G10
28	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SFPhvul.010G07
29	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SFPhvul.010G07
30		0 0 0 Phvul.008G12
31	myosin, putative	Phvul.001G03 PTHR13140:SFPhvul.001G03
32	Eukaryotic aspartyl protease family protein	Phvul.002G10 PTHR13683:SFPhvul.002G10
33	ABI five binding protein 3	Phvul.008G03 PTHR31413:SFPhvul.008G03
34	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
35	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
36	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SFPhvul.002G15
37	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SFPhvul.009G14
38	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SFPhvul.011G04
39	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
40	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SFPhvul.006G09
41	TIC-like	Phvul.001G15 PTHR34798:SFPhvul.001G15
42	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
43	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
44	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
45	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
46	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
47	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10



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2	O-fucosyltransferase family protein		Phvul.008G15 PF10250 - GDIPhvul.008G15
3	Arabidopsis thaliana protein of unknown function (DUF		Phvul.005G11 PTHR10388:SfPhvul.005G11
4	growth-regulating factor 1		Phvul.001G03 PTHR31602:SfPhvul.001G03
5			
6	N2,N2-dimethylguanosine tRNA methyltransferase		Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
7	N2,N2-dimethylguanosine tRNA methyltransferase		Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
8	NOD26-like intrinsic protein 5;1		Phvul.007G08 PTHR19139:SfPhvul.007G08
9			
10	high-affinity nickel-transport family protein		Phvul.009G11 PTHR33876:SfPhvul.009G11
11	WVD2-like 1		Phvul.006G10 PTHR31358:SfPhvul.006G10
12	WVD2-like 1		Phvul.006G10 PTHR31358:SfPhvul.006G10
13			
14	Plant-specific transcription factor YABBY family protein		Phvul.010G07 PTHR31675:SfPhvul.010G07
15	Plant-specific transcription factor YABBY family protein		Phvul.010G07 PTHR31675:SfPhvul.010G07
16		0	0 0 Phvul.008G12
17			
18	myosin, putative		Phvul.001G03 PTHR13140:SfPhvul.001G03
19	Eukaryotic aspartyl protease family protein		Phvul.002G10 PTHR13683:SfPhvul.002G10
20	ABI five binding protein 3		Phvul.008G03 PTHR31413:SfPhvul.008G03
21			
22	Leucine-rich repeat transmembrane protein kinase		Phvul.009G24 PF00069//PF0Phvul.009G24
23	receptor like protein 7		Phvul.004G09 PF00560//PF0Phvul.004G09
24	AT hook motif DNA-binding family protein		Phvul.002G15 PTHR31500:SfPhvul.002G15
25			
26	Nucleotide-diphospho-sugar transferases superfamily r		Phvul.009G14 PTHR10896:SfPhvul.009G14
27	polyol/monosaccharide transporter 5		Phvul.011G04 PTHR23500:SfPhvul.011G04
28	GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.006G02 PTHR22835//IPhvul.006G02
29	Eukaryotic aspartyl protease family protein		Phvul.006G09 PTHR13683:SfPhvul.006G09
30	TIC-like		Phvul.001G15 PTHR34798:SfPhvul.001G15
31			
32	Ribosomal protein S3 family protein		Phvul.007G23 K02985 - smalPhvul.007G23
33	receptor-like protein kinase 2		Phvul.004G03 PTHR27000:SfPhvul.004G03
34	receptor-like protein kinase 2		Phvul.004G03 PTHR27000:SfPhvul.004G03
35	HSP20-like chaperones superfamily protein		Phvul.007G15 PTHR33981:SfPhvul.007G15
36	HSP20-like chaperones superfamily protein		Phvul.007G15 PTHR33981:SfPhvul.007G15
37	aspartate/glutamate/uridylate kinase family protein		Phvul.007G10 PTHR21499//IPhvul.007G10
38	O-fucosyltransferase family protein		Phvul.008G15 PF10250 - GDIPhvul.008G15
39	Arabidopsis thaliana protein of unknown function (DUF		Phvul.005G11 PTHR10388:SfPhvul.005G11
40	growth-regulating factor 1		Phvul.001G03 PTHR31602:SfPhvul.001G03
41			
42	N2,N2-dimethylguanosine tRNA methyltransferase		Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
43	N2,N2-dimethylguanosine tRNA methyltransferase		Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
44	NOD26-like intrinsic protein 5;1		Phvul.007G08 PTHR19139:SfPhvul.007G08
45			
46	high-affinity nickel-transport family protein		Phvul.009G11 PTHR33876:SfPhvul.009G11
47	WVD2-like 1		Phvul.006G10 PTHR31358:SfPhvul.006G10
48	WVD2-like 1		Phvul.006G10 PTHR31358:SfPhvul.006G10
49			
50	Plant-specific transcription factor YABBY family protein		Phvul.010G07 PTHR31675:SfPhvul.010G07
51	Plant-specific transcription factor YABBY family protein		Phvul.010G07 PTHR31675:SfPhvul.010G07
52		0	0 0 Phvul.008G12
53			
54	myosin, putative		Phvul.001G03 PTHR13140:SfPhvul.001G03
55	Eukaryotic aspartyl protease family protein		Phvul.002G10 PTHR13683:SfPhvul.002G10
56	ABI five binding protein 3		Phvul.008G03 PTHR31413:SfPhvul.008G03
57			
58	Leucine-rich repeat transmembrane protein kinase		Phvul.009G24 PF00069//PF0Phvul.009G24
59	receptor like protein 7		Phvul.004G09 PF00560//PF0Phvul.004G09
60			

1		
2	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SFPhvul.002G15
3	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SFPhvul.009G14
4	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SFPhvul.011G04
5		
6	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
7	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SFPhvul.006G09
8	TIC-like	Phvul.001G15 PTHR34798:SFPhvul.001G15
9		
10	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
11	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
12	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
13		
14	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
15	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
16	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
17		
18	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
19	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SFPhvul.005G11
20	growth-regulating factor 1	Phvul.001G03 PTHR31602:SFPhvul.001G03
21		
22	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
23	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
24	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SFPhvul.007G08
25	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SFPhvul.009G11
26	WVD2-like 1	Phvul.006G10 PTHR31358:SFPhvul.006G10
27	WVD2-like 1	Phvul.006G10 PTHR31358:SFPhvul.006G10
28		
29	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SFPhvul.010G07
30	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SFPhvul.010G07
31		
32		0 0 0 Phvul.008G12
33	myosin, putative	Phvul.001G03 PTHR13140:SFPhvul.001G03
34		
35	Eukaryotic aspartyl protease family protein	Phvul.002G10 PTHR13683:SFPhvul.002G10
36	ABI five binding protein 3	Phvul.008G03 PTHR31413:SFPhvul.008G03
37	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
38	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
39		
40	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SFPhvul.002G15
41	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SFPhvul.009G14
42	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SFPhvul.011G04
43		
44	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
45	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SFPhvul.006G09
46	TIC-like	Phvul.001G15 PTHR34798:SFPhvul.001G15
47		
48	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
49	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
50	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SFPhvul.004G03
51		
52	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
53	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SFPhvul.007G15
54		
55	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
56	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
57	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SFPhvul.005G11
58	growth-regulating factor 1	Phvul.001G03 PTHR31602:SFPhvul.001G03
59		
60	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04



1				
2	NOD26-like intrinsic protein 5;1			Phvul.007G08 PTHR19139:SlPhvul.007G08
3	high-affinity nickel-transport family protein			Phvul.009G11 PTHR33876:SlPhvul.009G11
4	WVD2-like 1			Phvul.006G10 PTHR31358:SlPhvul.006G10
5	WVD2-like 1			Phvul.006G10 PTHR31358:SlPhvul.006G10
6	WVD2-like 1			Phvul.006G10 PTHR31358:SlPhvul.006G10
7	Plant-specific transcription factor YABBY family protein			Phvul.010G07 PTHR31675:SlPhvul.010G07
8	Plant-specific transcription factor YABBY family protein			Phvul.010G07 PTHR31675:SlPhvul.010G07
9				
10		0	0	0 Phvul.008G12
11	myosin, putative			Phvul.001G03 PTHR13140:SlPhvul.001G03
12	Eukaryotic aspartyl protease family protein			Phvul.002G10 PTHR13683:SlPhvul.002G10
13	ABI five binding protein 3			Phvul.008G03 PTHR31413:SlPhvul.008G03
14	ABI five binding protein 3			Phvul.008G03 PTHR31413:SlPhvul.008G03
15	Leucine-rich repeat transmembrane protein kinase			Phvul.009G24 PF00069//PF0Phvul.009G24
16	receptor like protein 7			Phvul.004G09 PF00560//PF0Phvul.004G09
17	receptor like protein 7			Phvul.004G09 PF00560//PF0Phvul.004G09
18	AT hook motif DNA-binding family protein			Phvul.002G15 PTHR31500:SlPhvul.002G15
19	Nucleotide-diphospho-sugar transferases superfamily			Phvul.009G14 PTHR10896:SlPhvul.009G14
20	polyol/monosaccharide transporter 5			Phvul.011G04 PTHR23500:SlPhvul.011G04
21	polyol/monosaccharide transporter 5			Phvul.011G04 PTHR23500:SlPhvul.011G04
22	GDSL-like Lipase/Acylhydrolase superfamily protein			Phvul.006G02 PTHR22835//IPhvul.006G02
23	Eukaryotic aspartyl protease family protein			Phvul.006G09 PTHR13683:SlPhvul.006G09
24	TIC-like			Phvul.001G15 PTHR34798:SlPhvul.001G15
25	TIC-like			Phvul.001G15 PTHR34798:SlPhvul.001G15
26	Ribosomal protein S3 family protein			Phvul.007G23 K02985 - smalPhvul.007G23
27	receptor-like protein kinase 2			Phvul.004G03 PTHR27000:SlPhvul.004G03
28	receptor-like protein kinase 2			Phvul.004G03 PTHR27000:SlPhvul.004G03
29	receptor-like protein kinase 2			Phvul.004G03 PTHR27000:SlPhvul.004G03
30	HSP20-like chaperones superfamily protein			Phvul.007G15 PTHR33981:SlPhvul.007G15
31	HSP20-like chaperones superfamily protein			Phvul.007G15 PTHR33981:SlPhvul.007G15
32	HSP20-like chaperones superfamily protein			Phvul.007G15 PTHR33981:SlPhvul.007G15
33	aspartate/glutamate/uridylate kinase family protein			Phvul.007G10 PTHR21499//IPhvul.007G10
34	O-fucosyltransferase family protein			Phvul.008G15 PF10250 - GDIPhvul.008G15
35	Arabidopsis thaliana protein of unknown function (DUF			Phvul.005G11 PTHR10388:SlPhvul.005G11
36	growth-regulating factor 1			Phvul.001G03 PTHR31602:SlPhvul.001G03
37	growth-regulating factor 1			Phvul.001G03 PTHR31602:SlPhvul.001G03
38	N2,N2-dimethylguanosine tRNA methyltransferase			Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
39	N2,N2-dimethylguanosine tRNA methyltransferase			Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
40	N2,N2-dimethylguanosine tRNA methyltransferase			Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
41	NOD26-like intrinsic protein 5;1			Phvul.007G08 PTHR19139:SlPhvul.007G08
42	high-affinity nickel-transport family protein			Phvul.009G11 PTHR33876:SlPhvul.009G11
43	WVD2-like 1			Phvul.006G10 PTHR31358:SlPhvul.006G10
44	WVD2-like 1			Phvul.006G10 PTHR31358:SlPhvul.006G10
45	WVD2-like 1			Phvul.006G10 PTHR31358:SlPhvul.006G10
46	Plant-specific transcription factor YABBY family protein			Phvul.010G07 PTHR31675:SlPhvul.010G07
47	Plant-specific transcription factor YABBY family protein			Phvul.010G07 PTHR31675:SlPhvul.010G07
48				
49		0	0	0 Phvul.008G12
50	myosin, putative			Phvul.001G03 PTHR13140:SlPhvul.001G03
51	myosin, putative			Phvul.001G03 PTHR13140:SlPhvul.001G03
52	Eukaryotic aspartyl protease family protein			Phvul.002G10 PTHR13683:SlPhvul.002G10
53	Eukaryotic aspartyl protease family protein			Phvul.002G10 PTHR13683:SlPhvul.002G10
54	ABI five binding protein 3			Phvul.008G03 PTHR31413:SlPhvul.008G03
55	ABI five binding protein 3			Phvul.008G03 PTHR31413:SlPhvul.008G03
56	Leucine-rich repeat transmembrane protein kinase			Phvul.009G24 PF00069//PF0Phvul.009G24
57	receptor like protein 7			Phvul.004G09 PF00560//PF0Phvul.004G09
58	receptor like protein 7			Phvul.004G09 PF00560//PF0Phvul.004G09
59	AT hook motif DNA-binding family protein			Phvul.002G15 PTHR31500:SlPhvul.002G15
60	AT hook motif DNA-binding family protein			Phvul.002G15 PTHR31500:SlPhvul.002G15
61	Nucleotide-diphospho-sugar transferases superfamily			Phvul.009G14 PTHR10896:SlPhvul.009G14
62	polyol/monosaccharide transporter 5			Phvul.011G04 PTHR23500:SlPhvul.011G04
63	polyol/monosaccharide transporter 5			Phvul.011G04 PTHR23500:SlPhvul.011G04
64	GDSL-like Lipase/Acylhydrolase superfamily protein			Phvul.006G02 PTHR22835//IPhvul.006G02
65	Eukaryotic aspartyl protease family protein			Phvul.006G09 PTHR13683:SlPhvul.006G09
66	Eukaryotic aspartyl protease family protein			Phvul.006G09 PTHR13683:SlPhvul.006G09

1		
2	TIC-like	Phvul.001G15 PTHR34798:SfPhvul.001G15
3	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
4	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
5	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
6	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
7	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
8	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
9	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
10	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SfPhvul.005G11
11	growth-regulating factor 1	Phvul.001G03 PTHR31602:SfPhvul.001G03
12	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
13	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
14	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SfPhvul.007G08
15	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SfPhvul.009G11
16	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
17	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
18	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
19	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
20		0 0 0 Phvul.008G12
21	myosin, putative	Phvul.001G03 PTHR13140:SfPhvul.001G03
22	Eukaryotic aspartyl protease family protein	Phvul.002G10 PTHR13683:SfPhvul.002G10
23	ABI five binding protein 3	Phvul.008G03 PTHR31413:SfPhvul.008G03
24	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
25	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
26	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SfPhvul.002G15
27	Nucleotide-diphospho-sugar transferases superfamily p	Phvul.009G14 PTHR10896:SfPhvul.009G14
28	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SfPhvul.011G04
29	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
30	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SfPhvul.006G09
31	TIC-like	Phvul.001G15 PTHR34798:SfPhvul.001G15
32	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
33	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
34	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
35	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
36	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
37	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
38	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
39	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SfPhvul.005G11
40	growth-regulating factor 1	Phvul.001G03 PTHR31602:SfPhvul.001G03
41	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
42	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
43	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SfPhvul.007G08
44	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SfPhvul.009G11
45	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
46	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
47	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
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2	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:Sf	Phvul.010G07	
3		0	0	0 Phvul.008G12
4	myosin, putative	Phvul.001G03PTHR13140:Sf	Phvul.001G03	
5	Eukaryotic aspartyl protease family protein	Phvul.002G10PTHR13683:Sf	Phvul.002G10	
6	ABI five binding protein 3	Phvul.008G03PTHR31413:Sf	Phvul.008G03	
7	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24PF00069//PF0	Phvul.009G24	
8	receptor like protein 7	Phvul.004G09PF00560//PF0	Phvul.004G09	
9	AT hook motif DNA-binding family protein	Phvul.002G15PTHR31500:Sf	Phvul.002G15	
10	Nucleotide-diphospho-sugar transferases superfamily γ	Phvul.009G14PTHR10896:Sf	Phvul.009G14	
11	polyol/monosaccharide transporter 5	Phvul.011G04PTHR23500:Sf	Phvul.011G04	
12	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02PTHR22835//I	Phvul.006G02	
13	Eukaryotic aspartyl protease family protein	Phvul.006G09PTHR13683:Sf	Phvul.006G09	
14	TIC-like	Phvul.001G15PTHR34798:Sf	Phvul.001G15	
15	Ribosomal protein S3 family protein	Phvul.007G23K02985 - smal	Phvul.007G23	
16	receptor-like protein kinase 2	Phvul.004G03PTHR27000:Sf	Phvul.004G03	
17	receptor-like protein kinase 2	Phvul.004G03PTHR27000:Sf	Phvul.004G03	
18	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:Sf	Phvul.007G15	
19	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:Sf	Phvul.007G15	
20	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10PTHR21499//I	Phvul.007G10	
21	O-fucosyltransferase family protein	Phvul.008G15PF10250 - GD	Phvul.008G15	
22	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11PTHR10388:Sf	Phvul.005G11	
23	growth-regulating factor 1	Phvul.001G03PTHR31602:Sf	Phvul.001G03	
24	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216 - tR	Phvul.004G04	
25	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216 - tR	Phvul.004G04	
26	NOD26-like intrinsic protein 5;1	Phvul.007G08PTHR19139:Sf	Phvul.007G08	
27	high-affinity nickel-transport family protein	Phvul.009G11PTHR33876:Sf	Phvul.009G11	
28	WVD2-like 1	Phvul.006G10PTHR31358:Sf	Phvul.006G10	
29	WVD2-like 1	Phvul.006G10PTHR31358:Sf	Phvul.006G10	
30	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:Sf	Phvul.010G07	
31	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:Sf	Phvul.010G07	
32		0	0	0 Phvul.008G12
33	myosin, putative	Phvul.001G03PTHR13140:Sf	Phvul.001G03	
34	Eukaryotic aspartyl protease family protein	Phvul.002G10PTHR13683:Sf	Phvul.002G10	
35	ABI five binding protein 3	Phvul.008G03PTHR31413:Sf	Phvul.008G03	
36	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24PF00069//PF0	Phvul.009G24	
37	receptor like protein 7	Phvul.004G09PF00560//PF0	Phvul.004G09	
38	AT hook motif DNA-binding family protein	Phvul.002G15PTHR31500:Sf	Phvul.002G15	
39	Nucleotide-diphospho-sugar transferases superfamily γ	Phvul.009G14PTHR10896:Sf	Phvul.009G14	
40	polyol/monosaccharide transporter 5	Phvul.011G04PTHR23500:Sf	Phvul.011G04	
41	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02PTHR22835//I	Phvul.006G02	
42	Eukaryotic aspartyl protease family protein	Phvul.006G09PTHR13683:Sf	Phvul.006G09	
43	TIC-like	Phvul.001G15PTHR34798:Sf	Phvul.001G15	
44	Ribosomal protein S3 family protein	Phvul.007G23K02985 - smal	Phvul.007G23	
45	receptor-like protein kinase 2	Phvul.004G03PTHR27000:Sf	Phvul.004G03	
46	receptor-like protein kinase 2	Phvul.004G03PTHR27000:Sf	Phvul.004G03	
47	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:Sf	Phvul.007G15	

1			
2	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:SfPhvul.007G15	
3	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10PTHR21499//IPhvul.007G10	
4	O-fucosyltransferase family protein	Phvul.008G15PF10250 - GDIPhvul.008G15	
5			
6	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11PTHR10388:SfPhvul.005G11	
7	growth-regulating factor 1	Phvul.001G03PTHR31602:SfPhvul.001G03	
8	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216 - tRIPhvul.004G04	
9			
10	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216 - tRIPhvul.004G04	
11	NOD26-like intrinsic protein 5;1	Phvul.007G08PTHR19139:SfPhvul.007G08	
12	high-affinity nickel-transport family protein	Phvul.009G11PTHR33876:SfPhvul.009G11	
13			
14	WVD2-like 1	Phvul.006G10PTHR31358:SfPhvul.006G10	
15	WVD2-like 1	Phvul.006G10PTHR31358:SfPhvul.006G10	
16	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:SfPhvul.010G07	
17			
18	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:SfPhvul.010G07	
19		0	0
20			0 Phvul.008G12
21	myosin, putative	Phvul.001G03PTHR13140:SfPhvul.001G03	
22	Eukaryotic aspartyl protease family protein	Phvul.002G10PTHR13683:SfPhvul.002G10	
23	ABI five binding protein 3	Phvul.008G03PTHR31413:SfPhvul.008G03	
24	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24PF00069//PF0Phvul.009G24	
25			
26	receptor like protein 7	Phvul.004G09PF00560//PF0Phvul.004G09	
27	AT hook motif DNA-binding family protein	Phvul.002G15PTHR31500:SfPhvul.002G15	
28	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14PTHR10896:SfPhvul.009G14	
29			
30	polyol/monosaccharide transporter 5	Phvul.011G04PTHR23500:SfPhvul.011G04	
31	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02PTHR22835//IPhvul.006G02	
32	Eukaryotic aspartyl protease family protein	Phvul.006G09PTHR13683:SfPhvul.006G09	
33	TIC-like	Phvul.001G15PTHR34798:SfPhvul.001G15	
34			
35	Ribosomal protein S3 family protein	Phvul.007G23K02985 - smalPhvul.007G23	
36	receptor-like protein kinase 2	Phvul.004G03PTHR27000:SfPhvul.004G03	
37			
38	receptor-like protein kinase 2	Phvul.004G03PTHR27000:SfPhvul.004G03	
39	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:SfPhvul.007G15	
40	HSP20-like chaperones superfamily protein	Phvul.007G15PTHR33981:SfPhvul.007G15	
41	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10PTHR21499//IPhvul.007G10	
42			
43	O-fucosyltransferase family protein	Phvul.008G15PF10250 - GDIPhvul.008G15	
44	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11PTHR10388:SfPhvul.005G11	
45	growth-regulating factor 1	Phvul.001G03PTHR31602:SfPhvul.001G03	
46	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216 - tRIPhvul.004G04	
47			
48	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G042.1.1.216 - tRIPhvul.004G04	
49	NOD26-like intrinsic protein 5;1	Phvul.007G08PTHR19139:SfPhvul.007G08	
50	high-affinity nickel-transport family protein	Phvul.009G11PTHR33876:SfPhvul.009G11	
51			
52	WVD2-like 1	Phvul.006G10PTHR31358:SfPhvul.006G10	
53	WVD2-like 1	Phvul.006G10PTHR31358:SfPhvul.006G10	
54			
55	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:SfPhvul.010G07	
56	Plant-specific transcription factor YABBY family protein	Phvul.010G07PTHR31675:SfPhvul.010G07	
57		0	0
58			0 Phvul.008G12
59	myosin, putative	Phvul.001G03PTHR13140:SfPhvul.001G03	
60	Eukaryotic aspartyl protease family protein	Phvul.002G10PTHR13683:SfPhvul.002G10	
	ABI five binding protein 3	Phvul.008G03PTHR31413:SfPhvul.008G03	



1		
2	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
3	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
4	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SfPhvul.002G15
5	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SfPhvul.009G14
6	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SfPhvul.011G04
7	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
8	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SfPhvul.006G09
9	TIC-like	Phvul.001G15 PTHR34798:SfPhvul.001G15
10	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
11	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
12	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
13	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
14	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
15	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
16	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
17	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SfPhvul.005G11
18	growth-regulating factor 1	Phvul.001G03 PTHR31602:SfPhvul.001G03
19	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
20	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
21	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SfPhvul.007G08
22	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SfPhvul.009G11
23	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
24	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
25	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
26	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
27		0 0 0 Phvul.008G12
28	myosin, putative	Phvul.001G03 PTHR13140:SfPhvul.001G03
29	Eukaryotic aspartyl protease family protein	Phvul.002G10 PTHR13683:SfPhvul.002G10
30	ABI five binding protein 3	Phvul.008G03 PTHR31413:SfPhvul.008G03
31	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
32	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
33	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SfPhvul.002G15
34	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SfPhvul.009G14
35	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SfPhvul.011G04
36	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
37	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SfPhvul.006G09
38	TIC-like	Phvul.001G15 PTHR34798:SfPhvul.001G15
39	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
40	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
41	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
42	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
43	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
44	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
45	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
46	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SfPhvul.005G11
47	growth-regulating factor 1	Phvul.001G03 PTHR31602:SfPhvul.001G03

1				
2	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tRIP	Phvul.004G04
3	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tRIP	Phvul.004G04
4	NOD26-like intrinsic protein 5;1	Phvul.007G08	PTHR19139:SF	Phvul.007G08
5	high-affinity nickel-transport family protein	Phvul.009G11	PTHR33876:SF	Phvul.009G11
6	WVD2-like 1	Phvul.006G10	PTHR31358:SF	Phvul.006G10
7	WVD2-like 1	Phvul.006G10	PTHR31358:SF	Phvul.006G10
8	Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:SF	Phvul.010G07
9	Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:SF	Phvul.010G07
10		0	0	0 Phvul.008G12
11	myosin, putative	Phvul.001G03	PTHR13140:SF	Phvul.001G03
12	Eukaryotic aspartyl protease family protein	Phvul.002G10	PTHR13683:SF	Phvul.002G10
13	ABI five binding protein 3	Phvul.008G03	PTHR31413:SF	Phvul.008G03
14	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24	PF00069//PF0	Phvul.009G24
15	receptor like protein 7	Phvul.004G09	PF00560//PF0	Phvul.004G09
16	AT hook motif DNA-binding family protein	Phvul.002G15	PTHR31500:SF	Phvul.002G15
17	Nucleotide-diphospho-sugar transferases superfamily γ	Phvul.009G14	PTHR10896:SF	Phvul.009G14
18	polyol/monosaccharide transporter 5	Phvul.011G04	PTHR23500:SF	Phvul.011G04
19	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02	PTHR22835//IP	Phvul.006G02
20	Eukaryotic aspartyl protease family protein	Phvul.006G09	PTHR13683:SF	Phvul.006G09
21	TIC-like	Phvul.001G15	PTHR34798:SF	Phvul.001G15
22	Ribosomal protein S3 family protein	Phvul.007G23	K02985 - smal	Phvul.007G23
23	receptor-like protein kinase 2	Phvul.004G03	PTHR27000:SF	Phvul.004G03
24	receptor-like protein kinase 2	Phvul.004G03	PTHR27000:SF	Phvul.004G03
25	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SF	Phvul.007G15
26	HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SF	Phvul.007G15
27	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10	PTHR21499//IP	Phvul.007G10
28	O-fucosyltransferase family protein	Phvul.008G15	PF10250 - GDIP	Phvul.008G15
29	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11	PTHR10388:SF	Phvul.005G11
30	growth-regulating factor 1	Phvul.001G03	PTHR31602:SF	Phvul.001G03
31	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tRIP	Phvul.004G04
32	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tRIP	Phvul.004G04
33	NOD26-like intrinsic protein 5;1	Phvul.007G08	PTHR19139:SF	Phvul.007G08
34	high-affinity nickel-transport family protein	Phvul.009G11	PTHR33876:SF	Phvul.009G11
35	WVD2-like 1	Phvul.006G10	PTHR31358:SF	Phvul.006G10
36	WVD2-like 1	Phvul.006G10	PTHR31358:SF	Phvul.006G10
37	Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:SF	Phvul.010G07
38	Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:SF	Phvul.010G07
39		0	0	0 Phvul.008G12
40	myosin, putative	Phvul.001G03	PTHR13140:SF	Phvul.001G03
41	Eukaryotic aspartyl protease family protein	Phvul.002G10	PTHR13683:SF	Phvul.002G10
42	ABI five binding protein 3	Phvul.008G03	PTHR31413:SF	Phvul.008G03
43	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24	PF00069//PF0	Phvul.009G24
44	receptor like protein 7	Phvul.004G09	PF00560//PF0	Phvul.004G09
45	AT hook motif DNA-binding family protein	Phvul.002G15	PTHR31500:SF	Phvul.002G15
46	Nucleotide-diphospho-sugar transferases superfamily γ	Phvul.009G14	PTHR10896:SF	Phvul.009G14
47	polyol/monosaccharide transporter 5	Phvul.011G04	PTHR23500:SF	Phvul.011G04



1		
2	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
3	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SfPhvul.006G09
4	TIC-like	Phvul.001G15 PTHR34798:SfPhvul.001G15
5		
6	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
7	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
8	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
9		
10	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
11	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
12	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
13		
14	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
15	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SfPhvul.005G11
16	growth-regulating factor 1	Phvul.001G03 PTHR31602:SfPhvul.001G03
17		
18	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
19	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
20	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SfPhvul.007G08
21		
22	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SfPhvul.009G11
23	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
24	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10
25		
26	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
27	Plant-specific transcription factor YABBY family protein	Phvul.010G07 PTHR31675:SfPhvul.010G07
28		0 0 0 Phvul.008G12
29		
30	myosin, putative	Phvul.001G03 PTHR13140:SfPhvul.001G03
31	Eukaryotic aspartyl protease family protein	Phvul.002G10 PTHR13683:SfPhvul.002G10
32	ABI five binding protein 3	Phvul.008G03 PTHR31413:SfPhvul.008G03
33		
34	Leucine-rich repeat transmembrane protein kinase	Phvul.009G24 PF00069//PF0Phvul.009G24
35	receptor like protein 7	Phvul.004G09 PF00560//PF0Phvul.004G09
36	AT hook motif DNA-binding family protein	Phvul.002G15 PTHR31500:SfPhvul.002G15
37		
38	Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14 PTHR10896:SfPhvul.009G14
39	polyol/monosaccharide transporter 5	Phvul.011G04 PTHR23500:SfPhvul.011G04
40	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02 PTHR22835//IPhvul.006G02
41	Eukaryotic aspartyl protease family protein	Phvul.006G09 PTHR13683:SfPhvul.006G09
42		
43	TIC-like	Phvul.001G15 PTHR34798:SfPhvul.001G15
44	Ribosomal protein S3 family protein	Phvul.007G23 K02985 - smalPhvul.007G23
45	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
46	receptor-like protein kinase 2	Phvul.004G03 PTHR27000:SfPhvul.004G03
47		
48	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
49	HSP20-like chaperones superfamily protein	Phvul.007G15 PTHR33981:SfPhvul.007G15
50		
51	aspartate/glutamate/uridylate kinase family protein	Phvul.007G10 PTHR21499//IPhvul.007G10
52	O-fucosyltransferase family protein	Phvul.008G15 PF10250 - GDIPhvul.008G15
53		
54	Arabidopsis thaliana protein of unknown function (DUF	Phvul.005G11 PTHR10388:SfPhvul.005G11
55	growth-regulating factor 1	Phvul.001G03 PTHR31602:SfPhvul.001G03
56		
57	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
58	N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04 2.1.1.216 - tRIPhvul.004G04
59	NOD26-like intrinsic protein 5;1	Phvul.007G08 PTHR19139:SfPhvul.007G08
60	high-affinity nickel-transport family protein	Phvul.009G11 PTHR33876:SfPhvul.009G11
	WVD2-like 1	Phvul.006G10 PTHR31358:SfPhvul.006G10

1				
2	WVD2-like 1			Phvul.006G10PTHR31358:SFPhvul.006G10
3	Plant-specific transcription factor YABBY family protein			Phvul.010G07PTHR31675:SFPhvul.010G07
4	Plant-specific transcription factor YABBY family protein			Phvul.010G07PTHR31675:SFPhvul.010G07
5				
6		0	0	0 Phvul.008G12
7	myosin, putative			Phvul.001G03PTHR13140:SFPhvul.001G03
8	Eukaryotic aspartyl protease family protein			Phvul.002G10PTHR13683:SFPhvul.002G10
9	ABI five binding protein 3			Phvul.008G03PTHR31413:SFPhvul.008G03
10	Leucine-rich repeat transmembrane protein kinase			Phvul.009G24PF00069//PF0Phvul.009G24
11	aspartate/glutamate/uridylate kinase family protein			Phvul.007G10PTHR21499//IPhvul.007G10
12	polyol/monosaccharide transporter 5			Phvul.011G04PTHR23500:SFPhvul.011G04
13	WVD2-like 1			Phvul.006G10PTHR31358:SFPhvul.006G10
14	WVD2-like 1			Phvul.006G10PTHR31358:SFPhvul.006G10
15	GDSL-like Lipase/Acylhydrolase superfamily protein			Phvul.006G02PTHR22835//IPhvul.006G02
16	receptor like protein 7			Phvul.004G09PF00560//PF0Phvul.004G09
17	AT hook motif DNA-binding family protein			Phvul.002G15PTHR31500:SFPhvul.002G15
18	Nucleotide-diphospho-sugar transferases superfamily p			Phvul.009G14PTHR10896:SFPhvul.009G14
19	Eukaryotic aspartyl protease family protein			Phvul.006G09PTHR13683:SFPhvul.006G09
20	TIC-like			Phvul.001G15PTHR34798:SFPhvul.001G15
21	Leucine-rich repeat transmembrane protein kinase			Phvul.009G24PF00069//PF0Phvul.009G24
22	phosphatidylinositol-4-phosphate 5-kinase 2			Phvul.009G12PTHR23086:SFPhvul.009G12
23	phosphatidylinositol-4-phosphate 5-kinase 2			Phvul.009G12PTHR23086:SFPhvul.009G12
24	HSP20-like chaperones superfamily protein			Phvul.007G15PTHR33981:SFPhvul.007G15
25	HSP20-like chaperones superfamily protein			Phvul.007G15PTHR33981:SFPhvul.007G15
26	O-fucosyltransferase family protein			Phvul.008G15PF10250 - GDIPhvul.008G15
27	Ribosomal protein S3 family protein			Phvul.007G23K02985 - smalPhvul.007G23
28	receptor-like protein kinase 2			Phvul.004G03PTHR27000:SFPhvul.004G03
29	receptor-like protein kinase 2			Phvul.004G03PTHR27000:SFPhvul.004G03
30	Arabidopsis thaliana protein of unknown function (DUF			Phvul.005G11PTHR10388:SFPhvul.005G11
31	growth-regulating factor 1			Phvul.001G03PTHR31602:SFPhvul.001G03
32	N2,N2-dimethylguanosine tRNA methyltransferase			Phvul.004G042.1.1.216 - tRIPhvul.004G04
33	N2,N2-dimethylguanosine tRNA methyltransferase			Phvul.004G042.1.1.216 - tRIPhvul.004G04
34	Eukaryotic aspartyl protease family protein			Phvul.002G10PTHR13683:SFPhvul.002G10
35	NOD26-like intrinsic protein 5;1			Phvul.007G08PTHR19139:SFPhvul.007G08
36	high-affinity nickel-transport family protein			Phvul.009G11PTHR33876:SFPhvul.009G11
37	Plant-specific transcription factor YABBY family protein			Phvul.010G07PTHR31675:SFPhvul.010G07
38	Plant-specific transcription factor YABBY family protein			Phvul.010G07PTHR31675:SFPhvul.010G07
39		0	0	0 Phvul.008G12
40	leucine-rich repeat transmembrane protein kinase fam			Phvul.007G02PF00560//PF0Phvul.007G02
41	fatty acid desaturase 5			Phvul.010G15K00507 - steaIPhvul.010G15
42	Protein of unknown function (DUF630 and DUF632)			Phvul.009G21PF04782 - ProPhvul.009G21
43	Integrase-type DNA-binding superfamily protein			Phvul.008G04PF00847 - AP2Phvul.008G04
44		0		Phvul.009G07K17968 - TRIAPhvul.009G07
45	embryo defective 2735		0	0 Phvul.001G19
46	embryo defective 2735		0	0 Phvul.001G19
47	Pentatricopeptide repeat (PPR) superfamily protein			Phvul.003G15PF01535//PF1Phvul.003G15
48	S-adenosyl-L-methionine-dependent methyltransferase			Phvul.009G03PTHR10108//IPhvul.009G03

1			
2	thioredoxin-dependent peroxidase 1		Phvul.004G16PTHR10430 - IPhvul.004G16
3	Protein prenyltransferase superfamily protein		Phvul.009G16PF13414 - TPRPhvul.009G16
4	Uncharacterised conserved protein UCP015417, vWA		Phvul.002G11PTHR31373:SfPhvul.002G11
5	alanine-2-oxoglutarate aminotransferase 2		Phvul.002G152.6.1.4 - GlyciPhvul.002G15
6	chloroplastic NIFS-like cysteine desulfurase		Phvul.002G274.4.1.16 - SelePhvul.002G27
7	SecY protein transport family protein		Phvul.011G16K10956 - protPhvul.011G16
8	NDH-dependent cyclic electron flow 1		Phvul.001G11PTHR11122:SfPhvul.001G11
9	rubredoxin family protein		Phvul.002G03PTHR17130 - IPhvul.002G03
10	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
11	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
12	ferredoxin 3		Phvul.007G02PTHR19370:SfPhvul.007G02
13	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
14	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
15	REF4-related 1		Phvul.006G15PTHR33739:SfPhvul.006G15
16	Alpha amylase family protein		Phvul.006G04PTHR10357:SfPhvul.006G04
17	cellulose synthase like G1		Phvul.005G00PTHR13301//IPhvul.005G00
18	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
19	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
20	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
21	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
22	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
23	cytochrome P450, family 76, subfamily C, polypeptide 4		Phvul.007G101.14.13.152 - Phvul.007G10
24	purine permease 1		Phvul.009G03PTHR31376:SfPhvul.009G03
25		0	0 Phvul.L00244
26		0	0 Phvul.L00244
27	vacuolar iron transporter 1		Phvul.008G07KOG4473 - UnPhvul.008G07
28	fatty acid desaturase 5		Phvul.010G15K00507 - steaiPhvul.010G15
29	Protein of unknown function (DUF630 and DUF632)		Phvul.009G21PF04782 - ProPhvul.009G21
30	Integrase-type DNA-binding superfamily protein		Phvul.008G04PF00847 - AP2Phvul.008G04
31		0	Phvul.009G07K17968 - TRIAPhvul.009G07
32	embryo defective 2735	0	0 Phvul.001G19
33	embryo defective 2735	0	0 Phvul.001G19
34	Pentatricopeptide repeat (PPR) superfamily protein		Phvul.003G15PF01535//PF1Phvul.003G15
35	S-adenosyl-L-methionine-dependent methyltransferase		Phvul.009G03PTHR10108//IPhvul.009G03
36	thioredoxin-dependent peroxidase 1		Phvul.004G16PTHR10430 - IPhvul.004G16
37	Protein prenyltransferase superfamily protein		Phvul.009G16PF13414 - TPRPhvul.009G16
38	Uncharacterised conserved protein UCP015417, vWA		Phvul.002G11PTHR31373:SfPhvul.002G11
39	alanine-2-oxoglutarate aminotransferase 2		Phvul.002G152.6.1.4 - GlyciPhvul.002G15
40	chloroplastic NIFS-like cysteine desulfurase		Phvul.002G274.4.1.16 - SelePhvul.002G27
41	SecY protein transport family protein		Phvul.011G16K10956 - protPhvul.011G16
42	NDH-dependent cyclic electron flow 1		Phvul.001G11PTHR11122:SfPhvul.001G11
43	rubredoxin family protein		Phvul.002G03PTHR17130 - IPhvul.002G03
44	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
45	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
46	ferredoxin 3		Phvul.007G02PTHR19370:SfPhvul.007G02
47	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11

1	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - IPhvul.010G11
2	REF4-related 1	Phvul.006G15PTHR33739:SfPhvul.006G15
3	Alpha amylase family protein	Phvul.006G04PTHR10357:SfPhvul.006G04
4	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
5	negative regulator of systemic acquired resistance (SNI	0 0 Phvul.003G05
6	negative regulator of systemic acquired resistance (SNI	0 0 Phvul.003G05
7	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - SphiPhvul.008G01
8	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - SphiPhvul.008G01
9	negative regulator of systemic acquired resistance (SNI	0 0 Phvul.003G05
10	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - IPhvul.007G10
11	purine permease 1	Phvul.009G03PTHR31376:SfPhvul.009G03
12		0 0 Phvul.L00244
13		0 0 Phvul.L00244
14	vacuolar iron transporter 1	Phvul.008G07KOG4473 - UnPhvul.008G07
15	fatty acid desaturase 5	Phvul.010G15K00507 - steaiPhvul.010G15
16	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - ProPhvul.009G21
17	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2Phvul.008G04
18		0 Phvul.009G07K17968 - TRIAPhvul.009G07
19	embryo defective 2735	0 0 Phvul.001G19
20	embryo defective 2735	0 0 Phvul.001G19
21	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1Phvul.003G15
22	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//IPhvul.009G03
23	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - IPhvul.004G16
24	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPRPhvul.009G16
25	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:SfPhvul.002G11
26	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - GlyciPhvul.002G15
27	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - SelePhvul.002G27
28	SecY protein transport family protein	Phvul.011G16K10956 - protPhvul.011G16
29	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:SfPhvul.001G11
30	rubredoxin family protein	Phvul.002G03PTHR17130 - IPhvul.002G03
31	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - NonPhvul.002G01
32	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - NonPhvul.002G01
33	ferredoxin 3	Phvul.007G02PTHR19370:SfPhvul.007G02
34	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - IPhvul.010G11
35	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - IPhvul.010G11
36	REF4-related 1	Phvul.006G15PTHR33739:SfPhvul.006G15
37	Alpha amylase family protein	Phvul.006G04PTHR10357:SfPhvul.006G04
38	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
39	negative regulator of systemic acquired resistance (SNI	0 0 Phvul.003G05
40	negative regulator of systemic acquired resistance (SNI	0 0 Phvul.003G05
41	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - SphiPhvul.008G01
42	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - SphiPhvul.008G01
43	negative regulator of systemic acquired resistance (SNI	0 0 Phvul.003G05
44	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - IPhvul.007G10
45	purine permease 1	Phvul.009G03PTHR31376:SfPhvul.009G03
46		0 0 Phvul.L00244

1			
2		0	0
3			0 Phvul.L00244
4	vacuolar iron transporter 1	Phvul.008G07KOG4473 - UnPhvul.008G07	
5	fatty acid desaturase 5	Phvul.010G15K00507 - steaPhvul.010G15	
6	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - ProPhvul.009G21	
7	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2Phvul.008G04	
8		0 Phvul.009G07K17968 - TRIAPhvul.009G07	
9			
10	embryo defective 2735		0 Phvul.001G19
11	embryo defective 2735		0 Phvul.001G19
12	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1Phvul.003G15	
13	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//IPhvul.009G03	
14	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - IPhvul.004G16	
15	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPRPhvul.009G16	
16	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:SFPhvul.002G11	
17	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - GlyciPhvul.002G15	
18	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - SelePhvul.002G27	
19	SecY protein transport family protein	Phvul.011G16K10956 - protPhvul.011G16	
20	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:SFPhvul.001G11	
21	rubredoxin family protein	Phvul.002G03PTHR17130 - IPhvul.002G03	
22	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - NonPhvul.002G01	
23	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - NonPhvul.002G01	
24	ferredoxin 3	Phvul.007G02PTHR19370:SFPhvul.007G02	
25	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - IPhvul.010G11	
26	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - IPhvul.010G11	
27	REF4-related 1	Phvul.006G15PTHR33739:SFPhvul.006G15	
28	Alpha amylase family protein	Phvul.006G04PTHR10357:SFPhvul.006G04	
29	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00	
30	negative regulator of systemic acquired resistance (SNI		0 Phvul.003G05
31	negative regulator of systemic acquired resistance (SNI		0 Phvul.003G05
32	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - SphiPhvul.008G01	
33	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - SphiPhvul.008G01	
34	negative regulator of systemic acquired resistance (SNI		0 Phvul.003G05
35	cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G101.14.13.152 - Phvul.007G10	
36	purine permease 1	Phvul.009G03PTHR31376:SFPhvul.009G03	
37		0	0 Phvul.L00244
38		0	0 Phvul.L00244
39			
40	vacuolar iron transporter 1	Phvul.008G07KOG4473 - UnPhvul.008G07	
41	fatty acid desaturase 5	Phvul.010G15K00507 - steaPhvul.010G15	
42	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - ProPhvul.009G21	
43	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2Phvul.008G04	
44		0 Phvul.009G07K17968 - TRIAPhvul.009G07	
45			
46	embryo defective 2735		0 Phvul.001G19
47	embryo defective 2735		0 Phvul.001G19
48	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1Phvul.003G15	
49	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//IPhvul.009G03	
50	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - IPhvul.004G16	
51	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPRPhvul.009G16	
52			
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58			
59			
60			



1			
2	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:SF	Phvul.002G11
3	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
4	chloroplatic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
5	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
6	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:SF	Phvul.001G11
7	rubredoxin family protein	Phvul.002G03PTHR17130 - I	Phvul.002G03
8	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
9	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
10	ferredoxin 3	Phvul.007G02PTHR19370:SF	Phvul.007G02
11	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
12	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
13	REF4-related 1	Phvul.006G15PTHR33739:SF	Phvul.006G15
14	Alpha amylase family protein	Phvul.006G04PTHR10357:SF	Phvul.006G04
15	cellulose synthase like G1	Phvul.005G00PTHR13301//I	Phvul.005G00
16	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
17	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
18	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sph	Phvul.008G01
19	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sph	Phvul.008G01
20	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
21	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 -	Phvul.007G10
22	purine permease 1	Phvul.009G03PTHR31376:SF	Phvul.009G03
23		0	0 Phvul.L00244
24		0	0 Phvul.L00244
25	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
26	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
27	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
28	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP	Phvul.008G04
29		0 Phvul.009G07K17968 - TRIA	Phvul.009G07
30	embryo defective 2735	0	0 Phvul.001G19
31	embryo defective 2735	0	0 Phvul.001G19
32	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
33	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
34	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
35	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPR	Phvul.009G16
36	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:SF	Phvul.002G11
37	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
38	chloroplatic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
39	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
40	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:SF	Phvul.001G11
41	rubredoxin family protein	Phvul.002G03PTHR17130 - I	Phvul.002G03
42	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
43	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
44	ferredoxin 3	Phvul.007G02PTHR19370:SF	Phvul.007G02
45	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
46	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
47	REF4-related 1	Phvul.006G15PTHR33739:SF	Phvul.006G15



1			
2	Alpha amylase family protein		Phvul.006G04PTHR10357:SfPhvul.006G04
3	cellulose synthase like G1		Phvul.005G00PTHR13301//IPhvul.005G00
4	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
5	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
6	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
7	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
8	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
9	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
10	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
11	cytochrome P450, family 76, subfamily C, polypeptide 4		Phvul.007G101.14.13.152 - IPhvul.007G10
12	cytochrome P450, family 76, subfamily C, polypeptide 4		Phvul.007G101.14.13.152 - IPhvul.007G10
13	purine permease 1		Phvul.009G03PTHR31376:SfPhvul.009G03
14		0	0 Phvul.L002444
15		0	0 Phvul.L002444
16	vacuolar iron transporter 1		Phvul.008G07KOG4473 - UnPhvul.008G07
17	vacuolar iron transporter 1		Phvul.008G07KOG4473 - UnPhvul.008G07
18	fatty acid desaturase 5		Phvul.010G15K00507 - steaIPhvul.010G15
19	Protein of unknown function (DUF630 and DUF632)		Phvul.009G21PF04782 - ProPhvul.009G21
20	Integrase-type DNA-binding superfamily protein		Phvul.008G04PF00847 - AP2Phvul.008G04
21	Integrase-type DNA-binding superfamily protein		Phvul.008G04PF00847 - AP2Phvul.008G04
22		0	Phvul.009G07K17968 - TRIAPhvul.009G07
23	embryo defective 2735	0	0 Phvul.001G19
24	embryo defective 2735	0	0 Phvul.001G19
25	embryo defective 2735	0	0 Phvul.001G19
26	Pentatricopeptide repeat (PPR) superfamily protein		Phvul.003G15PF01535//PF1Phvul.003G15
27	S-adenosyl-L-methionine-dependent methyltransferase 6		Phvul.009G03PTHR10108//IPhvul.009G03
28	thioredoxin-dependent peroxidase 1		Phvul.004G16PTHR10430 - IPhvul.004G16
29	thioredoxin-dependent peroxidase 1		Phvul.004G16PTHR10430 - IPhvul.004G16
30	Protein prenyltransferase superfamily protein		Phvul.009G16PF13414 - TPRPhvul.009G16
31	Uncharacterised conserved protein UCP015417, vWA		Phvul.002G11PTHR31373:SfPhvul.002G11
32	alanine-2-oxoglutarate aminotransferase 2		Phvul.002G152.6.1.4 - GlyciIPhvul.002G15
33	alanine-2-oxoglutarate aminotransferase 2		Phvul.002G152.6.1.4 - GlyciIPhvul.002G15
34	chloroplastic NIFS-like cysteine desulfurase		Phvul.002G274.4.1.16 - SelePhvul.002G27
35	SecY protein transport family protein		Phvul.011G16K10956 - protIPhvul.011G16
36	NDH-dependent cyclic electron flow 1		Phvul.001G11PTHR11122:SfPhvul.001G11
37	rubredoxin family protein		Phvul.002G03PTHR17130 - IPhvul.002G03
38	rubredoxin family protein		Phvul.002G03PTHR17130 - IPhvul.002G03
39	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
40	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
41	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
42	ferredoxin 3		Phvul.007G02PTHR19370:SfPhvul.007G02
43	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
44	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
45	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
46	REF4-related 1		Phvul.006G15PTHR33739:SfPhvul.006G15
47	Alpha amylase family protein		Phvul.006G04PTHR10357:SfPhvul.006G04
48	cellulose synthase like G1		Phvul.005G00PTHR13301//IPhvul.005G00
49	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
50	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
51	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
52	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
53	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
54	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
55	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
56	cytochrome P450, family 76, subfamily C, polypeptide 4		Phvul.007G101.14.13.152 - IPhvul.007G10
57	cytochrome P450, family 76, subfamily C, polypeptide 4		Phvul.007G101.14.13.152 - IPhvul.007G10
58	purine permease 1		Phvul.009G03PTHR31376:SfPhvul.009G03
59		0	0 Phvul.L002444
60		0	0 Phvul.L002444
	vacuolar iron transporter 1		Phvul.008G07KOG4473 - UnPhvul.008G07

1			
2	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
3	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
4	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP	Phvul.008G04
5			
6		0 Phvul.009G07K17968 - TRIA	Phvul.009G07
7	embryo defective 2735	0	0 Phvul.001G19
8	embryo defective 2735	0	0 Phvul.001G19
9			
10	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
11	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
12	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
13	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TP	Phvul.009G16
14	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:S	Phvul.002G11
15	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
16	chloroplatic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
17	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
18	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:S	Phvul.001G11
19	rubredoxin family protein	Phvul.002G03PTHR17130 - I	Phvul.002G03
20	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
21	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
22	ferredoxin 3	Phvul.007G02PTHR19370:S	Phvul.007G02
23	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
24	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
25	REF4-related 1	Phvul.006G15PTHR33739:S	Phvul.006G15
26	Alpha amylase family protein	Phvul.006G04PTHR10357:S	Phvul.006G04
27	cellulose synthase like G1	Phvul.005G00PTHR13301//I	Phvul.005G00
28	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
29	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
30	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sph	Phvul.008G01
31	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sph	Phvul.008G01
32	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
33	cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G101.14.13.152 -	Phvul.007G10
34	purine permease 1	Phvul.009G03PTHR31376:S	Phvul.009G03
35		0	0 Phvul.L00244
36		0	0 Phvul.L00244
37	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
38	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
39	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
40	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP	Phvul.008G04
41			
42		0 Phvul.009G07K17968 - TRIA	Phvul.009G07
43	embryo defective 2735	0	0 Phvul.001G19
44	embryo defective 2735	0	0 Phvul.001G19
45			
46	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
47	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
48	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
49	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TP	Phvul.009G16
50	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:S	Phvul.002G11
51	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15

1				
2	chloroplastic NIFS-like cysteine desulfurase			Phvul.002G274.4.1.16 - SelePhvul.002G27
3	SecY protein transport family protein			Phvul.011G16K10956 - protPhvul.011G16
4	NDH-dependent cyclic electron flow 1			Phvul.001G11PTHR11122:SFPhvul.001G11
5	rubredoxin family protein			Phvul.002G03PTHR17130 - IPhvul.002G03
6	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
7	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
8	ferredoxin 3			Phvul.007G02PTHR19370:SFPhvul.007G02
9	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
10	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
11	REF4-related 1			Phvul.006G15PTHR33739:SFPhvul.006G15
12	Alpha amylase family protein			Phvul.006G04PTHR10357:SFPhvul.006G04
13	cellulose synthase like G1			Phvul.005G00PTHR13301//IPhvul.005G00
14	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
15	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
16	dihydrosphingosine phosphate lyase			Phvul.008G014.1.2.27 - SphiPhvul.008G01
17	dihydrosphingosine phosphate lyase			Phvul.008G014.1.2.27 - SphiPhvul.008G01
18	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
19	cytochrome P450, family 76, subfamily C, polypeptide 4			Phvul.007G101.14.13.152 - Phvul.007G10
20	purine permease 1			Phvul.009G03PTHR31376:SFPhvul.009G03
21		0	0	Phvul.L00244
22		0	0	Phvul.L00244
23	vacuolar iron transporter 1			Phvul.008G07KOG4473 - UnPhvul.008G07
24	fatty acid desaturase 5			Phvul.010G15K00507 - steaiPhvul.010G15
25	Protein of unknown function (DUF630 and DUF632)			Phvul.009G21PF04782 - ProPhvul.009G21
26	Integrase-type DNA-binding superfamily protein			Phvul.008G04PF00847 - AP2Phvul.008G04
27		0		Phvul.009G07K17968 - TRIAPhvul.009G07
28	embryo defective 2735	0	0	Phvul.001G19
29	embryo defective 2735	0	0	Phvul.001G19
30	Pentatricopeptide repeat (PPR) superfamily protein			Phvul.003G15PF01535//PF1Phvul.003G15
31	S-adenosyl-L-methionine-dependent methyltransferase			Phvul.009G03PTHR10108//IPhvul.009G03
32	thioredoxin-dependent peroxidase 1			Phvul.004G16PTHR10430 - IPhvul.004G16
33	Protein prenyltransferase superfamily protein			Phvul.009G16PF13414 - TPRPhvul.009G16
34	Uncharacterised conserved protein UCP015417, vWA			Phvul.002G11PTHR31373:SFPhvul.002G11
35	alanine-2-oxoglutarate aminotransferase 2			Phvul.002G152.6.1.4 - GlyciPhvul.002G15
36	chloroplastic NIFS-like cysteine desulfurase			Phvul.002G274.4.1.16 - SelePhvul.002G27
37	SecY protein transport family protein			Phvul.011G16K10956 - protPhvul.011G16
38	NDH-dependent cyclic electron flow 1			Phvul.001G11PTHR11122:SFPhvul.001G11
39	rubredoxin family protein			Phvul.002G03PTHR17130 - IPhvul.002G03
40	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
41	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
42	ferredoxin 3			Phvul.007G02PTHR19370:SFPhvul.007G02
43	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
44	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
45	REF4-related 1			Phvul.006G15PTHR33739:SFPhvul.006G15
46	Alpha amylase family protein			Phvul.006G04PTHR10357:SFPhvul.006G04
47	cellulose synthase like G1			Phvul.005G00PTHR13301//IPhvul.005G00

1			
2	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
3	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
4	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
5	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
6	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
7	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
8	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - (Phvul.007G10	
9	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - (Phvul.007G10	
10	purine permease 1	Phvul.009G03PTHR31376:SF	Phvul.009G03
11		0	0 Phvul.L002444
12		0	0 Phvul.L002444
13			
14	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
15	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
16	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
17	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2	Phvul.008G04
18	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2	Phvul.008G04
19	Integrase-type DNA-binding superfamily protein	0 Phvul.009G07K17968 - TRIA	Phvul.009G07
20	embryo defective 2735	0	0 Phvul.001G19
21	embryo defective 2735	0	0 Phvul.001G19
22	embryo defective 2735	0	0 Phvul.001G19
23	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
24	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
25	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
26	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
27	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPR	Phvul.009G16
28	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:SF	Phvul.002G11
29	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
30	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
31	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
32	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
33	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
34	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:SF	Phvul.001G11
35	rubredoxin family protein	Phvul.002G03PTHR17130 - I	Phvul.002G03
36	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
37	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
38	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
39	ferredoxin 3	Phvul.007G02PTHR19370:SF	Phvul.007G02
40	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
41	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
42	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
43	REF4-related 1	Phvul.006G15PTHR33739:SF	Phvul.006G15
44	Alpha amylase family protein	Phvul.006G04PTHR10357:SF	Phvul.006G04
45	cellulose synthase like G1	Phvul.005G00PTHR13301//I	Phvul.005G00
46	cellulose synthase like G1	Phvul.005G00PTHR13301//I	Phvul.005G00
47	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
48	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
49	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
50	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
51	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
52	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
53	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
54	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - (Phvul.007G10	
55	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - (Phvul.007G10	
56	purine permease 1	Phvul.009G03PTHR31376:SF	Phvul.009G03
57		0	0 Phvul.L002444
58		0	0 Phvul.L002444
59	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
60	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21

1			
2	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2	Phvul.008G04
3		0 Phvul.009G07K17968 - TRIA	Phvul.009G07
4	embryo defective 2735	0	0 Phvul.001G19
5	embryo defective 2735	0	0 Phvul.001G19
6			
7	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
8	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
9			
10	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
11	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPR	Phvul.009G16
12	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:Sf	Phvul.002G11
13			
14	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
15	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
16	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
17			
18	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:Sf	Phvul.001G11
19	rubredoxin family protein	Phvul.002G03PTHR17130 - I	Phvul.002G03
20	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
21	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
22			
23	ferredoxin 3	Phvul.007G02PTHR19370:Sf	Phvul.007G02
24	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
25			
26	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
27	REF4-related 1	Phvul.006G15PTHR33739:Sf	Phvul.006G15
28	Alpha amylase family protein	Phvul.006G04PTHR10357:Sf	Phvul.006G04
29	cellulose synthase like G1	Phvul.005G00PTHR13301//I	Phvul.005G00
30			
31	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
32	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
33			
34	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sph	Phvul.008G01
35	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sph	Phvul.008G01
36	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
37			
38	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 - (	Phvul.007G10
39	purine permease 1	Phvul.009G03PTHR31376:Sf	Phvul.009G03
40		0	0 Phvul.L00244
41		0	0 Phvul.L00244
42			
43	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
44	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
45	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
46			
47	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP2	Phvul.008G04
48		0 Phvul.009G07K17968 - TRIA	Phvul.009G07
49	embryo defective 2735	0	0 Phvul.001G19
50	embryo defective 2735	0	0 Phvul.001G19
51			
52	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
53	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
54			
55	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
56	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPR	Phvul.009G16
57	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:Sf	Phvul.002G11
58			
59	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
60	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16



1				
2	NDH-dependent cyclic electron flow 1			Phvul.001G11PTHR11122:SfPhvul.001G11
3	rubredoxin family protein			Phvul.002G03PTHR17130 - IPhvul.002G03
4	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
5	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
6	ferredoxin 3			Phvul.007G02PTHR19370:SfPhvul.007G02
7	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
8	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
9	REF4-related 1			Phvul.006G15PTHR33739:SfPhvul.006G15
10	Alpha amylase family protein			Phvul.006G04PTHR10357:SfPhvul.006G04
11	cellulose synthase like G1			Phvul.005G00PTHR13301//IPhvul.005G00
12	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
13	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
14	dihydrosphingosine phosphate lyase			Phvul.008G014.1.2.27 - SphiPhvul.008G01
15	dihydrosphingosine phosphate lyase			Phvul.008G014.1.2.27 - SphiPhvul.008G01
16	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
17	cytochrome P450, family 76, subfamily C, polypeptide 4			Phvul.007G101.14.13.152 - IPhvul.007G10
18	purine permease 1			Phvul.009G03PTHR31376:SfPhvul.009G03
19		0	0	Phvul.L002444
20		0	0	Phvul.L002444
21	vacuolar iron transporter 1			Phvul.008G07KOG4473 - UnPhvul.008G07
22	fatty acid desaturase 5			Phvul.010G15K00507 - steaiPhvul.010G15
23	Protein of unknown function (DUF630 and DUF632)			Phvul.009G21PF04782 - ProPhvul.009G21
24	Integrase-type DNA-binding superfamily protein			Phvul.008G04PF00847 - AP2Phvul.008G04
25				0 Phvul.009G07K17968 - TRIAPhvul.009G07
26	embryo defective 2735	0	0	Phvul.001G19
27	embryo defective 2735	0	0	Phvul.001G19
28	Pentatricopeptide repeat (PPR) superfamily protein			Phvul.003G15PF01535//PF1Phvul.003G15
29	S-adenosyl-L-methionine-dependent methyltransferase			Phvul.009G03PTHR10108//IPhvul.009G03
30	thioredoxin-dependent peroxidase 1			Phvul.004G16PTHR10430 - IPhvul.004G16
31	Protein prenyltransferase superfamily protein			Phvul.009G16PF13414 - TPRPhvul.009G16
32	Uncharacterised conserved protein UCP015417, vWA			Phvul.002G11PTHR31373:SfPhvul.002G11
33	alanine-2-oxoglutarate aminotransferase 2			Phvul.002G152.6.1.4 - GlyciiPhvul.002G15
34	chloroplastic NIFS-like cysteine desulfurase			Phvul.002G274.4.1.16 - SelePhvul.002G27
35	SecY protein transport family protein			Phvul.011G16K10956 - protiPhvul.011G16
36	NDH-dependent cyclic electron flow 1			Phvul.001G11PTHR11122:SfPhvul.001G11
37	rubredoxin family protein			Phvul.002G03PTHR17130 - IPhvul.002G03
38	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
39	Protein kinase superfamily protein			Phvul.002G012.7.11.1 - NonPhvul.002G01
40	ferredoxin 3			Phvul.007G02PTHR19370:SfPhvul.007G02
41	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
42	transducin family protein / WD-40 repeat family protei			Phvul.010G11PTHR13950 - IPhvul.010G11
43	REF4-related 1			Phvul.006G15PTHR33739:SfPhvul.006G15
44	Alpha amylase family protein			Phvul.006G04PTHR10357:SfPhvul.006G04
45	cellulose synthase like G1			Phvul.005G00PTHR13301//IPhvul.005G00
46	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
47	negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05



1			
2	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
3	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
4	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
5	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 -	Phvul.007G10
6	purine permease 1	Phvul.009G03PTHR31376:Sf	Phvul.009G03
7			
8		0	0 Phvul.L00244
9			
10		0	0 Phvul.L00244
11	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
12	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
13	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
14	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP	Phvul.008G04
15			
16		0	Phvul.009G07K17968 - TRIA
17			Phvul.009G07
18	embryo defective 2735	0	0 Phvul.001G19
19	embryo defective 2735	0	0 Phvul.001G19
20	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15PF01535//PF1	Phvul.003G15
21	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03PTHR10108//I	Phvul.009G03
22	thioredoxin-dependent peroxidase 1	Phvul.004G16PTHR10430 - I	Phvul.004G16
23	Protein prenyltransferase superfamily protein	Phvul.009G16PF13414 - TPR	Phvul.009G16
24	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11PTHR31373:Sf	Phvul.002G11
25	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G152.6.1.4 - Glyci	Phvul.002G15
26	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G274.4.1.16 - Sele	Phvul.002G27
27	SecY protein transport family protein	Phvul.011G16K10956 - prot	Phvul.011G16
28	NDH-dependent cyclic electron flow 1	Phvul.001G11PTHR11122:Sf	Phvul.001G11
29	rubredoxin family protein	Phvul.002G03PTHR17130 - I	Phvul.002G03
30	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
31	Protein kinase superfamily protein	Phvul.002G012.7.11.1 - Non	Phvul.002G01
32	ferredoxin 3	Phvul.007G02PTHR19370:Sf	Phvul.007G02
33	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
34	transducin family protein / WD-40 repeat family protei	Phvul.010G11PTHR13950 - I	Phvul.010G11
35	REF4-related 1	Phvul.006G15PTHR33739:Sf	Phvul.006G15
36	Alpha amylase family protein	Phvul.006G04PTHR10357:Sf	Phvul.006G04
37	cellulose synthase like G1	Phvul.005G00PTHR13301//I	Phvul.005G00
38	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
39	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
40	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
41	dihydrosphingosine phosphate lyase	Phvul.008G014.1.2.27 - Sphi	Phvul.008G01
42	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
43	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G101.14.13.152 -	Phvul.007G10
44	purine permease 1	Phvul.009G03PTHR31376:Sf	Phvul.009G03
45			
46		0	0 Phvul.L00244
47			
48		0	0 Phvul.L00244
49	vacuolar iron transporter 1	Phvul.008G07KOG4473 - Un	Phvul.008G07
50	fatty acid desaturase 5	Phvul.010G15K00507 - stea	Phvul.010G15
51	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21PF04782 - Pro	Phvul.009G21
52	Integrase-type DNA-binding superfamily protein	Phvul.008G04PF00847 - AP	Phvul.008G04
53			
54		0	Phvul.009G07K17968 - TRIA
55			Phvul.009G07

1			
2	embryo defective 2735	0	0 Phvul.001G19
3	embryo defective 2735	0	0 Phvul.001G19
4	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15 PF01535//PF1	Phvul.003G15
5	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03 PTHR10108//I	Phvul.009G03
6	thioredoxin-dependent peroxidase 1	Phvul.004G16 PTHR10430 - I	Phvul.004G16
7	Protein prenyltransferase superfamily protein	Phvul.009G16 PF13414 - TPR	Phvul.009G16
8	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11 PTHR31373:SF	Phvul.002G11
9	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15 2.6.1.4 - Glyci	Phvul.002G15
10	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27 4.4.1.16 - Sele	Phvul.002G27
11	SecY protein transport family protein	Phvul.011G16 K10956 - prot	Phvul.011G16
12	NDH-dependent cyclic electron flow 1	Phvul.001G11 PTHR11122:SF	Phvul.001G11
13	rubredoxin family protein	Phvul.002G03 PTHR17130 - I	Phvul.002G03
14	Protein kinase superfamily protein	Phvul.002G01 2.7.11.1 - Non	Phvul.002G01
15	Protein kinase superfamily protein	Phvul.002G01 2.7.11.1 - Non	Phvul.002G01
16	ferredoxin 3	Phvul.007G02 PTHR19370:SF	Phvul.007G02
17	transducin family protein / WD-40 repeat family protei	Phvul.010G11 PTHR13950 - I	Phvul.010G11
18	transducin family protein / WD-40 repeat family protei	Phvul.010G11 PTHR13950 - I	Phvul.010G11
19	REF4-related 1	Phvul.006G15 PTHR33739:SF	Phvul.006G15
20	Alpha amylase family protein	Phvul.006G04 PTHR10357:SF	Phvul.006G04
21	cellulose synthase like G1	Phvul.005G00 PTHR13301//I	Phvul.005G00
22	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
23	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
24	dihydrosphingosine phosphate lyase	Phvul.008G01 4.1.2.27 - Sph	Phvul.008G01
25	dihydrosphingosine phosphate lyase	Phvul.008G01 4.1.2.27 - Sph	Phvul.008G01
26	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
27	cytochrome P450, family 76, subfamily C, polypeptide 4	Phvul.007G10 1.14.13.152 -	Phvul.007G10
28	purine permease 1	Phvul.009G03 PTHR31376:SF	Phvul.009G03
29		0	0 Phvul.L00244
30		0	0 Phvul.L00244
31	vacuolar iron transporter 1	Phvul.008G07 KOG4473 - Un	Phvul.008G07
32	fatty acid desaturase 5	Phvul.010G15 K00507 - stea	Phvul.010G15
33	Protein of unknown function (DUF630 and DUF632)	Phvul.009G21 PF04782 - Pro	Phvul.009G21
34	Integrase-type DNA-binding superfamily protein	Phvul.008G04 PF00847 - AP	Phvul.008G04
35		0 Phvul.009G07 K17968 - TRIA	Phvul.009G07
36	embryo defective 2735	0	0 Phvul.001G19
37	embryo defective 2735	0	0 Phvul.001G19
38	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15 PF01535//PF1	Phvul.003G15
39	S-adenosyl-L-methionine-dependent methyltransferase	Phvul.009G03 PTHR10108//I	Phvul.009G03
40	thioredoxin-dependent peroxidase 1	Phvul.004G16 PTHR10430 - I	Phvul.004G16
41	Protein prenyltransferase superfamily protein	Phvul.009G16 PF13414 - TPR	Phvul.009G16
42	Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11 PTHR31373:SF	Phvul.002G11
43	alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15 2.6.1.4 - Glyci	Phvul.002G15
44	chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27 4.4.1.16 - Sele	Phvul.002G27
45	SecY protein transport family protein	Phvul.011G16 K10956 - prot	Phvul.011G16
46	NDH-dependent cyclic electron flow 1	Phvul.001G11 PTHR11122:SF	Phvul.001G11
47	rubredoxin family protein	Phvul.002G03 PTHR17130 - I	Phvul.002G03

1			
2	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
3	Protein kinase superfamily protein		Phvul.002G012.7.11.1 - NonPhvul.002G01
4	ferredoxin 3		Phvul.007G02PTHR19370:SfPhvul.007G02
5			
6	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
7	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
8	REF4-related 1		Phvul.006G15PTHR33739:SfPhvul.006G15
9			
10	Alpha amylase family protein		Phvul.006G04PTHR10357:SfPhvul.006G04
11	cellulose synthase like G1		Phvul.005G00PTHR13301//IPhvul.005G00
12	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
13	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
14	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
15	dihydrosphingosine phosphate lyase		Phvul.008G014.1.2.27 - SphiPhvul.008G01
16			
17	negative regulator of systemic acquired resistance (SNI	0	0 Phvul.003G05
18	cytochrome P450, family 76, subfamily C, polypeptide 4		Phvul.007G101.14.13.152 - (Phvul.007G10
19	purine permease 1		Phvul.009G03PTHR31376:SfPhvul.009G03
20			
21			
22		0	0 Phvul.L00244
23		0	0 Phvul.L00244
24	vacuolar iron transporter 1		Phvul.008G07KOG4473 - UnPhvul.008G07
25	fatty acid desaturase 5		Phvul.010G15K00507 - steaPhvul.010G15
26	Protein prenyltransferase superfamily protein		Phvul.009G16PF13414 - TPRPhvul.009G16
27	Protein of unknown function (DUF630 and DUF632)		Phvul.009G21PF04782 - ProPhvul.009G21
28	ferredoxin 3		Phvul.007G02PTHR19370:SfPhvul.007G02
29			
30	Integrase-type DNA-binding superfamily protein		Phvul.008G04PF00847 - AP2Phvul.008G04
31			0 Phvul.009G07K17968 - TRIAPhvul.009G07
32			
33	embryo defective 2735	0	0 Phvul.001G19
34	embryo defective 2735	0	0 Phvul.001G19
35			
36	AMP-dependent synthetase and ligase family protein		Phvul.009G16PTHR24096:SfPhvul.009G16
37	Pentatricopeptide repeat (PPR) superfamily protein		Phvul.003G15PF01535//PF1Phvul.003G15
38	MAC/Perforin domain-containing protein		Phvul.L00374(PF01823 - MAPhvul.L00374(
39	MAC/Perforin domain-containing protein		Phvul.L00374(PF01823 - MAPhvul.L00374(
40			
41	S-adenosyl-L-methionine-dependent methyltransferas		Phvul.009G03PTHR10108//IPhvul.009G03
42	thioredoxin-dependent peroxidase 1		Phvul.004G16PTHR10430 - IPhvul.004G16
43	Uncharacterised conserved protein UCP015417, vWA		Phvul.002G11PTHR31373:SfPhvul.002G11
44	alanine-2-oxoglutarate aminotransferase 2		Phvul.002G152.6.1.4 - GlyciPhvul.002G15
45	chloroplastic NIFS-like cysteine desulfurase		Phvul.002G274.4.1.16 - SelePhvul.002G27
46	SecY protein transport family protein		Phvul.011G16K10956 - protPhvul.011G16
47	cation exchanger 1		Phvul.006G06K07300 - Ca2+Phvul.006G06
48			
49	NDH-dependent cyclic electron flow 1		Phvul.001G11PTHR11122:SfPhvul.001G11
50	rubredoxin family protein		Phvul.002G03PTHR17130 - IPhvul.002G03
51			
52	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
53	transducin family protein / WD-40 repeat family protei		Phvul.010G11PTHR13950 - IPhvul.010G11
54			
55	C2 calcium/lipid-binding plant phosphoribosyltransfera		Phvul.002G15PTHR10024:SfPhvul.002G15
56	Plant invertase/pectin methylesterase inhibitor superfc		Phvul.009G22PTHR31707:SfPhvul.009G22
57			
58	Protein of unknown function (DUF630) ;Protein of unkr		Phvul.002G10PF04782 - ProPhvul.002G10
59	FASCICLIN-like arabinoogalactan 9		Phvul.005G09PTHR32077:SfPhvul.005G09
60	basic helix-loop-helix (bHLH) DNA-binding superfamily		Phvul.003G18PTHR12565:SfPhvul.003G18

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2	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:Sf	Phvul.003G18
3	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132://I	Phvul.003G12
4	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132://I	Phvul.003G12
5	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - Perc	Phvul.006G07
6	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - Perc	Phvul.006G07
7	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nucl	Phvul.008G28
8	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:Sf	Phvul.007G16
9	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:Sf	Phvul.007G16
10	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680://I	Phvul.001G26
11	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:Sf	Phvul.006G09
12	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:Sf	Phvul.006G09
13	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:Sf	Phvul.006G09
14	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:Sf	Phvul.003G03
15		0	0
16		0	0
17	P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10PTHR10799://I	Phvul.003G10
18	P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10PTHR10799://I	Phvul.003G10
19	binding	Phvul.002G26PTHR23315:Sf	Phvul.002G26
20	binding	Phvul.002G26PTHR23315:Sf	Phvul.002G26
21	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA	Phvul.002G29
22	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA	Phvul.002G29
23	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA	Phvul.002G29
24	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:Sf	Phvul.007G15
25	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:Sf	Phvul.007G15
26	RING/U-box superfamily protein	Phvul.002G00PTHR10044:Sf	Phvul.002G00
27	RING/U-box superfamily protein	Phvul.002G00PTHR10044:Sf	Phvul.002G00
28	cellulose synthase like G1	Phvul.005G00PTHR13301://I	Phvul.005G00
29	RING/U-box superfamily protein	Phvul.002G00PTHR10044:Sf	Phvul.002G00
30	RING/U-box superfamily protein	Phvul.002G00PTHR10044:Sf	Phvul.002G00
31	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493://I	Phvul.008G24
32	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850://I	Phvul.007G20
33	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850://I	Phvul.007G20
34	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
35	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
36	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
37	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
38	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
39	RING/U-box superfamily protein	Phvul.003G18PTHR22763:Sf	Phvul.003G18
40	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
41	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
42	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
43	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956://I	Phvul.006G16
44	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
45	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
46	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
47	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - Perc	Phvul.005G05
48	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
49	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
50	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
51	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - Perc	Phvul.005G05
52	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phos	Phvul.002G11
53	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY	Phvul.008G10
54	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY	Phvul.008G10
55	protein binding	Phvul.008G07PTHR33601:Sf	Phvul.008G07
56	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:Sf	Phvul.003G26
57	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
58	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
59	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
60	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08



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2	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
3	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
4	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
5	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
6	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
7	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
8	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22PTHR31707:SFPhvul.009G22
9	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10PF04782 - ProPhvul.002G10
10	FASCICLIN-like arabinoogalactan 9	Phvul.005G09PTHR32077:SFPhvul.005G09
11	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
12	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
13	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
14	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
15	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - PercPhvul.006G07
16	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
17	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SFPhvul.007G16
18	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
19	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
20	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
21	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SFPhvul.003G03
22		0 0 0 Phvul.009G00
23	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//IPhvul.003G10
24	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//IPhvul.003G10
25	binding	Phvul.002G26PTHR23315:SFPhvul.002G26
26	binding	Phvul.002G26PTHR23315:SFPhvul.002G26
27	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
28	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
29	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SFPhvul.007G15
30	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
31	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
32	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
33	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
34	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
35	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
36	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
37	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
38	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
39	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
40	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SFPhvul.003G18
41	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
42	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
43	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
44	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
45	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
46	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
47	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
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2	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
3	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
4	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phosPhvul.002G11
5	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY Phvul.008G10
6	protein binding	Phvul.008G07 PTHR33601:SfPhvul.008G07
7	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SfPhvul.003G26
8	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
9	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
10	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
11	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
12	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
13	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20 K01530 - phosPhvul.009G20
14	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
15	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
16	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20 K01530 - phosPhvul.009G20
17	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
18	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22 PTHR31707:SfPhvul.009G22
19	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10 PF04782 - Pro Phvul.002G10
20	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SfPhvul.005G09
21	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SfPhvul.003G18
22	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SfPhvul.003G18
23	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
24	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
25	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
26	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nuclPhvul.008G28
27	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SfPhvul.007G16
28	serine hydroxymethyltransferase 4	Phvul.001G26 PTHR11680//IPhvul.001G26
29	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
30	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
31	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03 PTHR15245:SfPhvul.003G03
32		0 0 0 Phvul.009G00
33	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10 PTHR10799//IPhvul.003G10
34	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10 PTHR10799//IPhvul.003G10
35	binding	Phvul.002G26 PTHR23315:SfPhvul.002G26
36	binding	Phvul.002G26 PTHR23315:SfPhvul.002G26
37	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
38	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
39	phytochrome interacting factor 3-like 5	Phvul.007G15 PTHR12565:SfPhvul.007G15
40	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
41	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
42	cellulose synthase like G1	Phvul.005G00 PTHR13301//IPhvul.005G00
43	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
44	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24 PTHR21493//IPhvul.008G24
45	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20 PTHR11850//IPhvul.007G20
46	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
47	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15



1		
2	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
3	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
4	RING/U-box superfamily protein	Phvul.003G18 PTHR22763:SFPhvul.003G18
5		
6	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
7	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
8	Protein of unknown function (DUF616)	Phvul.006G16 PTHR12956//IPhvul.006G16
9		
10	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
11	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
12	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
13		
14	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
15	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
16	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
17		
18	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phosPhvul.002G11
19	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY Phvul.008G10
20	protein binding	Phvul.008G07 PTHR33601:SFPhvul.008G07
21		
22	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SFPhvul.003G26
23	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
24	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
25		
26	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
27	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
28	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
29		
30	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
31	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SFPhvul.005G15
32	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SFPhvul.005G15
33		
34	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
35	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
36	Plant invertase/pectin methylesterase inhibitor superfamily protein	Phvul.009G22 PTHR31707:SFPhvul.009G22
37	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10 PF04782 - ProPhvul.002G10
38		
39	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SFPhvul.005G09
40	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18 PTHR12565:SFPhvul.003G18
41	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18 PTHR12565:SFPhvul.003G18
42		
43	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
44	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
45	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
46		
47	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nuclPhvul.008G28
48	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SFPhvul.007G16
49	serine hydroxymethyltransferase 4	Phvul.001G26 PTHR11680//IPhvul.001G26
50		
51	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SFPhvul.006G09
52	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SFPhvul.006G09
53	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03 PTHR15245:SFPhvul.003G03
54		
55		0 0 0 Phvul.009G00
56	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10 PTHR10799//IPhvul.003G10
57	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10 PTHR10799//IPhvul.003G10
58		
59	binding	Phvul.002G26 PTHR23315:SFPhvul.002G26
60	binding	Phvul.002G26 PTHR23315:SFPhvul.002G26
	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29

1		
2	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
3	phytochrome interacting factor 3-like 5	Phvul.007G15 PTHR12565:SfPhvul.007G15
4	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
5	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
6	cellulose synthase like G1	Phvul.005G00 PTHR13301//IPhvul.005G00
7	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
8		
9		
10	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24 PTHR21493//IPhvul.008G24
11	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20 PTHR11850//IPhvul.007G20
12	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
13	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
14	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
15	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
16	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
17	RING/U-box superfamily protein	Phvul.003G18 PTHR22763:SfPhvul.003G18
18	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
19	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
20	Protein of unknown function (DUF616)	Phvul.006G16 PTHR12956//IPhvul.006G16
21	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
22	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
23	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
24	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
25	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
26	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
27	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
28	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
29	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
30	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phosPhvul.002G11
31	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY Phvul.008G10
32	protein binding	Phvul.008G07 PTHR33601:SfPhvul.008G07
33	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SfPhvul.003G26
34	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
35	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
36	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
37	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
38	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
39	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20 K01530 - phosPhvul.009G20
40	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
41	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
42	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20 K01530 - phosPhvul.009G20
43	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
44	Plant invertase/pectin methylesterase inhibitor superf	Phvul.009G22 PTHR31707:SfPhvul.009G22
45	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10 PF04782 - Pro Phvul.002G10
46	FASCICLIN-like arabinoogalactan 9	Phvul.005G09 PTHR32077:SfPhvul.005G09
47	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SfPhvul.003G18
48	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SfPhvul.003G18
49	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
50	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
51	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
52	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nuclPhvul.008G28
53	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SfPhvul.007G16

1		
2	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
3	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
4	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
5	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SfPhvul.003G03
6		0 0 0 Phvul.009G00
7		
8	P-loop containing nucleoside triphosphate hydrolases	sPhvul.003G10PTHR10799//IPhvul.003G10
9	P-loop containing nucleoside triphosphate hydrolases	sPhvul.003G10PTHR10799//IPhvul.003G10
10	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
11	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
12	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
13	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
14	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SfPhvul.007G15
15	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
16	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
17	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
18	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
19	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
20	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
21	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
22	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
23	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
24	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
25	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SfPhvul.003G18
26	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
27	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
28	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
29	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
30	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
31	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
32	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
33	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
34	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
35	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
36	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MYPhvul.008G10
37	protein binding	Phvul.008G07PTHR33601:SfPhvul.008G07
38	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SfPhvul.003G26
39	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
40	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
41	gigantea protein (GI)	Phvul.004G08K12124 - GIG#Phvul.004G08
42	gigantea protein (GI)	Phvul.004G08K12124 - GIG#Phvul.004G08
43	gigantea protein (GI)	Phvul.004G08K12124 - GIG#Phvul.004G08
44	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
45	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
46	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
47	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
48	gigantea protein (GI)	Phvul.004G08K12124 - GIG#Phvul.004G08

1	Plant invertase/pectin methylesterase inhibitor superfamily	Phvul.009G22 PTHR31707:SF	Phvul.009G22
2	Protein of unknown function (DUF630) ;Protein of unknown function	Phvul.002G10 PF04782 - Pro	Phvul.002G10
3	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SF	Phvul.005G09
4	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SF	Phvul.003G18
5	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SF	Phvul.003G18
6	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132://I	Phvul.003G12
7	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132://I	Phvul.003G12
8	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - Perc	Phvul.006G07
9	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nucle	Phvul.008G28
10	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SF	Phvul.007G16
11	serine hydroxymethyltransferase 4	Phvul.001G26 PTHR11680://I	Phvul.001G26
12	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SF	Phvul.006G09
13	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SF	Phvul.006G09
14	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03 PTHR15245:SF	Phvul.003G03
15		0	0
16		0	0
17	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10 PTHR10799://I	Phvul.003G10
18	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10 PTHR10799://I	Phvul.003G10
19	binding	Phvul.002G26 PTHR23315:SF	Phvul.002G26
20	binding	Phvul.002G26 PTHR23315:SF	Phvul.002G26
21	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA	Phvul.002G29
22	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA	Phvul.002G29
23	phytochrome interacting factor 3-like 5	Phvul.007G15 PTHR12565:SF	Phvul.007G15
24	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SF	Phvul.002G00
25	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SF	Phvul.002G00
26	cellulose synthase like G1	Phvul.005G00 PTHR13301://I	Phvul.005G00
27	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SF	Phvul.002G00
28	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24 PTHR21493://I	Phvul.008G24
29	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20 PTHR11850://I	Phvul.007G20
30	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
31	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
32	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
33	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
34	RING/U-box superfamily protein	Phvul.003G18 PTHR22763:SF	Phvul.003G18
35	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
36	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
37	Protein of unknown function (DUF616)	Phvul.006G16 PTHR12956://I	Phvul.006G16
38	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
39	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
40	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05
41	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
42	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
43	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05
44	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phos	Phvul.002G11
45	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY	Phvul.008G10
46	protein binding	Phvul.008G07 PTHR33601:SF	Phvul.008G07
47	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SF	Phvul.003G26



1		
2	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
3	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
4	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
5	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
6	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
7	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
8	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
9	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
10	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
11	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
12	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
13	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
14	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
15	Plant invertase/pectin methylesterase inhibitor superfamily	Phvul.009G22PTHR31707:SFPhvul.009G22
16	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10PF04782 - ProPhvul.002G10
17	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10PF04782 - ProPhvul.002G10
18	FASCICLIN-like arabinogalactan 9	Phvul.005G09PTHR32077:SFPhvul.005G09
19	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
20	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
21	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
22	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
23	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
24	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - PercPhvul.006G07
25	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - PercPhvul.006G07
26	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
27	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SFPhvul.007G16
28	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
29	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
30	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
31	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
32	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
33	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SFPhvul.003G03
34	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SFPhvul.003G03
35	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10PTHR10799//IPhvul.003G10
36	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10PTHR10799//IPhvul.003G10
37	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10PTHR10799//IPhvul.003G10
38	binding	Phvul.002G26PTHR23315:SFPhvul.002G26
39	binding	Phvul.002G26PTHR23315:SFPhvul.002G26
40	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
41	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
42	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
43	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SFPhvul.007G15
44	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
45	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
46	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
47	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
48	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
49	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
50	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
51	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
52	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
53	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
54	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
55	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
56	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
57	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SFPhvul.003G18
58	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SFPhvul.003G18
59	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
60	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16

1			
2	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SF	Phvul.007G15
3	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SF	Phvul.007G15
4	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - Perc	Phvul.005G05
5			
6	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SF	Phvul.007G15
7	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SF	Phvul.007G15
8	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - Perc	Phvul.005G05
9			
10	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phos	Phvul.002G11
11	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY	Phvul.008G10
12	protein binding	Phvul.008G07PTHR33601:SF	Phvul.008G07
13			
14	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SF	Phvul.003G26
15	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
16	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://I	Phvul.008G07
17	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
18	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
19	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
20			
21	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phos	Phvul.009G20
22			
23	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SF	Phvul.005G15
24	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SF	Phvul.005G15
25			
26	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phos	Phvul.009G20
27	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
28	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22PTHR31707:SF	Phvul.009G22
29	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10PF04782 - Pro	Phvul.002G10
30			
31	FASCICLIN-like arabinoogalactan 9	Phvul.005G09PTHR32077:SF	Phvul.005G09
32	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SF	Phvul.003G18
33	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SF	Phvul.003G18
34			
35	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132://I	Phvul.003G12
36	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132://I	Phvul.003G12
37			
38	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - Perc	Phvul.006G07
39	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nucl	Phvul.008G28
40	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SF	Phvul.007G16
41	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680://I	Phvul.001G26
42			
43	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SF	Phvul.006G09
44	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SF	Phvul.006G09
45	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SF	Phvul.003G03
46			
47		0 0 0	Phvul.009G00
48	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799://I	Phvul.003G10
49	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799://I	Phvul.003G10
50			
51	binding	Phvul.002G26PTHR23315:SF	Phvul.002G26
52	binding	Phvul.002G26PTHR23315:SF	Phvul.002G26
53	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA	Phvul.002G29
54	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA	Phvul.002G29
55			
56	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SF	Phvul.007G15
57	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SF	Phvul.002G00
58	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SF	Phvul.002G00
59	cellulose synthase like G1	Phvul.005G00PTHR13301://I	Phvul.005G00
60	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SF	Phvul.002G00



1			
2	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//I	Phvul.008G24
3	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//I	Phvul.007G20
4	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
5	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
6	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
7	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
8	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
9	RING/U-box superfamily protein	Phvul.003G18PTHR22763:Sf	Phvul.003G18
10	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
11	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
12	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//I	Phvul.006G16
13	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
14	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
15	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05
16	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
17	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
18	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05
19	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
20	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:Sf	Phvul.007G15
21	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05
22	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phos	Phvul.002G11
23	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY	Phvul.008G10
24	protein binding	Phvul.008G07PTHR33601:Sf	Phvul.008G07
25	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:Sf	Phvul.003G26
26	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//I	Phvul.008G07
27	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//I	Phvul.008G07
28	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
29	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
30	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
31	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phos	Phvul.009G20
32	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:Sf	Phvul.005G15
33	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:Sf	Phvul.005G15
34	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phos	Phvul.009G20
35	gigantea protein (GI)	Phvul.004G08K12124 - GIG	Phvul.004G08
36	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22PTHR31707:Sf	Phvul.009G22
37	Protein of unknown function (DUF630) ;Protein of unkn	Phvul.002G10PF04782 - Pro	Phvul.002G10
38	FASCICLIN-like arabinoogalactan 9	Phvul.005G09PTHR32077:Sf	Phvul.005G09
39	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:Sf	Phvul.003G18
40	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:Sf	Phvul.003G18
41	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//I	Phvul.003G12
42	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//I	Phvul.003G12
43	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - Perc	Phvul.006G07
44	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nucl	Phvul.008G28
45	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:Sf	Phvul.007G16
46	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//I	Phvul.001G26
47	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:Sf	Phvul.006G09
48	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:Sf	Phvul.006G09
49	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:Sf	Phvul.003G03
50		0	0
51		0	0
52	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//I	Phvul.003G10

1		
2	P-loop containing nucleoside triphosphate hydrolases	sPhvul.003G10PTHR10799//IPhvul.003G10
3	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
4	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
5	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
6	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
7	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SfPhvul.007G15
8	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
9	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
10	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
11	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
12	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
13	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
14	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
15	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
16	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
17	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
18	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
19	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
20	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
21	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
22	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
23	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SfPhvul.003G18
24	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
25	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
26	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
27	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
28	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
29	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
30	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
31	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
32	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
33	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
34	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
35	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
36	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY Phvul.008G10
37	protein binding	Phvul.008G07PTHR33601:SfPhvul.008G07
38	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SfPhvul.003G26
39	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
40	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
41	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
42	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
43	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
44	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
45	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
46	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
47	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
48	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
49	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22PTHR31707:SfPhvul.009G22
50	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10PF04782 - ProPhvul.002G10
51	FASCICLIN-like arabinogalactan 9	Phvul.005G09PTHR32077:SfPhvul.005G09
52	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
53	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
54	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12

1		
2	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
3	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
4	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nuclIPhvul.008G28
5	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SFPhvul.007G16
6	serine hydroxymethyltransferase 4	Phvul.001G26 PTHR11680//IPhvul.001G26
7	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SFPhvul.006G09
8	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SFPhvul.006G09
9	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03 PTHR15245:SFPhvul.003G03
10		0 0 0 Phvul.009G00
11		
12		
13		
14	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10 PTHR10799//IPhvul.003G10
15	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10 PTHR10799//IPhvul.003G10
16	binding	Phvul.002G26 PTHR23315:SFPhvul.002G26
17	binding	Phvul.002G26 PTHR23315:SFPhvul.002G26
18	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA :Phvul.002G29
19	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA :Phvul.002G29
20	phytochrome interacting factor 3-like 5	Phvul.007G15 PTHR12565:SFPhvul.007G15
21	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SFPhvul.002G00
22	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SFPhvul.002G00
23	cellulose synthase like G1	Phvul.005G00 PTHR13301//IPhvul.005G00
24	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SFPhvul.002G00
25	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24 PTHR21493//IPhvul.008G24
26	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20 PTHR11850//IPhvul.007G20
27	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
28	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
29	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
30	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
31	RING/U-box superfamily protein	Phvul.003G18 PTHR22763:SFPhvul.003G18
32	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
33	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
34	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
35	Protein of unknown function (DUF616)	Phvul.006G16 PTHR12956//IPhvul.006G16
36	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
37	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
38	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
39	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
40	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SFPhvul.007G15
41	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
42	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phosPhvul.002G11
43	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY Phvul.008G10
44	protein binding	Phvul.008G07 PTHR33601:SFPhvul.008G07
45	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SFPhvul.003G26
46	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
47	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
48	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
49	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
50	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
51	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20 K01530 - phosPhvul.009G20

1	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SF	Phvul.005G15
2	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SF	Phvul.005G15
3	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phos	Phvul.009G20
4	gigantea protein (GI)	Phvul.004G08 K12124 - GIG	Phvul.004G08
5	Plant invertase/pectin methylesterase inhibitor superfamily	Phvul.009G22 PTHR31707:SF	Phvul.009G22
6	Protein of unknown function (DUF630) ;Protein of unknown function	Phvul.002G10 PF04782 - Pro	Phvul.002G10
7	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SF	Phvul.005G09
8	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SF	Phvul.003G18
9	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SF	Phvul.003G18
10	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132://I	Phvul.003G12
11	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132://I	Phvul.003G12
12	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - Perc	Phvul.006G07
13	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nucl	Phvul.008G28
14	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SF	Phvul.007G16
15	serine hydroxymethyltransferase 4	Phvul.001G26 PTHR11680://I	Phvul.001G26
16	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SF	Phvul.006G09
17	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SF	Phvul.006G09
18	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03 PTHR15245:SF	Phvul.003G03
19		0	0
20		0	0
21	P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10 PTHR10799://I	Phvul.003G10
22	P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10 PTHR10799://I	Phvul.003G10
23	binding	Phvul.002G26 PTHR23315:SF	Phvul.002G26
24	binding	Phvul.002G26 PTHR23315:SF	Phvul.002G26
25	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA	Phvul.002G29
26	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA	Phvul.002G29
27	phytochrome interacting factor 3-like 5	Phvul.007G15 PTHR12565:SF	Phvul.007G15
28	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SF	Phvul.002G00
29	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SF	Phvul.002G00
30	cellulose synthase like G1	Phvul.005G00 PTHR13301://I	Phvul.005G00
31	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SF	Phvul.002G00
32	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24 PTHR21493://I	Phvul.008G24
33	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20 PTHR11850://I	Phvul.007G20
34	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
35	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
36	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
37	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
38	RING/U-box superfamily protein	Phvul.003G18 PTHR22763:SF	Phvul.003G18
39	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
40	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
41	Protein of unknown function (DUF616)	Phvul.006G16 PTHR12956://I	Phvul.006G16
42	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
43	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
44	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05
45	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
46	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SF	Phvul.007G15
47	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - Perc	Phvul.005G05



1		
2	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
3	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY Phvul.008G10
4	protein binding	Phvul.008G07PTHR33601:SfPhvul.008G07
5	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SfPhvul.003G26
6	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
7	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
8	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
9	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
10	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
11	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
12	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
13	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
14	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
15	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
16	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22PTHR31707:SfPhvul.009G22
17	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10PF04782 - Pro Phvul.002G10
18	FASCICLIN-like arabinoogalactan 9	Phvul.005G09PTHR32077:SfPhvul.005G09
19	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
20	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
21	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
22	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
23	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - PercPhvul.006G07
24	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
25	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SfPhvul.007G16
26	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
27	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
28	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
29	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SfPhvul.003G03
30		0 0 0 Phvul.009G00
31	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//IPhvul.003G10
32	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//IPhvul.003G10
33	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
34	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
35	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
36	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
37	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SfPhvul.007G15
38	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
39	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
40	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
41	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
42	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
43	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
44	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
45	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
46	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
47	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
48	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15

1		
2	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SfPhvul.003G18
3	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
4	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
5	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
6	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
7	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
8	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
9	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
10	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
11	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
12	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
13	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
14	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
15	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
16	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY Phvul.008G10
17	protein binding	Phvul.008G07PTHR33601:SfPhvul.008G07
18	protein binding	Phvul.008G07PTHR33601:SfPhvul.008G07
19	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SfPhvul.003G26
20	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
21	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
22	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
23	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
24	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
25	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
26	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
27	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
28	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
29	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
30	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
31	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
32	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
33	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
34	Plant invertase/pectin methylesterase inhibitor superfamily protein	Phvul.009G22PTHR31707:SfPhvul.009G22
35	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10PF04782 - ProPhvul.002G10
36	FASCICLIN-like arabinogalactan 9	Phvul.005G09PTHR32077:SfPhvul.005G09
37	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18PTHR12565:SfPhvul.003G18
38	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18PTHR12565:SfPhvul.003G18
39	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18PTHR12565:SfPhvul.003G18
40	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
41	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
42	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
43	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
44	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
45	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SfPhvul.007G16
46	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SfPhvul.007G16
47	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
48	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
49	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
50	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
51	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SfPhvul.003G03
52		0 0 0 Phvul.009G00
53	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10PTHR10799//IPhvul.003G10
54	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10PTHR10799//IPhvul.003G10
55	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10PTHR10799//IPhvul.003G10
56	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
57	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
58	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
59	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
60	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SfPhvul.007G15



1		
2	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
3	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
4	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
5		
6	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
7	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
8	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
9		
10	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
11	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
12	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
13	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
14	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
15	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SFPhvul.003G18
16	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
17	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
18	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
19	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
20	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
21	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
22	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
23	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
24	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
25	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
26	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
27	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
28	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
29	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY Phvul.008G10
30	protein binding	Phvul.008G07PTHR33601:SFPhvul.008G07
31	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SFPhvul.003G26
32	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
33	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
34	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
35	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
36	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
37	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
38	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
39	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
40	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
41	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
42	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
43	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
44	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
45	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
46	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
47	Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22PTHR31707:SFPhvul.009G22
48	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10PF04782 - ProPhvul.002G10
49	FASCICLIN-like arabinogalactan 9	Phvul.005G09PTHR32077:SFPhvul.005G09
50		
51	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
52	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
53	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
54	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
55	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
56	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
57	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
58	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SFPhvul.007G16
59	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
60	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09

1		
2	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
3	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SfPhvul.003G03
4		0 0 0 Phvul.009G00
5		
6	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//IPhvul.003G10
7	P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10PTHR10799//IPhvul.003G10
8	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
9	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
10	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
11	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA :Phvul.002G29
12	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SfPhvul.007G15
13	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
14	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
15	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
16	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
17	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
18	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
19	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
20	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
21	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
22	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
23	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SfPhvul.003G18
24	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
25	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
26	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
27	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
28	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
29	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
30	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
31	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
32	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
33	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
34	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY Phvul.008G10
35	protein binding	Phvul.008G07PTHR33601:SfPhvul.008G07
36	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SfPhvul.003G26
37	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
38	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155//IPhvul.008G07
39	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
40	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
41	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
42	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
43	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
44	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
45	ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20K01530 - phosPhvul.009G20
46	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
47	Plant invertase/pectin methylesterase inhibitor superf	Phvul.009G22PTHR31707:SfPhvul.009G22
48	Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10PF04782 - ProPhvul.002G10

1		
2	FASCICLIN-like arabinogalactan 9	Phvul.005G09PTHR32077:SFPhvul.005G09
3	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
4	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SFPhvul.003G18
5	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132://IPhvul.003G12
6	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132://IPhvul.003G12
7	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - PercPhvul.006G07
8	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
9	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SFPhvul.007G16
10	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680://IPhvul.001G26
11	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
12	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SFPhvul.006G09
13	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SFPhvul.003G03
14		0 0 0 Phvul.009G00
15	P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10PTHR10799://IPhvul.003G10
16	P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10PTHR10799://IPhvul.003G10
17	binding	Phvul.002G26PTHR23315:SFPhvul.002G26
18	binding	Phvul.002G26PTHR23315:SFPhvul.002G26
19	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
20	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
21	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SFPhvul.007G15
22	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
23	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
24	cellulose synthase like G1	Phvul.005G00PTHR13301://IPhvul.005G00
25	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SFPhvul.002G00
26	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493://IPhvul.008G24
27	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850://IPhvul.007G20
28	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
29	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
30	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
31	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
32	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SFPhvul.003G18
33	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
34	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
35	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956://IPhvul.006G16
36	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
37	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
38	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
39	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
40	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SFPhvul.007G15
41	Peroxidase superfamily protein	Phvul.005G051.11.1.7 - PercPhvul.005G05
42	phosphatidylinositolglycan-related	Phvul.002G11K03858 - phosPhvul.002G11
43	myb-like HTH transcriptional regulator family protein	Phvul.008G10PF14379 - MY Phvul.008G10
44	protein binding	Phvul.008G07PTHR33601:SFPhvul.008G07
45	SAUR-like auxin-responsive protein family	Phvul.003G26PTHR31374:SFPhvul.003G26
46	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://IPhvul.008G07
47	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07PTHR23155://IPhvul.008G07

1		
2	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
3	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
4	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
5	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
6	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
7	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
8	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
9	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SfPhvul.005G15
10	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
11	gigantea protein (GI)	Phvul.004G08K12124 - GIG/Phvul.004G08
12	Plant invertase/pectin methylesterase inhibitor superfamily	Phvul.009G22PTHR31707:SfPhvul.009G22
13	Plant invertase/pectin methylesterase inhibitor superfamily	Phvul.009G22PTHR31707:SfPhvul.009G22
14	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10PF04782 - ProPhvul.002G10
15	FASCICLIN-like arabinogalactan 9	Phvul.005G09PTHR32077:SfPhvul.005G09
16	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
17	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
18	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18PTHR12565:SfPhvul.003G18
19	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
20	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
21	Nucleotide-sugar transporter family protein	Phvul.003G12PTHR11132//IPhvul.003G12
22	Peroxidase superfamily protein	Phvul.006G071.11.1.7 - PercPhvul.006G07
23	Nucleoporin, Nup133/Nup155-like	Phvul.008G28K14300 - nuclPhvul.008G28
24	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SfPhvul.007G16
25	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SfPhvul.007G16
26	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
27	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
28	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
29	homolog of yeast sucrose nonfermenting 4	Phvul.006G09PTHR13780:SfPhvul.006G09
30	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SfPhvul.003G03
31		0 0 0 Phvul.009G00
32	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10PTHR10799//IPhvul.003G10
33	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10PTHR10799//IPhvul.003G10
34	P-loop containing nucleoside triphosphate hydrolases superfamily	Phvul.003G10PTHR10799//IPhvul.003G10
35	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
36	binding	Phvul.002G26PTHR23315:SfPhvul.002G26
37	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
38	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
39	RNA cyclase family protein	Phvul.002G296.5.1.4 - RNA Phvul.002G29
40	phytochrome interacting factor 3-like 5	Phvul.007G15PTHR12565:SfPhvul.007G15
41	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
42	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
43	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
44	cellulose synthase like G1	Phvul.005G00PTHR13301//IPhvul.005G00
45	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
46	RING/U-box superfamily protein	Phvul.002G00PTHR10044:SfPhvul.002G00
47	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24PTHR21493//IPhvul.008G24
48	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20PTHR11850//IPhvul.007G20
49	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
50	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
51	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
52	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
53	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
54	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
55	RING/U-box superfamily protein	Phvul.003G18PTHR22763:SfPhvul.003G18
56	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
57	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
58	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
59	Protein of unknown function (DUF616)	Phvul.006G16PTHR12956//IPhvul.006G16
60	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15
	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15PTHR24320:SfPhvul.007G15



1		
2	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
3	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
4	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
5	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
6	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
7	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phosPhvul.002G11
8	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY Phvul.008G10
9	protein binding	Phvul.008G07 PTHR33601:SfPhvul.008G07
10	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SfPhvul.003G26
11	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
12	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
13	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
14	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
15	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
16	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
17	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
18	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
19	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
20	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
21	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
22	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
23	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
24	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
25	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
26	Plant invertase/pectin methylesterase inhibitor superfamily protein	Phvul.009G22 PTHR31707:SfPhvul.009G22
27	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10 PF04782 - ProPhvul.002G10
28	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SfPhvul.005G09
29	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SfPhvul.005G09
30	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18 PTHR12565:SfPhvul.003G18
31	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18 PTHR12565:SfPhvul.003G18
32	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Phvul.003G18 PTHR12565:SfPhvul.003G18
33	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
34	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
35	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
36	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
37	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nuclPhvul.008G28
38	ubiquitin-protein ligase 4	Phvul.007G16 PTHR11254:SfPhvul.007G16
39	serine hydroxymethyltransferase 4	Phvul.001G26 PTHR11680//IPhvul.001G26
40	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
41	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
42	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
43	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03 PTHR15245:SfPhvul.003G03
44		0 0 0 Phvul.009G00
45	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10 PTHR10799//IPhvul.003G10
46	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10 PTHR10799//IPhvul.003G10
47	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Phvul.003G10 PTHR10799//IPhvul.003G10
48	binding	Phvul.002G26 PTHR23315:SfPhvul.002G26
49	binding	Phvul.002G26 PTHR23315:SfPhvul.002G26
50	binding	Phvul.002G26 PTHR23315:SfPhvul.002G26
51	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
52	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
53	RNA cyclase family protein	Phvul.002G29 6.5.1.4 - RNA Phvul.002G29
54	phytochrome interacting factor 3-like 5	Phvul.007G15 PTHR12565:SfPhvul.007G15
55	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
56	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
57	cellulose synthase like G1	Phvul.005G00 PTHR13301//IPhvul.005G00
58	cellulose synthase like G1	Phvul.005G00 PTHR13301//IPhvul.005G00
59	RING/U-box superfamily protein	Phvul.002G00 PTHR10044:SfPhvul.002G00
60	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24 PTHR21493//IPhvul.008G24
	KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20 PTHR11850//IPhvul.007G20

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2	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
3	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
4	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
5	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
6	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
7	RING/U-box superfamily protein	Phvul.003G18 PTHR22763:SfPhvul.003G18
8	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
9	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
10	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
11	Protein of unknown function (DUF616)	Phvul.006G16 PTHR12956//IPhvul.006G16
12	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
13	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
14	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
15	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
16	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
17	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
18	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15 PTHR24320:SfPhvul.007G15
19	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
20	phosphatidylinositolglycan-related	Phvul.002G11 K03858 - phosPhvul.002G11
21	myb-like HTH transcriptional regulator family protein	Phvul.008G10 PF14379 - MY Phvul.008G10
22	protein binding	Phvul.008G07 PTHR33601:SfPhvul.008G07
23	SAUR-like auxin-responsive protein family	Phvul.003G26 PTHR31374:SfPhvul.003G26
24	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
25	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
26	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
27	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
28	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
29	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
30	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
31	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
32	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
33	gigantea protein (GI)	Phvul.004G08 K12124 - GIG/Phvul.004G08
34	Peroxidase superfamily protein	Phvul.006G07 1.11.1.7 - PercPhvul.006G07
35	Nucleoporin, Nup133/Nup155-like	Phvul.008G28 K14300 - nuclPhvul.008G28
36	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
37	Plant invertase/pectin methylesterase inhibitor superfamily	Phvul.009G22 PTHR31707:SfPhvul.009G22
38	homolog of yeast sucrose nonfermenting 4	Phvul.006G09 PTHR13780:SfPhvul.006G09
39	Protein of unknown function (DUF630) ;Protein of unknown function (DUF630)	Phvul.002G10 PF04782 - ProPhvul.002G10
40	FASCICLIN-like arabinogalactan 9	Phvul.005G09 PTHR32077:SfPhvul.005G09
41	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SfPhvul.003G18
42	basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18 PTHR12565:SfPhvul.003G18
43	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
44	Nucleotide-sugar transporter family protein	Phvul.003G12 PTHR11132//IPhvul.003G12
45	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
46	Peroxidase superfamily protein	Phvul.005G05 1.11.1.7 - PercPhvul.005G05
47	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
48	Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07 PTHR23155//IPhvul.008G07
49	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20 K01530 - phosPhvul.009G20
50	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15
51	Plant regulator RWP-RK family protein	Phvul.005G15 PTHR32002:SfPhvul.005G15



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2	ATPase E1-E2 type family protein / haloacid dehalogenase	Phvul.009G20K01530 - phosPhvul.009G20
3	Plant regulator RWP-RK family protein	Phvul.005G15PTHR32002:SFPhvul.005G15
4	Leucine-rich repeat transmembrane protein kinase family	Phvul.009G112.7.11.1 - NonPhvul.009G11
5	heavy metal atpase 1	Phvul.003G24PTHR24093:SFPhvul.003G24
6	Polynucleotide adenyltransferase family protein	Phvul.002G28PTHR13734:SFPhvul.002G28
7	Polynucleotide adenyltransferase family protein	Phvul.002G28PTHR13734:SFPhvul.002G28
8	Polynucleotide adenyltransferase family protein	Phvul.002G28PTHR13734:SFPhvul.002G28
9	Polynucleotide adenyltransferase family protein	Phvul.002G28PTHR13734:SFPhvul.002G28
10	sucrose phosphate synthase 1F	Phvul.003G17PTHR12526//IPhvul.003G17
11	Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.011G17PF01535//PF1Phvul.011G17
12	dolichol phosphate-mannose biosynthesis regulatory p	Phvul.003G28K09658 - dolichPhvul.003G28
13	ubiquitin-protein ligase 4	Phvul.007G16PTHR11254:SFPhvul.007G16
14	Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03PTHR15245:SFPhvul.003G03
15	serine hydroxymethyltransferase 4	Phvul.001G26PTHR11680//IPhvul.001G26
16	CRINKLY4 related 3	Phvul.001G24PTHR27003:SFPhvul.001G24
17	cation exchanger 1	Phvul.006G06K07300 - Ca2+Phvul.006G06
18	UDP-Glycosyltransferase superfamily protein	Phvul.008G14PTHR11926:SFPhvul.008G14
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1 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip  
2 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip  
3 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip  
4 Cell wall organo caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629  
5 not assigned.ε (original description: pacid=37171837 transcript=Phvul.006G169300.1 locus=Phvul.C  
6 not assigned.r no hits & (original description: pacid=37164135 transcript=Phvul.007G164800.1 locu  
7 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip  
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12 Cell wall organo caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629  
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15 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip  
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17 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip  
18 Cell wall organo caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629  
19 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C  
20 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu  
21 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
22 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C  
23 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu  
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26 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu  
27 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu  
28 Solute transport:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri  
29 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C  
30 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu  
31 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
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51 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
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60 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
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6 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
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12 Solute transp cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri  
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24 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
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41 RNA biosynth transcription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C  
42 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu  
43 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971  
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47 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu  
48 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio  
49 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio  
50 RNA biosynth transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv  
51 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07  
52 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C  
53 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C  
54 Solute transp anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317  
55 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph  
56 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu



1 Solute transp  
2 solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00  
3 Chromatin or $\xi$ chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=  
4 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G  
5 not assigned. $\epsilon$  (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C  
6 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu  
7 RNA biosynth $\xi$ transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph  
8 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu  
9 not assigned. $\epsilon$  (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C  
10 External stim $\xi$ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio  
11 External stim $\xi$ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio  
12 RNA biosynth $\xi$ transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv  
13 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07  
14 not assigned. $\epsilon$  (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C  
15 not assigned. $\epsilon$  (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C  
16 Solute transp  
17 anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317  
18 Amino acid m  
19 serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph  
20 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu  
21 Solute transp  
22 solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00  
23 Chromatin or $\xi$ chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=  
24 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G  
25 not assigned. $\epsilon$  (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C  
26 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu  
27 RNA biosynth $\xi$ transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph  
28 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu  
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49 not assigned.ç (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C  
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16 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
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21 Solute transpc transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009  
22 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
23 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
24 RNA biosynth transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
25 RNA biosynth transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
26 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu  
27 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C  
28 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C  
29 RNA biosynth transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans  
30 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2  
31 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C  
32 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C  
33 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009  
34 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran:  
35 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C  
36 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09  
37 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu  
38 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=  
39 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
40 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
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42 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu  
43 RNA biosynth transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.  
44 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C  
45 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C  
46 RNA biosynth component GRF of GRF-GIF transcriptional complex (original description: pacid=3716



1 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
2 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
3 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
4 Solute transp; Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip  
5 Solute transp; transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009  
6 Cytoskeleton ; microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
7 Cytoskeleton ; microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
8 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
9 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
10 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu  
11 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C  
12 Protein home; pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10  
13 RNA biosynth; transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans  
14 Protein modif; protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2  
15 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C  
16 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C  
17 Cell wall orga; xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009  
18 Solute transp; polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran  
19 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C  
20 Protein home; pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09  
21 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu  
22 Protein biosyr; component RPS3 of SSU proteome (original description: pacid=37164640 transcript=  
23 Protein modif; protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
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25 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu  
26 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu  
27 RNA biosynth; transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.  
28 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C  
29 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C  
30 RNA biosynth; component GRF of GRF-GIF transcriptional complex (original description: pacid=3716  
31 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
32 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
33 Solute transp; Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip  
34 Solute transp; transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009  
35 Cytoskeleton ; microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
36 Cytoskeleton ; microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
37 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
38 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
39 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu  
40 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C  
41 Protein home; pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10  
42 RNA biosynth; transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans  
43 Protein modif; protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2  
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45 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C  
46 Cell wall orga; xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009  
47 Solute transp; polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran

1 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C  
2 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09  
3 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu  
4 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=  
5 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
6 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
7 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu  
8 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu  
9 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.  
10 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C  
11 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C  
12 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716  
13 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
14 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
15 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip  
16 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009  
17 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
18 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
19 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
20 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
21 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu  
22 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C  
23 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10  
24 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans  
25 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2  
26 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C  
27 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C  
28 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009  
29 Solute transpcpolyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran  
30 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C  
31 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09  
32 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu  
33 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=  
34 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
35 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
36 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu  
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38 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.  
39 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C  
40 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C  
41 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716  
42 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
43 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
44 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip  
45 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009  
46 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript

1 Cytoskeleton (microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
2 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
3 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
4 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu  
5 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C  
6 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C  
7 RNA biosynthetranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans  
8 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G  
9 RNA biosynthetranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.  
10 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran  
11 Cytoskeleton (microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript  
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14 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C  
15 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C  
16 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009  
17 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09  
18 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu  
19 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G  
20 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37151  
21 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37151  
22 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu  
23 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu  
24 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C  
25 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=  
26 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
27 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G  
28 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C  
29 RNA biosynthecomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716  
30 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
31 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra  
32 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C  
33 Solute transpc Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip  
34 Solute transpc transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009  
35 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
36 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C  
37 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu  
38 Protein modif protein kinase (LRR-III) (original description: pacid=37166830 transcript=Phvul.007G  
39 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip  
40 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C  
41 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t  
42 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip  
43 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu  
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45 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C  
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1 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0  
2 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu  
3 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu  
4 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=  
5 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu  
6 Protein transl subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip  
7 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998  
8 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu  
9 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q  
10 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q  
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15 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006  
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17 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714  
18 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714  
19 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv  
20 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv  
21 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714  
22 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6\_catro : 434.0) &  
23 Solute transp organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph  
24 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl  
25 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl  
26 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G0  
27 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip  
28 not assigned.a (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C  
29 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 i  
30 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip  
31 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu  
32 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu  
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35 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0  
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37 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu  
38 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=  
39 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu  
40 Protein transl subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip  
41 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998  
42 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu  
43 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q  
44 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q  
45 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C  
46 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu

1 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu  
2 RNA biosynthcomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ  
3 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006  
4 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C  
5 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714  
6 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714  
7 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv  
8 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv  
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10 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6\_catro : 434.0) &  
11 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph  
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15 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip  
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18 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip  
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22 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C  
23 Redox homeo type-2 peroxidoredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0  
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28 Protein translsunit alpha of co-translational insertion system Sec61 subcomplex (original descrip  
29 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998ε  
30 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu  
31 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε  
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33 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C  
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46 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio  
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29 Solute transpP4-type ATPase component ALA of phospholipid flippase complex (original descriptio  
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41 v.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &  
42 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)  
43 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &  
44 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {  
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46 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2  
47 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)  
48 v.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &  
49 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)  
50 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai  
51 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500  
52 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500  
53 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &  
54 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &  
55 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro  
56 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei  
57 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers  
58 v.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &  
59 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)  
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009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2



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2     js=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)  
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4     js=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)  
5     011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai  
6     n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500  
7     n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500  
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9     011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai  
10     011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro  
11     008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei  
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13     .002G073200.1 locus=Phvul.002G073200 ID=Phvul.002G073200.1.v2.1 annot-version=v2.1) &  
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16     ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &  
17     js=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)  
18     01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &  
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21     009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2  
22     004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol  
23     002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
24     G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &  
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27     93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &  
28     il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &  
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30     ;037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
31     ;037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
32     js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)  
33     js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)  
34     .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &  
35     008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39  
36     005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=  
37     59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno  
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40     pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1  
41     9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &  
42     t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
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44     010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
45     010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
46     js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)

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3 transcript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v  
4 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &  
5 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol  
6 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
7 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &  
8 transcript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v  
9 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C  
10 093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &  
11 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &  
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17 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &  
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19 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=  
20 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno  
21 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version  
22 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version  
23 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1  
24 09G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &  
25 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
26 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
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28 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
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30 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana  
31 005200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &  
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34 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol  
35 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
36 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &  
37 transcript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v  
38 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C  
39 093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &  
40 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &  
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42 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
43 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
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45 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)  
46 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &



1 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39  
2 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=  
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6 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1  
7 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &  
8 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1) &  
9 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
10 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
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13 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar  
14 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &  
15 nscript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v  
16 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &  
17 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol  
18 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
19 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &  
20 nscript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=  
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22 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &  
23 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &  
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31 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=  
32 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno  
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41 s=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)  
42 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar  
43 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &  
44 nscript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v  
45 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &  
46 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol

1 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
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4 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (  
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12 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno  
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25 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &  
26 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol  
27 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
28 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &  
29 nscript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=  
30 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C  
31 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &  
32 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &  
33 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &  
34 :037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
35 :037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
36 :s=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)  
37 :s=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)  
38 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &  
39 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39  
40 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=  
41 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno  
42 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version  
43 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version  
44 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1  
45 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &  
46 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)

1 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
2 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
3 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
4 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)  
5 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana  
6 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &  
7 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v  
8 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &  
9 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &  
10 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v  
11 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
12 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)  
13 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C  
14 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol  
15 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p  
16 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &  
17 093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &  
18 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &  
19 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &  
20 1870 transcript=Phvul.009G121200.2 locus=Phvul.009G121200 ID=Phvul.009G121200.2.v2.1 annot-  
21 1870 transcript=Phvul.009G121200.2 locus=Phvul.009G121200 ID=Phvul.009G121200.2.v2.1 annot-  
22 us=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)  
23 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)  
24 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39  
25 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &  
26 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &  
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28 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=  
29 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno  
30 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version  
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32 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &  
33 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1  
34 09G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &  
35 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
36 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &  
37 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)  
38 029900.1 locus=Phvul.007G029900 ID=Phvul.007G029900.1.v2.1 annot-version=v2.1) &  
39 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
40 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
41 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
42 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
43 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
44 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
45 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
46 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas



1 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
2 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
3 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
4 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
5 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
6 tion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1  
7 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
8 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
9 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
10 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
11 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
12 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
13 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
14 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0  
15 06G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &  
16 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
17 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
18 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
19 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
20 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
21 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
22 t Enzyme classification.EC\_1 oxidoreductases.EC\_1.14 oxidoreductase acting on paired donor with in  
23 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
24 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
25 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
26 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
27 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
28 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
29 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
30 tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
31 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
32 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
33 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
34 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
35 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
36 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
37 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
38 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
39 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
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41 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
42 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
43 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
44 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
45 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
46 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)





1 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
2  
3 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
4 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
5 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (  
6 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
7 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
8 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
9 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
10 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
11 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase  
12 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
13 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
14 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
15 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
16 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
17 on: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166  
18 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
19 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
20 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
21 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
22 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
23 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
24 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
25 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0  
26 05G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &  
27 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
28 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
29 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
30 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
31 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
32 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
33 t, Enzyme classification.EC\_1 oxidoreductases.EC\_1.14 oxidoreductase acting on paired donor with i  
34 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
35 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
36 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
37 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
38 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
39 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (  
40 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
41 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
42 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
43 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
44 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
45 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase  
46 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
47 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
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49  
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1  
2 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
3 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
4 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
5  
6 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166  
7 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
8  
9 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
10  
11 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
12 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
13 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
14 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
15 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
16 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0  
17 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &  
18 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
19 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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26 t Enzyme classification.EC\_1 oxidoreductases.EC\_1.14 oxidoreductase acting on paired donor with i  
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29 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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34 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
35 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
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42 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
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53  
54 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
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56 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
57 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
58 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
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60 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
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4 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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13 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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16 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
17 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
18 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
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22 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
23 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
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30 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
31 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
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38 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
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45 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
46 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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48 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &

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3 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
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6 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
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8 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
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13 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
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15 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
16 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
17 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
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24 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
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37 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
38 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
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40 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
41 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
42 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
43 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
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46 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &



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5 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
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7 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
8 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
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16 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
17 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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24 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
25 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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27 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
28 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
29 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
30 otion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
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32 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
33 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
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35 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
36 js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
37 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
38 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
39 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
40 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1  
41 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
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43 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
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45 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
46 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
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50 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

1 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
2 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
3 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
4 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
5 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
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8 ul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
9 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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11 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
12 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
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17 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
18 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
19 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
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22 us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
23 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
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27 us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
28 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
29 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
30 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
31 us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
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35 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
36 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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42 ul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
43 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
44 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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46 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
47 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C



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2 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
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6 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
7 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
8 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
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14 200.1.v2.1 annot-version=v2.1) & transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
15 us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
16 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
17 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
18 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
19 us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
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22 006G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &  
23 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
24 003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
25 003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
26 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
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28 003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
29 t Enzyme classification.EC\_1 oxidoreductases.EC\_1.14 oxidoreductase acting on paired donor with in  
30 ul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
31 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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34 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
35 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
36 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
37 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
38 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
39 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
40 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
41 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
42 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
43 us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
44 us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
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46 us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
47 option: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166

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2 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
3 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
4 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
5 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
6 J7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
7 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
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12 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
13 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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17 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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19 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
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21 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
22 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
23 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
24 J09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
25 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
26 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
27 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
28 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
29 J03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
30 J09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase  
31 J04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
32 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
33 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
34 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
35 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
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37 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
38 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
39 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
40 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
41 J7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
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46 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
47 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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7 Phvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
8 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
9 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
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11 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
12 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
13 Phvul.009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
14 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
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18 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
19 Phvul.003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
20 Phvul.009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase  
21 Phvul.004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
22 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
23 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
24 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
25 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
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29 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver  
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31 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)  
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33 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
34 3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
35 Phvul.007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &  
36 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)  
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42 Phvul.005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
43 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
44 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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46 Phvul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
47 Phvul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &  
48 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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50 t; Enzyme classification.EC\_1 oxidoreductases.EC\_1.14 oxidoreductase acting on paired donor with i  
51 Phvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &  
52 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
53 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)  
54  
55 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &  
56 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)  
57 Phvul.009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
58 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi  
59 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079  
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3 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)  
4 J03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi  
5 J09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas  
6 J04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &  
7 js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)  
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9 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)  
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11 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &  
12 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)  
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28 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno  
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60 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)



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3edl4|y1154\_arath : 415.0) & Enzyme classification.EC\_2 transferases.EC\_2.7 transferase transferri  
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 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis  
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 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho  
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 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1  
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 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
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7 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &  
8 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
9 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1  
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11 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &  
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35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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7 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis  
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1 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote  
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 12 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C  
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47 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabid

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34 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
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40 008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)  
41 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50  
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27 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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30 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
31 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1  
32 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
33 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
34 us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)  
35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
36 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
37 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
38 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
39 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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41 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168  
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44 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50  
45 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote  
46 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

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3 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300  
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6 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &  
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8 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600  
9 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300  
10 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &  
11 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (  
12 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1  
13 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &  
14 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &  
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16 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &  
17 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis  
18 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an  
19 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1  
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21 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;  
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37 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &  
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41 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
42 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1  
43 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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1 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
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8 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50  
9 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote  
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19 022600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &  
20 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (  
21 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1  
22 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &  
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24 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &  
25 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &  
26 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis  
27 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an  
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32 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio  
33 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &  
34 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {  
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38 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase  
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43 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1  
44 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabid  
45 js=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)  
46 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

1 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
2 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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11 006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)  
12 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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14 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
15 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
16 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
17 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32  
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19 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168  
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21 008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)  
22 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50  
23 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote  
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33 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis  
34 008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an  
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37 n: pacid=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;  
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39 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1  
40 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &  
41 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &  
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43 003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) ;  
44 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
45 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid  
46 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote  
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7 rs=Phvul.002G283000 ID=Phvul.002G283000.4.v2.1 annot-version=v2.1)  
8 rs=Phvul.002G283000 ID=Phvul.002G283000.4.v2.1 annot-version=v2.1)  
9 .003G170100.1 locus=Phvul.003G170100 ID=Phvul.003G170100.1.v2.1 annot-version=v2.1) &  
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52 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25\_arath : 146.0)  
53 ion=v2.1) &  
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26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq\_arath : 910.0)

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6 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591\_arath : 1384.0)  
7 0.2.v2.1 annot-version=v2.1) &  
8 0.2.v2.1 annot-version=v2.1) &  
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11 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591\_arath : 1384.0)  
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14 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7\_arath : 356.0)  
15 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25\_arath : 146.0)  
16 iion=v2.1) &  
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28 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq\_arath : 910.0)  
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30 rprotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5\_arath : 201.0)  
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47 98|rrt1\_arath : 178.0)  
48 =Arabidopsis thaliana (sp|q9lsz0|apo4\_arath : 369.0)  
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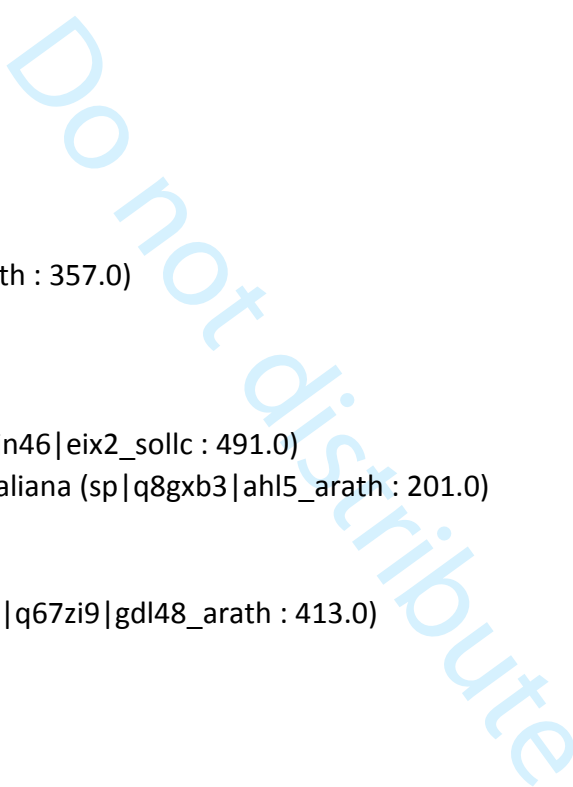
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53 OS=Arabidopsis thaliana (sp|q93yu8|nrg2\_arath : 155.0)  
54 ion=v2.1) &  
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60 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341\_arath : 1019.0)  
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13 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph  
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34 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32\_pea : 207.0)  
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38 OS=Gossypium hirsutum (sp|p0ch30|ring1\_goshi : 103.0)  
39 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32\_pea : 207.0)  
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47 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32\_pea : 207.0)  
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 46 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32\_pea : 207.0)  
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13 3G283500 ID=Phvul.003G283500.1.v2.1 annot-version=v2.1) &

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**Supplementary Table 4:** Primers used for qPCR experiments

<b>cDNA</b>	<b>Gene reference no.</b>	<b>Function</b>	<b>Primer sequence</b>
UBI	CV543388	Ubiquitin	GAGGATGGTCGCACCCTGGCT CCCTCCTTGTCTGAATCTTA
EF1- $\alpha$	GI151368189	Elongation factor 1 $\alpha$	CAAGGATCTCAAGCGTGGTTTCG TGGGAGGTGTGGCAATCAAGC
WRK72	Phvul.003G068700	WRKY72 TF	CCATTCCTGGGGCATCTTTG TGATTGCTTTGGTTGCAGCT