



HAL
open science

Grape@GnpIS: Overview of the GnpIS grape genomics and genetics integrative resource

Nacer Mohellibi, Nathalie Choisne, Aminah A. Keliet, Daphné Verdelet, Françoise Alfama, Guillaume Merceron, Célia Michotey, Amandine Launay, Thomas Letellier, Raphaël Flores, et al.

► **To cite this version:**

Nacer Mohellibi, Nathalie Choisne, Aminah A. Keliet, Daphné Verdelet, Françoise Alfama, et al.. Grape@GnpIS: Overview of the GnpIS grape genomics and genetics integrative resource. 23. Plant and Animal Genome (PAG XXIII), Jan 2015, San Diego, Californie, United States. pp.24 slides. hal-02741780

HAL Id: hal-02741780

<https://hal.inrae.fr/hal-02741780>

Submitted on 3 Jun 2020

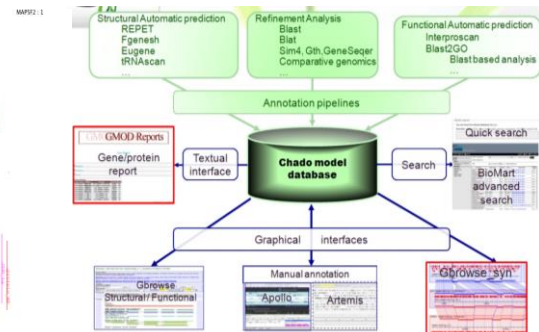
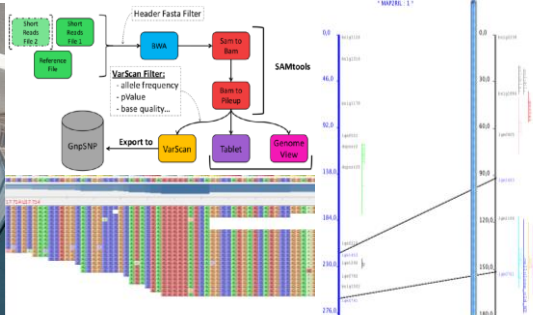
HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Grape@GnplS

Overview of the GnplS Grape Genomics & Genetics Integrative Resource

Nacer Mohellibi

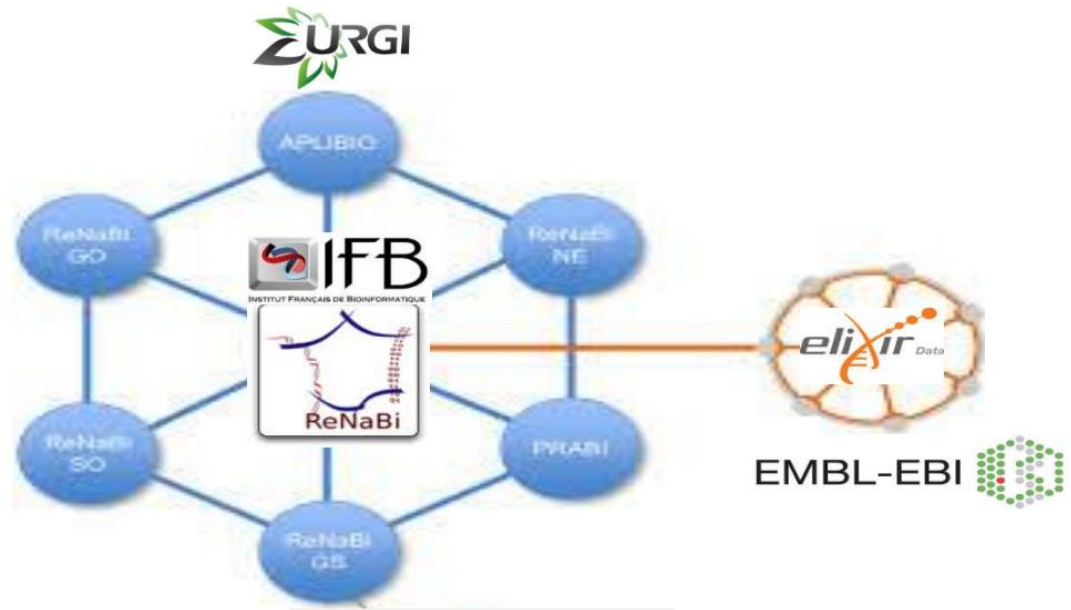




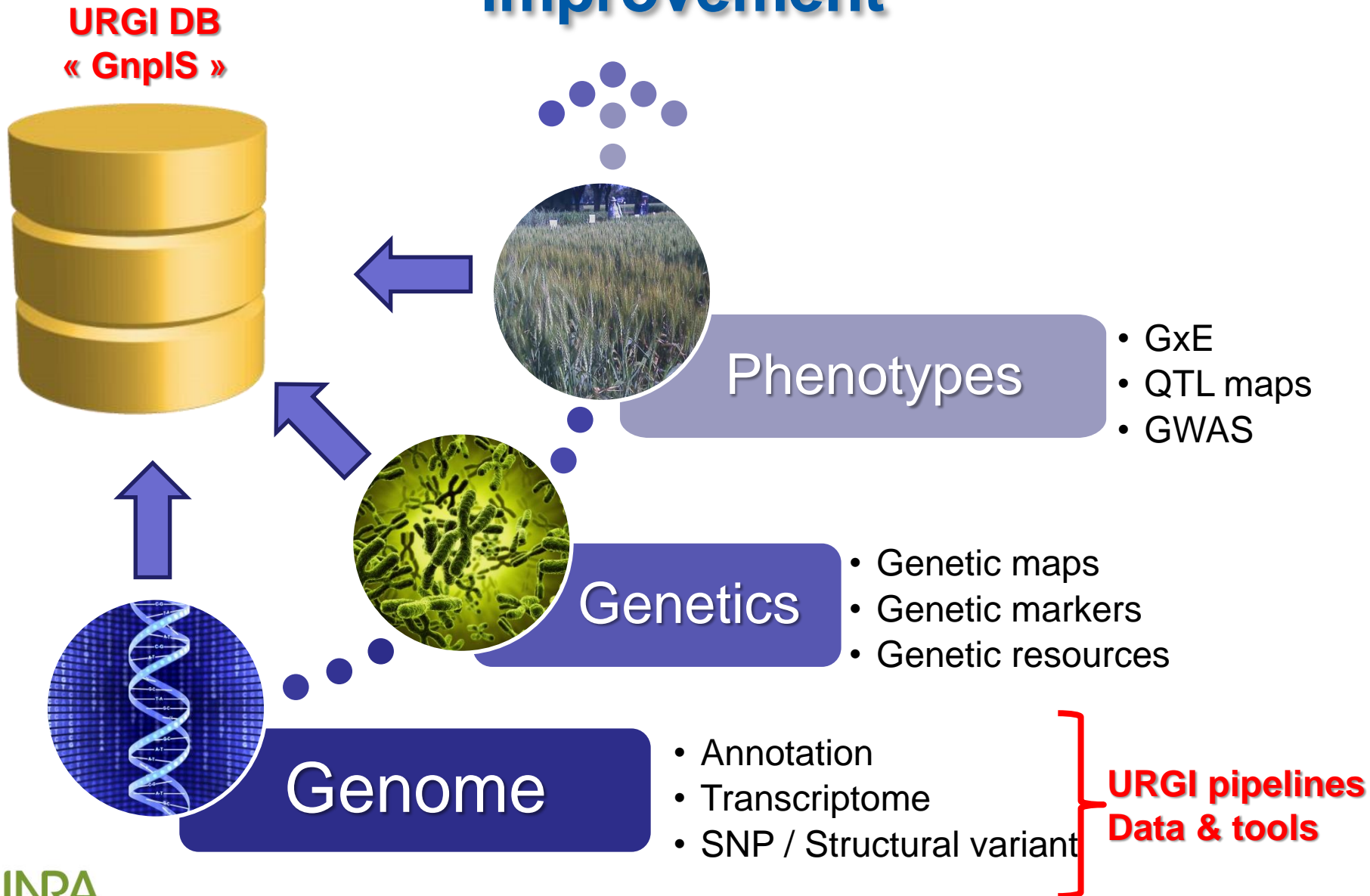
ABOUT URGI

<https://urgi.versailles.inra.fr>

The screenshot shows the URGI website header with the logo and the text "PLANT AND FUNGI DATA INTEGRATION". A navigation bar includes links for Platform, Research, Projects, Data, Tools, and Species. A search bar is present with an "OK" button. A "Register" link is in the top right. A "WHAT'S NEW?" section features an RSS icon and a news item dated 21 Nov 2014: "2A physical map is now available" with subtext "2AS and 2AL physical maps are now". A sidebar lists categories: Taxon, Sequence, Genetic maps, Polymorphisms, Phenotype, and Association. Below the navigation bar, there is a descriptive paragraph in English and a corresponding paragraph in French, both with an "About" link below them.



A bioinformatic platform for crop improvement



GnplS Overview

Transversal portal

Global search

QUICK SEARCH No restriction

WVF52

You can find the indexed data list [here](#).

Examples: [WJ](#), [WVF52](#), [gene_arabidopsis](#), [AY109603](#), [xwmc430](#)

ADVANCED TOOLS

Genomes
Genome annotation data. GnpGenome.

Taxons
Taxonomic data.

Sequences
NGS projects description. GnpSeq.

Genetic maps
Genetic maps and QTLs. GnpMap.

Polymorphisms
Molecular polymorphism. GnpSNP.

Phenotypes
Phenotypic and environmental experiments. Ephesis.

Genetic resources
Plant genetic resources data. Siregal.

Arrays
Expression data. GnpArray.

GrapeMine

Biomart

Galaxy

Thematic portals

genome

taxonomy

maps

polymorphisms

phenotypes

Genetic resources

GnpMap / Taxon: Triticum aestivum

GnpSeq / Run: STEWALXX

Genetic resources

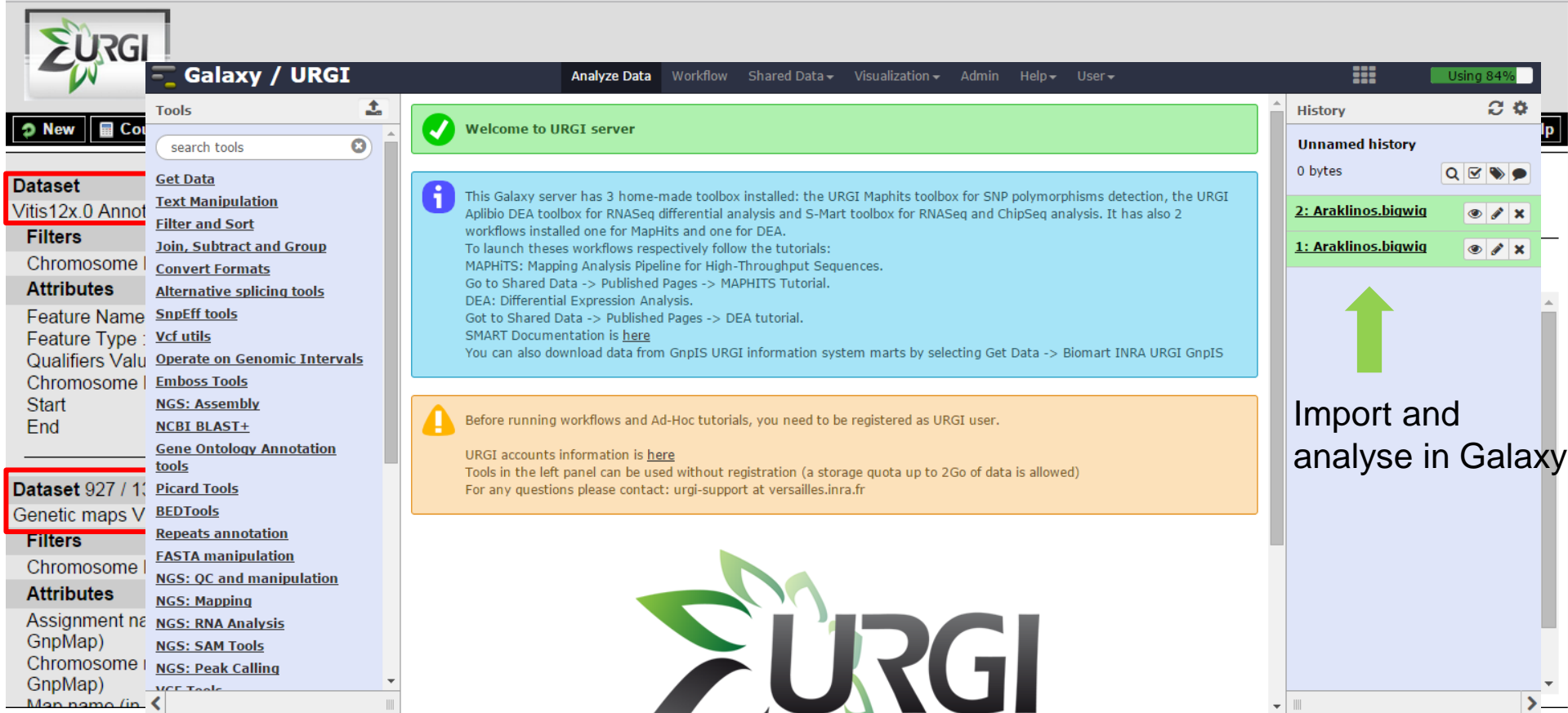
Transversal portal - quicksearch



The screenshot displays the GnpIS (Genetic and Genomic Information System) interface. At the top, it features the GnpIS logo and the text "GENETIC AND GENOMIC INFORMATION SYSTEM". A search bar is prominently displayed with "WIF52" entered and highlighted by a red box. Below the search bar, there are two tabs for "Vitis (8X) genome" and "Vitis (12X) genome", with the latter being selected. The search results show "Features (1)" for "WIF52" with a four-star rating. Below the results, it indicates "1 items found, displaying 1 to 1 | Display 10 results per page". The interface also includes a "SEARCH" button, a "FEEDBACK" link, and a section for "ADVANCED TOOLS" with buttons for "BIOMART", "GALA...", and "INTERMINE".

<https://urgi.versailles.inra.fr/gnpis/>

Transversal portal Biomart & Galaxy



Dataset
Vitis12x.0 Annot

Filters
Chromosome
Attributes
Feature Name
Feature Type
Qualifiers Value
Chromosome
Start
End

Dataset 927 / 1; Genetic maps V
Filters
Chromosome
Attributes
Assignment name
GnpMap)
Chromosome
GnpMap)
Map name (in

Tools
search tools

Get Data
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Alternative splicing tools
Snpeff tools
Vcf utils
Operate on Genomic Intervals
Emboss Tools
NGS: Assembly
NCBI BLAST+
Gene Ontology Annotation tools
Picard Tools
BEDTools
Repeats annotation
FASTA manipulation
NGS: QC and manipulation
NGS: Mapping
NGS: RNA Analysis
NGS: SAM Tools
NGS: Peak Calling
VCF Tools

Welcome to URGI server

This Galaxy server has 3 home-made toolbox installed: the URGI Maphits toolbox for SNP polymorphisms detection, the URGI Aplibio DEA toolbox for RNASeq differential analysis and S-Mart toolbox for RNASeq and ChipSeq analysis. It has also 2 workflows installed one for MapHits and one for DEA.
To launch these workflows respectively follow the tutorials:
MAPHITS: Mapping Analysis Pipeline for High-Throughput Sequences.
Go to Shared Data -> Published Pages -> MAPHITS Tutorial.
DEA: Differential Expression Analysis.
Got to Shared Data -> Published Pages -> DEA tutorial.
SMART Documentation is [here](#)
You can also download data from GnpIS URGI information system marts by selecting Get Data -> Biomart INRA URGI GnpIS

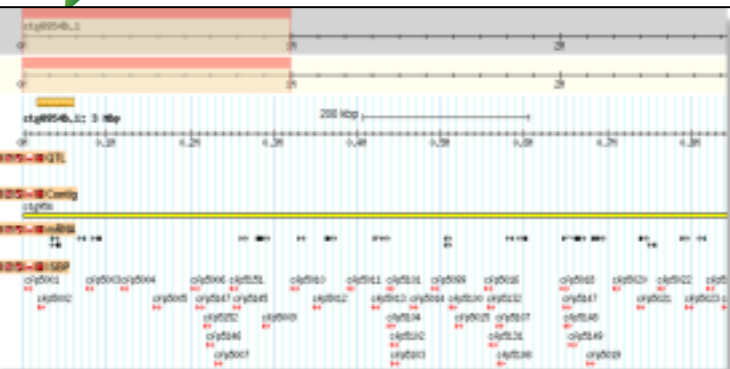
Before running workflows and Ad-Hoc tutorials, you need to be registered as URGI user.
URGI accounts information is [here](#)
Tools in the left panel can be used without registration (a storage quota up to 2Go of data is allowed)
For any questions please contact: urgi-support@versailles.inra.fr

History
Unnamed history
0 bytes
2: Araklinos.bigwig
1: Araklinos.bigwig

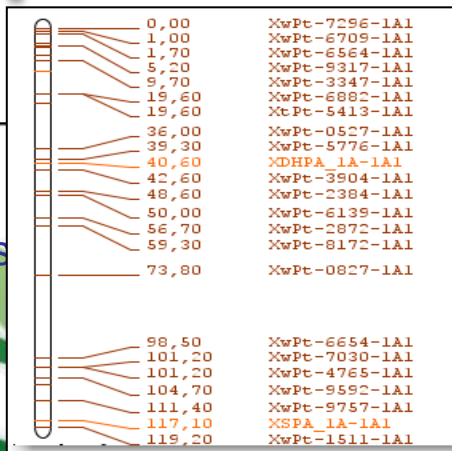
Import and analyse in Galaxy

→ Integration of Genomic and Genetics data for Vitis markers in chr. 18

Thematic portals



Genome
Vitis 8X
& 12X
(annotations
Genoscope
and CRIBI)



Sequencing
Metadata & Files
Resequencing runs:
2 public / 13 private

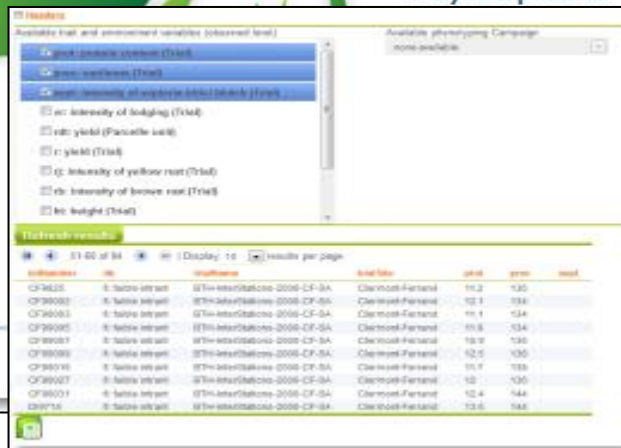
Genetic Resources
10,459 Vitis accessions



Genetic Maps & Markers
27 Vitis genetic maps

Genetic maps
Genetic maps and QTLs

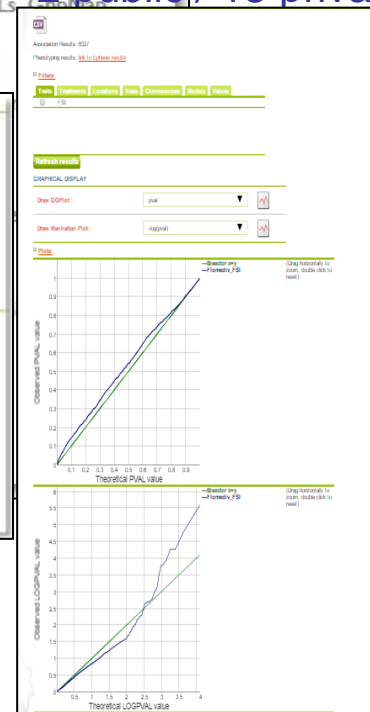
Polymorphisms



Phenotyping 1 trial

Polymorphism (genotypes of
>1100 accessions for > 14000
markers)

Nacer Mohellibi



GWAS (in progress)

Genotyping form

Back to form

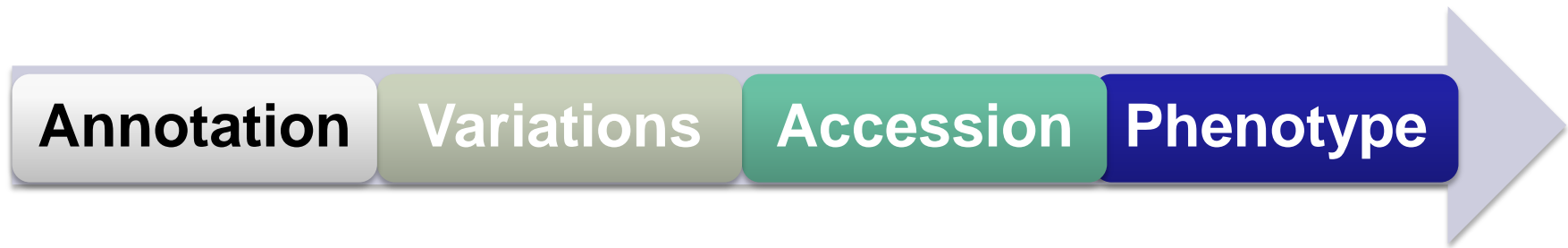
GENOTYPING RESULTS

Marker	Accession	Genotype type	Genotype	Quality type	Quality	Experiment	Marker set
chr18_814711_A_G	Wildbachertruebbau	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	LAIREN	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	SENA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	TROUSSEAU NOIR	genotype	AG			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	LADO	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	ALJURELHAG	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	Zaubertschwarz	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	Delledonora	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	TOURIGAFRANCA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina
chr18_814711_A_G	JAVORSEBS	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina

GENOTYPING MATRIX

Marker \ Accession	ALBILLA	Adreuli skekana	ALARJUE	ALCA? ON	AIREN	ALLAREN	ALEDO	Adreuli tetri	ALMERIA NERA
chr18_882766_A_G	GG	AA	AA	AA	AG				
chr18_758407_C_T	CC				CC	CC	CC	CC	CC
chr18_816244_A_G			AA			AA		AG	AA
chr18_750791_C_T		TC		CC		CC	CC	CC	CC
chr18_715339_C_T		TC		CC	CC	CC	TT	CC	CC
chr18_814711_A_G	AA	AA	AA	AA	AA	AA			

1 Workflow / 2 use cases

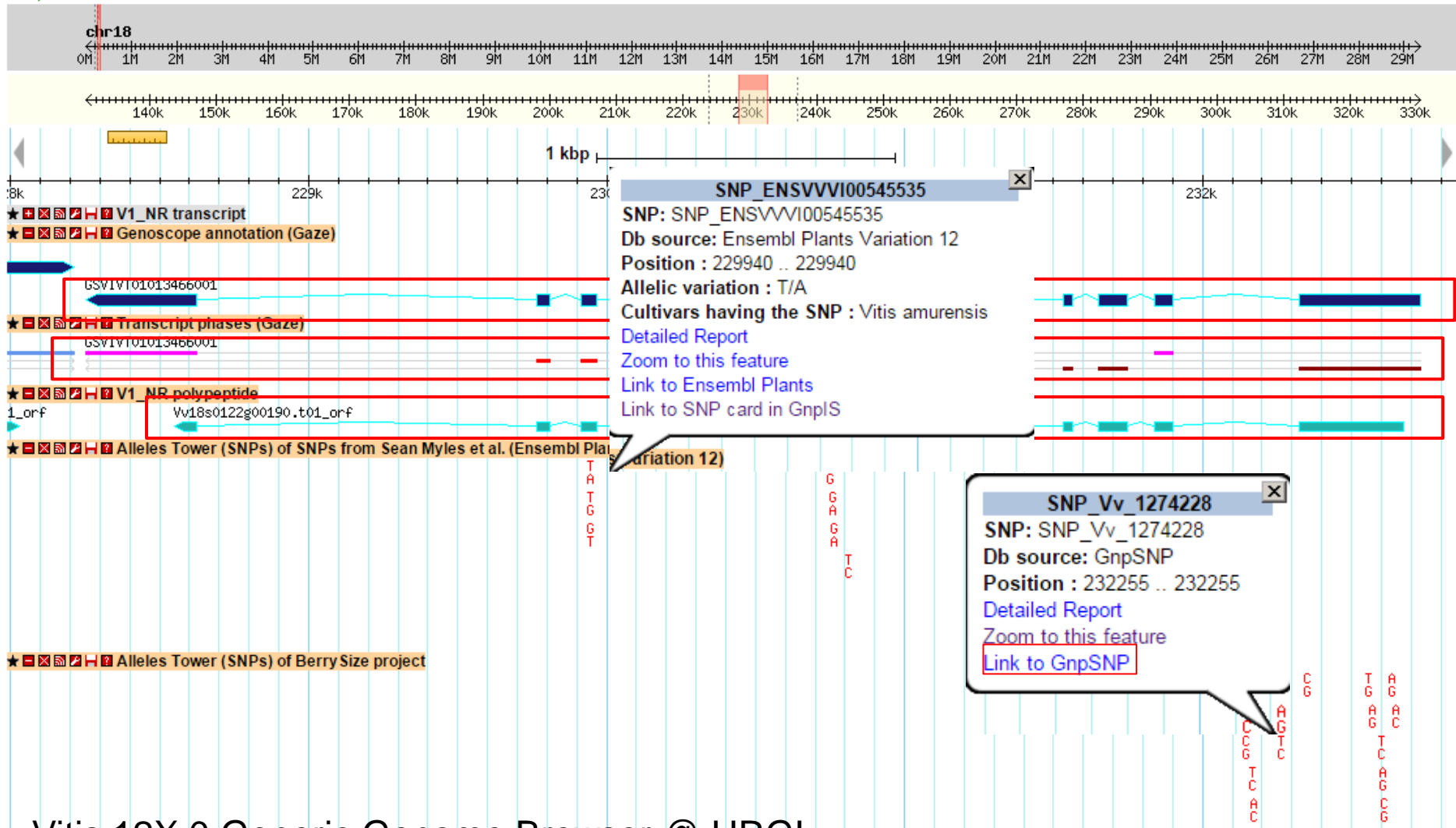




Use case 1: Zoom on a gene in Flb Locus

The screenshot displays the GnpIS (Genetic and Genomic Information System) interface. At the top, the URGI logo and the text "GnpIS GENETIC AND GENOMIC INFORMATION SYSTEM" are visible. On the left, a navigation menu includes "Log in", "Main" (with a home icon), "GNPIS HOME", "Searches" (with a magnifying glass icon), "QUICK SEARCH", "ADVANCED TOOLS", "Documentation" (with a book icon), "USER GUIDE", "NEWS", and "RELEASE NOTES". The main content area shows a search form with a dropdown menu set to "All species", a text input field containing "GSVIVG01013466001", and a "SUBMIT" button. Below the search form, a green button labeled "Vitis (12X) genome" is highlighted. Underneath, a section titled "Features (2)" lists two entries: "GSVIVG01013466001" with five yellow stars, and "GSVIVT01013466001" with four stars (one greyed out). Below the list, it says "2 items found, displaying 1 to 2 | Display 10 results per page". At the bottom of the search results, there is another identical search form with the same input and "SUBMIT" button.

GnpIS QuickSearch: <https://urgi.versailles.inra.fr/gnpis/>




Vitis 12X.0 Generic Genome Browser @ URGI:
https://urgi.versailles.inra.fr/gb2/gbrowse/vitis_12x_pub




SNP details

Polymorphic locus card

DETAILS

Name :	Vv_1274238
Ref. Sequences :	Major allele of variants in VVC2972A-bat 
Position on ref. seq. :	512
Source :	GnpSNP

COMPLEMENTS

Type :	SNP
Sequence variation :	C/G 
Linked with variations :	VVC2972A_512_45  View list
Linked with lines :	294Mtp1  View list




MAPPING INFORMATIONS (NGS)

Reference Genome :	Vitis vinifera 12X
Taxon (mapping) :	Vitis vinifera L.
Chromosome :	chr18
Mapping position :	176646

EXTERNAL REFERENCES

Database	Reference name	Reference value
Vitis vinifera 12x Genome Browser	name	SNP Vv_1274238

SEQUENCES

5' flanker on ref.seq. :	>Vv_1274238-5' TGGGCCCCAGAAGACCATCACTCTTCTCTCCAGAGGCGAGGCTGTACCACATCACCCCTAAGGTATCATCCTCCCAATC TTTTCTTTCTTTCTTTGTTCTCTCCTCGATTGAAAAACCTCTTTCAGTCCATCTGAAATCCACCTCCCTAGACT TCCGAGTTCCTATTAAATCCATTCAATTCCCTAACTCATCGCTACCGAATTCCTAAATTTGCTTGGGTCT GCTTCTACTT	
3' flanker on ref.seq. :	>Vv_1274238-3' TTATTAATTCATAATTAATTTGTGCTATTTTTCTTTTTCAAAAAAAAA	
Genomic context on ref. seq. :	>Vv_1274238-genomic_context TGGGCCCCAGAAGACCATCACTCTTCTCTCCAGAGGCGAGGCTGTACCACATCACCCCTAAGGTATCATCCTCCCAATC TTTTCTTTCTTTCTTTGTTCTCTCCTCGATTGAAAAACCTCTTTCAGTCCATCTGAAATCCACCTCCCTAGACT TCCGAGTTCCTATTAAATCCATTCAATTCCCTAACTCATCGCTACCGAATTCCTAAATTTGCTTGGGTCT GCTTCTACTT[C/G]TTATTAATTCATAATTAATTTGTGCTATTTTTCTTTTTCAAAAAAAAA	

Sequence variations of the locus

Sequence variation results

RESULTS



1 2 3 4 | 31 items found, displaying 1 to 10 | Display results per page

#	Name	Type	Project	Experiment	Line	Ref. sequence	Position on ref. seq.	Gene/marker name
1	VVC2972A_512_10	SNP	BerrySize	VVC2972A-batch1	9006Mtp1	Major allele of variants in VVC2972A-batch1	512	VVC2972A
2	VVC2972A_512_11	SNP	BerrySize	VVC2972A-batch1	8056Mtp1	Major allele of variants in VVC2972A-batch1	512	VVC2972A
3	VVC2972A_512_12	SNP	BerrySize	VVC2972A-batch1	6541Mtp4	Major allele of variants in VVC2972A-batch1	512	VVC2972A
4	VVC2972A_512_16	SNP	BerrySize	VVC2972A-batch1	8010Mtp1	Major allele of variants in VVC2972A-batch1	512	VVC2972A
5	VVC2972A_512_18	SNP	BerrySize	VVC2972A-batch1	8003Mtp1	Major allele of variants in VVC2972A-batch1	512	VVC2972A

Resequencing batch genotypes summary

Genotype table

RESULTS

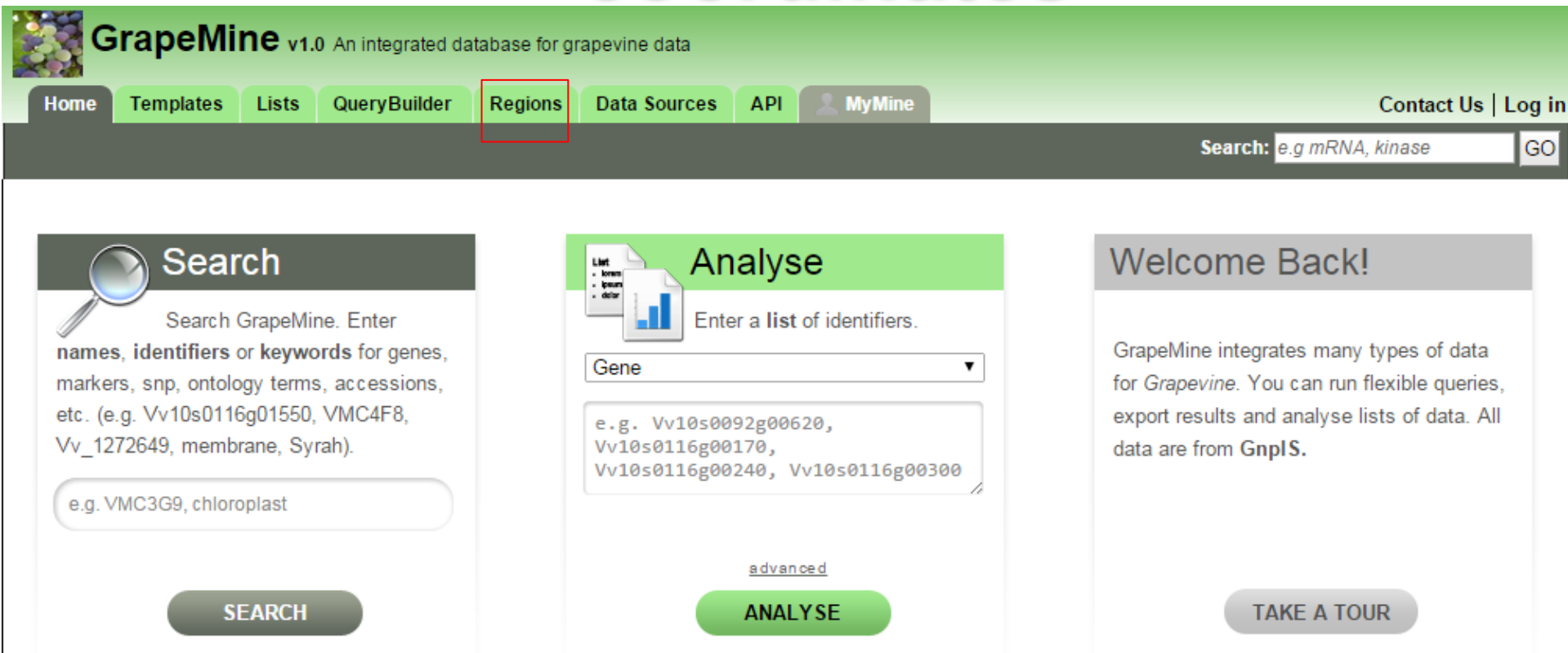


1 2 3 4 ▶ ▶ | 36 items found, displaying 1 to 10 | Display results per page

The experiment [VVC2972A-batch1](#) contains 32 marker(s).

Positions	4	15	17	21	23	46	51	53	84	99	176	283	303	321	340	346	360	391	396	427	482	487
Ref. Sequence Major allele of variants in VVC2972A-batch1	A	G	G	A	DEL	G	G	T	G	G	A	C	C	T	T	DEL	IN	C	C	G	C	T
Genotype Taxon 9006Mtp1 Vitis riparia cv. Riparia Gloire de Montpellier	A	G	G	G	-----	G	G	T	G	G	A	C	C	T	C	-	G	C	C	A	C	T
Genotype Taxon 0Mtp567 Vitis vinifera L.	A	G	G	A	TTCTGGTATTGGCGTTGGC	G	G	C/T	G	G	A/C	C	C	T	T	T	-	C	C	G	C	T
Genotype Taxon 0Mtp636 Vitis vinifera L.	A	G	G	A	TTCTGGTATTGGCGTTGGC	G	G	C/T	G	G	A/C	C	C	T	T	T	-	C/T	C	G	C	T
Genotype Taxon 1498Mtp1 Vitis vinifera subsp. vinifera cv. Espadelleiro into	A	G	G	A	TTCTGGTATTGGCGTTGGC	G	G	T	G	G	A/C	C	C	T	T	T	-	C	C	G	C	T
Genotype Taxon 225Mtp2 Vitis vinifera subsp. vinifera cv. César	A	G	G	A	TTCTGGTATTGGCGTTGGC	G	G	T	G	G	A	C	C	T	T	T	-	C	C	G	C	T
Genotype Taxon 0Mtp1323 Vitis vinifera L.	A	G	G	A	TTCTGGTATTGGCGTTGGC	G	G	C	G	G	C	C	C	T	T	T	-	C	C	G	C	T
Genotype Taxon 8500Mtp23 Vitis vinifera L.	A	G	G	A	TTCTGGTATTGGCGTTGGC	G	G	T	G	G	A	C	C	T	C/T	T	n/a	n/a	n/a	n/a	n/a	n/a

Use case 2: Enter by genome coordinates



GrapeMine v1.0 An integrated database for grapevine data

Home Templates Lists QueryBuilder **Regions** Data Sources API MyMine Contact Us | Log in

Search: GO

Search

Search GrapeMine. Enter names, identifiers or keywords for genes, markers, snp, ontology terms, accessions, etc. (e.g. Vv10s0116g01550, VMC4F8, Vv_1272649, membrane, Syrah).

SEARCH

Analyse

Enter a list of identifiers.

Gene

e.g. Vv10s0092g00620,
Vv10s0116g00170,
Vv10s0116g00240, Vv10s0116g00300

[advanced](#)

ANALYSE

Welcome Back!

GrapeMine integrates many types of data for *Grapevine*. You can run flexible queries, export results and analyse lists of data. All data are from **GnplS**.

TAKE A TOUR

GrapeMine: <http://urgi.versailles.inra.fr/GrapeMine/begin.do>

*More details on InterMine functionalities
Wheat3BMine Poster #654: Letellier T. et al.
and computer demo: January 13th 11:00 am*

GrapeMine: Region form

Search for features within Genomic Regions

Search for features that overlap a list of genome coordinates you enter or upload, e.g. **chr1:20..10000000**

[Genome coordinates help](#)

1. Select Organism: *genome build: not available*

2. Select Feature Types:

Exon

Gene

Indel

Marker

mRNA

Polypeptide

SNP

3. Type/Paste in genomic regions in base coordinate interbase coordinate

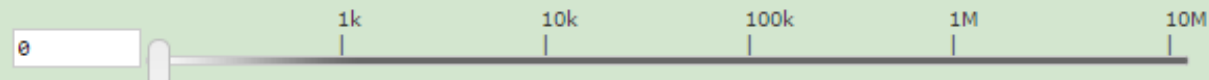
[\(click to see an example\)](#)

chr18:745,960..749,094

or Upload genomic regions from a .txt file...

Aucun fichier choisi

4. Extend your regions at both sides:





Selected organism: *V. vinifera* Hide
 Selected feature types: Exon, Marker, SNP, Gene, mRNA, Indel, Polypeptide

Export for all regions: or Create List by feature type: Page size << First < Prev | Next > Last >>

GENOME REGION	FEATURE	FEATURE TYPE	LOCATION
chr18:745960..749094 <input type="button" value="FASTA..."/> <input type="button" value="TAB"/> <input type="button" value="CSV"/> <input type="button" value="GFF3"/> <input type="button" value="FASTA"/> <input type="button" value="BED"/> <input type="button" value="GALAXY"/> Create List by <input type="text" value="Exon"/> <input type="button" value="Go"/>	Vv18s0122g01060 Vv18s0122g01060	Gene ^o	chr18:745960..749094
	Vv18s0122g01060.t01 Vv18s0122g01060.t01	mRNA ^o	chr18:745960..749094
	Vv18s0122g01060.t01.e6 Vv18s0122g01060.t01.e6	Exon ^o	chr18:745960..746164
	Vv18s0122g01060_orf Vv18s0122g01060_orf	Gene ^o	chr18:746021..748732
	Vv18s0122g01060.t01_orf Vv18s0122g01060.t01_orf	mRNA ^o	chr18:746021..748732
	Vv18s0122g01060.t01.p01_orf Vv18s0122g01060.t01.p01_orf	Polypeptide ^o	chr18:746021..748732
	Vv18s0122g01060.t01.e6_orf Vv18s0122g01060.t01.e6_orf	Exon ^o	chr18:746021..746164
	Vv18s0122g01060.t01.p01 Vv18s0122g01060.t01.p01	Polypeptide ^o	chr18:746021..748732
	Vv18s0122g01060.t01.e5_orf Vv18s0122g01060.t01.e5_orf	Exon ^o	chr18:746643..746760
	Vv18s0122g01060.t01.e5 Vv18s0122g01060.t01.e5	Exon ^o	chr18:746643..746760
indel_Vv_1273703 Vv_1273703	Indel ^o	chr18:746783..746783	
SNP_Vv_1273492 Vv_1273492	SNP ^o	chr18:746825..746825	
SNP_Vv_1273728 Vv_1273728	SNP ^o	chr18:746843..746843	
SNP_Vv_1273483 Vv_1273483	SNP ^o	chr18:746849..746849	
SNP_Vv_1273475 Vv_1273475	SNP ^o	chr18:746864..746864	
SNP_Vv_1273711 Vv_1273711	SNP ^o	chr18:746864..746864	
SNP_Vv_1273463 Vv_1273463	SNP ^o	chr18:746883..746883	

Genes,
transcripts,
ORFs

Indels

SNPs

Zoom on a SNP

SNP : **SNP_Vv_1273492** *V. vinifera*

DB identifier	Vv_1273492	Organism . Name	Vitis vinifera
Allele	A/G	Gnpsnpid	1273492
Taxon	Vitis vinifera L.		

[SHARE](#)

Genome feature

Region:	SNP	Length:	1
Location:	chr18:746825-746825 forward strand		

Overlapping Features

Genome features that overlap coordinates of this SNP
 Genes: 2, mRNAs: 2, Polypeptides: 2

[Show all in a table »](#)

Lists

This SNP isn't in any lists. Upload a list.

External Links

[Browse URGI VITIS12X](#)
[GNP-SNP URGI VITIS12X](#)

1 Organism

Name	Taxon Id
Vitis vinifera	29760

1 Data Sets

Name	URL
markersvitis12X	

List of the species concerned by this marker

Genotype results

AVAILABLE GENOTYPES



1 2 3 4 ▶ ▶ | 34 items found, displaying 1 to 10 | Display 10 ▼ results per page

#	Genotype name	Taxon
1	2082Mtp1	Vitis vinifera subsp vinifera cv. Mehdik
2	9006Mtp1	Vitis riparia cv. Riparia Gloire de Montpellier
3	0Mtp567	Vitis vinifera L.
4	0Mtp636	Vitis vinifera L.
5	8011Mtp12	Vitis berlandieri Planch.
6	225Mtp2	Vitis vinifera subsp vinifera cv. César
7	0Mtp1323	Vitis vinifera L.
8	8003Mtp1	Vitis amurensis Ruprecht
9	324Mtp1	Vitis vinifera subsp vinifera cv. Cabernet franc
10	1186Mtp1	Vitis vinifera subsp vinifera cv. Chirai obak

Diversity in *V. vinifera* in the chr18: 700K-800k region (1)

GnplS genotyping form: <https://urgi.versailles.inra.fr/GnpSNP/snp/genotyping/form.do>

Genotyping

↓

Accessions
Markers

Add accessions by genus

Add accessions by panel

Add accessions by name

Selected accessions

Accession

Adreuli ske

Adreuli tetr

AIREN

ALARIJE

ALARJVER

ALBILLA

ALBILLO D

Genotyping form

Show results

Accessions
Markers

Marker set

Select your marker sets

Markers

Custom marker set

chr18_715339_C_T
 chr18_750761_C_T
 chr18_758407_C_T
 chr18_814711_A_G
 chr18_816244_A_G
 chr18_882766_A_G

Selected markers

1-6 of 6

Marker	Marker type	Taxon	Remove
chr18_715339_C_T	SNP	Vitis vinifera L.	✘
chr18_750761_C_T	SNP	Vitis vinifera L.	✘
chr18_758407_C_T	SNP	Vitis vinifera L.	✘
chr18_814711_A_G	SNP	Vitis vinifera L.	✘

Diversity in *V. vinifera* in the chr18: 700K-800k region (2)

Genotyping form

[Back to form](#)

GENOTYPING RESULTS

1-10 of 560

Marker

- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)
- [chr18_814711_A_G](#)

GENOTYPING MATRIX

1 - 100 of 6

	A	B	C	D	E	F	G	H	I
1	markerName	AccessionName	Genotype type	Genotype	Quality type	Quality	Experiment	Genotyping array	
2	chr18_814711_A_G	Wildbacherfruehblau	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
3	chr18_814711_A_G	LAIREN	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
4	chr18_814711_A_G	SENA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
5	chr18_814711_A_G	TROUSSEAU NOIR	genotype	AG			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
6	chr18_814711_A_G	LADO	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
7	chr18_814711_A_G	ALVARELHAO	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
8	chr18_814711_A_G	Tauberschwarz	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
9	chr18_814711_A_G	Oeilladenoire	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
10	chr18_814711_A_G	TOURIGAFRANCA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
11	chr18_814711_A_G	Javorweiss	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
12	chr18_814711_A_G	TrincadeiradasPratas	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
13	chr18_814711_A_G	DERECHERO DE MUNIES	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
14	chr18_814711_A_G	MIGUELDEARCO	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
15	chr18_814711_A_G	Heunischrot	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
16	chr18_814711_A_G	TARRAGONI	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
17	chr18_814711_A_G	E32 07	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
18	chr18_814711_A_G	FORCALLAT TINTA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
19	chr18_814711_A_G	Savagninblanc	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
20	chr18_814711_A_G	VERDIL	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
21	chr18_814711_A_G	CONCA D???ORO	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
22	chr18_814711_A_G	Limnio	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
23	chr18_814711_A_G	ZALEMA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
24	chr18_814711_A_G	BERMEJUELA	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	
25	chr18_814711_A_G	Bakatorroz	genotype	AA			GrapeReSeq_illumina_20K_experiment	GrapeReSeq_illumina_20K	

CSV

Marker \ Accession	ALBILLA	Adreuli skelkana	ALARIEJE	ALCA? ON	AIREN	ALLAREN	ALEDO	Adreuli tetri	ALMERIA NERA
chr18_882766_A_G	GG	AA	AA	AA	AG				
chr18_758407_C_T	CC				CC	CC	CC	CC	CC
chr18_816244_A_G			AA			AA		AG	AA
chr18_750761_C_T	TC	TC		CC		CC	CC	CC	CC
chr18_715339_C_T	TC				CC	CC	TT	CC	
chr18_814711_A_G	AA	AA	AA	AA		AA			

Prospects

- **Jbrowse based on the Vitis12X.2 assembly**

Learn more about this assembly:

<https://urgi.versailles.inra.fr/Species/Vitis/Data-Sequences/Genome-sequences>

- **Add GWAS Vitis data (INRA)**



Available soon: Vitis GWAS data

More details on GnpAsso:
Poster #1128
Computer demo
January 13th 10:30 am

GnpIS Genetic Association form:

<https://urgi.versailles.inra.fr/association/association/welcome.do>

Association

DETAILS

Number of association analyses:	2
Number of panels:	1
Number of chromosomes:	13
Number of associated markers:	6327
Number of associated traits:	2
Number of phenotyping treatments:	0
Number of phenotyping years:	1

GRAPHICAL DISPLAY

Draw QQPlot :

pval



Draw Manhattan Plot:

$-\log(pval)$



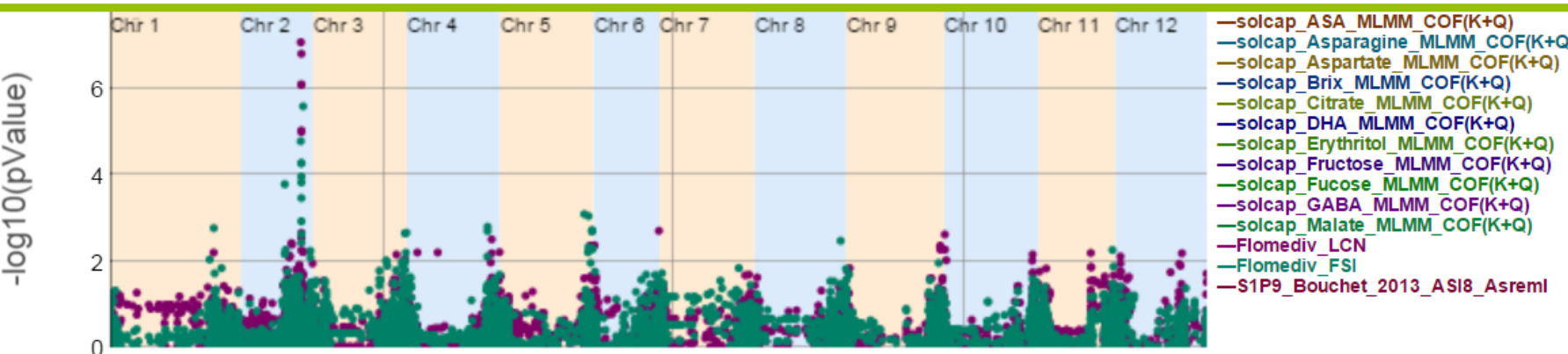
Plots:

Draw Manhattan Plot:

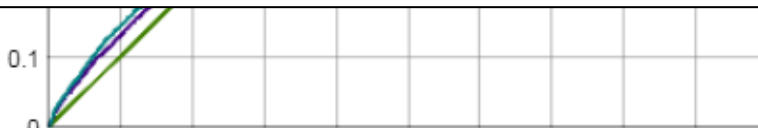
$-\log(pval)$



Plots:



Position of markers by chromosome



Acknowledgments

- URG I TEAM



- INRA PARTNERS
INRA EPGV, INRA AGAP,
INRA URGV...

- PROJECT PARTNERS
GrapereSeq, Muscares,
SNPGrapeMap...



THANK YOU FOR YOUR ATTENTION!



Contact: nacer.mohellibi@versailles.inra.fr