Targeted mRNA oxidation regulates sunflower seed dormancy alleviation during dry after-ripening

Jeremie Bazin, Nicolas Langlade, Patrick P. Vincourt, Sandrine Arribat, Sandrine Balzergue, Hayat El-Maarouf-Bouteau, Christophe Bailly

To cite this version:

Jeremie Bazin, Nicolas Langlade, Patrick P. Vincourt, Sandrine Arribat, Sandrine Balzergue, et al.. Targeted mRNA oxidation regulates sunflower seed dormancy alleviation during dry after-ripening. The Plant cell, 2011, 23 (6), pp.2196-2208. 10.1105/tpc.111.086694 . hal-02652604

HAL Id: hal-02652604
https://hal.inrae.fr/hal-02652604v1

Submitted on 29 May 2020

Supplemental Data. Bazin et al. (2011). Plant Cell 10.1105/tpc.111

Supplemental Dataset 1. Microarray data showing differentially oxidized tr

Gene set of differentially oxidized transcripts among dormant (Dox) and non-dormant (NDox) arra
Columns show Affymetrix probe set ID (A and B), AGI code for each probe set (C), best BLAST
Log2 intensity ratio Dox/NDox (I), P-value of the corresponding Bonferroni test (J).

Gene		AGI code
HuAJ412623	Heli084312_x_st	
HuAJ539665	Heli051458_st	IPR001128:Cytochrome P450
HuAJ539777	Heli028589_st	IPR004265:Plant disease resistance response pr
HuAJ539857	Heli050180_st	IPR010683:Protein of unknown function DUF126
HuAJ539963	Heli029605_st	
HuAJ541254	Heli031562_st	
HuAJ541589	Heli052313_st	
HuAJ827844	Heli054040_st	
HuBQ909276	Heli035946_st	IPR003821:1-deoxy-D-xylulose 5-phosphate redu
HuBQ909346	Heli055535_st	
HuBQ911112	Heli050393_st	IPR005804:Fatty acid desaturase, type 1
HuBQ912010	Heli046157_st	
HuBQ912781	Heli011004_st	IPR002672:Ribosomal protein L28e
HuBQ912783	Heli049518_st	IPR001752:Kinesin, motor region
HuBQ913099	Heli004956_x_st	IPR010987:Glutathione S-transferase, C-terminal
HuBQ913694	Heli078760_st	Unknown Protein
HuBQ913873	Heli017391_st	IPR000347:Plant metallothionein, family 15
HuBQ914329	Heli029672_st	IPR011009:Protein kinase-like
HuBQ914424	Heli034012_st	IPR004993:GH3 auxin-responsive promoter
HuBQ915430	Heli050995_st	
HuBQ917096	Heli033728_st	IPR015414:SNARE associated Golgi protein
HuBQ917214	Heli044162_st	IPR001128:Cytochrome P450
HuBQ966288	Heli052851_st	IPR002085:Alcohol dehydrogenase superfamily,
HuBQ966869	Heli050698_st	IPR007114:Major facilitator superfamily
HuBQ967737	Heli052110_st	
HuBQ968258	Heli048630_st	IPR001878:Zinc finger, CCHC-type
HuBQ971026	Heli032354_st	IPR000266:Ribosomal protein S17
HuBQ971297	Heli045795_st	IPR015706:RNA-directed DNA polymerase (rever
HuBQ971814	Heli030058_x_st	IPR001806:Ras GTPase
HuBQ972080	Heli055676_st	IPR011009:Protein kinase-like
HuBQ972117	Heli037119_st	IPR011009:Protein kinase-like
HuBQ972132	Heli035305_st	
HuBQ973138	Heli044681_x_st	
HuBQ974239	Heli048759_st	
HuBQ975625	Heli049597_st	IPR001128:Cytochrome P450
HuBQ976517	Heli072152_st	
HuBQ976635	Heli055652_st	IPR001757:ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/
HuBQ976959	Heli029319_x_st	IPR002198:Short-chain dehydrogenase/reductas
HuBQ977592	Heli051140_st	IPR008480:Protein of unknown function DUF761,
HuBQ977974	Heli042892_st	IPR015947:PUA-like
HuBQ977996	Heli053515_st	
HuBQ978521	Heli051822_st	
HuBU015901	Heli028859_st	IPR003883:Extensin-like protein
HuBU018106	Heli045595_st	IPR004240:Nonaspanin (TM9SF)
HuBU021058	Heli002578_x_st	IPR000528:Plant lipid transfer protein/Par allerge
HuBU021463	Heli049222_st	IPR001993:Mitochondrial substrate carrier
HuBU021545	Heli054724_x_st	
HuBU021566	Heli027313_st	IPR001344:Chlorophyll A-B binding protein
HuBU021936	Heli002765_x_st	IPR000528:Plant lipid transfer protein/Par allerge

HuBU024381	Heli002606_x_st	IPR000528:Plant lipid transfer protein/Par allerge
HuBU025426	Heli053878_st	IPR001128:Cytochrome P450
HuBU026042	Heli064004_st	
HuBU026138	Heli052618_st	
HuBU027143	Heli040546_st	IPR011084:DNA repair metallo-beta-lactamase
HuBU027455	Heli015269_st	IPR000136:Oleosin
HuBU028230	Heli039952_st	IPR011009:Protein kinase-like
HuBU028730	Heli049602_st	IPR001128:Cytochrome P450
HuBU030479	Heli037273_st	IPR000846:Dihydrodipicolinate reductase
HuBU031891	Heli042260_x_st	IPR011992:EF-Hand type
HuBU036198	Heli047898_st	
HuBU036482	Heli042963_st	
HuCD846190	Heli029523_st	IPR015706:RNA-directed DNA polymerase (rever
HuCD849310	Heli002795_st	IPR000077:Ribosomal protein L39e
HuCD849720	Heli018381_st	
HuCD852613	Heli002799_x_st	IPR000077:Ribosomal protein L39e
HuCD852698	Heli049378_st	IPR001128:Cytochrome P450
HuCD853647	Heli007511_x_st	IPR003612:Plant lipid transfer protein/seed stora
HuCD854396	Heli029606_st	IPR015157:Translation machinery associated TM
HuCD854414	Heli034353_st	IPR001892:Ribosomal protein S13
HuCD857474	Heli086244_st	Unknown Protein
HuCL00001C046	Heli009077_x_st	IPR013128:Peptidase C1A, papain
HuCL00001C087	Heli001459_x_st	IPR000916:Bet v I allergen
HuCL00001C098	Heli026075_x_st	IPR003612:Plant lipid transfer protein/seed stora
HuCL00001C290	Heli001487_st	IPR000916:Bet v I allergen
HuCL00001C303	Heli013051_st	
HuCL00001C390	Heli055067_st	
HuCL00001C420	Heli058013_x_st	
HuCL00001C425	Heli012496_x_st	IPR015659:Proline oxidase
HuCL00001C444	Heli005077_x_st	IPR001106:Phenylalanine/histidine ammonia-lyas
HuCL00001C497	Heli021774_st	IPR000136:Oleosin
HuCL00001C529	Heli000051_x_st	IPR001106:Phenylalanine/histidine ammonia-lyas
HuCL00001C548	Heli059313_st	IPR007186:Plant invertase/pectin methylesterase
HuCL00001C624	Heli006139_st	IPR011008:Dimeric alpha-beta barrel
HuCL00001C636	Heli009071_x_st	IPR013128:Peptidase C1A, papain
HuCL00001C821	Heli025044_st	IPR001938:Thaumatin, pathogenesis-related
HuCL00001C830	Heli055295_x_st	
HuCL00001C866	Heli012623_x_st	IPR003607:Metal-dependent phosphohydrolase,
HuCL00003C003	Heli031805_x_st	IPR006426:Asparagine synthase, glutamine-hydr
HuCL00003C004	Heli060118_st	
HuCL00003C007	Heli000151_x_st	IPR006426:Asparagine synthase, glutamine-hydr
HuCL00040C004	Heli006005_st	IPR006044:11-S plant seed storage protein
HuCL00042C002	Heli004077_x_st	IPR004038:Ribosomal protein L7Ae/L30e/S12e/G
HuCL00046C001	Heli002824_st	IPR000484:Photosynthetic reaction centre, L and
HuCL00074C003	Heli006670_x_st	IPR013770:Plant lipid transfer protein and hydrop
HuCL00078C001	Heli003016_x_st	IPR001395:Aldo/keto reductase
HuCL00091C003	Heli009262_x_st	IPR001128:Cytochrome P450
HuCL00100C004	Heli050828_st	
HuCL00136C001	Heli003028_x_st	IPR002198:Short-chain dehydrogenase/reductase
HuCL00146C001	Heli000544_x_st	IPR005804:Fatty acid desaturase, type 1
HuCL00146C002	Heli000467_x_st	IPR005804:Fatty acid desaturase, type 1
HuCL00146C005	Heli000532_x_st	IPR005804:Fatty acid desaturase, type 1
HuCL00146C008	Heli000548_x_st	IPR005804:Fatty acid desaturase, type 1
HuCL00176C002	Heli045692_x_st	
HuCL00191C002	Heli000369_st	IPR004809:Glutamine synthetase type I
HuCL00219C003	Heli007215_x_st	IPR014746:Glutamine synthetase/guanido kinase
HuCL00241C011	Heli056501_x_st	

HuCL00259C002	Heli048512_st	IPR008985:Concanavalin A-like lectin/glucanase
HuCL00339C002	Heli009385_st	
HuCL00347C001	Heli029963_x_st	IPR005819:Histone H5
HuCL00377C001	Heli009174_x_st	IPR015891:Cyclophilin-like
HuCL00384C002	Heli003793_st	IPR000308:14-3-3 protein
HuCL00395C001	Heli006554_st	IPR004809:Glutamine synthetase type I
HuCL00395C003	Heli025576_x_st	IPR014746:Glutamine synthetase/guanido kinase
HuCL00406C001	Heli000571_st	IPR005804:Fatty acid desaturase, type 1
HuCL00421C003	Heli010179_st	
HuCL00421C004	Heli027739_st	
HuCL00442C001	Heli014910_x_st	IPR012020:AB-hydrolase YheT, putative
HuCL00480C002	Heli006910_st	IPR005132:Rare lipoprotein A
HuCL00510C005	Heli030998_st	IPR007114:Major facilitator superfamily
HuCL00552C001	Heli000675_st	IPR000092:Polyprenyl synthetase
HuCL00598C002	Heli004659_st	IPR006183:6-phosphogluconate dehydrogenase
HuCL00695C001	Heli010602_st	IPR002528:Multi antimicrobial extrusion protein
HuCL00701C001	Heli037941_st	IPR007114:Major facilitator superfamily
HuCL00701C002	Heli007098_st	IPR003663:Sugar transporter
HuCL00722C002	Heli059407_st	Unknown Protein
HuCL00741C001	Heli009179_st	IPR001179:Peptidyl-prolyl cis-trans isomerase, F
HuCL00753C003	Heli001603_x_st	IPR010987:Glutathione S-transferase, C-terminal
HuCL00761C001	Heli005482_st	IPR008354:Bacterial glucose-fructose oxidoreduc
HuCL00791C002	Heli060140_st	
HuCL00815C001	Heli000468_st	IPR005804:Fatty acid desaturase, type 1
HuCL00852C001	Heli009807_x_st	IPR001564:Nucleoside diphosphate kinase, core
HuCL00859C003	Heli003020_x_st	IPR002085:Alcohol dehydrogenase superfamily,
HuCL00974C001	Heli000019_x_st	IPR003593:AAA+ ATPase, core
HuCL00974C002	Heli055842_x_st	
HuCL01009C001	Heli006393_st	IPR001251:Cellular retinaldehyde-binding/triple f
HuCL01023C003	Heli003464_st	IPR003441:No apical meristem (NAM) protein
HuCL01049C002	Heli008064_st	IPR001395:Aldo/keto reductase
HuCL01146C001	Heli005390_st	IPR010255:Haem peroxidase
HuCL01168C001	Heli008919_st	IPR000741:Fructose-bisphosphate aldolase, clas
HuCL01188C001	Heli000663_st	IPR008030:NmrA-like
HuCL01200C001	Heli000892_x_st	
HuCL01208C001	Heli027171_x_st	IPR001030:Aconitase/3-isopropylmalate dehydrat
HuCL01208C003	Heli031810_st	IPR006251:Homoaconitase/3-isopropylmalate de
HuCL01240C001	Heli006961_x_st	IPR001128:Cytochrome P450
HuCL01320C001	Heli009090_st	IPR000073:Alpha/beta hydrolase fold-1
HuCL01383C001	Heli008233_st	IPR006094:FAD linked oxidase, N-terminal
HuCL01383C002	Heli043337_st	IPR012951:Berberine/berberine-like
HuCL01439C001	Heli003314_st	IPR013921:TATA-binding related factor
HuCL01764C002	Heli059327_st	
HuCL01793C001	Heli000121_st	IPR001023:Heat shock protein Hsp70
HuCL01890C002	Heli010180_x_st	IPR002528:Multi antimicrobial extrusion protein
HuCL01891C001	Heli042212_st	IPR000873:AMP-dependent synthetase and ligas
HuCL02086C001	Heli007410_st	IPR005132:Rare lipoprotein A
HuCL02221C001	Heli007795_st	IPR000473:Ribosomal protein L36
HuCL02264C001	Heli008168_st	IPR001461:Peptidase A1
HuCL02340C001	Heli010337_st	IPR001128:Cytochrome P450
HuCL02362C001	Heli005915_x_st	IPR007114:Major facilitator superfamily
HuCL02387C001	Heli006867_st	IPR001509:NAD-dependent epimerase/dehydrat
HuAJ412616	Heli043523_st	IPR001464:Annexin
HuCL02514C001	Heli008176_st	IPR013657:UAA transporter
HuCL02608C004	Heli059509_st	
HuCL02614C001	Heli000033_st	IPR004147:ABC-1
HuCL02666C001	Heli004667_x_st	IPR000301:CD9/CD37/CD63 antigen

HuCL02671C001	Heli003794_st	IPR005804:Fatty acid desaturase, type 1
HuCL02782C001	Heli011118_st	IPR005804:Fatty acid desaturase, type 1
HuCL02799C001	Heli006895_st	IPR001063:Ribosomal protein L22/L17
HuCL02813C001	Heli004730_st	IPR000109:TGF-beta receptor, type I/II extracellul
HuCL02835C001	Heli024267_st	IPR000915:Ribosomal protein L6E
HuCL02850C001	Heli010656_st	IPR000136:Oleosin
HuCL02924C001	Heli000341_st	IPR001128:Cytochrome P450
HuCL03008C002	Heli036518_st	IPR002085:Alcohol dehydrogenase superfamily, z
HuCL03103C001	Heli013772_st	IPR003340:Transcriptional factor B3
HuCL03419C001	Heli000574_st	IPR003657:DNA-binding WRKY
HuCL03507C001	Heli016404_st	IPR006590:RNA polymerase II, Rpb4, core
HuCL03612C001	Heli028185_st	IPR001128:Cytochrome P450
HuCL03632C001	Heli012607_st	IPR001757:ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/C
HuCL03969C001	Heli012625_st	IPR001938:Thaumatin, pathogenesis-related
HuCL03990C001	Heli056297_x_st	
HuCL04046C001	Heli006559_x_st	IPR005123:2OG-Fe(II) oxygenase
HuCL04063C001	Heli020652_x_st	IPR001106:Phenylalanine/histidine ammonia-lyas
HuCL04258C001	Heli010077_st	IPR009743:Hs1pro-1, C-terminal
HuCL04259C002	Heli005048_st	IPR001848:Ribosomal protein S10
HuCL04294C001	Heli010750_st	IPR005477:Deoxyxylulose-5-phosphate synthase
HuCL04298C001	Heli005655_st	IPR012392:Very-long-chain 3-ketoacyl-CoA synth
HuCL04300C002	Heli022176_st	
HuCL04453C001	Heli027537_st	IPR011009:Protein kinase-like
HuCL04689C001	Heli027539_st	IPR011051:Cupin, RmlC-type
HuCL04692C001	Heli006706_st	IPR003663:Sugar transporter
HuCL04738C001	Heli014977_st	
HuCL04739C001	Heli003467_st	IPR002085:Alcohol dehydrogenase superfamily, z
HuCL04770C001	Heli003600_st	IPR003480:Transferase
HuCL04825C001	Heli007876_st	IPR005150:Cellulose synthase
HuCL04865C001	Heli007046_st	IPR004843:Metallophosphoesterase
HuCL05007C001	Heli012645_st	IPR001862:Membrane attack complex componen
HuCL05096C001	Heli003446_x_st	IPR013216:Methyltransferase type 11
HuCL05257C001	Heli005580_st	IPR002946:Intracellular chloride channel
HuCL05288C001	Heli015325_st	IPR003106:Leucine zipper, homeobox-associated
HuCL05425C001	Heli008741_st	IPR006094:FAD linked oxidase, N-terminal
HuCL05495C001	Heli009761_st	IPR001853:DSBA oxidoreductase
HuCL05793C001	Heli004259_st	IPR002213:UDP-glucuronosyl/UDP-glucosyltrans
HuCL05870C002	Heli027786_st	IPR002213:UDP-glucuronosyl/UDP-glucosyltrans
HuCL05947C001	Heli005249_st	IPR002198:Short-chain dehydrogenase/reductase
HuCL05959C001	Heli009626_x_st	IPR001087:Lipolytic enzyme, G-D-S-L
HuCL05991C002	Heli006143_st	IPR001349:Cytochrome c oxidase, subunit VIa
HuCL06193C001	Heli009006_st	IPR005828:General substrate transporter
HuCL06197C001	Heli010548_st	IPR004827:Basic-leucine zipper (bZIP) transcripti
HuCL06529C001	Heli059967_st	
HuCL06706C001	Heli014130_st	IPR002086:
HuCL06854C001	Heli004678_st	IPR002946:Intracellular chloride channel
HuCL06855C001	Heli037030_st	IPR007650:Protein of unknown function DUF581
HuCL06973C001	Heli025196_st	
HuCL07004C001	Heli006552_st	IPR003726:Homocysteine S-methyltransferase
HuCL07092C001	Heli021634_st	IPR001128:Cytochrome P450
HuCL07400C001	Heli035513_st	IPR003656:Zinc finger, BED-type predicted
HuCL07459C001	Heli059028_st	
HuCL07672C002	Heli011459_st	IPR004843:Metallophosphoesterase
HuCL07795C001	Heli007188_st	IPR002198:Short-chain dehydrogenase/reductase
HuCL07815C001	Heli006796_st	IPR003480:Transferase
HuCL07844C001	Heli019720_st	IPR013090:Phospholipase A2, active site
HuCL07863C001	Heli000586_st	IPR002085:Alcohol dehydrogenase superfamily, z

HuCL07937C001	Heli052576_st	IPR001709:Flavoprotein pyridine nucleotide cytoc
HuCL08087C001	Heli058989_st	IPR005050:Early nodulin 93 ENOD93 protein
HuCL08178C002	Heli033801_x_st	IPR013083:Zinc finger, RING/FYVE/PHD-type
HuCL08219C001	Heli024260_st	IPR002213:UDP-glucuronosyl/UDP-glucosyltrans
HuCL08399C001	Heli005500_st	IPR007273:SCAMP
HuCL08462C001	Heli012547_st	IPR001128:Cytochrome P450
HuCL08567C001	Heli008977_st	
HuCL08591C001	Heli012473_st	
HuCL08618C001	Heli022437_st	IPR003311:AUX/IAA protein
HuCL08694C001	Heli007541_st	IPR011230:Phosphoesterase At2g46880
HuCL08712C001	Heli027635_st	IPR000873:AMP-dependent synthetase and ligas
HuCL08761C001	Heli059534_st	
HuCL08893C001	Heli001767_st	
HuCL09064C001	Heli011107_st	IPR007114:Major facilitator superfamily
HuCL09187C001	Heli030475_st	IPR013057:Amino acid transporter, transmembra
HuCL09248C001	Heli035049_st	IPR001734:Na+/solute symporter
HuCL09288C001	Heli020461_st	IPR013128:Peptidase C1A, papain
HuCL09313C001	Heli051275_st	
HuCL09324C001	Heli006713_st	IPR013057:Amino acid transporter, transmembra
HuCL09620C001	Heli014007_st	IPR011009:Protein kinase-like
HuCL09645C001	Heli007348_st	IPR000073:Alpha/beta hydrolase fold-1
HuCL09884C001	Heli003104_st	IPR001128:Cytochrome P450
HuCL09896C001	Heli007560_st	
HuCL09981C001	Heli001312_st	IPR001806:Ras GTPase
HuCL10352C002	Heli059763_st	
HuCL10582C001	Heli022208_st	IPR013601:FAE1/Type III polyketide synthase-lik
HuCL10608C001	Heli019183_st	IPR002528:Multi antimicrobial extrusion protein
HuCL10742C001	Heli022507_st	IPR001902:Sulphate anion transporter
HuCL10757C001	Heli009851_st	IPR011991:Winged helix repressor DNA-binding
HuCL11043C001	Heli011735_st	IPR000537:UbiA prenyltransferase
HuCL11279C001	Heli017131_st	IPR001395:Aldo/keto reductase
HuCL11373C001	Heli014774_st	IPR000109:TGF-beta receptor, type I/II extracellu
HuCL11402C001	Heli028879_st	IPR013057:Amino acid transporter, transmembra
HuCL11558C001	Heli003532_st	
HuCL11673C001	Heli049233_st	IPR007185:DNA polymerase epsilon subunit B
HuCL11938C001	Heli060020_st	
HuCL12044C001	Heli001973_st	
HuCL12142C001	Heli045497_st	
HuCL12178C002	Heli035259_st	IPR004345:TB2/DP1 and HVA22 related protein
HuCL12264C001	Heli060145_st	
HuCL12331C001	Heli007700_st	IPR006734:Protein of unknown function DUF597
HuCL12533C001	Heli040322_st	IPR012328:Chalcone and stilbene synthases, C-
HuCL12656C001	Heli028766_st	IPR005814:Aminotransferase class-III
HuCL12751C001	Heli054232_st	
HuCL13045C001	Heli011608_st	IPR002198:Short-chain dehydrogenase/reductas
HuCL13071C001	Heli016897_st	IPR000109:TGF-beta receptor, type I/II extracellu
HuCL13196C001	Heli059608_st	
HuCL13255C001	Heli055631_st	IPR008896:Ycf1
HuCL13466C001	Heli019368_st	IPR004776:Auxin efflux carrier
HuCL13763C001	Heli060103_st	
HuCL13773C001	Heli027628_st	IPR005379:Region of unknown function XH
HuCL13928C001	Heli046601_st	IPR001128:Cytochrome P450
HuCL13987C001	Heli039417_st	IPR013083:Zinc finger, RING/FYVE/PHD-type
HuCL14020C001	Heli050091_st	
HuCL14238C001	Heli008390_st	IPR000528:Plant lipid transfer protein/Par allerge
HuCL14447C001	Heli025081_st	IPR013601:FAE1/Type III polyketide synthase-lik
HuCL14658C001	Heli038898_st	IPR000873:AMP-dependent synthetase and ligas

HuCL15068C001	Heli011324_st	IPR006689:ARF/SAR superfamily
HuCL15223C001	Heli037017_x_st	IPR011046:WD40 repeat-like
HuCL15234C001	Heli058598_st	
HuCL15411C001	Heli019205_st	IPR013771:Bifunctional trypsin/alpha-amylase inh
HuCL15527C001	Heli032135_st	IPR001362:Glycoside hydrolase, family 32
HuCL15620C001	Heli058632_st	
HuCL15743C001	Heli031577_st	
HuCL16006C001	Heli055480_st	
HuCL16722C001	Heli059427_st	
HuCL17112C001	Heli016810_x_st	
HuCL17138C001	Heli010576_st	IPR005513:Late embryogenesis abundant (LEA)
HuCL17256C001	Heli038267_st	IPR011009:Protein kinase-like
HuCL17274C001	Heli046188_st	IPR011046:WD40 repeat-like
HuCL17371C001	Heli059347_st	
HuCL17527C001	Heli056046_st	
HuCL17538C001	Heli033119_st	IPR005475:Transketolase, central region
HuCL17581C001	Heli059991_st	
HuCL17582C001	Heli058560_st	
HuCL17709C001	Heli059771_st	
HuCL17912C001	Heli059003_st	
HuCL18694C001	Heli013524_st	IPR013785:Aldolase-type TIM barrel
HuCL18817C001	Heli050950_st	
HuCL18828C001	Heli014149_st	IPR000246:Peptidase T2, asparaginase 2
HuCL19240C001	Heli058200_st	
HuCL19652C001	Heli057774_st	
HuCL20634C001	Heli014467_st	IPR001128:Cytochrome P450
HuCL21027C001	Heli034373_st	IPR007185:DNA polymerase epsilon subunit B
HuCL21198C001	Heli019453_st	IPR010530:B12D
HuCL21215C001	Heli045826_st	IPR011009:Protein kinase-like
HuCL21340C001	Heli016848_st	IPR002198:Short-chain dehydrogenase/reductas
HuCL21477C001	Heli058616_st	IPR011261:RNA polymerase, dimerisation
HuCL21777C001	Heli024811_st	IPR000559:Formate-tetrahydrofolate ligase, FTH
HuCL22060C001	Heli059652_st	
HuCX944071	Heli021073_st	IPR001344:Chlorophyll A-B binding protein
HuCX944517	Heli027213_st	Unknown Protein
HuCX944565	Heli045755_st	IPR002213:UDP-glucuronosyl/UDP-glucosyltrans
HuCX946896	Heli049598_st	IPR000595:Cyclic nucleotide-binding
HuCX947280	Heli044537_st	IPR002259:Delayed-early response protein/equili
HuDY906325	Heli053081_st	IPR001128:Cytochrome P450
HuDY907326	Heli061146_st	
HuDY907709	Heli035021_x_st	
HuDY909263	Heli035347_st	IPR011527:ABC transporter, transmembrane regi
HuDY909281	Heli062950_st	
HuDY910362	Heli045698_st	IPR000767:Disease resistance protein
HuDY912139	Heli021460_x_st	IPR001196:Ribosomal protein L15
HuDY913288	Heli038016_st	IPR002213:UDP-glucuronosyl/UDP-glucosyltrans
HuDY913384	Heli063048_st	
HuDY913880	Heli062695_st	
HuDY917639	Heli062611_st	
HuDY918037	Heli060770_st	
HuDY921713	Heli048127_st	
HuDY923350	Heli051519_st	IPR002226:Catalase
HuDY924121	Heli038945_st	
HuDY924254	Heli061284_st	
HuDY925086	Heli019531_st	IPR001461:Peptidase A1
HuDY926953	Heli002754_x_st	IPR008389:ATPase, V0 complex, subunit H
HuDY927618	Heli042553_st	IPR002213:UDP-glucuronosyl/UDP-glucosyltrans

HuDY929082	Heli048136_st	IPR000109:TGF-beta receptor, type I/II extracellul
HuDY931634	Heli041193_x_st	
HuDY929689	Heli072953_st	
HuBU027997	Heli069754_st	
HuCD851021	Heli093861_st	
HuCD846043	Heli092737_st	
HuBQ977464	Heli075069_st	
HuBU023339	Heli076972_st	
	Heli094166_st	
HuCD852425	Heli091577_st	
	Heli089180_st	
HuCD852298	Heli090405_x_st	
HuBU017389	Heli078463_st	
HuBU032080	Heli076600_st	
HuBQ970964	Heli076629_st	
HuBQ910296	Heli076080_st	
HuAJ827826	Heli094007_st	
HuDY913318	Heli077080_st	
	Heli087221_st	
	Heli093372_st	
HuCD851582	Heli093707_x_st	
HuBQ911418	Heli070941_st	
HuCD853572	Heli079621_st	
HuBU024452	Heli072735_st	
HuCX945526	Heli092681_st	
HuBQ975685	Heli077792_st	
HuBQ978422	Heli077196_st	IPR000608:Ubiquitin-conjugating enzyme, E2
HuDY904064	Heli073617_st	
HuAJ541683	Heli094869_st	
	Heli082819_x_st	
HuBU025621	Heli070963_st	IPR013026:Tetratricopeptide region
HuBU026401	Heli071773_st	
HuBG734526	Heli071065_st	
HuCD853913	Heli081467_st	
HuBU034537	Heli065782_st	IPR000554:Ribosomal protein S7e
	Heli093023_st	
HuBU034963	Heli077398_st	
HuCD856086	Heli095331_st	
	Heli088468_st	
	Heli092646_st	
HuDY909608	Heli075141_st	
HuCD849422	Heli088538_st	
HuDY917886	Heli078652_st	
HuCD850512	Heli090135_x_st	
HuCD850603	Heli091751_st	
HuBQ972016	Heli071901_st	
	Heli081832_st	
HuCD848060	Heli081507_st	
HuBQ973266	Heli077132_st	
HuCX943552	Heli092871_st	
HuCD855994	Heli092208_st	
HuCD850431	Heli088836_st	
HuDY910648	Heli077527_st	
HuDY909583	Heli075997_st	
	Heli088329_st	
HuCD856379	Heli093304_st	
HuDY930774	Heli075737_st	

HuDY906332	Heli071579_st	
	Heli087886_st	IPR003757:Photosystem I reaction centre, subuni
	Heli092482_st	
HuDY919080	Heli078346_st	
HuBQ913502	Heli078326_st	
HuBQ974282	Heli075461_st	
HuBU024906	Heli078046_st	
HuBQ975845	Heli076534_x_st	
HuBU019516	Heli072116_st	
HuBQ977597	Heli078076_st	
HuAJ827855	Heli093560_st	
HuDY909462	Heli076462_st	
HuBU672031	Heli087858_st	
HuAJ437740	Heli083248_st	
HuBQ976535	Heli071747_st	
HuBQ977134	Heli070358_st	
HuBU030424	Heli071033_st	IPR000490:Glycoside hydrolase, family 17
HuBQ974552	Heli075520_st	
HuBQ976364	Heli077904_st	
HuBQ916964	Heli071844_st	
HuDY909584	Heli076641_x_st	
	Heli093737_st	
HuDY931121	Heli076099_st	
HuBQ977895	Heli071572_st	
HuCD848620	Heli081947_st	
HuBQ973378	Heli072227_st	
HuBU028537	Heli075401_st	
HuBQ978061	Heli077015_st	
HuCX943622	Heli092221_st	
HuBQ972643	Heli075551_st	
	Heli091224_st	
HuBU029163	Heli066197_st	
HuCX943626	Heli092112_st	
	AFFX-r2-Bs-phe-M_	Control Sequence
HuBQ966308	Heli076305_st	
HuBQ970682	Heli067225_st	IPR006706:Extensin-like region
HuDY909508	Heli076826_st	
HuBU019689	Heli072176_st	
HuBQ974493	Heli072092_st	
HuBQ911082	Heli077288_st	
	Heli082003_st	
HuBU032024	Heli076708_st	
HuCX943633	Heli095381_st	
HuCX943520	Heli088386_st	
HuBU032785	Heli075856_st	
HuDY908969	Heli078770_st	
	Heli093986_st	
HuDY930989	Heli072995_st	
HuAJ542298	Heli086016_st	
HuCD847425	Heli092382_st	
HuBQ969223	Heli070981_st	
HuBQ912370	Heli071871_st	
HuBQ978936	Heli076795_x_st	
	Heli082880_st	
	Heli094717_st	
HuCX945174	Heli092600_st	
HuCX943621	Heli093179_st	

HuBU025043	Heli077369_st
HuDY909535	Heli078740_st
HuBQ916728	Heli074493_st
HuBQ916756	Heli078790_st
HuBU022799	Heli073727_st
HuCD852315	Heli078868_st
HuDY921637	Heli077821_st
HuBU015557	Heli073861_st
	Heli092031_st
HuBQ972381	Heli078166_st
HuBQ911753	Heli076916_st
HuBU022212	Heli071108_st
HuBQ909788	Heli073066_x_st
HuBQ979410	Heli077452_st
HuBU015985	Heli073571_st
HuBQ972594	Heli074898_st

1.086694

anscripts during dry after-ripening

ys.

esults against TAIR database (Annotation, D), Log2 intensity of array NDox1 (E), NDox2 (F), Dox1 (G), Dox2 (H)

Annotation	**NDox1**
Unknown Protein	6,27
AT4G27800.3:protein phosphatase 2C PPH1 / PP2C PPH1 (PPH1) chr4:13852411-138	8,89
AT5G49040.1:disease resistance-responsive protein-related / dirigent protein-related ch	5,73
AT1G13500.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13530.1)	4,77
	4,91
	9,28
AT4G33050.2:EDA39 (embryo sac development arrest 39)	7,04
	3,57
ctoisomerase	5,23
AT1G48410.2:AGO1 (ARGONAUTE 1) chr1:17889953-17895560 REVERSE	4,56
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	4,49
	6,75
AT2G19730.3:60S ribosomal protein L28 (RPL28A) chr2:8518834-8520077 FORWARD	5,24
AT5G47820.2:FRA1 (FRAGILE FIBER 1)	7,77
-like	7,37
Unknown Protein	8,64
AT3G09390.1:MT2A (METALLOTHIONEIN 2A) chr3:2889743-2890194 REVERSE	8,14
AT1G56120.1:leucine-rich repeat family protein / protein kinase family protein chr1:209	4,43
AT5G54510.1:DFL1 (DWARF IN LIGHT 1)	6,46
	4,43
AT4G17790.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71940.1)	7,74
AT3G48300.1:CYP71A23 (cytochrome P450, family 71, subfamily A, polypeptide 23)	6,71
AT4G37990.1:ELI3-2 (ELICITOR-ACTIVATED GENE 3) chr4:17855958-17857382 FOR	7,77
AT2G16130.1:mannitol transporter, putative chr2:7009404-7011125 FORWARD	7,69
AT3G55270.1 : MKP1 (MKP1); MAP kinase phosphatase	7,86
AT2G28910.1:CXIP4 (CAX INTERACTING PROTEIN 4)	5,87
AT4G30800.1:40S ribosomal protein S11 (RPS11B) chr4:15001222-15002398 FORWA	4,57
se transcriptase), related	6,48
IPR013753:Ras	4,25
AT2G16250.1:leucine-rich repeat transmembrane protein kinase, putative chr2:704676	7,88
AT1G70520.1:protein kinase family protein chr1:26588551-26590997 REVERSE	5,67
AT5G06090.1:ATGPAT7/GPAT7 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 7	4,55
	4,07
AT3G62250.1:UBQ5 (UBIQUITIN 5)	7,17
AT5G63450.1:CYP94B1 (cytochrome P450, family 94, subfamily B, polypeptide 1)	8,10
Unknown Protein	5,79
AT1G63440.1:HMA5 (HEAVY METAL ATPASE 5)	9,31
AT4G11410.1:short-chain dehydrogenase/reductase (SDR) family protein chr4:694512	4,71
AT1G61260.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G11220.1)	5,94
	7,55
	7,48
	4,16
	6,32
AT2G01970.1:endomembrane protein 70, putative chr2:452196-454818 REVERSE	4,15
AT5G59310.1:LTP4 (LIPID TRANSFER PROTEIN 4)	5,78
IPR002113:Adenine nucleotide translocator 1	5,79
AT5G16370.1:AMP-binding protein, putative chr5:5356826-5358484 REVERSE	7,05
AT2G34420.1:LHB1B2 (Photosystem II light harvesting complex gene 1.5)	4,52
AT5G59310.1:LTP4 (LIPID TRANSFER PROTEIN 4)	7,96

AT5G59310.1:LTP4 (LIPID TRANSFER PROTEIN 4)	4,61
AT2G30490.1:ATC4H (CINNAMATE-4-HYDROXYLASE) chr2:13000938-13002760 RE	4,69
	9,61
AT1G71720.1:S1 RNA-binding domain-containing protein chr1:26987406-26989555 FO	3,00
AT2G45700.1:sterile alpha motif (SAM) domain-containing protein chr2:18834290-1883	7,09
AT3G27660.1:OLEO4 (OLEOSIN4) chr3:10245088-10246058 FORWARD	9,16
AT2G23450.1:protein kinase family protein chr2:9996006-9998324 REVERSE	10,05
AT2G30490.1:ATC4H (CINNAMATE-4-HYDROXYLASE) chr2:13000938-13002760 RE	4,62
AT3G59890.1:dihydrodipicolinate reductase family protein chr3:22135474-22137468 RE	6,32
	11,90
AT3G62250.1:UBQ5 (UBIQUITIN 5)	5,88
	7,38
se transcriptase), related	6,92
AT4G31985.1:60S ribosomal protein L39 (RPL39C) chr4:15469937-15470372 FORWA	4,65
AT4G09550.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G73790.1)	4,44
AT4G31985.1:60S ribosomal protein L39 (RPL39C) chr4:15469937-15470372 FORWA	6,86
AT2G34500.1:CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide 1)	6,61
AT4G30880.1:protease inhibitor/seed storage/lipid transfer protein (LTP) family protein (	5,71
AT1G15270.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G16040.1)	3,97
AT4G09800.1:RPS18C (S18 RIBOSOMAL PROTEIN)	6,25
Unknown Protein	9,69
AT5G60360.1:AALP (ARABIDOPSIS ALEURAIN-LIKE PROTEASE)	10,07
AT1G24020.1:Bet v I allergen family protein chr1:8500642-8501447 REVERSE	7,75
AT2G10940.2:protease inhibitor/seed storage/lipid transfer protein (LTP) family protein (	7,80
AT1G24020.1:Bet v I allergen family protein chr1:8500642-8501447 REVERSE	7,28
	5,93
AT1G74470.1:geranylgeranyl reductase chr1:27994909-27996506 FORWARD	8,38
AT2G25670.2:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32610.1)	6,63
AT3G30775.1:ERD5 (EARLY RESPONSIVE TO DEHYDRATION 5, PROLINE OXIDAS	7,71
AT2G37040.1:PAL1 (PHE AMMONIA LYASE 1)	7,71
AT3G01570.1:glycine-rich protein / oleosin chr3:222159-222785 REVERSE	9,32
AT2G37040.1:PAL1 (PHE AMMONIA LYASE 1)	10,88
AT5G62360.1:invertase/pectin methylesterase inhibitor family protein chr5:25057925-25	5,81
AT5G22580.1:Identical to Protein At5g22580 [Arabidopsis Thaliana] (GB:Q9FK81)	3,78
AT5G60360.1:AALP (ARABIDOPSIS ALEURAIN-LIKE PROTEASE)	7,61
AT4G11650.1:ATOSM34 (OSMOTIN 34) chr4:7025121-7026107 REVERSE	7,06
AT2G37040.1:PAL1 (PHE AMMONIA LYASE 1)	8,62
HD region	6,54
IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	6,98
	8,08
IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	10,16
IPR011051:Cupin, RmlC-type	8,93
AT1G36240.1:60S ribosomal protein L30 (RPL30A) chr1:13616102-13617445 FORWA	9,62
IPR000932:Photosystem antenna protein-like	7,88
AT5G38170.1:protease inhibitor/seed storage/lipid transfer protein (LTP) family protein (	6,36
AT1G60710.1:ATB2	10,12
AT4G37340.1:CYP81D3 (cytochrome P450, family 81, subfamily D, polypeptide 3)	4,29
	3,63
AT4G23420.2:short-chain dehydrogenase/reductase (SDR) family protein chr4:1222629	5,65
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	8,11
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	5,19
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	6,31
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	7,02
AT1G24440.1:protein binding / zinc ion binding chr1:8662328-8663765 FORWARD	4,35
AT5G35630.3:GS2 (GLUTAMINE SYNTHETASE 2) chr5:13848450-13850469 FORWA	7,18
AT1G66200.1:ATGSR2 (Arabidopsis thaliana glutamine synthase clone R2)	5,24
	6,62

AT3G52600.2:ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2)	8,69
AT1G15740.1:leucine-rich repeat family protein chr1:5411504-5414539 FORWARD	2,69
AT1G06760.1:histone H1, putative chr1:2076686-2077615 REVERSE	8,76
AT5G58710.1:ROC7 (rotamase CyP 7)	7,85
AT2G42590.2:GRF9 (General regulatory factor 9)	7,86
AT5G37600.1:ATGSR1 (Arabidopsis thaliana glutamine synthase clone R1)	7,47
AT5G37600.1:ATGSR1 (Arabidopsis thaliana glutamine synthase clone R1)	9,89
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	7,60
AT2G36630.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25737.1)	6,79
AT2G36630.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25737.1)	5,27
	6,08
IPR007112:Expansin 45, endoglucanase-like	4,93
AT3G13050.1:transporter-related chr3:4176873-4178875 FORWARD	7,96
AT5G47770.1:FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1)	7,63
IPR006398:2-hydroxy-3-oxopropionate reductase	5,38
AT1G12950.1:MATE efflux family protein chr1:4419847-4422460 FORWARD	9,31
AT3G18830.1:ATPLT5 (POLYOL TRANSPORTER 5)	8,48
IPR005828:General substrate transporter	7,72
Unknown Protein	8,64
AT3G25220.1:FKBP15-1 (FK506-binding protein 15 kD-1)	8,07
-like	5,49
tase	6,76
	7,84
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	6,95
AT4G23900.1:nucleoside diphosphate kinase 4 (NDK4) chr4:12424515-12426328 FOR	10,78
IPR006140:D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	7,63
IPR013525:ABC-2 type transporter	9,10
AT1G15210.1:ATPDR7/PDR7 (PLEIOTROPIC DRUG RESISTANCE 7)	6,05
ınction, C-terminal	9,99
AT4G27410.2:RD26 (RESPONSIVE TO DESSICATION 26)	10,42
AT1G60690.1:aldo/keto reductase family protein chr1:22353557-22355333 REVERSE	10,84
AT1G73680.1:pathogen-responsive alpha-dioxygenase, putative chr1:27707882-27711	8,33
AT2G01140.1:fructose-bisphosphate aldolase, putative chr2:95005-96490 REVERSE	9,17
AT4G39230.1:isoflavone reductase, putative chr4:18266018-18267598 REVERSE	5,65
AT1G28190.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12340.1)	5,98
IPR015936:Homoaconitase/3-isopropylmalate dehydratase, small/large subunit	7,10
IPR015936:Homoaconitase/3-isopropylmalate dehydratase, small/large subunit	9,79
	6,67
	4,81
IPR012951:Berberine/berberine-like	7,86
AT4G20830.2:FAD-binding domain-containing protein chr4:11155497-11157119 FORW	4,85
AT2G28230.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G09070.1)	9,51
AT4G02930.1 : elongation factor Tu	6,18
AT5G02500.1:HSC70-1 (heat shock cognate 70 kDa protein 1)	11,22
AT5G52450.1:MATE efflux protein-related chr5:21306268-21308975 REVERSE	10,23
AT5G16370.1:AMP-binding protein, putative chr5:5356826-5358484 REVERSE	6,87
IPR007118:Expansin/Lol pI	11,52
AT5G20180.2:ribosomal protein L36 family protein chr5:6811314-6811912 FORWARD	9,59
AT1G03220.1:extracellular dermal glycoprotein, putative / EDGP, putative chr1:787143-	6,75
AT4G36220.1: FAH1 (FERULATE-5-HYDROXYLASE 1)	10,60
AT5G13750.1:ZIFL1 (ZINC INDUCED FACILITATOR-LIKE 1)	9,84
AT5G42800.1:DFR (DIHYDROFLAVONOL 4-REDUCTASE)	5,14
AT1G68090.1:ANNAT5 (ANN5, ANNEXIN ARABIDOPSIS 5)	5,88
	9,85
	6,48
AT3G07700.2:ABC1 family protein chr3:2459702-2463247 REVERSE	6,68
AT3G45600.1:TET3 (TETRASPANIN3) chr3:16744958-16746839 REVERSE	6,53

AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	7,32
AT3G12120.2:FAD2 (FATTY ACID DESATURASE 2) chr3:3860598-3861749 REVERS	8,14
AT1G67430.1:60S ribosomal protein L17 (RPL17B) chr1:25265872-25267290 FORWAI	7,22
AT1G32450.1:proton-dependent oligopeptide transport (POT) family protein chr1:11715	6,47
AT1G18540.1:60S ribosomal protein L6 (RPL6A) chr1:6377441-6378541 REVERSE	3,07
AT4G25140.1:OLEO1 (OLEOSIN1) chr4:12900508-12901269 FORWARD	11,41
AT1G13080.1:CYP71B2 (CYTOCHROME P450 71B2)	9,56
AT4G37970.1:mannitol dehydrogenase, putative chr4:17849666-17852139 FORWARD	11,09
AT3G26790.1:FUS3 (FUSCA 3)	9,55
AT1G80840.1:WRKY40 (WRKY DNA-binding protein 40)	5,45
	5,79
AT3G48320.1:CYP71A21 (cytochrome P450, family 71, subfamily A, polypeptide 21)	4,91
IPR006534:Plasma-membrane proton-efflux P-type ATPase	7,04
IPR002160:Proteinase inhibitor I3, Kunitz legume	9,35
	8,30
AT1G14130.1:2-oxoglutarate-dependent dioxygenase, putative chr1:4836038-4837037	7,91
AT2G37040.1:PAL1 (PHE AMMONIA LYASE 1)	5,80
IPR009869:Hs1pro-1, N-terminal	6,89
AT5G62300.2:40S ribosomal protein S20 (RPS20C) chr5:25038614-25039461 REVER	7,71
IPR009014:Transketolase, C-terminal/Pyruvate-ferredoxin oxidoreductase, domain II	7,41
AT1G01120.1:KCS1 (3-KETOACYL-COA SYNTHASE 1)	6,37
AT5G49410.2:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G73940.1)	9,20
AT1G56140.1:leucine-rich repeat family protein / protein kinase family protein chr1:210	8,85
	7,04
IPR005828:General substrate transporter	9,91
AT3G27210.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40860.1)	6,62
IPR006058:2Fe-2S ferredoxin, iron-sulphur binding site	5,56
AT1G03940.1:transferase family protein chr1:1009541-1010950 REVERSE	8,40
AT4G23990.1:ATCSLG3 (Cellulose synthase-like G3)	7,74
AT2G39840.1:TOPP4 (Type one serine/threonine protein phosphatase 4)	7,22
AT4G24290.2:similar to NSL1 (NECROTIC SPOTTED LESIONS 1) [Arabidopsis thalian	7,55
IPR013705:Sterol methyltransferase C-terminal	5,72
IPR004046:Glutathione S-transferase, C-terminal	4,22
IPR009057:Homeodomain-like	5,78
IPR012951:Berberine/berberine-like	6,82
IPR012336:Thioredoxin-like fold	7,68
AT4G15550.1:IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE)	7,07
AT1G22380.1:transcription factor/ transferase, transferring glycosyl groups chr1:790051	6,06
AT3G03980.1:short-chain dehydrogenase/reductase (SDR) family protein chr3:103179	10,13
IPR013830:Esterase, SGNH hydrolase-type	6,20
AT4G37830.1:cytochrome c oxidase-related chr4:17787666-17788756 REVERSE	7,01
IPR005829:Sugar transporter superfamily	7,04
AT5G24800.1:BZO2H2 (basic leucine zipper O2 homolog 2)	8,44
	6,55
IPR012394:Aldehyde dehydrogenase NAD(P)-dependent	6,44
IPR004046:Glutathione S-transferase, C-terminal	8,99
AT5G20700.1:senescence-associated protein-related chr5:7006180-7007005 REVERS	8,01
AT3G03280.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G17350.1)	6,24
AT3G63250.1:ATHMT-2/HMT-2	8,75
AT4G31940.1:CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4)	9,43
	9,35
	3,59
AT3G52780.1:ATPAP20/PAP20	6,34
AT4G13180.1:short-chain dehydrogenase/reductase (SDR) family protein chr4:765736	6,09
AT4G13840.1:transferase family protein chr4:8014084-8016322 REVERSE	5,78
	7,78
AT1G22430.2:oxidoreductase/ zinc ion binding chr1:7919224-7921583 FORWARD	8,83

IPR001834:NADH:cytochrome b5 reductase (CBR)	6,02
	8,16
AT5G05830.1:zinc finger (C3HC4-type RING finger) family protein chr5:1755911-17568	9,60
AT2G36790.1:UGT73C6 (UDP-glucosyl transferase 73C6)	5,63
AT1G61250.1:SC3 (SECRETORY CARRIER 3)	8,83
AT3G26210.1:CYP71B23 (cytochrome P450, family 71, subfamily B, polypeptide 23)	7,01
AT3G14880.1:similar to DOG1 (DELAY OF GERMINATION 1) [Arabidopsis thaliana] (T/	6,89
AT2G26110.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G26130.1)	3,86
AT3G15540.1:IAA19 (indoleacetic acid-induced protein 19)	4,69
AT5G63140.1:ATPAP29/PAP29 (purple acid phosphatase 29)	8,86
AT5G16370.1:AMP-binding protein, putative chr5:5356826-5358484 REVERSE	8,07
	6,92
	8,16
AT3G47420.1:glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permeas	6,87
AT5G40780.2:LHT1 (LYSINE HISTIDINE TRANSPORTER 1)	7,87
	7,45
AT1G09850.1:XBCP3 (XYLEM BARK CYSTEINE PEPTIDASE 3)	6,68
AT1G02660.1:lipase class 3 family protein chr1:572187-574746 REVERSE	5,04
ne	6,31
AT2G30040.1:MAPKKK14 (Mitogen-activated protein kinase kinase kinase 14)	6,79
	3,87
AT4G31940.1:CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4)	6,38
AT1G04985.1:similar to OSJNBa0043A12.17 [Oryza sativa (japonica cultivar-group)] (GI	8,42
IPR002078:RNA polymerase sigma factor 54, interaction	7,52
	7,76
AT2G26250.1:FDH (FIDDLEHEAD)	7,70
AT5G52450.1:MATE efflux protein-related chr5:21306268-21308975 REVERSE	8,24
AT5G10180.1:AST68 (Sulfate transporter 2.1) chr5:3193226-3196819 FORWARD	6,26
AT4G36990.1:HSF4 (HEAT SHOCK FACTOR 4)	8,03
IPR003439:ABC transporter related	7,18
AT1G60710.1:ATB2	7,12
lar region	6,25
AT5G40780.2:LHT1 (LYSINE HISTIDINE TRANSPORTER 1)	7,11
	6,04
AT1G67630.1:DNA polymerase alpha subunit B family chr1:25348236-25351950 REVE	5,64
	4,98
AT4G16695.1:unknown protein chr4:9394281-9395273 FORWARD	6,28
AT5G32482.1:zinc knuckle (CCHC-type) family protein chr5:12132212-12133237 FORV	9,86
AT5G42560.2:abscisic acid-responsive HVA22 family protein chr5:17032931-17034197	7,89
	10,33
AT4G17900.1:zinc-binding family protein chr4:9946059-9947710 FORWARD	8,99
AT2G26640.1:beta-ketoacyl-CoA synthase, putative chr2:11337172-11338701 FORWA	8,41
AT3G22200.1:POP2 (POLLEN-PISTIL INCOMPATIBILITY 2)	7,87
AT4G36520.1:trichohyalin-related chr4:17230592-17235438 REVERSE	6,01
AT3G61220.1:short-chain dehydrogenase/reductase (SDR) family protein chr3:2267400	5,63
lar region	6,97
	5,83
ATCG01000.1:Identical to Putative membrane protein ycf1 (ycf1-B) [Arabidopsis Thalian	9,60
AT5G65980.1:auxin efflux carrier family protein chr5:26409670-26411458 FORWARD	6,28
	5,40
AT1G13790.1:XH/XS domain-containing protein / XS zinc finger domain-containing prote	7,86
AT5G35715.1:CYP71B8 (cytochrome P450, family 71, subfamily B, polypeptide 8)	9,61
AT3G63530.2:BB (BIG BROTHER)	7,65
AT5G05860.1 : UGT76C2 (UDP-glucosyl transferase 76C2)	9,42
AT4G33355.1:lipid binding chr4:16067101-16067572 FORWARD	4,92
AT1G68530.2:CUT1 (CUTICULAR 1)	5,76
AT5G16370.1:AMP-binding protein, putative chr5:5356826-5358484 REVERSE	7,60

IPR006689:ARF/SAR superfamily	4,71
AT3G15980.3:coatomer protein complex, subunit beta 2 (beta prime), putative chr3:541	5,05
	6,70
ıibitor	7,13
AT3G52600.1:ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2)	7,41
	3,39
AT4G37030.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G12680.1)	7,82
	6,86
	4,20
AT5G19860.1:similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55265.1)	4,35
AT1G32560.1:late embryogenesis abundant group 1 domain-containing protein / LEA gr	8,41
IPR015742:Calcium/calmodulin-dependent protein kinase II isoform	5,21
AT1G15750.4:TPL/WSIP1 (WUS-INTERACTING PROTEIN 1) chr1:5415081-5420354 F	7,77
	6,30
AT2G39430.1:disease resistance-responsive protein-related / dirigent protein-related ch	5,79
AT4G15560.1:CLA1 (CLOROPLASTOS ALTERADOS 1) chr4:8884216-8887252 FORV	6,24
	6,38
	3,65
	5,19
	6,27
AT1G76690.1:OPR2 (12-oxophytodienoate reductase 2)	6,89
	8,74
AT3G16150.1:L-asparaginase, putative / L-asparagine amidohydrolase, putative chr3:54	7,79
	9,49
	7,99
AT5G25120.1:CYP71B11 (cytochrome P450, family 71, subfamily B, polypeptide 11)	8,43
	6,53
AT3G48140.1:senescence-associated protein, putative chr3:17789456-17790284 FORV	5,63
AT5G23720.3:PHS1 (PROPYZAMIDE-HYPERSENSITIVE 1)	8,69
AT3G51680.1:short-chain dehydrogenase/reductase (SDR) family protein chr3:1918460	6,53
	8,09
AT1G50480.1:THFS (10-FORMYLTETRAHYDROFOLATE SYNTHETASE)	10,30
	7,52
AT3G54890.4:LHCA1 chr3:20350859-20351900 REVERSE	7,88
Unknown Protein	9,63
AT1G05680.1:UDP-glucoronosyl/UDP-glucosyl transferase family protein chr1:1703195	10,15
AT5G54250.2:ATCNGC4 (DEFENSE, NO DEATH 2)	6,30
AT1G02630.2:equilibrative nucleoside transporter, putative (ENT8) chr1:561007-56238	7,74
AT2G45560.2:CYP76C1 (cytochrome P450, family 76, subfamily C, polypeptide 1)	4,20
	7,27
AT3G47340.2:ASN1 (DARK INDUCIBLE 6) chr3:17449430-17452028 REVERSE	4,25
AT3G28345.1:ABC transporter family protein chr3:10595158-10600012 REVERSE	8,74
	6,34
AT4G27190.1:disease resistance protein (NBS-LRR class), putative chr4:13620983-136	6,76
AT3G25920.1:RPL15 (ribosomal protein L15) chr3:9492505-9493795 REVERSE	6,59
AT5G05900.1:UDP-glucoronosyl/UDP-glucosyl transferase family protein chr5:1774514	4,86
	5,31
	5,73
	6,11
	7,94
AT5G02970.1:hydrolase, alpha/beta fold family protein chr5:695389-697410 FORWAR	5,72
AT4G35090.2:CAT2 (CATALASE 2)	4,25
	4,64
	5,09
	9,01
AT5G55290.1:ATP synthase subunit H family protein chr5:22440263-22441312 REVER	4,69
AT1G05560.1:UGT1 (UDP-glucosyl transferase 75B1)	4,73

AT1G68570.1:proton-dependent oligopeptide transport (POT) family protein chr1:25750	9,79
AT5G19440.1:cinnamyl-alcohol dehydrogenase, putative (CAD) chr5:6556495-6558125	7,94
	6,57
	8,06
	6,64
	4,59
	5,14
	5,34
	4,94
	4,65
	4,76
	8,22
	4,96
	6,45
	7,06
	10,47
	5,50
	5,35
	4,13
	7,85
	3,67
	9,90
	8,20
	4,21
	5,77
	7,01
AT3G52560.1:MMZ4 (MMS ZWEI HOMOLOGE 4)	5,34
	4,21
	10,63
	8,80
	5,97
	4,75
	5,08
	6,35
AT3G02560.2:40S ribosomal protein S7 (RPS7B) chr3:542348-543175 FORWARD	6,32
	4,42
	6,81
	5,52
	4,69
	4,06
	8,21
	5,00
	5,71
	3,02
AT5G59845.1:gibberellin-regulated family protein chr5:24128669-24129034 FORWARD	5,10
	3,45
	5,92
	3,81
	3,91
	4,94
	2,73
	4,21
	3,00
	4,21
	4,42
	4,03
	3,72

	4,64
AT4G12800.1:PSAL (photosystem I subunit L) chr4:7521466-7522490 FORWARD	4,17
	5,98
	4,64
	7,29
	3,14
	3,92
	7,40
AT2G01630.2:glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative chr2:2	6,24
	3,46
	6,55
	4,87
	4,07
	7,75
AT2G44730.1:transcription factor chr2:18444522-18445640 REVERSE	11,04
	8,15
AT3G55430.1:glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative chr3:2	3,51
	7,48
	2,74
AT5G61960.2:AML1 (ARABIDOPSIS MEI2-LIKE PROTEIN 1)	4,53
	6,34
	3,67
	6,25
	4,76
	4,38
	3,54
	5,24
	9,91
	4,99
	8,01
	6,27
	5,01
	3,24
B. subtilis /GEN=pheA /DB_XREF=gb:M24537.1 /NOTE=SIF corresponding to nucleotid	3,20
	4,06
	7,22
	3,73
	7,13
	4,55
	8,35
	8,74
	6,69
	5,93
	4,09
	6,37
	5,95
	5,47
	5,33
	5,89
	5,23
	3,51
	7,26
	7,38
	8,04
	2,99
	5,69
	4,35

4,77
3,34
5,67
5,16
8,64
5,08
5,06
6,31
3,57
4,58
4,89
6,68
5,62
8,18
6,97
7,69

NDox2	Dox1	Dox2	NDox vs dox	Bonferroni
6,40	4,53	4,82	-4,07	0,00E+0
8,92	4,91	5,05	-3,92	0,00E+0
5,97	5,18	4,76	-3,25	1,23E-4
5,38	4,32	4,17	-2,95	1,11E-3
4,29	3,72	3,71	-2,90	1,32E-4
9,21	8,31	8,63	-2,78	8,57E-3
7,08	5,51	5,94	-2,60	0,00E+0
3,63	4,50	4,91	-2,33	6,33E-9
4,53	6,18	5,93	-2,18	2,03E-10
4,19	5,13	5,27	-1,93	1,30E-3
4,83	5,43	5,96	-1,87	2,02E-7
6,94	6,28	5,76	-1,87	1,30E-3
4,48	4,46	3,79	-1,81	3,41E-2
7,74	8,51	8,61	-1,77	3,08E-3
7,51	6,40	6,35	-1,76	4,48E-8
8,62	5,90	6,17	-1,75	0,00E+0
8,03	7,21	7,09	-1,72	1,42E-5
4,81	3,52	3,64	-1,71	1,36E-7
6,56	5,31	5,48	-1,66	3,23E-9
4,27	4,84	5,46	-1,60	2,97E-3
7,94	8,48	9,11	-1,54	5,97E-6
6,58	5,54	6,02	-1,53	3,35E-4
7,55	6,21	6,34	-1,50	0,00E+0
7,64	6,40	6,75	-1,50	1,15E-8
7,80	6,40	6,26	-1,49	0,00E+0
5,19	6,57	6,45	-1,49	2,69E-6
3,93	4,81	5,20	-1,43	1,65E-2
6,46	5,72	5,36	-1,43	1,98E-5
4,22	3,99	2,99	-1,43	2,13E-2
8,05	8,36	9,12	-1,40	8,47E-3
5,50	4,71	4,50	-1,40	1,69E-6
4,68	5,28	5,42	-1,40	3,04E-2
4,45	4,81	5,30	-1,38	3,87E-3
6,87	7,50	8,11	-1,38	5,24E-3
8,05	7,54	6,89	-1,38	2,71E-4
5,56	4,18	4,09	-1,36	0,00E+0
9,39	8,50	8,74	-1,35	4,41E-2
4,84	3,85	3,79	-1,34	5,99E-6
6,16	5,12	4,89	-1,32	8,74E-8
8,12	8,28	9,20	-1,31	5,15E-5
7,65	8,23	8,59	-1,29	6,72E-4
4,55	4,71	5,53	-1,29	1,32E-2
6,39	5,91	5,32	-1,28	2,52E-2
4,58	4,80	5,62	-1,28	6,12E-4
6,10	7,88	7,26	-1,24	0,00E+0
6,16	4,97	4,73	-1,24	2,28E-9
7,09	6,05	6,32	-1,22	1,43E-4
4,53	5,12	5,43	-1,21	1,86E-2
7,93	9,07	9,36	-1,21	0,00E+0

4,59	5,67	5,35	-1,19	3,62E-5
4,64	5,45	5,81	-1,17	4,17E-6
9,55	10,53	10,28	-1,17	1,09E-3
3,37	3,78	4,58	-1,17	1,13E-6
7,19	6,26	6,35	-1,16	8,88E-4
9,12	10,40	10,54	-1,16	0,00E+0
10,13	8,68	8,88	-1,15	0,00E+0
4,54	5,52	5,76	-1,14	5,26E-8
6,17	7,76	7,61	-1,13	0,00E+0
11,91	10,94	10,96	-1,13	7,58E-6
6,13	6,40	7,09	-1,12	2,31E-2
6,98	6,40	6,34	-1,11	2,17E-3
6,81	6,08	5,90	-1,11	2,08E-4
4,95	5,31	6,31	-1,10	6,35E-7
4,85	5,21	5,63	-1,09	1,01E-2
7,06	6,41	5,92	-1,09	4,95E-3
6,53	5,70	5,56	-1,09	1,34E-5
5,85	6,68	6,71	-1,08	4,17E-5
3,65	3,25	2,91	-1,08	4,45E-2
6,85	5,34	6,02	-1,07	2,85E-4
9,47	7,69	8,04	-1,07	0,00E+0
10,27	9,32	9,50	-1,06	1,23E-2
7,89	7,00	6,70	-1,06	3,48E-6
7,77	7,06	7,03	-1,06	2,80E-2
7,24	6,41	6,47	-1,05	1,75E-3
5,87	7,01	6,76	-1,05	1,42E-6
8,28	9,13	9,23	-1,05	5,57E-4
6,73	7,13	7,70	-1,04	3,24E-2
7,55	8,52	8,36	-1,03	2,04E-3
7,71	8,75	8,78	-1,03	7,50E-8
9,12	10,07	10,03	-1,02	1,28E-3
10,88	9,43	9,46	-1,01	0,00E+0
5,66	6,69	6,62	-1,00	2,80E-5
4,56	3,32	3,28	-1,00	2,12E-4
7,69	6,40	7,44	-0,99	3,51E-2
7,10	7,94	8,12	-0,99	8,83E-6
8,65	6,66	6,25	-0,99	0,00E+0
6,54	5,39	5,70	-0,99	9,73E-7
6,95	8,01	8,11	-0,99	9,94E-9
7,96	8,76	8,82	-0,99	8,34E-3
10,18	11,21	11,26	-0,99	5,99E-8
9,00	10,55	10,47	-0,98	0,00E+0
9,77	8,89	8,84	-0,98	1,05E-3
7,86	8,81	8,68	-0,98	2,07E-4
6,62	5,60	5,39	-0,97	1,12E-6
10,08	9,19	9,02	-0,97	1,34E-6
4,50	6,05	5,73	-0,97	0,00E+0
3,35	4,40	4,32	-0,96	2,60E-4
5,62	4,70	4,64	-0,96	4,98E-6
8,05	6,34	6,29	-0,96	0,00E+0
5,56	4,49	4,56	-0,96	5,30E-4
6,25	5,17	5,55	-0,96	2,99E-5
7,08	5,82	5,71	-0,95	0,00E+0
4,54	3,85	3,51	-0,95	9,39E-3
7,29	5,81	5,86	-0,95	0,00E+0
5,30	6,10	6,14	-0,95	4,30E-4
6,58	7,60	7,42	-0,95	4,34E-5

8,49	7,22	7,33	-0,94	0,00E+0
2,59	3,12	3,66	-0,94	2,11E-2
8,88	7,90	7,98	-0,94	1,46E-4
7,94	7,06	7,08	-0,94	1,36E-3
7,80	7,09	7,00	-0,94	5,43E-3
7,46	6,41	6,33	-0,94	9,55E-9
9,98	8,90	9,06	-0,93	6,34E-6
7,63	8,39	8,53	-0,93	6,22E-4
6,88	5,88	5,80	-0,93	1,18E-6
6,03	6,40	6,64	-0,93	2,66E-4
6,14	5,21	5,11	-0,92	8,03E-6
4,92	3,55	3,49	-0,92	0,00E+0
8,00	7,11	7,27	-0,92	4,58E-3
7,52	6,19	6,20	-0,92	0,00E+0
5,43	4,66	4,56	-0,91	4,14E-3
9,31	8,15	8,21	-0,91	1,60E-9
8,35	6,94	7,02	-0,90	0,00E+0
7,65	6,84	6,87	-0,90	1,13E-3
8,47	6,73	6,86	-0,90	0,00E+0
8,20	7,21	7,23	-0,89	4,15E-5
5,33	4,47	4,42	-0,89	5,12E-6
6,78	5,55	5,70	-0,88	8,75E-10
8,16	8,94	8,60	-0,88	1,19E-2
6,82	6,00	6,04	-0,88	2,69E-4
10,82	10,08	10,01	-0,88	1,86E-2
7,51	6,51	6,52	-0,87	6,20E-8
9,15	7,25	7,26	-0,87	0,00E+0
5,97	4,99	5,46	-0,87	6,28E-3
10,05	9,01	9,15	-0,87	1,26E-5
10,40	11,30	11,21	-0,87	6,74E-4
10,79	10,07	10,05	-0,87	1,93E-2
8,30	9,11	9,12	-0,87	3,40E-3
9,21	8,42	8,40	-0,87	6,19E-3
5,77	4,82	4,92	-0,86	7,42E-4
6,03	5,19	5,35	-0,86	3,01E-2
7,11	6,39	6,34	-0,86	3,06E-2
9,82	9,00	8,97	-0,86	1,67E-3
6,72	5,88	5,91	-0,86	3,14E-3
5,00	4,29	4,05	-0,86	2,87E-2
7,84	8,79	8,65	-0,85	2,59E-4
4,78	5,55	5,67	-0,85	4,40E-3
9,38	10,39	10,07	-0,85	6,14E-3
5,70	4,73	3,95	-0,85	0,00E+0
11,21	10,45	10,51	-0,85	2,80E-2
10,20	8,73	8,72	-0,85	0,00E+0
7,02	5,95	6,22	-0,85	3,13E-4
11,50	10,17	10,37	-0,84	7,00E-12
9,74	8,89	8,98	-0,84	3,33E-2
6,79	5,31	5,24	-0,84	0,00E+0
10,59	9,03	9,16	-0,84	0,00E+0
9,83	8,67	8,66	-0,84	2,59E-10
5,35	6,15	6,17	-0,84	4,47E-5
5,52	5,21	4,54	-0,83	1,23E-3
9,86	8,99	9,05	-0,83	7,77E-4
6,44	5,62	5,25	-0,83	2,50E-7
6,70	5,91	5,98	-0,83	2,21E-2
6,67	6,02	5,72	-0,83	3,27E-2

7,22	6,34	6,22	-0,83	1,52E-6
8,16	7,08	6,87	-0,83	1,75E-10
7,21	6,43	6,48	-0,83	1,29E-2
6,36	7,38	7,32	-0,83	1,54E-5
3,12	3,83	4,09	-0,83	2,91E-4
11,45	12,17	12,28	-0,83	4,29E-3
9,61	5,46	5,56	-0,82	0,00E+0
11,07	9,68	9,76	-0,82	0,00E+0
9,53	10,35	10,38	-0,82	1,32E-3
5,76	4,71	4,83	-0,82	8,70E-4
5,86	4,75	4,76	-0,82	3,97E-8
4,75	3,99	4,04	-0,82	2,02E-3
7,06	6,13	6,03	-0,82	3,37E-6
9,43	8,58	8,60	-0,82	3,16E-3
8,32	9,12	9,01	-0,81	1,51E-2
7,88	7,00	7,05	-0,81	2,46E-4
6,07	5,06	5,01	-0,81	5,38E-5
6,98	6,19	6,18	-0,81	1,86E-2
7,67	6,96	6,87	-0,80	7,46E-3
7,43	6,21	6,31	-0,80	3,85E-10
6,44	7,30	7,37	-0,80	2,00E-5
9,19	8,58	8,25	-0,80	6,35E-3
8,81	7,91	7,85	-0,80	8,31E-6
7,01	8,39	8,45	-0,80	0,00E+0
9,95	9,15	9,18	-0,79	1,20E-2
6,53	5,78	5,64	-0,79	2,94E-4
5,67	4,96	4,81	-0,79	3,61E-2
8,41	7,44	7,42	-0,79	2,45E-6
7,71	6,40	6,47	-0,79	0,00E+0
7,08	6,10	6,33	-0,78	1,21E-5
7,49	6,62	6,74	-0,78	7,55E-4
5,77	4,97	5,01	-0,78	1,94E-2
3,87	3,33	3,29	-0,78	2,89E-2
5,83	5,03	4,98	-0,78	3,16E-3
6,94	5,56	5,33	-0,78	0,00E+0
7,70	8,61	8,60	-0,78	3,20E-5
7,19	6,16	6,22	-0,77	1,21E-5
6,15	5,39	5,35	-0,77	3,23E-2
10,25	9,30	9,54	-0,77	8,32E-3
6,30	5,14	5,19	-0,77	1,46E-8
7,27	8,20	7,93	-0,77	2,14E-5
7,17	5,87	5,93	-0,77	3,50E-11
8,40	7,62	7,66	-0,77	6,04E-3
6,86	7,47	7,62	-0,76	7,06E-4
6,47	7,23	7,22	-0,76	8,36E-3
9,02	7,86	8,00	-0,76	3,05E-8
8,13	9,29	9,39	-0,76	0,00E+0
6,32	5,40	5,01	-0,76	2,27E-8
8,77	7,98	8,01	-0,76	1,05E-2
9,43	7,52	7,72	-0,76	0,00E+0
9,34	10,13	10,02	-0,76	3,32E-2
4,13	4,38	5,04	-0,76	4,13E-4
6,63	5,49	5,68	-0,76	6,59E-5
6,20	5,15	5,16	-0,76	1,29E-6
5,84	5,03	5,06	-0,76	1,23E-2
7,82	6,46	6,71	-0,76	1,40E-11
8,90	6,09	6,09	-0,75	0,00E+0

6,33	5,28	5,47	-0,75	3,57E-3
8,37	9,32	9,03	-0,75	4,27E-5
9,60	10,35	10,33	-0,75	2,96E-2
5,79	4,96	4,84	-0,75	2,57E-3
8,95	7,87	7,96	-0,75	3,06E-6
7,13	5,14	5,14	-0,75	0,00E+0
6,77	7,66	7,72	-0,75	3,93E-4
4,11	4,66	5,00	-0,75	5,44E-4
4,86	5,75	5,92	-0,75	7,85E-8
8,94	7,96	8,04	-0,74	8,48E-5
8,09	7,08	6,97	-0,74	6,69E-8
6,76	5,75	5,84	-0,74	1,05E-7
8,20	7,55	7,35	-0,74	3,76E-2
7,02	7,81	7,97	-0,74	9,43E-6
7,89	6,67	6,75	-0,74	2,31E-10
7,50	6,25	6,38	-0,74	3,99E-10
6,71	5,41	5,51	-0,74	7,00E-12
4,47	6,35	5,62	-0,73	7,00E-12
6,28	5,28	5,16	-0,73	2,62E-8
6,86	8,16	8,29	-0,73	0,00E+0
3,86	4,77	4,61	-0,73	1,54E-3
6,27	5,39	5,54	-0,73	3,76E-4
8,35	7,59	7,58	-0,73	3,11E-3
7,48	6,62	6,76	-0,73	2,39E-3
7,51	6,82	6,69	-0,73	1,76E-4
7,62	8,94	9,00	-0,73	0,00E+0
8,16	6,66	6,24	-0,73	0,00E+0
6,51	5,36	5,70	-0,73	4,33E-4
8,01	7,01	7,19	-0,73	2,97E-5
7,20	4,87	4,86	-0,73	0,00E+0
7,28	6,26	6,50	-0,73	1,51E-3
6,19	5,42	5,51	-0,73	1,48E-2
7,31	5,09	5,59	-0,72	0,00E+0
6,14	5,34	5,40	-0,72	4,64E-2
5,65	4,89	4,95	-0,72	4,51E-2
4,99	5,84	5,65	-0,72	1,45E-2
6,31	5,64	5,50	0,72	4,52E-2
9,78	8,89	9,10	0,72	1,38E-3
7,92	7,13	7,00	0,72	6,33E-4
10,48	9,54	9,81	0,73	4,44E-2
8,90	8,21	8,15	0,73	1,01E-2
8,44	7,47	7,52	0,73	1,92E-5
7,87	6,89	6,88	0,73	2,22E-6
6,08	5,03	5,03	0,73	4,86E-7
5,83	4,68	5,12	0,73	9,80E-4
7,01	5,75	5,68	0,73	0,00E+0
6,02	5,29	4,84	0,73	3,36E-4
9,46	10,35	10,18	0,73	2,73E-2
6,21	5,17	5,26	0,73	1,95E-7
5,92	6,35	6,55	0,73	3,97E-3
7,88	7,14	7,10	0,73	1,69E-2
9,86	6,16	6,81	0,74	0,00E+0
7,77	6,90	6,83	0,74	5,52E-4
9,57	7,67	8,25	0,74	0,00E+0
4,89	6,06	5,96	0,74	5,73E-9
5,68	6,89	6,80	0,74	2,40E-9
7,45	6,49	6,76	0,74	7,14E-5

5,12	4,23	3,61	0,74	1,40E-6
5,15	4,31	4,18	0,74	4,33E-4
6,94	6,34	5,78	0,74	1,41E-2
7,00	7,96	7,91	0,74	2,79E-4
7,17	6,39	6,30	0,75	1,20E-5
4,09	2,91	3,11	0,75	3,54E-2
7,77	6,64	6,65	0,75	7,28E-10
6,40	5,40	5,28	0,75	0,00E+0
4,71	3,52	3,17	0,75	5,56E-9
4,48	3,60	3,75	0,75	2,82E-2
8,37	9,10	9,14	0,75	3,38E-2
5,05	4,34	4,06	0,75	1,92E-5
7,74	6,96	6,90	0,76	1,37E-3
5,88	5,13	5,39	0,76	1,07E-3
5,83	4,92	5,24	0,76	3,99E-2
6,35	4,87	4,97	0,76	0,00E+0
6,37	5,48	5,09	0,76	1,40E-8
3,09	5,34	4,97	0,76	0,00E+0
4,99	6,18	6,46	0,76	7,00E-12
6,40	7,18	7,02	0,76	1,27E-2
7,00	5,71	5,96	0,76	5,43E-9
8,70	7,61	7,79	0,76	4,12E-7
7,91	8,53	8,67	0,76	1,91E-2
9,53	10,46	10,34	0,76	1,07E-4
8,06	8,79	8,79	0,76	1,27E-2
8,34	5,26	5,62	0,77	0,00E+0
6,73	5,77	5,75	0,77	2,77E-4
6,02	5,19	4,91	0,77	1,02E-2
8,54	9,51	9,47	0,77	1,32E-4
6,35	5,22	4,96	0,77	0,00E+0
8,06	8,79	9,02	0,77	1,13E-3
10,32	11,21	11,27	0,77	2,34E-5
7,66	8,35	8,56	0,77	2,94E-4
7,95	8,88	9,17	0,77	4,64E-9
9,71	6,64	6,88	0,77	0,00E+0
9,96	8,16	8,52	0,77	0,00E+0
6,66	7,78	7,68	0,78	0,00E+0
7,68	8,51	8,74	0,78	3,95E-5
4,86	5,22	5,45	0,78	3,34E-3
7,12	8,82	8,22	0,79	0,00E+0
4,44	5,36	5,07	0,79	2,21E-4
8,80	7,76	7,68	0,79	8,66E-8
6,38	7,25	7,36	0,79	1,03E-5
6,93	7,70	7,82	0,79	4,28E-5
6,30	5,70	5,68	0,79	1,38E-2
4,82	4,05	4,07	0,79	5,72E-3
5,24	6,17	6,33	0,80	2,52E-6
5,69	6,67	6,35	0,80	3,38E-3
6,10	6,75	6,92	0,80	3,93E-2
8,04	8,91	8,58	0,80	1,91E-2
5,97	6,26	7,27	0,80	2,37E-5
4,48	5,54	4,76	0,80	5,46E-3
4,79	5,35	5,63	0,80	9,07E-3
5,17	6,27	6,03	0,80	4,21E-7
8,96	8,05	8,13	0,81	7,29E-5
5,18	6,00	5,39	0,81	1,23E-2
4,77	3,66	3,44	0,81	6,30E-11

9,74	8,91	8,99	0,82	1,72E-3
7,78	7,06	7,12	0,82	1,03E-2
6,73	5,20	5,30	0,82	0,00E+0
8,03	6,76	6,92	0,82	2,80E-11
6,44	5,50	5,59	0,82	1,19E-6
4,41	3,30	3,74	0,82	1,90E-6
4,92	3,97	4,18	0,83	5,86E-6
5,29	4,17	4,56	0,83	8,21E-6
5,23	4,10	4,18	0,83	9,90E-6
5,05	3,55	4,28	0,83	1,88E-5
4,78	3,65	4,06	0,83	3,59E-5
8,08	7,37	7,11	0,83	3,63E-5
4,35	4,07	3,50	0,83	2,33E-4
6,60	5,93	5,39	0,83	2,52E-4
7,01	6,64	5,73	0,84	4,39E-4
10,47	9,47	9,76	0,84	4,59E-4
5,73	4,95	4,59	0,84	5,43E-4
5,01	4,80	3,88	0,84	8,30E-4
4,42	3,77	3,12	0,84	1,08E-3
7,58	6,46	7,32	0,85	1,16E-3
3,86	2,75	3,13	0,85	1,25E-3
9,85	9,03	9,07	0,85	1,28E-3
8,18	7,44	7,34	0,85	2,73E-3
4,36	3,78	3,21	0,85	5,12E-3
5,62	5,26	4,58	0,85	7,37E-3
7,06	6,22	6,32	0,85	1,23E-2
5,81	4,83	4,79	0,85	1,29E-2
4,01	3,29	3,41	0,86	1,29E-2
10,76	9,91	9,96	0,86	1,52E-2
8,71	8,19	7,81	0,86	1,56E-2
6,43	5,34	5,55	0,86	1,57E-2
5,39	4,51	4,14	0,86	2,02E-2
4,88	4,61	3,85	0,86	2,08E-2
6,34	5,57	5,63	0,86	2,09E-2
6,24	5,42	5,67	0,87	3,25E-2
4,65	3,78	3,83	0,87	3,53E-2
6,80	6,43	5,72	0,87	4,10E-2
5,51	5,02	4,56	0,87	4,80E-2
5,06	5,53	5,65	0,87	4,97E-2
4,13	4,69	4,95	0,87	4,90E-2
8,58	9,11	9,13	0,88	4,73E-2
5,01	5,42	6,03	0,88	4,34E-2
5,85	6,01	7,00	0,88	4,19E-2
3,47	3,75	4,20	0,88	3,92E-2
4,97	5,55	5,98	0,88	3,74E-2
3,59	4,35	4,15	0,89	3,62E-2
6,02	6,60	6,80	0,89	3,40E-2
3,54	4,33	4,48	0,89	3,28E-2
3,96	4,28	5,06	0,89	3,25E-2
5,19	5,54	6,06	0,90	3,20E-2
2,42	3,09	3,53	0,90	2,90E-2
3,79	4,64	4,84	0,90	2,82E-2
3,19	4,04	3,63	0,91	2,43E-2
4,22	4,91	5,01	0,91	2,40E-2
3,82	4,98	4,74	0,91	2,31E-2
3,86	4,75	4,64	0,91	2,27E-2
3,85	4,41	4,65	0,91	1,98E-2

5,05	5,20	5,99	0,91	1,87E-2
4,04	4,80	4,92	0,91	1,60E-2
5,79	6,85	6,43	0,91	1,55E-2
4,15	4,64	5,67	0,91	1,49E-2
7,64	8,14	8,32	0,92	1,26E-2
2,85	3,65	3,86	0,92	1,23E-2
3,96	4,39	5,02	0,92	1,23E-2
6,99	7,94	7,98	0,92	1,13E-2
5,46	6,75	6,49	0,93	1,08E-2
3,15	4,20	3,95	0,93	1,03E-2
6,21	6,83	7,47	0,93	9,72E-3
5,01	5,58	5,85	0,93	9,39E-3
4,30	4,60	5,33	0,93	8,08E-3
7,87	8,68	8,51	0,94	6,42E-3
11,39	11,86	12,13	0,94	5,73E-3
8,57	8,83	9,48	0,94	3,96E-3
3,64	4,27	4,47	0,95	3,94E-3
7,54	8,05	8,57	0,95	3,82E-3
2,78	3,25	3,87	0,95	3,01E-3
4,10	4,90	5,35	0,95	2,50E-3
6,56	6,97	7,56	0,95	1,91E-3
4,40	4,29	5,42	0,95	1,59E-3
6,79	6,91	7,77	0,96	1,58E-3
4,68	5,28	5,81	0,97	1,35E-3
4,14	4,91	5,26	0,97	1,28E-3
3,87	4,50	4,57	0,98	1,28E-3
5,14	5,63	6,41	0,98	1,16E-3
9,90	10,76	10,71	0,99	9,07E-4
4,98	5,89	5,75	0,99	8,96E-4
8,06	8,71	9,06	0,99	4,71E-4
5,62	6,58	7,01	0,99	4,55E-4
5,02	5,86	5,88	1,00	4,38E-4
3,28	4,03	4,20	1,00	4,33E-4
3,53	4,09	4,36	1,01	3,75E-4
4,25	5,01	5,02	1,01	3,28E-4
7,51	8,14	8,32	1,02	3,21E-4
3,90	4,22	5,15	1,03	2,09E-4
6,93	8,02	7,79	1,03	1,68E-4
5,14	5,43	6,02	1,05	1,64E-4
8,12	8,61	9,62	1,05	1,57E-4
8,69	9,63	9,56	1,06	1,47E-4
7,08	7,50	8,03	1,06	1,21E-4
5,35	6,36	6,70	1,06	1,11E-4
3,90	4,69	5,08	1,06	1,06E-4
6,79	7,33	7,62	1,09	7,81E-5
6,12	6,80	7,08	1,10	6,06E-5
6,01	6,41	6,87	1,10	5,85E-5
5,21	6,03	6,32	1,11	5,21E-5
5,53	6,05	7,19	1,11	5,10E-5
5,26	6,25	6,08	1,12	3,23E-5
3,78	4,65	4,51	1,12	2,05E-5
7,40	7,86	8,67	1,17	1,53E-5
7,15	8,30	8,11	1,23	1,29E-5
8,16	9,01	9,09	1,23	9,13E-6
3,44	4,14	4,18	1,24	9,00E-6
5,53	6,69	6,44	1,25	7,31E-6
4,22	5,03	5,48	1,26	2,95E-6

5,04	5,94	5,85	1,27	1,54E-6
3,22	4,13	4,41	1,27	1,44E-6
5,62	6,85	6,42	1,29	1,35E-6
4,66	5,72	6,10	1,31	8,37E-7
8,96	9,67	9,94	1,33	7,07E-7
5,18	6,06	6,25	1,33	2,77E-7
5,26	5,99	6,44	1,35	6,08E-8
5,63	6,96	7,11	1,39	4,89E-8
3,59	4,70	4,65	1,40	1,08E-8
4,55	5,65	5,73	1,44	2,55E-9
5,26	6,04	6,60	1,49	7,00E-12
7,31	8,14	8,34	1,51	7,00E-12
5,12	6,62	6,70	1,55	0,00E+0
8,28	9,58	9,57	1,56	0,00E+0
6,74	8,13	8,58	1,63	0,00E+0
7,57	9,26	9,12	1,79	0,00E+0