

# transPLANT

## First User training workshop : Tutorial on GnplS

November 13th 2012, INRA Versailles

Delphine Steinbach, INRA URGI





A screenshot of the GNPIS PORTAL interface. At the top, there's a navigation bar with links: GnpMap, GnpSeq, GnpGenome, GnpArray, GnpProt, SIRGal, Ephesis. Below this is a large green banner with the text "GNPIS PORTAL" and a right-pointing arrow. Underneath is a blue banner with the text "SPECIES" and a right-pointing arrow. The main content area shows a wheat field image with several arrows pointing to different genomic and bioinformatics tools: structural variants, genomics, TE annotation, molecular evolution, Tranposable Elements; REPET package, Pipelines, heterochromatin, TE classification.



# URGI, an INRA research unit

URGI, a  
Bioinformatics  
facility  
ISO-9001:2008



<http://urgi.versailles.inra.fr>  
<http://urgi.versailles.inra.fr/Platform>  
<http://urgi.versailles.inra.fr/gnpis>

# Missions and services

- Develop an information system for genetics and genomics data of plant and fungi (from genotype to phenotype)
- Develop pipelines for data analysis corresponding to URGI expertise and fields of research
- Maintain a repository with integrated data for plants and fungi of interest for INRA
- Provide a support for large collaborative project (data management, genome annotation, and data analysis)
- Provide tools, training and expertise for its users
- Provide computer resources for its collaborators



**URGI Web site**  
**<http://urgi.versailles.inra.fr>**





# INRA URGI Web site

## <http://urgi.versailles.inra.fr>

FEEDBACK | CONTACT | SITE MAP | ABOUT US Register

URGI - Unité de Recherche Génomique Info is a research unit in genomics and bioinformatics at Institut National de la Recherche Agronomique (INRA), dedicated to plants and crop parasites. The URGI research activity covers genome structure and dynamics. URGI hosts a [bioinformatics platform](#), which belongs to the French national network of bioinformatics platforms ([ReNaBi](#)).

L'URGI est une unité de recherche en génomique et bio-informatique de l'Institut National de la Recherche Agronomique (INRA), dédiée à la génomique des plantes et de leurs pathogènes. Son [activité de recherche](#) porte sur la structure et la dynamique du génome. L'unité héberge une [plate-forme bioinformatique](#) appartenant au REseau NAtional des plateformes Bio-informatiques ([ReNaBi](#)).

**EVENT & PUBLICATIONS**

**20 Nov 2012 User committee for Siregal project :**  
The User Scientific Committee for Siregal project (GnpIS genetic resource module) will take place ...

**05 Nov 2012 3 newcomers :**  
URGI team welcomes 3 engineers:  
• Blissam Alissaoui in ...

**31 Oct 2012 First User transPLANT training workshop at URGI campus :**  
First User transPLANT european training workshop will be held at INRA URGI Campus, from ...

**11 Oct 2012 talk on the new Galaxy workflow dedicated to RNASeq NGS ...**  
COM (talks)  
Pasteur institute, 11th of October 2012  
...

**11 Oct 2012 URGI bioinformatics platform talk: last news and updates ...**  
COM (talks)  
Pasteur institute, the 11th of October  
...

**11 Oct 2012 Presentation of GnpIS Information system at Apilbio annual meeting ...**  
COM (talks)  
Institut Pasteur. The meeting was organized by Ivan

**WHAT'S NEW ?**

**06 Nov 2012 New Zea mays ZmB73 V2 genome browser.**  
The private Zea mays ZmB73 Genome annotation is now available.  
...

**06 Nov 2012 Phenotype: data submission**  
Phenotyping data submison is now available.  
...

**26 Oct 2012 ISO 9001 certification**  
The Management System of URGI has been approved by LRQA (Lloyd's Register Quality Assurance) ...

**08 Oct 2012 Tools: link from Blast Results to Gbrowse**  
We provide a new link between Blast results launched via the Mobyle framework (

**11 Sep 2012 Data insertion: new forage accessions**  
152 Tall Fescue (Forage) accessions have been inserted in Siregal, ...

**04 Sep 2012 URGI platform unavailability 09/05/12 12-13PM**  
Our internet provider informed us of a short network interruption September the 5th ...

**SEARCH** **OK** **RSS**

**GNPIS PORTAL**

**SPECIES**

**RESEARCH**

**MORE... >** **MORE... >**



# Data content of GnpIS

## Data submission files

[Platform](#)   [Research](#)   [Projects](#)   **Data**   [Tools](#)   [Species](#)

SEARCH

OK

### Data

You are here : [Home](#) / [Home URGi](#) / Data

- [Transposable elements](#)
- [Genome](#)
- [Mapping](#)
- [Polymorphism](#)
- [Phenotype](#)
- [Genetic collections](#)
- [NGS sequences](#)
- [Transcriptome](#)
- [Sequences](#)
- [All Free access banks](#)
- [All registered access banks](#)

### Data

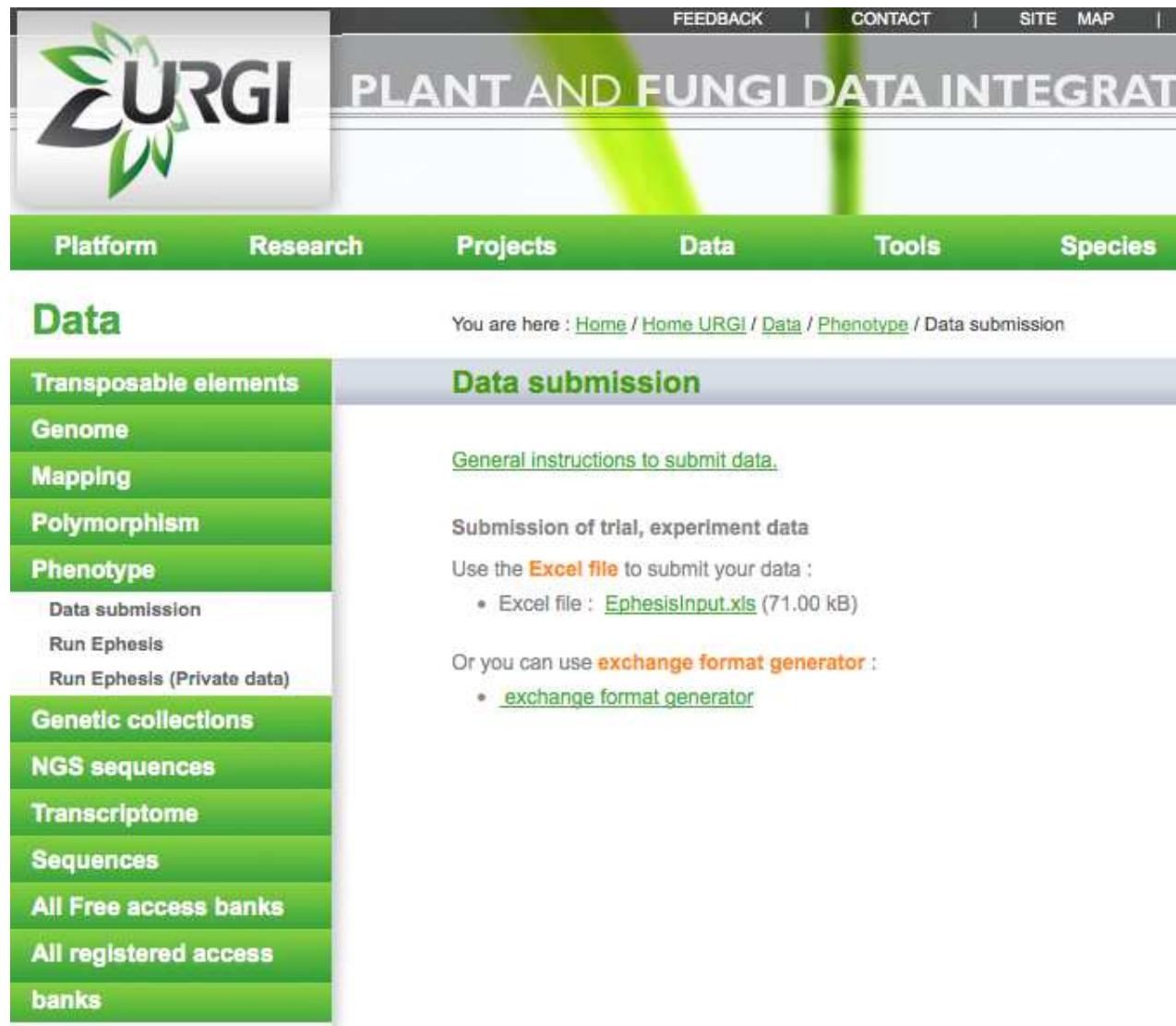
To submit data (registered access to download and to submit files) :

- Step 1 : Download templates files according to the type of data.
- Step 2 : Fill the templates corresponding to your data (see below)
- Step 3 : Submit delimited and text files through our Web site or contact us.

Different types of files are available according to the type of data :

Types of data	How to submit	Access to data	
		Public access	Registered access
Genome annotation data			
Mapping			
Polymorphisms			
Phenotype			
Genetic resources			
NGS sequences			
Transcriptome			
Sequences			

# A new \*\* template \*\* to submit phenotyping data



The screenshot shows the URGI website interface. At the top, there is a navigation bar with links for FEEDBACK, CONTACT, SITE MAP, and a search bar. Below the navigation bar is a banner with the text "PLANT AND FUNGI DATA INTEGRATION". The main menu includes links for Platform, Research, Projects, Data, Tools, and Species. On the left, there is a sidebar under the heading "Data" containing links for Transposable elements, Genome, Mapping, Polymorphism, Phenotype, Genetic collections, NGS sequences, Transcriptome, Sequences, All Free access banks, and All registered access banks. The main content area shows the "Data submission" section, which includes instructions for submitting data via Excel or exchange format generator, and a link to the submission file "EphesisInput.xls".

Contributors:

- Ephesis
- BreedWheat (Arvalis)
- Transplant Projects

Coord. C. Pommier & al. URGI

 INRA

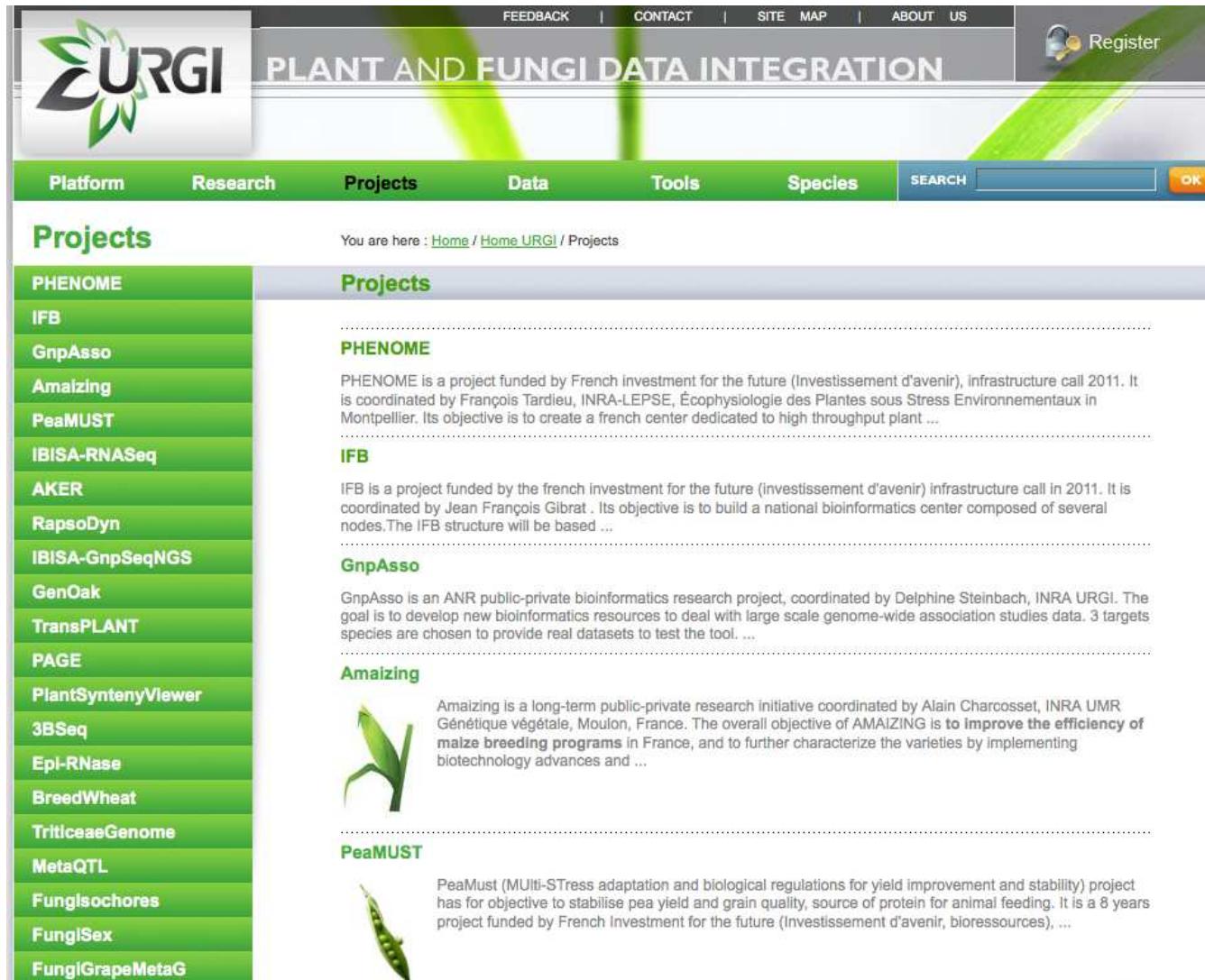
# Full genomic sequence data (Gbrowse / chado or BioSeqFeature)

Platform	Research	Projects	Data	Tools	Species	SEARCH	OK														
<b>Data</b>																					
You are here : <a href="#">Home</a> / <a href="#">Home URG! / Data / Genome</a> / Genome data access																					
<a href="#">Transposable elements</a> <a href="#">Genome</a> Genome data access Data submission Species		<b>Genome data access</b> <table border="1"> <tbody> <tr> <td><i>Agaricus subrefescens</i></td> <td>           GBrowse: <a href="#">Agaricus subrefescens functional isotig annotation</a>            Genome Report System: <a href="#">Agaricus subrefescensisotigs annotation report</a> </td> </tr> <tr> <td><i>Arabidopsis thaliana</i></td> <td>           GBrowse: <a href="#">Transnet - Arabis alpina GBrowse II (registered)</a>            GBrowse_syn: Synteny between <i>A. thaliana</i>, <i>A. lyrata</i> and <i>A. alpina</i> (registered)            Apollo: <a href="#">Distributed manual annotation system</a> </td> </tr> <tr> <td><i>Arabidopsis thaliana</i></td> <td>           GBrowse: <a href="#">epiRNaseIII - Arabidopsis thaliana GBrowse II (registered)</a>            GBrowse: <a href="#">RIP-Seq - Arabidopsis thaliana GBrowse II (registered)</a>            GBrowse: <a href="#">Arabidopsis thaliana TAIR V10</a> </td> </tr> <tr> <td><i>Vitis vinifera</i></td> <td>           GBrowse: <a href="#">Vitis vinifera (12X) Genome Browser</a>            GBrowse_syn: Synteny between <i>Vitis</i> 12X and <i>Vitis</i> 8X            GBrowse: <a href="#">Vitis vinifera (8X) Genome Browser</a>            GBrowse : <a href="#">Vitis vinifera (12X) Muscaries Genome Browser (registered)</a>            Gbrowse : <a href="#">Vitis vinifera (12X) Vitaroma Genome Browser (registered)</a>            Apollo: <a href="#">Distributed manual annotation system</a> </td> </tr> <tr> <td><i>Triticum aestivum</i></td> <td>           GBrowse: <a href="#">Wheat physical map viewer v4.0</a>            GBrowse: <a href="#">Wheat annotation viewer v2.0</a> </td> </tr> <tr> <td><i>Botrytis cinerea</i> T4</td> <td>           GBrowse: <a href="#">Botrytis cinerea T4 automated functional gene annotation</a>            GBrowse: <a href="#">Botrytis cinerea T4 genome annotation</a>            GBrowse_syn: Synteny between <i>Botrytis cinerea</i> T4/B05.10 and <i>Sclerotinia sclerotiorum</i>            Apollo: <a href="#">manual curation/validation of Botrytis cinerea T4 genes</a>            Genome Report System: <a href="#">Botrytis cinerea T4 genes annotation report</a> </td> </tr> <tr> <td><i>Botrytis cinerea</i> B0510</td> <td>           GBrowse: <a href="#">Botrytis cinerea B05.10 automated functional gene annotation</a>            GBrowse_syn: Synteny between <i>Botrytis cinerea</i> T4/B05.10 and <i>Sclerotinia sclerotiorum</i>            Genome Report System: <a href="#">Botrytis cinerea B05.10 genes annotation report</a> </td> </tr> </tbody> </table>						<i>Agaricus subrefescens</i>	GBrowse: <a href="#">Agaricus subrefescens functional isotig annotation</a> Genome Report System: <a href="#">Agaricus subrefescensisotigs annotation report</a>	<i>Arabidopsis thaliana</i>	GBrowse: <a href="#">Transnet - Arabis alpina GBrowse II (registered)</a> GBrowse_syn: Synteny between <i>A. thaliana</i> , <i>A. lyrata</i> and <i>A. alpina</i> (registered) Apollo: <a href="#">Distributed manual annotation system</a>	<i>Arabidopsis thaliana</i>	GBrowse: <a href="#">epiRNaseIII - Arabidopsis thaliana GBrowse II (registered)</a> GBrowse: <a href="#">RIP-Seq - Arabidopsis thaliana GBrowse II (registered)</a> GBrowse: <a href="#">Arabidopsis thaliana TAIR V10</a>	<i>Vitis vinifera</i>	GBrowse: <a href="#">Vitis vinifera (12X) Genome Browser</a> GBrowse_syn: Synteny between <i>Vitis</i> 12X and <i>Vitis</i> 8X GBrowse: <a href="#">Vitis vinifera (8X) Genome Browser</a> GBrowse : <a href="#">Vitis vinifera (12X) Muscaries Genome Browser (registered)</a> Gbrowse : <a href="#">Vitis vinifera (12X) Vitaroma Genome Browser (registered)</a> Apollo: <a href="#">Distributed manual annotation system</a>	<i>Triticum aestivum</i>	GBrowse: <a href="#">Wheat physical map viewer v4.0</a> GBrowse: <a href="#">Wheat annotation viewer v2.0</a>	<i>Botrytis cinerea</i> T4	GBrowse: <a href="#">Botrytis cinerea T4 automated functional gene annotation</a> GBrowse: <a href="#">Botrytis cinerea T4 genome annotation</a> GBrowse_syn: Synteny between <i>Botrytis cinerea</i> T4/B05.10 and <i>Sclerotinia sclerotiorum</i> Apollo: <a href="#">manual curation/validation of Botrytis cinerea T4 genes</a> Genome Report System: <a href="#">Botrytis cinerea T4 genes annotation report</a>	<i>Botrytis cinerea</i> B0510	GBrowse: <a href="#">Botrytis cinerea B05.10 automated functional gene annotation</a> GBrowse_syn: Synteny between <i>Botrytis cinerea</i> T4/B05.10 and <i>Sclerotinia sclerotiorum</i> Genome Report System: <a href="#">Botrytis cinerea B05.10 genes annotation report</a>
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# Full genomic sequence data (Gbrowse / chado or BioSeqFeature)

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<i>Leptosphaeria</i>	<a href="#">GBrowse: <i>Leptosphaeria maculans</i> JN3 automated functional gene annotation</a> <a href="#">GBrowse: <i>Leptosphaeria maculans</i> JN3 genome annotation</a> <a href="#">GBrowse_syn: Synteny between <i>Leptosphaeria</i> complex genomes (registered)</a> <a href="#">Apollo: manual curation/validation of <i>Leptosphaeria maculans</i> JN3 genes</a> <a href="#">Genome Report System: <i>Leptosphaeria maculans</i> JN3 genes annotation report</a>
<i>Microbotryum violaceum</i>	<a href="#">GBrowse: <i>Microbotryum</i> Sex Chromosomes (registered)</a>
<i>Tuber Melanosporum</i>	<a href="#">Apollo: manual curation/validation of <i>Tuber Melanosporum</i> genes</a>
<i>Venturia Inaequalis</i>	<a href="#">GBrowse: <i>Venturia Inaequalis</i> genome annotation (registered)</a> <a href="#">Genome Report System: <i>Venturia Inaequalis</i> gene annotation report (registered)</a>
<i>Populus trichocarpa</i>	<a href="#">GBrowse: <i>Populus trichocarpa</i> Genome browser (V1 genome version)</a> <a href="#">GBrowse: <i>Populus trichocarpa</i> Genome browser (registered) (V1 genome version)</a> <a href="#">GBrowse: <i>Populus trichocarpa</i> Genome browser V2.0</a>
<i>Zea mays</i> ZmB73 V2	<a href="#">GBrowse: <i>Zea mays</i> ZmB73 Genome annotation</a> <a href="#">GBrowse: <i>Zea mays</i> ZmB73 Genome annotation (registered)</a>
<i>Malus x domestica</i>	<a href="#">GBrowse: <i>Malus x domestica</i> Genome browser (registered)</a>
<i>Solanum lycopersicum</i> (iTAG 2.3)	<a href="#">GBrowse: <i>Solanum lycopersicum</i> (iTAG 2.3) Genome Browser (registered)</a>
<i>Wheat, Maize, Rice, Sorghum</i>	<a href="#">Plant synteny viewer (registered)</a>
<i>Pisum sativum</i> L.	<a href="#">Gbrowse: <i>Pisum sativum</i> Genome Browser (registered)</a>
<i>Medicago truncatula</i>	<a href="#">Gbrowse: <i>Medicago truncatula</i> Genome Browser (registered)</a> <a href="#">Gbrowse: <i>Medicago truncatula</i> GenomeBrowser on physical map (registered)</a>

# Access data by our projects list



The screenshot shows the URGI website interface. At the top, there is a navigation bar with links for FEEDBACK, CONTACT, SITE MAP, ABOUT US, and a Register button. Below the navigation bar, the title "PLANT AND FUNGI DATA INTEGRATION" is displayed. The main content area has a green header bar with tabs for Platform, Research, Projects, Data, Tools, Species, and a search bar. The "Projects" tab is selected. On the left, a sidebar lists various projects: PHENOME, IFB, GnpAsso, Amaizing, PeaMUST, IBISA-RNASeq, AKER, RapsoDyn, IBISA-GnpSeqNGS, GenOak, TransPLANT, PAGE, PlantSyntenyViewer, 3BSeq, Epi-RNase, BreedWheat, TriticeaeGenome, MetaQTL, FungiSochores, FungiSex, and FungiGrapeMetaG. The main content area displays detailed information for each project, including a brief description and a small image related to the project. For example, the PHENOME project is described as a French investment for the future infrastructure call 2011, coordinated by François Tardieu at INRA-LEPSE. The IFB project is described as a French investment for the future infrastructure call 2011, coordinated by Jean François Gibrat. The GnpAsso project is described as an ANR public-private bioinformatics research project, coordinated by Delphine Steinbach at INRA URGI. The Amaizing project is described as a long-term public-private research initiative coordinated by Alain Charcosset at INRA UMR Génétique végétale. The PeaMUST project is described as a Multi-STress adaptation and biological regulations for yield improvement and stability project.

FEEDBACK | CONTACT | SITE MAP | ABOUT US | Register

PLANT AND FUNGI DATA INTEGRATION

Platform Research Projects Data Tools Species SEARCH OK

## Projects

You are here : Home / Home URGI / Projects

Projects	Projects
PHENOME	PHENOME
IFB	IFB
GnpAsso	GnpAsso
Amaizing	Amaizing
PeaMUST	PeaMUST
IBISA-RNASeq	IBISA-RNASeq
AKER	AKER
RapsoDyn	RapsoDyn
IBISA-GnpSeqNGS	IBISA-GnpSeqNGS
GenOak	GenOak
TransPLANT	TransPLANT
PAGE	PAGE
PlantSyntenyViewer	PlantSyntenyViewer
3BSeq	3BSeq
Epi-RNase	Epi-RNase
BreedWheat	BreedWheat
TriticeaeGenome	TriticeaeGenome
MetaQTL	MetaQTL
FungiSochores	FungiSochores
FungiSex	FungiSex
FungiGrapeMetaG	FungiGrapeMetaG

**PHENOME**  
PHENOME is a project funded by French investment for the future (Investissement d'avenir), infrastructure call 2011. It is coordinated by François Tardieu, INRA-LEPSE, Écophysiologie des Plantes sous Stress Environnementaux in Montpellier. Its objective is to create a french center dedicated to high throughput plant ...

**IFB**  
IFB is a project funded by the french investment for the future (investissement d'avenir) infrastructure call in 2011. It is coordinated by Jean François Gibrat . Its objective is to build a national bioinformatics center composed of several nodes.The IFB structure will be based ...

**GnpAsso**  
GnpAsso is an ANR public-private bioinformatics research project, coordinated by Delphine Steinbach, INRA URGI. The goal is to develop new bioinformatics resources to deal with large scale genome-wide association studies data. 3 targets species are chosen to provide real datasets to test the tool. ...

**Amaizing**  
Amaizing is a long-term public-private research initiative coordinated by Alain Charcosset, INRA UMR Génétique végétale, Moulon, France. The overall objective of AMAIZING is to improve the efficiency of maize breeding programs in France, and to further characterize the varieties by implementing biotechnology advances and ...

**PeaMUST**  
PeaMust (Multi-STress adaptation and biological regulations for yield improvement and stability) project has for objective to stabilise pea yield and grain quality, source of protein for animal feeding. It is a 8 years project funded by French Investment for the future (Investissement d'avenir, bioressources), ...

# Genoplante : our first big project : 2000-2005 ) : maize, wheat, pea, rape... ESTs markers, QTLs, microarrays...

Collaboration with  
Rhobio  
(BayerCropscience,  
Biogemma)  
and INRA Moulon  
(maize)  
and GDEC (Wheat)

Database dvpt,  
data integration  
D. Steinbach & al.

**Genoplante**

 GENOPLANTE is a federative programme for plant genomics research in France.

Since its creation in 1999, this programme has made it possible to fund research on the genomes of crop plants (wheat, maize, rice, pea, rapeseed and sunflower) and also on the model genome of the species *Arabidopsis*. Its objective has also been to support research for the creation of tools for genomic research (BAC libraries, microsatellites, SNP, etc.) or functional genome analysis (collections of insertion mutants, TILLING technology, etc.) or in the field of high throughput biology (tools for analysing the transcriptome, proteome and metabolome, etc.). Over hundred projects have been funded by the ministries of research and agriculture during the two first phases.

A new initiative was launched in April 2005 to maintain the competitiveness of French research in this strategic field to the year 2010. This initiative, called GENOPLANTE 2010, is to last for six years and involves seven members working together on the basis of fair cooperation between the private and public sectors:

- From the public sector: INRA, CNRS, CIRAD and IRD.
- From the private sector: BIOGEMMA, ARVALIS Institut du Végétal (Arvalis plant institute) and SOFIPROTEOL.

This programme is now supported by the French national research agency (ANR: Agence Nationale de la Recherche) which calls for projects and takes funding decisions. The annual budget that was announced for the programme for the next few years is in the region of 30 M euros, including 12 M euros in the form of grants from the ANR. GENOPLANTE 2010 is thus entering a new phase in its development, focusing on four strategic objectives:

- To determine and then validate gene function on a large scale in crop species that are cultivated in France (wheat, maize, rapeseed, sunflower and pea crops) in order to:
  1. improve the quality and safety of agricultural products;
  2. minimise the impact on the environment, in particular by reducing inputs;
  3. increase the agricultural productivity of crop species and their tolerance to climatic variation.
- To promote widely the use of the tools that have already been developed, and to develop new technologies, in particular in the fields where France is still lagging behind, such as proteomics and metabolomics research.
- To broaden research and its applications to other important species for which professionals have expressed an interest, for example tomato, potato, grape, trees, cocoa and coffee.
- To build a genuine partnership at the European level, so that GENOPLANTE can be an important link in the construction of a European biotechnology and plant genomics platform, and to seek new reciprocal alliances at the international level (with Canada, China, USA and Australia).

The programme also aims to increase the efficiency of its policy to protect and exploit results, while still sharing its findings through publication in high quality international journals. The essential aim of the SAS GENOPLANTE VALOR, which was set up in 2001 as an equal partnership between public and private members, is to own, manage and exploit the patent rights of the results obtained from the GENOPLANTE programme.

GENOPLANTE 2010 is an open programme, which aims to encourage joint research projects between both public (European projects etc.) and private partners and participate in ERA-PG.

# TriticeaeGenome project : physical maps – genetics maps, QTLs

FP7

Coord:

C. Feuillet & al.

First collaboration with  
K. Mayer team

and N. Stein for barley

Data integration  
at URGI  
M Alaux & al.

**TriticeaeGenome**

**Improvement of Triticeae genomics**

TriticeaeGenome project is a european EC 7th Framework Program (-Food, Agriculture and Fisheries) project, where INRA URGI platform is in partnership. TriticeaeGenome goal is to improve the genomics of Triticeae (wheat, barley). It is a large collaborative international project coordinated by C. Feuillet, INRA Clermont-Ferrand.

**Links:**

- [Wheat data at URGI](#)
- [Barley data at MIPS](#)
- [TriticeaeGenome project presentation](#)
- [TriticeaeGenome collaborative workspace \(project members only\)](#)

**Project data summary:**

Data	Provider	Status	Public	Registered
<b>Wheat</b>				
Physical map 3B v1 and v2	E. Paux (INRA GDEC, France)	done		
Physical map 1BL v1 and v2	R. Philippe (INRA GDEC, France)	done		
Physical map 1AS v1	J. Breen & T. Wicker (IPB, Zurich)	v1		
Physical map 3DS v1	J. Bartos & J. Dolozel (IEB, CZH)	v1		
Physical map 1BS v1	Z. Frenkel & A. Korol (Haifa, Israel)	v1		
Genetic maps and markers : Neighbour3B, Neighbour1BL, SSR, ISBP.	P. Leroy & P. Sourdille (INRA GDEC, France)	done		
QTL : TOR107	M. Bogard & J. Le Gouis (INRA GDEC, France)	done		
QTL : CF9107xToisondorxQuebon	M. Bogard & J. Le Gouis (INRA GDEC, France)	done		
<b>Barley</b>				

**Applications**



# TriticeaeGenome project

Physical map 3DS v1	J. Bartos & J. Dolozel (IEB, CZH)	v1	
Physical map 1BS v1	Z. Frenkel & A. Korol (Haifa, Israel)	v1	
Genetic maps and markers : Neighbour3B, Neighbour1BL, SSR, ISBP.	P. Leroy & P. Sourdille (INRA GDEC, France)	done	
QTL : TOR107	M. Bogard & J. Le Gouis (INRA GDEC, France)	done	
QTL : CF9107xTolsendorxQuebon	M. Bogard & J. Le Gouis (INRA GDEC, France)	done	
<b>Barley</b>			
Genetic maps and markers : Stein consensus, Close Illumina consensus, Sato transcriptmap.	N. Stein (IPK, Germany)	done	

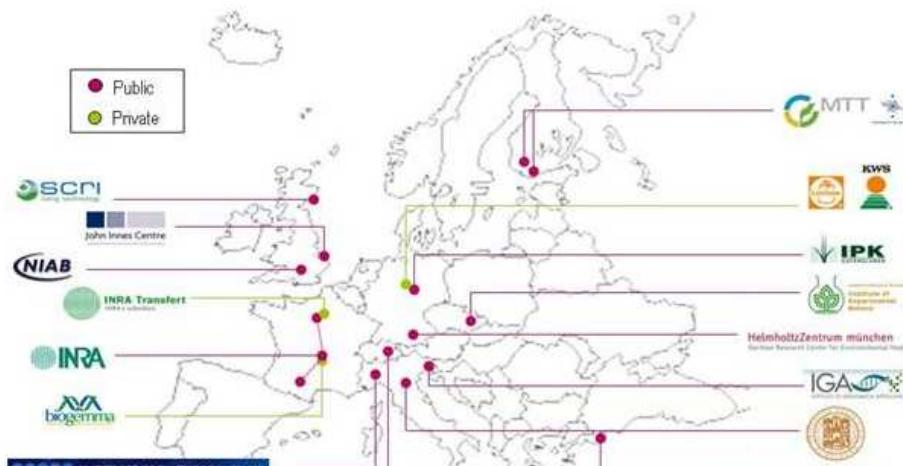
## Project data submission:

For data submission and help, please contact us ([michael.alaux\[at\]versailles.inra.fr](mailto:michael.alaux[at]versailles.inra.fr),

[Link to submission files formats](#).

Duration: **01/01/2008 to 31/12/2011**

Coordinator: **Catherine Feuillet**



# Wheat: 3Bseq project : the first wheat chromosome sequence : 2010-2012

ANR  
French  
national  
Agency

Coord:  
C. Feuillet & al.

Data integration  
at URG  
M Alaux & al.

**PLANT AND FUNGI DATA INTEGRATION**

FEEDBACK | CONTACT | SITE MAP | ABOUT US Register

SEARCH  OK

**Projects**

You are here : [Home](#) / [Home URG](#) / [Projects](#) / [3BSeq](#)

**3BSeq**

**Sequencing, annotation and characterization of the bread wheat chromosome 3B**

3BSeq is a flagship project funded by the [ANR](#) and [France Agrimer](#) for a duration of 3 years (2010-2013). The website and data from the 3BSEQ project are hosted by URG together with all the other wheat resources.

The aim of 3BSeq is to sequence, annotate and characterization the bread wheat chromosome 3B. The project is coordinated by C. Feuillet, INRA Clermont-Ferrand.

3BSEQ is supported by the competitiveness cluster [Céréales Vallée](#).

Duration: **01/01/2010** to **31/12/2012**

Coordinator: [Catherine Feuillet](#)

Partner 1 : [INRA GDEC](#) (Clermont-Ferrand)  
 Etienne Paux, Frédéric Choulet, Philippe Leroy, Pierre Sourdille, Nicolas Guilhot, Lise Pingault, Josquin Daron, Natasha Glover, Sébastien Theil, Camille Rustenholz, Catherine Feuillet ([catherine.feuillet@clermont.inra.fr](mailto:catherine.feuillet@clermont.inra.fr))

Partner 2: [CEA Génoscope](#) (Evry)  
 Julie Poulain, Adriana Alberti, Jean-Marc Aury, Arnaud Couloux, Patrick Wincker ([pwincker@genoscope.cns.fr](mailto:pwincker@genoscope.cns.fr))

Partner 3: [INRA URG](#) (Versailles)  
 Michael Alaux, Olivier Inizan, Erik Kimmel, Véronique Jamilloux, Isabelle Luyten, Sébastien Reboux, Delphine Steinbach, Hadi Quesneville ([hadi.quesneville@versailles.inra.fr](mailto:hadi.quesneville@versailles.inra.fr))

URGI contact: Michael Alaux ([michael.alaux@versailles.inra.fr](mailto:michael.alaux@versailles.inra.fr))

Links:



# 3Bseq project

## Links:

[Wheat at URGI](#)

## Documents:

Project Documents in [Alfresco](#) 

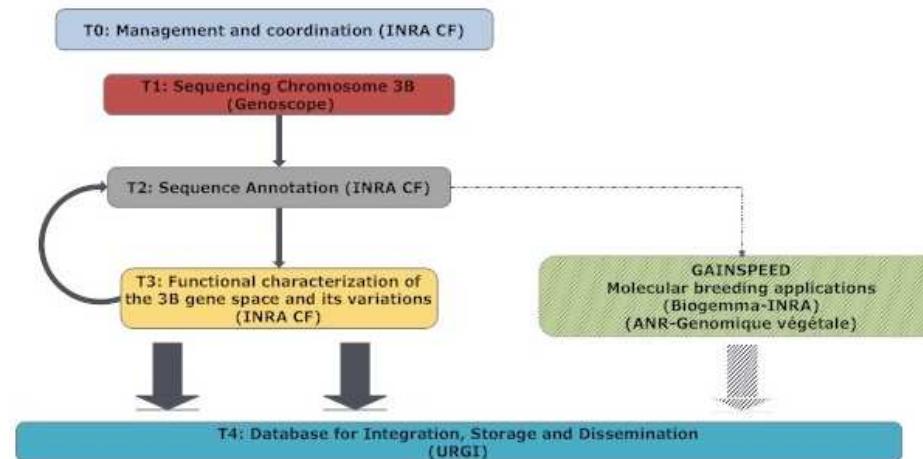
To share documents with other 3BSeq project members, use our electronic documents management software Alfresco.

To access to the Alfresco tool use your Alfresco login/password.

To ask for an account on the Alfresco tool, please contact us ([urgi-contact@versailles.inra.fr](mailto:urgi-contact@versailles.inra.fr)).

## Description:

3BSEQ is organized in 4 scientific tasks and a management task (T0) represented below:



## In 3BSEQ:

- T0 is focused on management of the project and aims at ensuring coordination between the partners, achievements of the objectives, dissemination of the results, and coordination at the international level with other projects within the International Wheat Genome Sequencing Consortium (IWGSC). Further, it will inform and organize annual meetings (at the PAG meeting every January) with the External advisory board. The Task is lead by INRA Clermont-Ferrand (Partner 1).
- T1 is dedicated to the sequencing of chromosome 3B and is led by Genoscope (Partner 2), the [French National Sequencing Center](#). Genoscope will be in charge of developing the strategy, producing the sequence, and assembling it into scaffolds that represent chromosome 3B.
- T2 is led by Partner 1 and concerns the annotation of the sequence that will be produced in T1. Annotation will be done using a combination of automated tools already in place / [TriAnnot pipeline](#) and programs developed for the



# Breedwheat project : 2012 – 2018 :

## genotyping, phenotyping, association studies, genomic selection

ANR  
French  
national  
Agency  
'Bioressources'

Investment for the  
future call

Coord:  
C. Feuillet & al.

Data integration  
at URGI  
M Alaux & al.



**BreedWheat**

**Breeding for economically and environmentally sustainable wheat varieties: an integrated approach from genomics to selection.**

BREEDWHEAT project is a long-term public-private research initiative coordinated by Catherine Feuillet from INRA-GDEC. In total, 39 M€ is being invested over 9 years by 26 French partners, including 11 private companies, to develop and use efficient genome sequence-based tools and new methodologies for breeding wheat varieties with improved quality, sustainability, and productivity.

*"Our goal is focused singularly on accelerating genetic gain to create new, high-yielding, wheat varieties that will meet current and future global challenges in wheat production"* Catherine Feuillet.

Duration: 01/09/2011 to 01/09/2020

Coordinator: Catherine Feuillet

Laboratories / Institutions:

- UMR GDEC, INRA Clermont-Ferrand
- UPR BIA, INRA Angers-Nantes
- U EPGV, INRA Versailles-Grignon
- UPR CNRGV, INRA Toulouse
- UMR GV, INRA Le Moulon
- UR URGI, INRA Versailles-Grignon
- UPR CPP, INRA Versailles-Grignon
- UMR GAEI, INRA Grenoble
- UMR BF, INRA Bordeaux
- UMR EGC, INRA Grignon
- UMR LIMOS, UBP Clermont-Ferrand
- UMR EMMAH, INRA Avignon
- UMR Agronomie, INRA Versailles-Grignon
- GEVES
- Céréales Vallée

Companies:

- ARVALIS-Institut du végétal
- RAGT 2n
- BIOPLANTE
- BIOGEMMA
- LIMAGRAIN EUROPE
- SYNGENTA
- AGRI OBTENTIONS S.A.
- MOMONT
- CAUSSADE SEMENCES
- BAYER SAS-Bayer CropScience
- SECOBRA Recherches



# Access by Species

Platform	Research	Projects	Data	Tools	Species	SEARCH <input type="text"/>	OK
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**Species**

You are here : [Home](#) / [Home URG](#) / Species

Vitis	<b>Species</b>
-------	----------------

You find here, the main species stored in the URG repository

**Vitis**



Why develop grape genomics?  
The International Grape Genome Program (IGGP, launched in 2001) aims at coordinating the international efforts for the development of genomic resources for the *Vitis* genus. During the last four years, more than 380 000 complete or partial sequences ...

**Wheat**



No one can be a statesman who is entirely ignorant of the problems of wheat (Socrates, 470-399BC).  
...

**Botrytis cinerea genome project**



Ascomycete *Botryotinia fuckeliana* (sexual stage of the teleomorph *Botryotinia fuckeliana*) is a necrotrophic fungus that causes grey mould disease on a very broad host range (more than 200 plant species) and inflicts serious crop losses worldwide. Known as polyphagous, *B. cinerea* is actually a ...

**Leptosphaeria maculans genome project**



*Leptosphaeria maculans* 'brassicae' (Lmb) is the ascomycete fungus that causes "stem canker" (also termed "Blackleg") on oilseed rape, *Brassica napus*, and numerous other crucifers (Rouxel et al. 2011). It is representative of an important genus of fungal phytopathogens, the Dothideomycetes, of which six ...

# Access by Species

[Platform](#)   [Research](#)   [Projects](#)   [Data](#)   [Tools](#)   [Species](#)

## Species

### Vitis

### Wheat

Sequence Repository

Demo

FAQ

Projects

Data

Tools

Triannot Pipeline

Deletion Bins

Publications

Links

### Botrytis

### Leptosphaeria

### Microbotryum

### Venturia

### Arabidopsis

### Oryza

### Populus

### Malze

### Medicago

### Pisum

### Flax

You are here : [Home](#) / [Home URGi](#) / [Species](#) / [Wheat](#) / Data

## Data

	free access data		registered access data
--	------------------	--	------------------------

Sequence survey		
Physical maps : 3B (v1 v2), 1BL (v1 v2), 1AS, 1AL, 3DS and 3DL		
Annotations : 13 contigs of 3B		
Deletion bins of 3B chromosome		
Genetic maps		
QTL, MetaQTL		
Markers		
Genetic resources		
EST		
SNP		

## Data summary (2012)

Public data

Genetic maps	26
Physical maps	3
Reference sequence chromosomes	1
Survey sequence chromosomes	21
QTL	324



## URGI main software developments :

1) GnplS: plant and fungal information system

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

2) REPET: tools, libraries, pipelines

3) GALAXY Workflows



## 2) Pipelines

### 3) Galaxy toolsworkflows

Galaxy  
tools  
S-Mart  
(RNASeq),  
MAPHITS

Pipelines  
Repeat detection,  
annotation  
REPET  
Plant, fungal

Pipelines  
Polymorphism (SNP)  
+ SNP integration in  
GnPlS

Galaxy  
workflows  
Bacterial  
Rna  
(Aplibio proj.)  
END

Pipelines  
Gene annotation  
(fungi)  
structural,  
functional

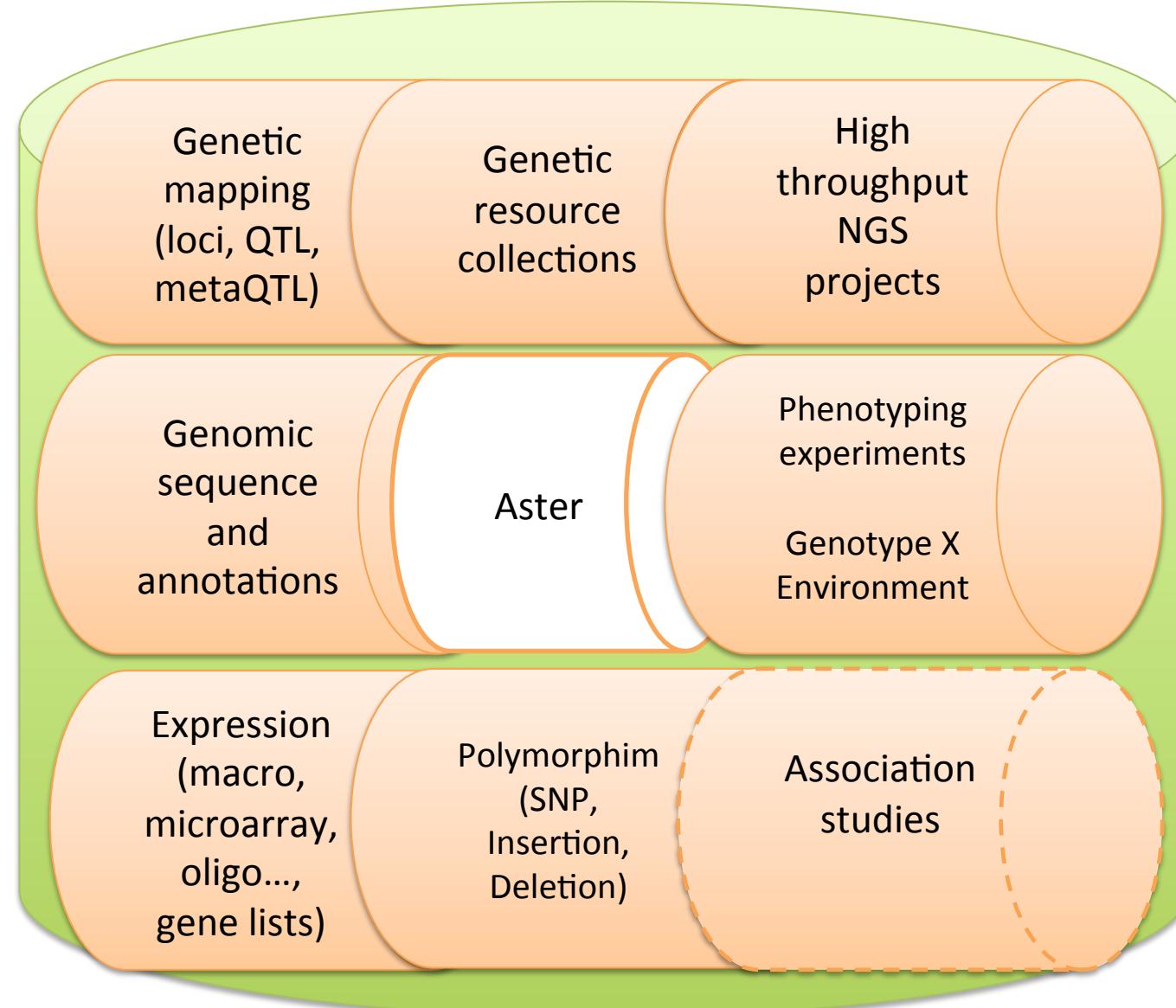
Segmental  
duplication  
Pipeline  
*(TransPlant proj.)*

Galaxy  
workflow  
RNA-Seq  
DiffExp analysis  
*(Aplibio Proj)*

Pipelines  
Gene annotation  
(OakSeq proj.)  
STARTING

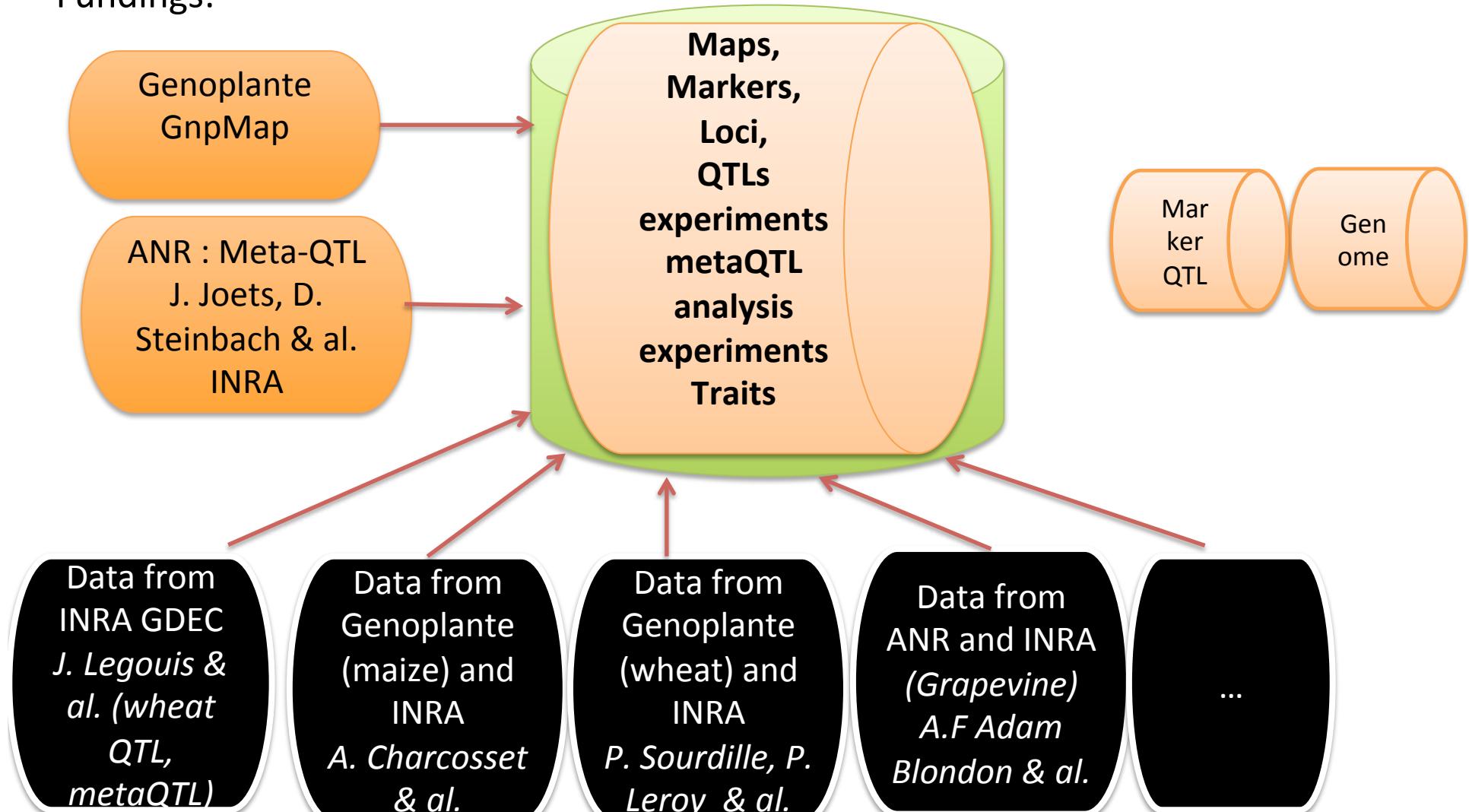
*Guided assembly  
pipeline*  
*(TransPlant proj.)*  
*IN PROGRESS*

# 1) GnplS – a modular multi-cores multispecies database, with a core module



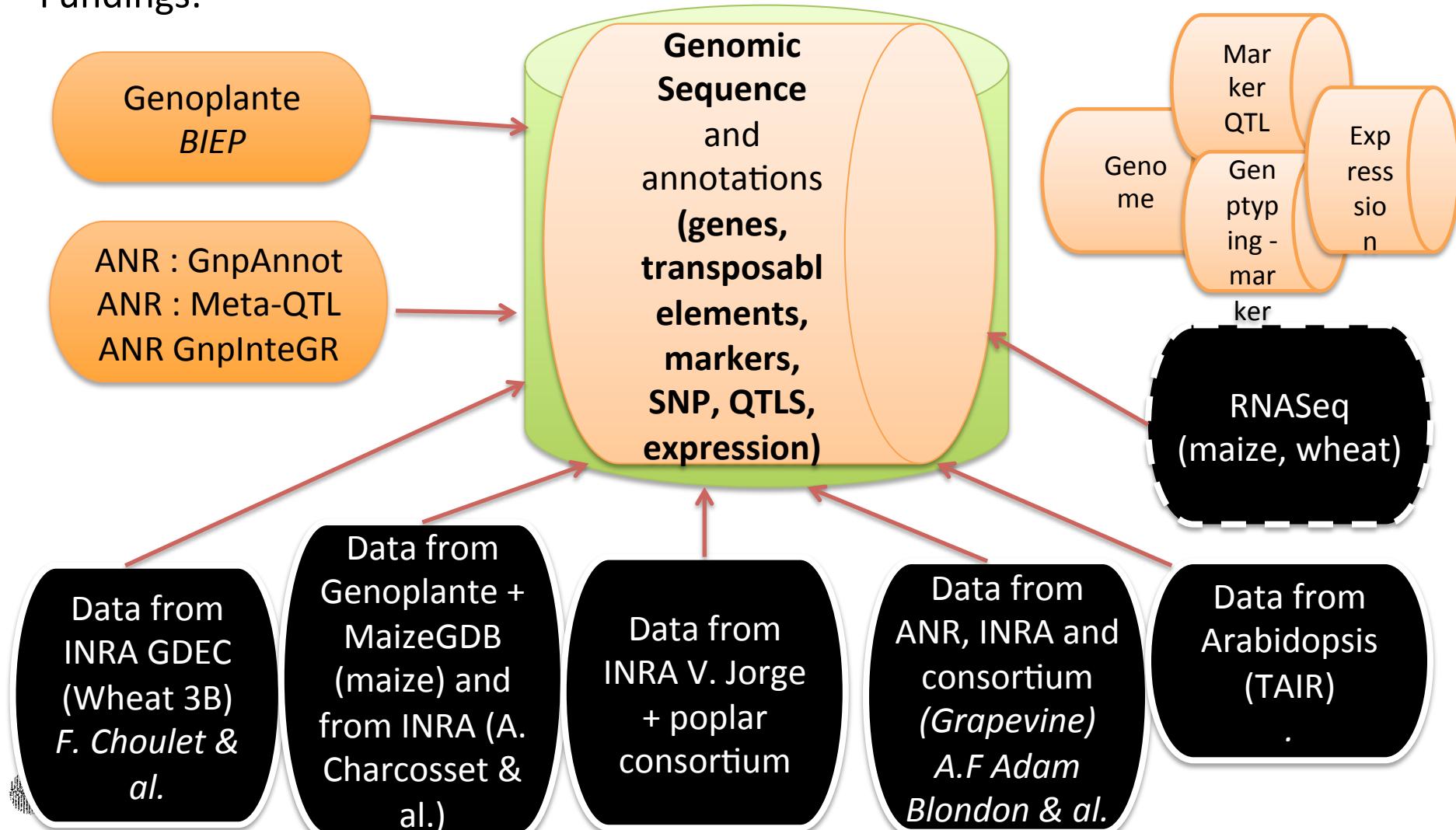
# GnpIS: the genetic mapping module

Fundings:



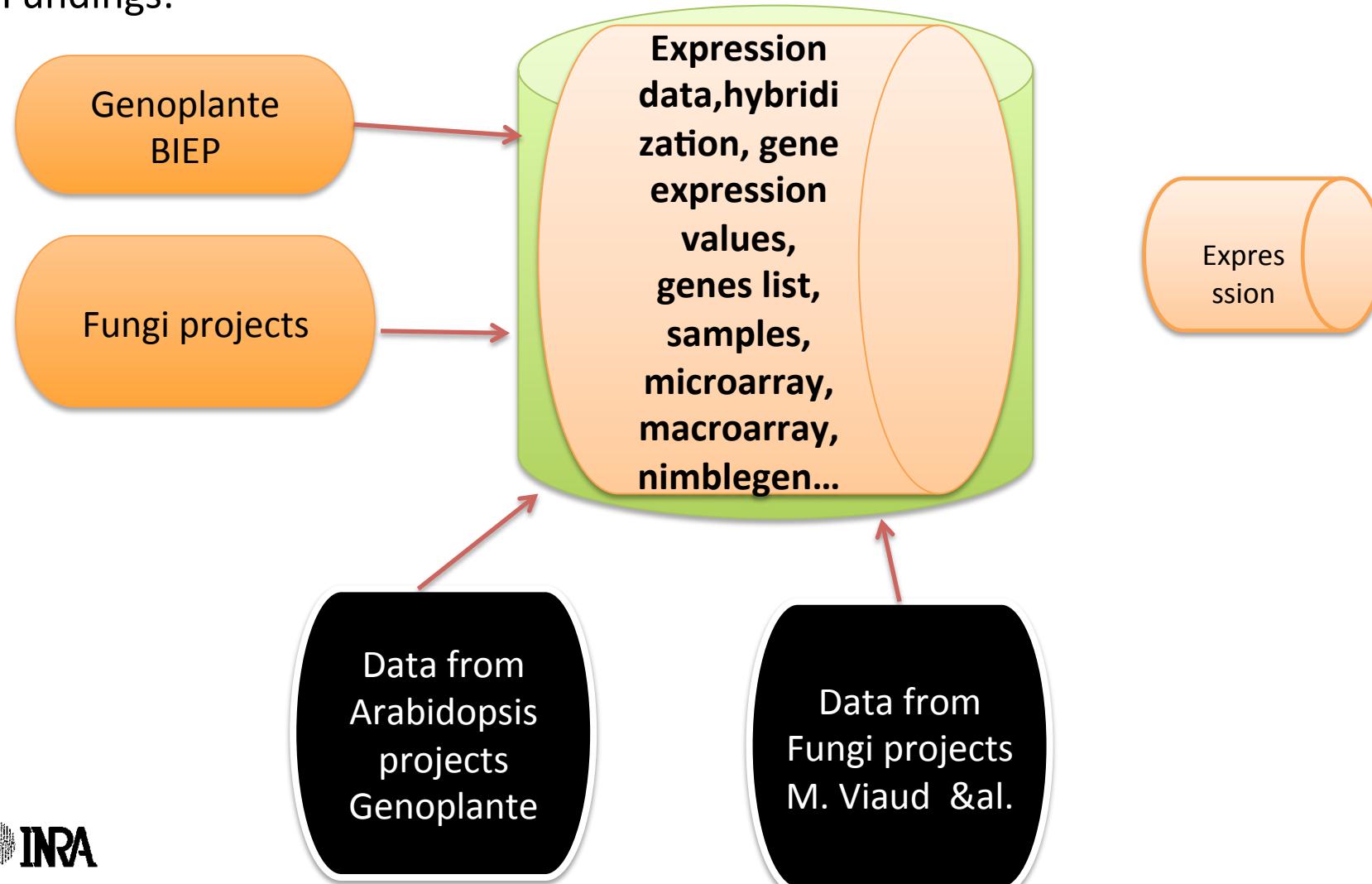
# GnplIS: the genomic annotations module : an ‘integrator’ module

Fundings:



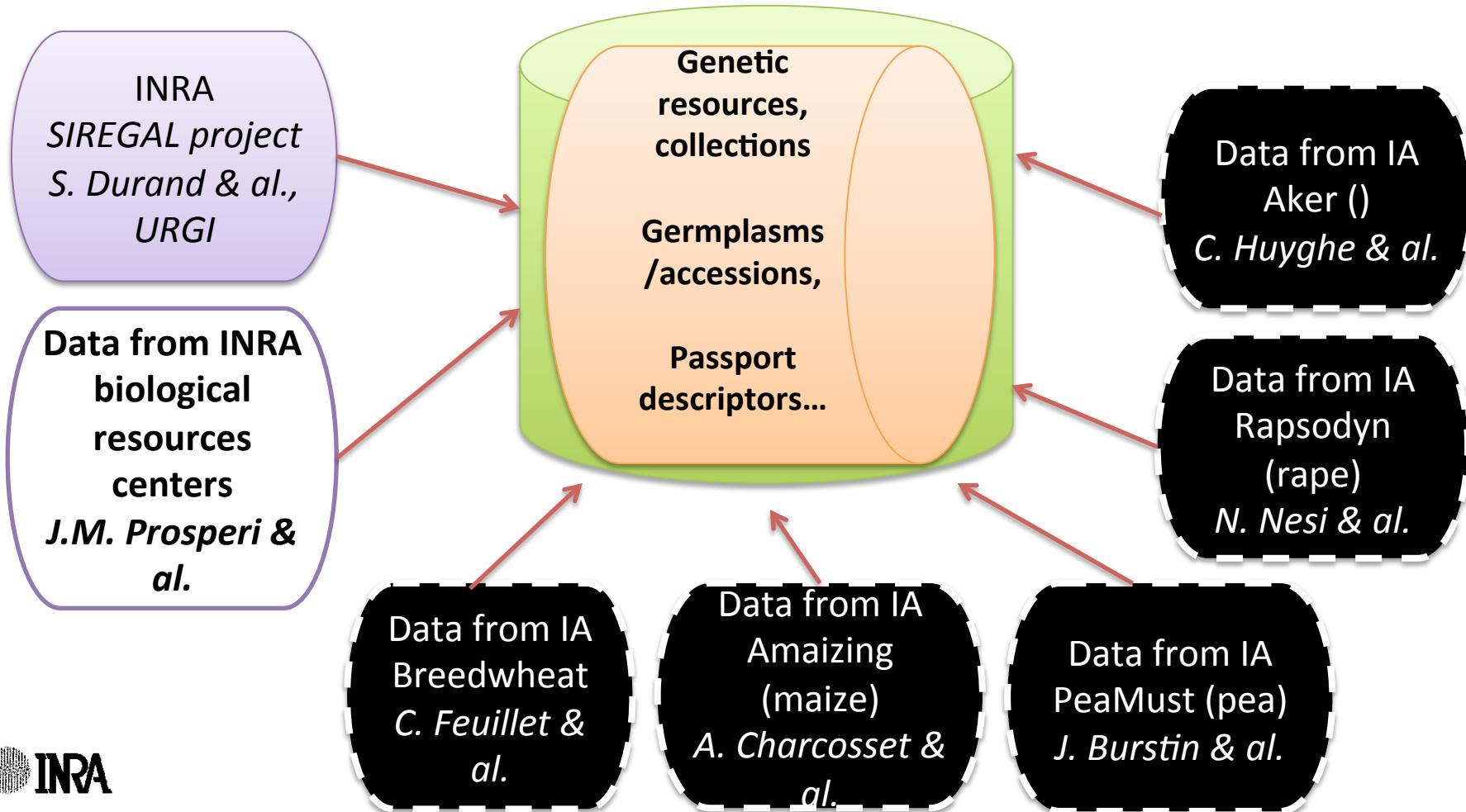
# GnpIS: the expression data module

Fundings:



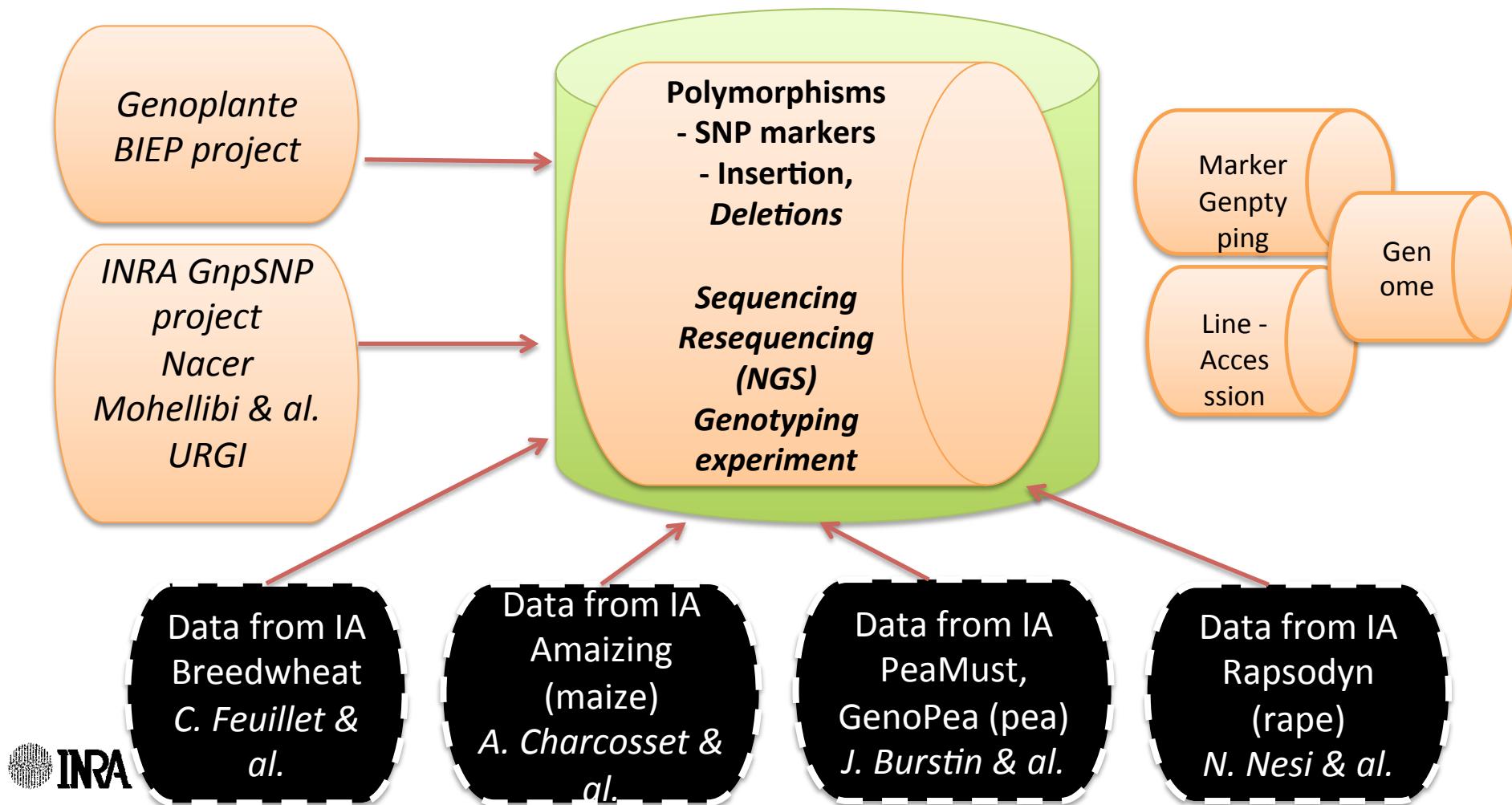
# GnpIS : the genetic resource module

Fundings:



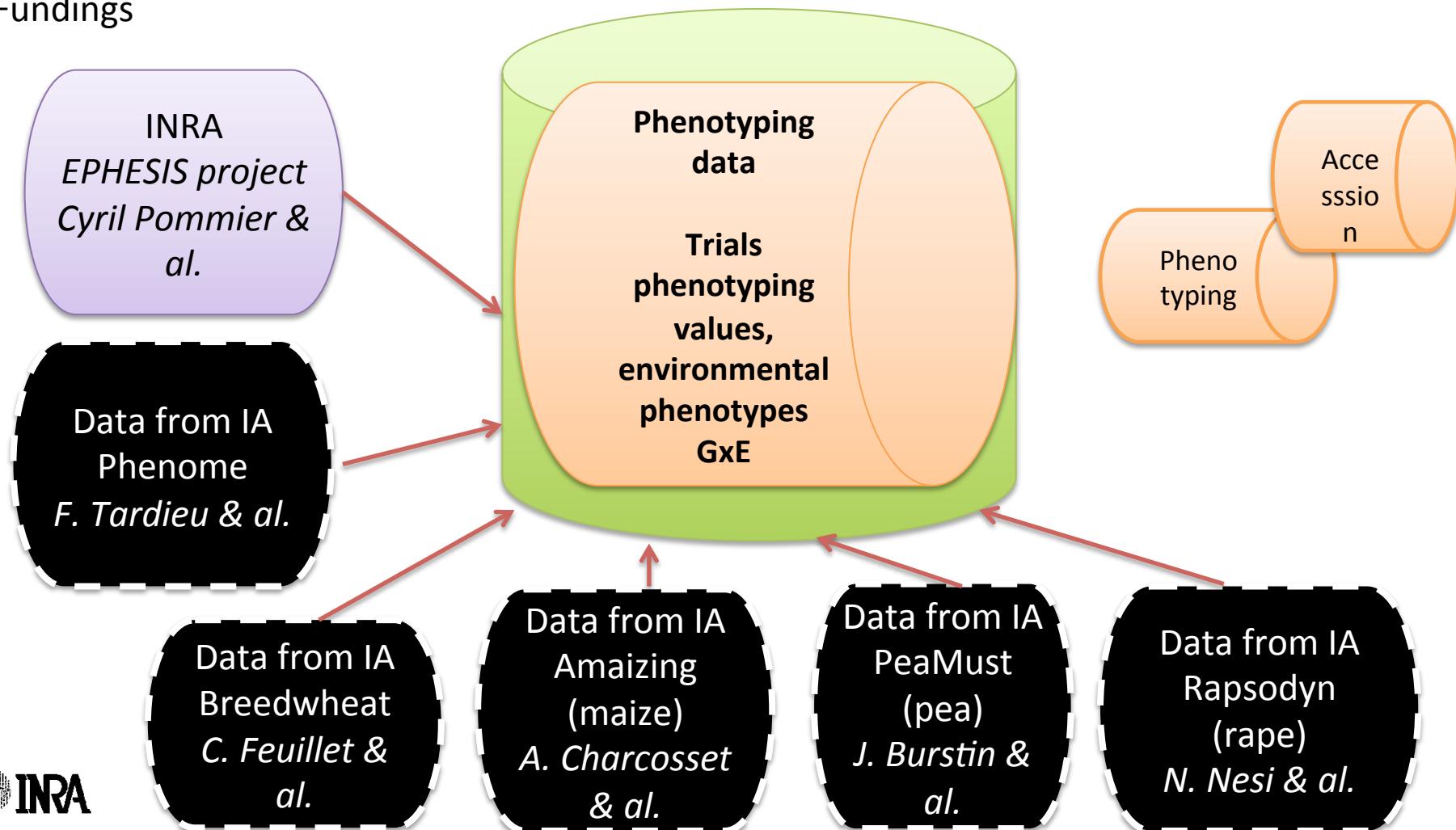
# GnplIS: the polymorphism module

Fundings :



# GnpIS : the phenotypic module

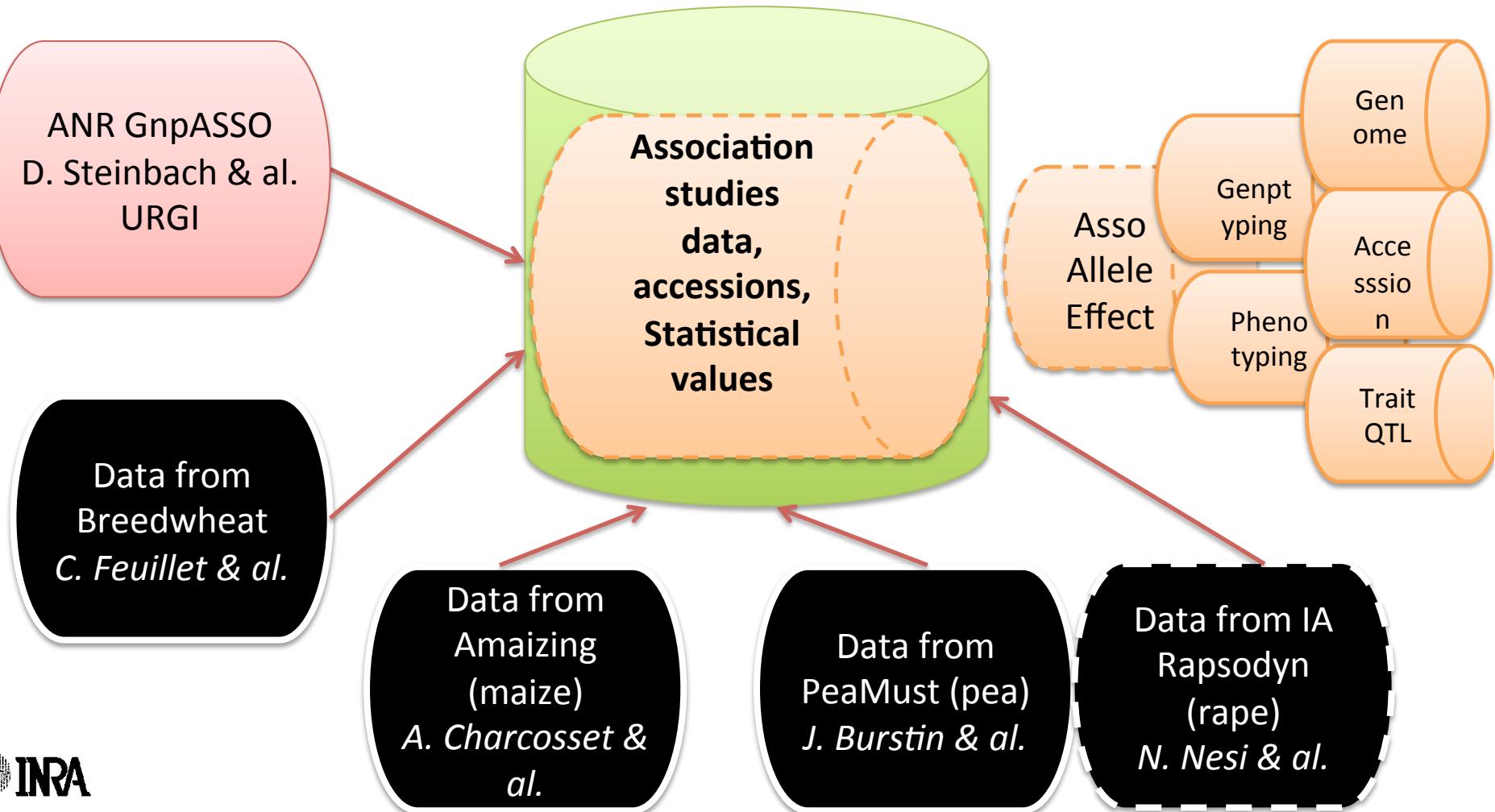
## Fundings



Fundings

# GnpIS : 2011-2013 (*restricted access*)

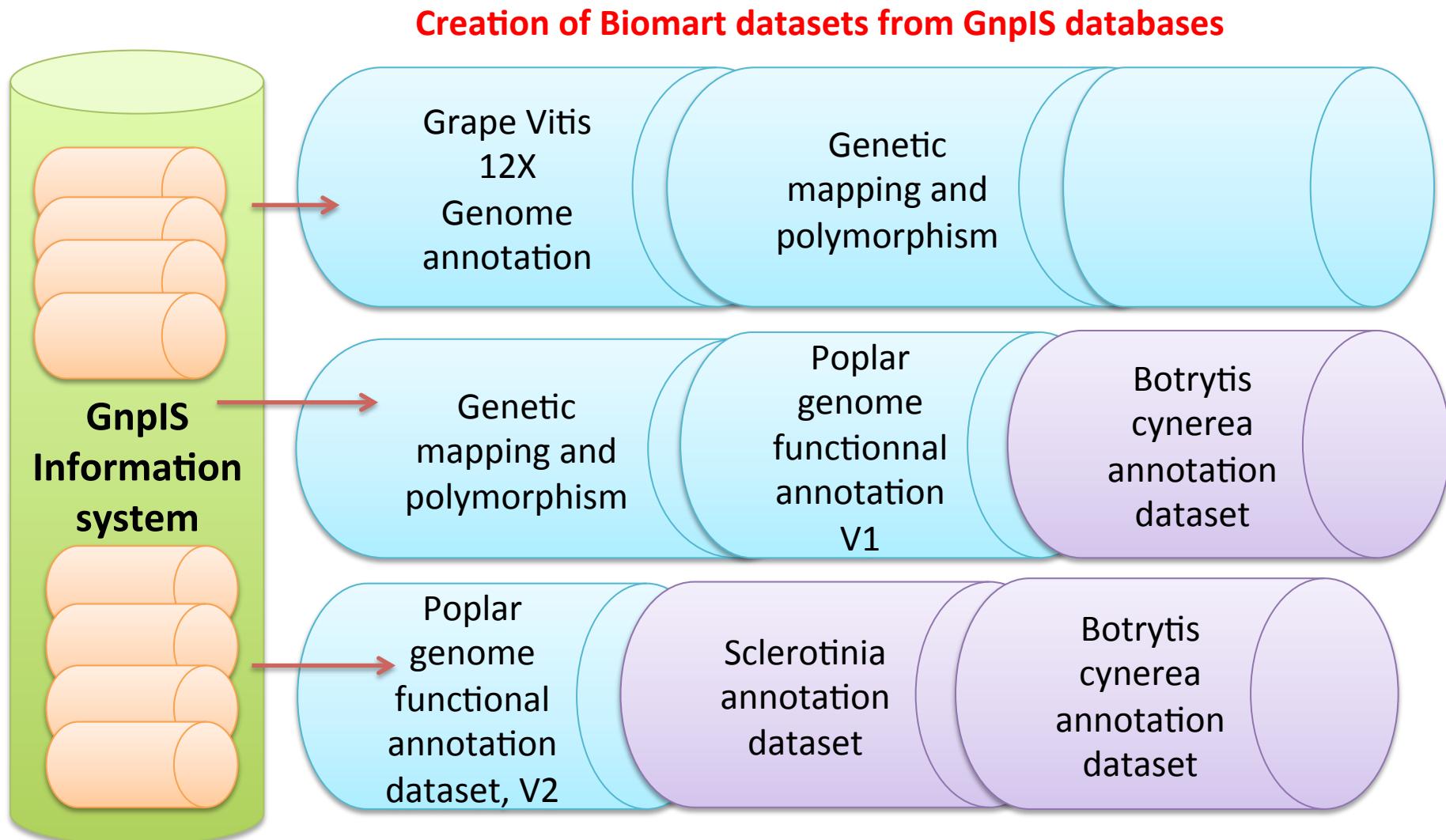
## The association studies module: the second ‘integrator’ module



# GnplIS is also a generator of datamarts



# GnplS: Datamarts



**GnplIS is also a generator of  
indexfiles for HibernateSearch  
- Lucene engine  
our Quick Search Query tool**



**GnplS is a generator :**  
**- for transPlant index for the  
virtual transPlants database**



**- for the LAILABS engine**



# GnplS – Query tools.



# To access the data: 4 types of query tools connected together

**QUICK SEARCH** Species

Xwmc430

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

Examples: VvI, VVf52, gene, arabidopsis, AF109603, Xwmc430

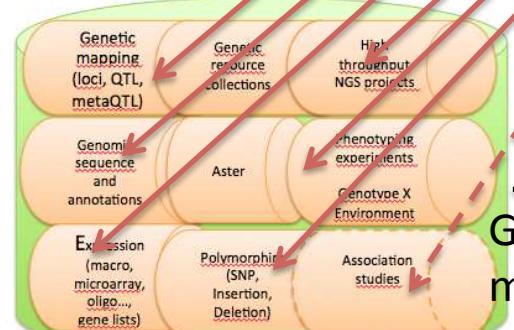


**Global query  
'as a google  
search'**

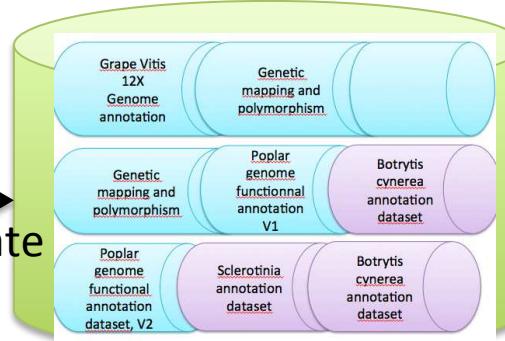
Specific queries  
built with  
Query builders

**Biomart** query  
with filters settings

**Galaxy query**

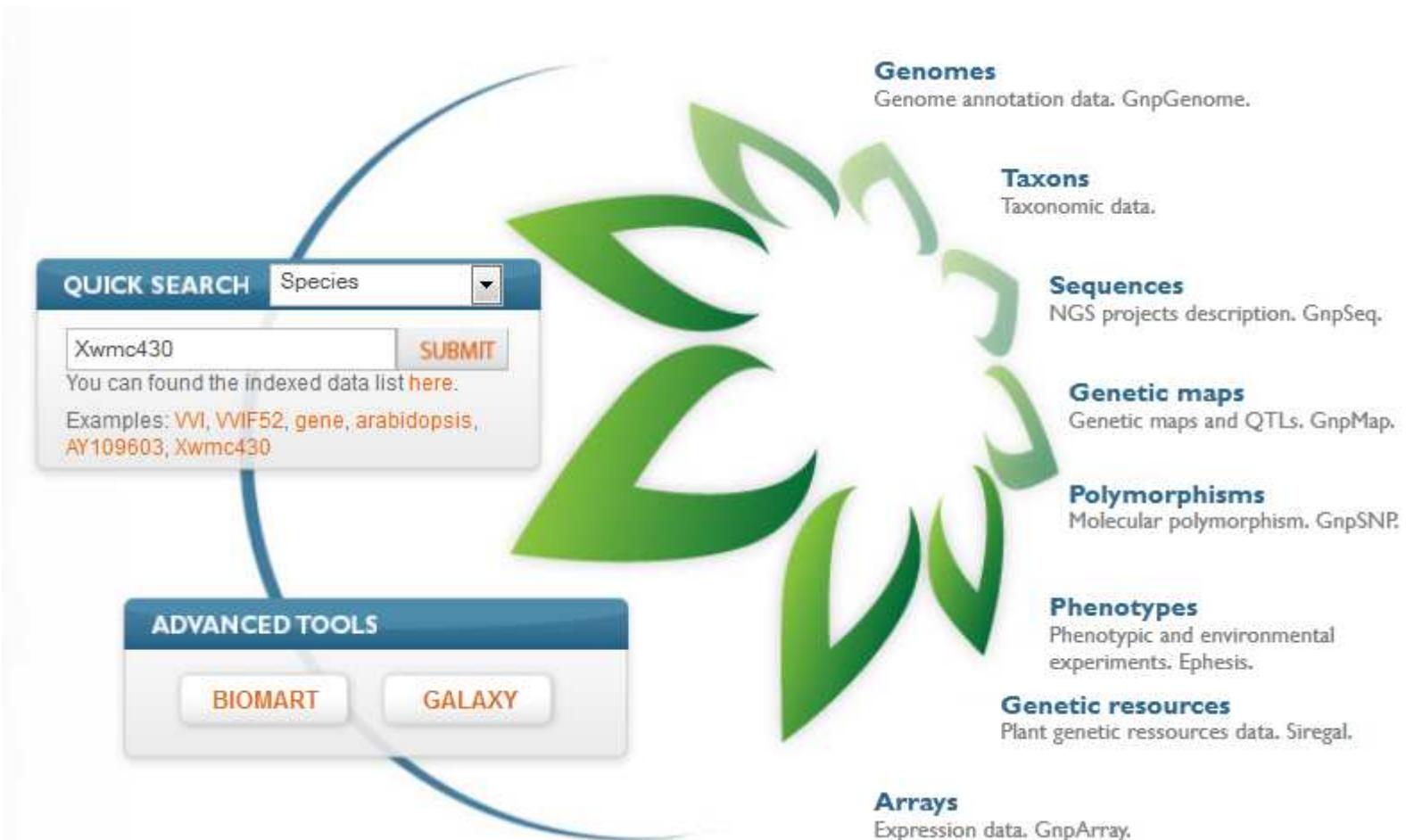


Make data available



# A unique portal for query:

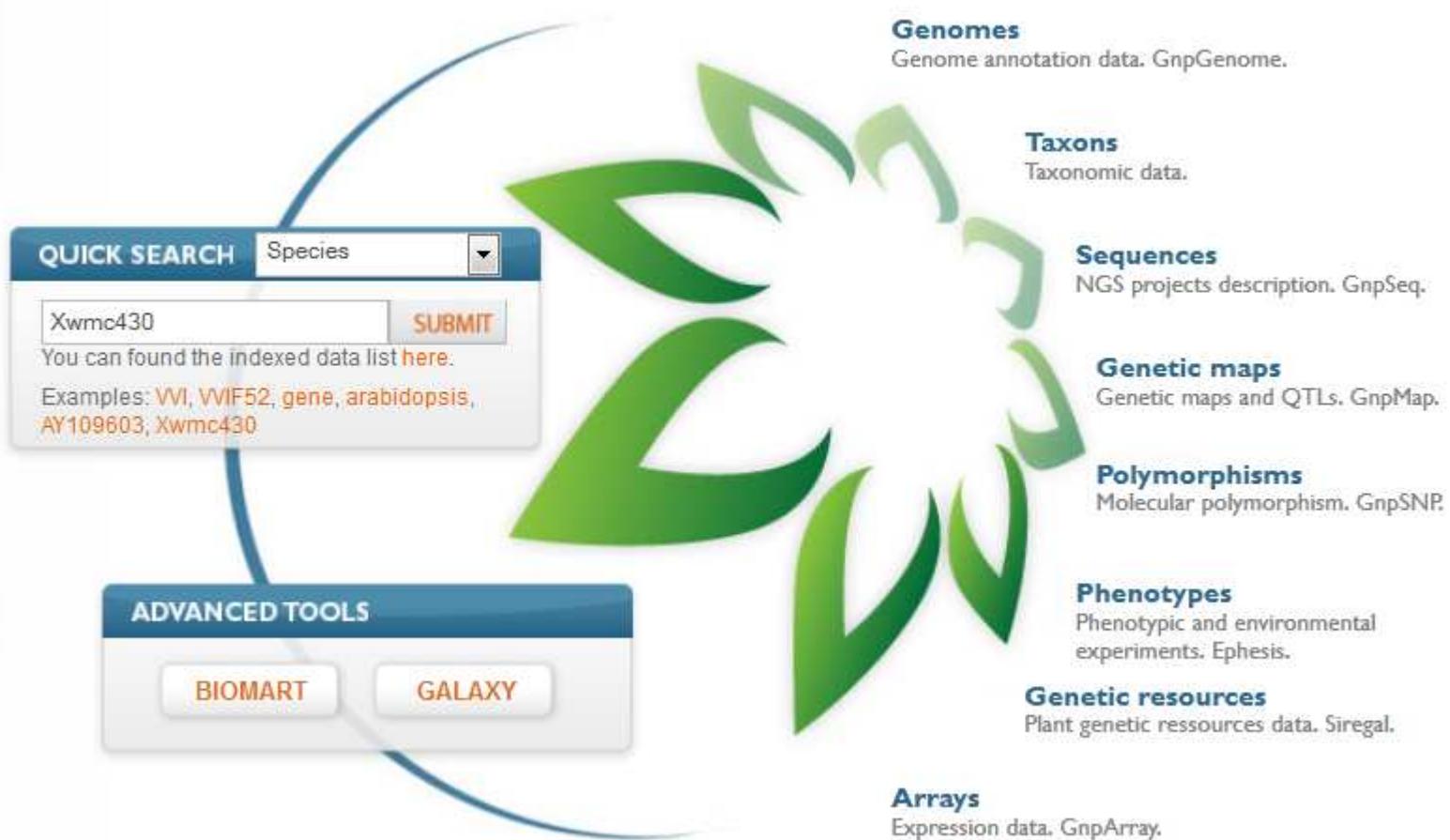
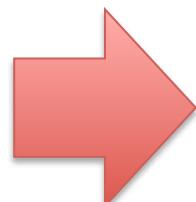
<http://urgi.versailles.inra.fr/gnpis>



# Multiple scenarios for Queries !

- Built according different types of user needs :
  - **Genetic mapping oriented needs:**
    - ‘get info by marker, marker name, marker localisation’,
    - get info by QTL, by trait....
  - **Genomic annotation oriented needs:** ‘get info by gene name, localisation, by ontology term (GO...)...
  - **Expression oriented needs:** ‘get info by gene lists or gene name’...
  - **Association studies needs:** ‘get info by association studies results’, marker, line, allele, statistical values...
  - **Germplasm needs :** get info by germplasm passport descriptors, values of evaluations, material availability...
  - **Phenotyping needs:** get info by phenotypic variables, ontology terms, by place, evaluation date, by environment (climate, soil....)
  - **By combining scenarios to cross queries all the database**

# Query : The Quick Search tool (Lucene indexes)



**Genomes**  
Genome annotation data. GnpGenome.

**Taxons**  
Taxonomic data.

**Sequences**  
NGS projects description. GnpSeq.

**Genetic maps**  
Genetic maps and QTLs. GnpMap.

**Polymorphisms**  
Molecular polymorphism. GnpSNP.

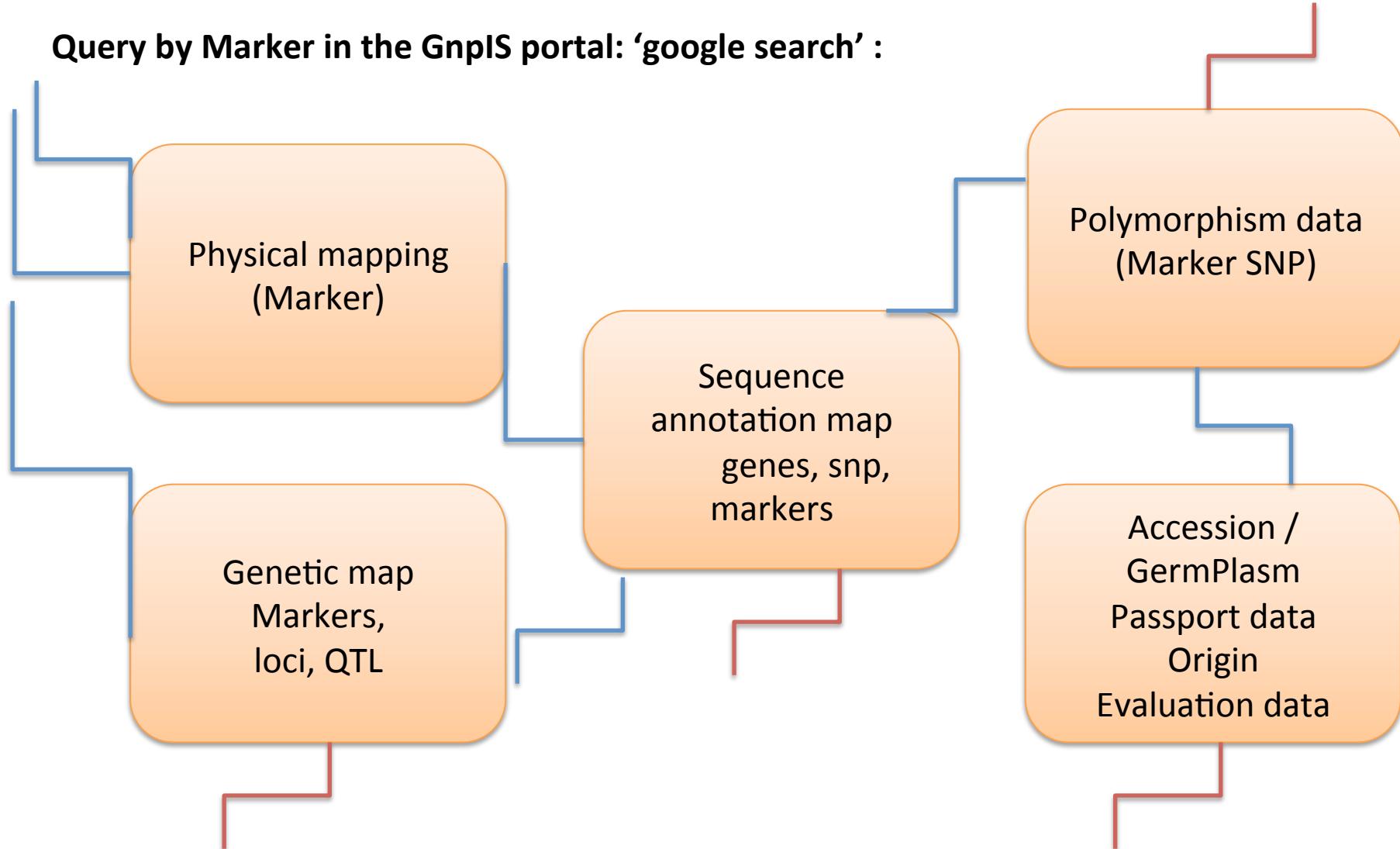
**Phenotypes**  
Phenotypic and environmental experiments. Ephesis.

**Genetic resources**  
Plant genetic resources data. Siregal.

**Arrays**  
Expression data. GnpArray.

# User Query scenario

Query by Marker in the GnpIS portal: 'google search' :



# Query made on a marker name results: 3 hits (physical maps, genetic map)

Species  Xwmc430

**Wheat physical map: 3B v1**   **Wheat physical map: 3B v2**   **Genetic mapping**

**Features (1)**

Xwmc430-3B ★★★★  
-

1 items found, displaying 1 to 1 | Display

Species  Xwmc430

**Markers 3B v1**  
Xwmc430-3B

**Contig 3B v1**  
ctg6

**Belongs to the Bin 3B v1**  
3BS8-0.78-0.87

**BACs 3B v1**  
3B\_101\_J20  
3B\_037\_K10  
3B\_023\_A14  
3B\_101\_L21  
3B\_040\_I22

# Query made on a marker name results: hit on genetic map

Species  Xwmc430

**Wheat physical map: 3B v1**   **Wheat physical map: 3B v2**   **Genetic mapping**

**Loci (2)**

Xwmc430-3B	★★★★★
Xwmc430-5B	★★★★★

2 items found, displaying 1 to 2 | Display  results per page

**GnpMap / Locus card**

**LOCUS DETAILS**

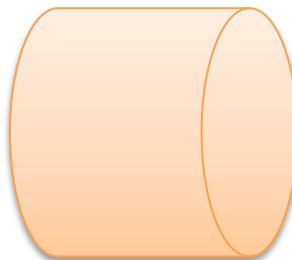
Locus name :	Xwmc430-3B
Marker name :	WMC430
Marker type :	SSR
Gene function (manual annotation) :	-

**ASSIGNMENTS**

Assignments number : 2

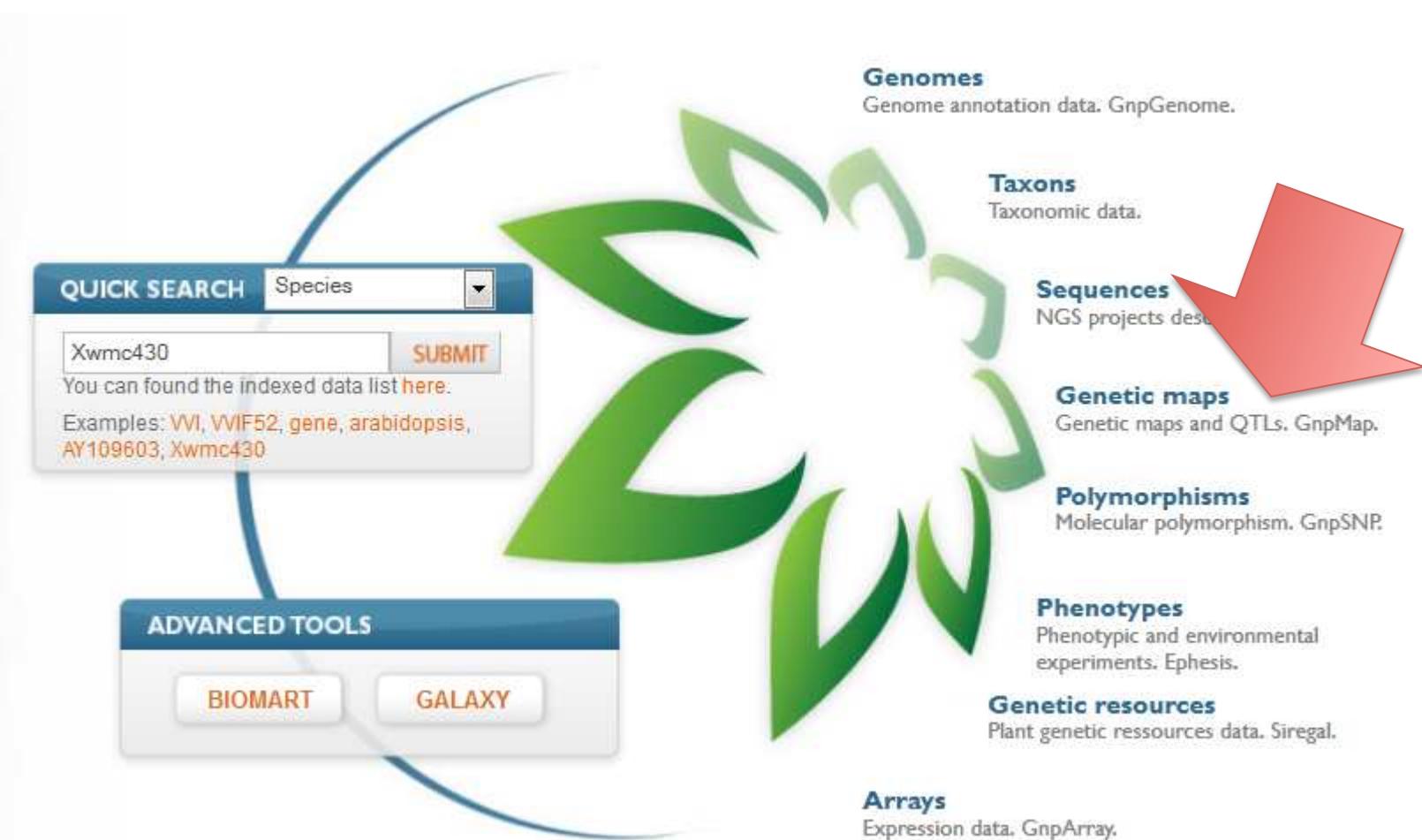
Map name	Reliability / (source map name)	Linkage group	Bin	Distance
SupBW_071212	non_framework	3B	-	3.1
TaVirtualPop01_071219	non_framework	3B	-	3.0

# GnplS – Genetic mapping data query specific interface



- to browse genetic or cytogenetic maps for several species
- to query by markers, maps, trait, QTL
- to display and compare several genetic maps
- to link common markers or loci together
- to integrate reference or consensus maps
- to store anchoring data from pooling experiments

# GnplS – Genetic mapping data dedicated module



# GnplIS: SPECIFIC QUERIES:

## 8 types of query (map, loci, qtl, MetaQTLs, marker, trait...)



**GnplIS**  
GENETIC AND GENOMIC INFORMATION SYSTEM

EN FR FEEDBACK

### Connexion

#### Principal

- INTERFACE TEXTUELLE
- MAPCOMPARATOR

#### Recherches globales

- TAXONS

#### Recherches

- CARTE
- LOCI
- QTL
- METAQTL
- MARQUEUR
- POOL
- XREF
- TRAIT

#### Documentation

- GUIDE DE L'UTILISATEUR
- FAQ
- NOUVEAUTÉS
- NOTES DE VERSION

#### GnplIS

- SOUMISSION
- GNPIS
- EPHESES

## GnpMap interface

Welcome on the textual part of the GnpMap interface.

The extended query forms allow to search and retrieve precise information, by using all the provided query parameters.

Some of the result pages offer the ability to export the query results in order to work on them in our own laboratory.

#### QUERY TYPES

- [Query on map](#)
- [Query on loci](#)
- [Query on QTL](#)
- [Query on MetaQTLs](#)
- [Query on marker](#)
- [Query on pool](#)
- [Query on crosslinks](#)
- [Query on trait](#)

### News

#### 03 APRIL 2012

GnpMap 2.6.0 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

##### Changements:

- restrictions dynamique sur le formulaire de recherche de MetaQTL
- intégration complète de BioMercator
- correction de bugs

#### 06 MARCH 2012

GnpMap 2.5.9 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

##### Changements:

- amélioration de l'interface des MetaQTLs
- mise en place de web services
- correction de bugs

#### 12 JANUARY 2012

GnpMap 2.5.8 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

##### Changements:

- amélioration de l'interface des MetaQTLs
- correction de bugs

#### 07 NOVEMBER 2011

GnpMap 2.5.7 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

##### Changements:

- nouveau design

#### 12 OCTOBER 2011

GnpMap 2.5.6 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.





# Map QUERY BUILDER

Step 1: select species

Step 2: select map

[Aide] Taxons

- Brassica napus L.*
- Hordeum vulgare*
- Oryza sativa*
- Sorghum bicolor*
- Triticum aestivum*
- Vitis vinifera L.*
- Zea mays L.*
- All

Selectionner

TABLE DES CARTES

Nom	Population	Taxon
ARE_050606	ARE	<i>Triticum aestivum</i>
AXO_050428	AXO	<i>Triticum aestivum</i>
CF9107xToisondorxQuebon	CFQUE-TORQUE-TOR107	<i>Triticum aestivum</i>
CtCs_040630	CtCs	<i>Triticum aestivum</i>
DEL_050308	Deletion	<i>Triticum aestivum</i>
Ditelo_050308	NT_DT	<i>Triticum aestivum</i>
ITMI_040618	ITMI	<i>Triticum aestivum</i>
Neighbour1BL_110314	Ta_virtual_1BL	<i>Triticum aestivum</i>
Neighbour3B_080407	TaVirtualPop03	<i>Triticum aestivum</i>
NulliTetra_050308	NT_DT	<i>Triticum aestivum</i>
ReCS_090305	ReCS	<i>Triticum aestivum</i>
RER_040618	RER	<i>Triticum aestivum</i>
RER_050614	RER	<i>Triticum aestivum</i>
RLAc_071219	RLAc	<i>Triticum aestivum</i>
SOds_071219	SOds	<i>Triticum aestivum</i>
SumStoa_090225	SumStoa	<i>Triticum aestivum</i>
SupBW_071212	SupBW	<i>Triticum aestivum</i>
TaVirtualPop01_071219	TaVirtualPop01	<i>Triticum aestivum</i>
TaVirtualPop02_090219	TaVirtualPop02	<i>Triticum aestivum</i>
TOR107_101010	TOR107	<i>Triticum aestivum</i>
TXO_050621	TXO	<i>Triticum aestivum</i>
Wheat_ISBP_RefMap_110101	ISBP_Ref	<i>Triticum aestivum</i>

# Details on the map: TOR107\_101010

## GnpMap / Carte

### DÉTAILS SUR LA CARTE

Nom :	TOR107_101010
Type de carte :	genetic
Date :	10/10/2010
Taxon :	Triticum aestivum
Population :	TOR107
Soumise par :	BOGARD Matthieu
Fichier de génotype :	
Fichier image :	
Nombre de groupes de liaison :	29
Nombre de loci :	475
Nombre de QTL :	104
Nombre de QTL non projetés :	104
Nombre de MetaQTL :	4

# Get all loci from this map

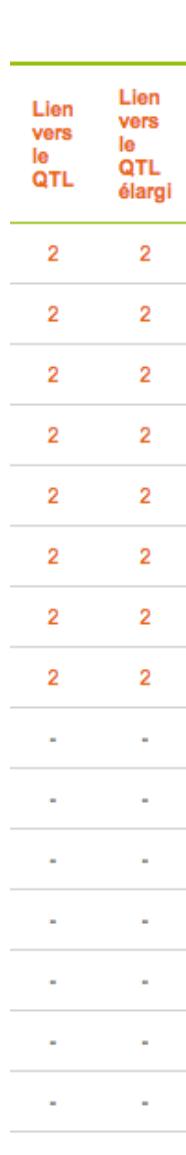
GnpMap / Loci

## RESULTS

?

1 2 3 4 5 ➡ | 475 items trouvés, affichage de 1 à 20 | Afficher   résultats par page

#	Nom	Nom du locus	Nom du marqueur	Protocole	Type de marqueur	Origine du marqueur	But	Fonction du gène (annotation manuelle)	Fiabilité/(nom de la carte d'origine)	Groupe de liaison	Bin	Distance
1	TOR107_101010	XwPt-1973-1B	wPt1973	-	DArT	genomic DNA	-	-	-	1B	-	0.0
2	TOR107_101010	XtPt-6091-1B	tPt6091	-	DArT	genomic DNA	-	-	-	1B	-	0.8
3	TOR107_101010	XwPt-1786-1B	wPt1786	-	DArT	genomic DNA	-	-	-	1B	-	0.8
4	TOR107_101010	XwPt-1672-1B	wPt1672	-	DArT	genomic DNA	-	-	-	1B	-	0.8
5	TOR107_101010	XwPt-5577-1B	wPt5577	-	DArT	genomic DNA	-	-	-	1B	-	7.0
6	TOR107_101010	XwPt-1313-1B	wPt1313	-	DArT	genomic DNA	-	-	-	1B	-	7.0
7	TOR107_101010	XwPt-8245-1B	wPt8245	-	DArT	genomic DNA	-	-	-	1B	-	7.0
8	TOR107_101010	XwPt-1770-1B	wPt1770	-	DArT	genomic DNA	-	-	-	1B	-	7.0
9	TOR107_101010	XG1P_1B-1B	G1P_1B	-	SNP	genomic DNA	-	-	-	1B	-	13.2
10	TOR107_101010	X44220_3B-1B	44220_3B	-	SNP	genomic DNA	-	-	-	1B	-	17.0
11	TOR107_101010	XwPt-4688-1B	wPt4688	-	DArT	genomic DNA	-	-	-	1B	-	36.3
12	TOR107_101010	XwPt-2526-1B	wPt2526	-	DArT	genomic DNA	-	-	-	1B	-	37.8
13	TOR107_101010	XwPt-4129-1B	wPt4129	-	DArT	genomic DNA	-	-	-	1B	-	37.8
14	TOR107_101010	XwPt-0944-1B	wPt0944	-	DArT	genomic DNA	-	-	-	1B	-	37.8
15	TOR107_101010	XwPt-3475-1B	wPt3475	-	DArT	genomic DNA	-	-	-	1B	-	37.8
16	TOR107_101010	XwPt-4532-1B	wPt4532	-	DArT	genomic DNA	-	-	-	1B	-	37.8
17	TOR107_101010	XwPt-5061-1B	wPt5061	-	DArT	genomic DNA	-	-	-	1B	-	44.0
18	TOR107_101010	XwPt-9809-1B	wPt9809	-	DArT	genomic DNA	-	-	-	1B	-	47.8



# Colocalisation between marker and QTLs

## GnpMap / QTL results

### RESULTS



2 items trouvés, affichage de 1 à 2 | Afficher

résultats par page

#	QTL name	Theme	Trait	Trait description	Map	Groupe de liaison	LOD	R2	Distance	From	to	Fiabilité(nom de la carte d'origine)	Link to loci	Link to loci large
1	ONSEN_ms.9.NI_1B	Senescence	ONSEN	date of the onset of the senescing phase	TOR107_101010	1B	4	4	0	0	8	unprojected	8	8
2	ONSEN_ms.9.Np_1B	Senescence	ONSEN	date of the onset of the senescing phase	TOR107_101010	1B	5	8	0	0	10	unprojected	8	8



Select loci

# QTL card : ONSEN\_ms.9.NI\_1B

## GnpMap / QTL card

### QTL DETAILS

QTL name :	ONSEN_ms.9.NI_1B
QTL detection :	composite interval mapping
Measure :	ONSEN_ms.9.NI
Experimentation :	ms.9.NI
Trait name :	ONSEN

### ASSOCIATED EFFECTS

Effects number : 1

Effect type	Effect value	Standard deviation	Line name	Min effect value	Max effect value	Short remark
additive	-26.64	-	unknown	-	-	-

### ASSOCIATED ASSIGNMENTS

Assignments number : 1

Map name	Linkage group	LOD	R2	Distance	From	To	Reliability / (source map name)	Link to loci	Link to loci large
TOR107_101010	1B	4	4	0	0	8	unprojected	8	8

# Details on QTL detection

## GnpMap / QTL detection card

### QTL DETECTION DETAILS

**Method :** composite interval mapping

**Date :** 2009

**Software :** Rqtl

**Parameters :** unknown

**Detection threshold :** 5% genomewide

**Ic criteria :** LOD -1 drop off

**Epistasis :**

**R2 global :** 59.0

**R2 corrected :**

**Number of QTL detected :** 4

**Description :**

**Short remark :**

**Contact :** BOGARD

**Map :** TOR107\_101010

**Measure :** ONSEN\_ms.9.NI

**Trait :** ONSEN

### ASSOCIATED QTLS

Number of QTL: 4

**QTL**

# Details on QTL Measure

## GnpMap / Measure card

### MEASURE DETAILS

Measure :	ONSEN_ms.9.NI
Unit :	?C days
Description :	date of the onset of leaf senescence during grain filling
Trait :	ONSEN
Experimentation :	ms.9.NI

### ASSOCIATED MEASURE VALUES

Number of measure values: 1

Synthesis method	Mean	h2 value	Short remark
-	-	-	ONSEN

### ASSOCIATED QTL DETECTIONS

Number of QTL detections: 1

Method	Date	Parameters	Description	Detection threshold	R2 global	R2 corrected	Number of QTL assignments
composite interval mapping	2009	unknown	-	5% genomewide	59.0	-	4



# Detail on QTL experiment

## GnpMap / Experiment card

### EXPERIMENT DETAILS

Experiment name :	ms.9.NI
Synthesis method :	mean
Vp Tc :	
Population :	TOR107
Culture conditions :	low N supply

### ASSOCIATED MEASURES

Number of measures: 6

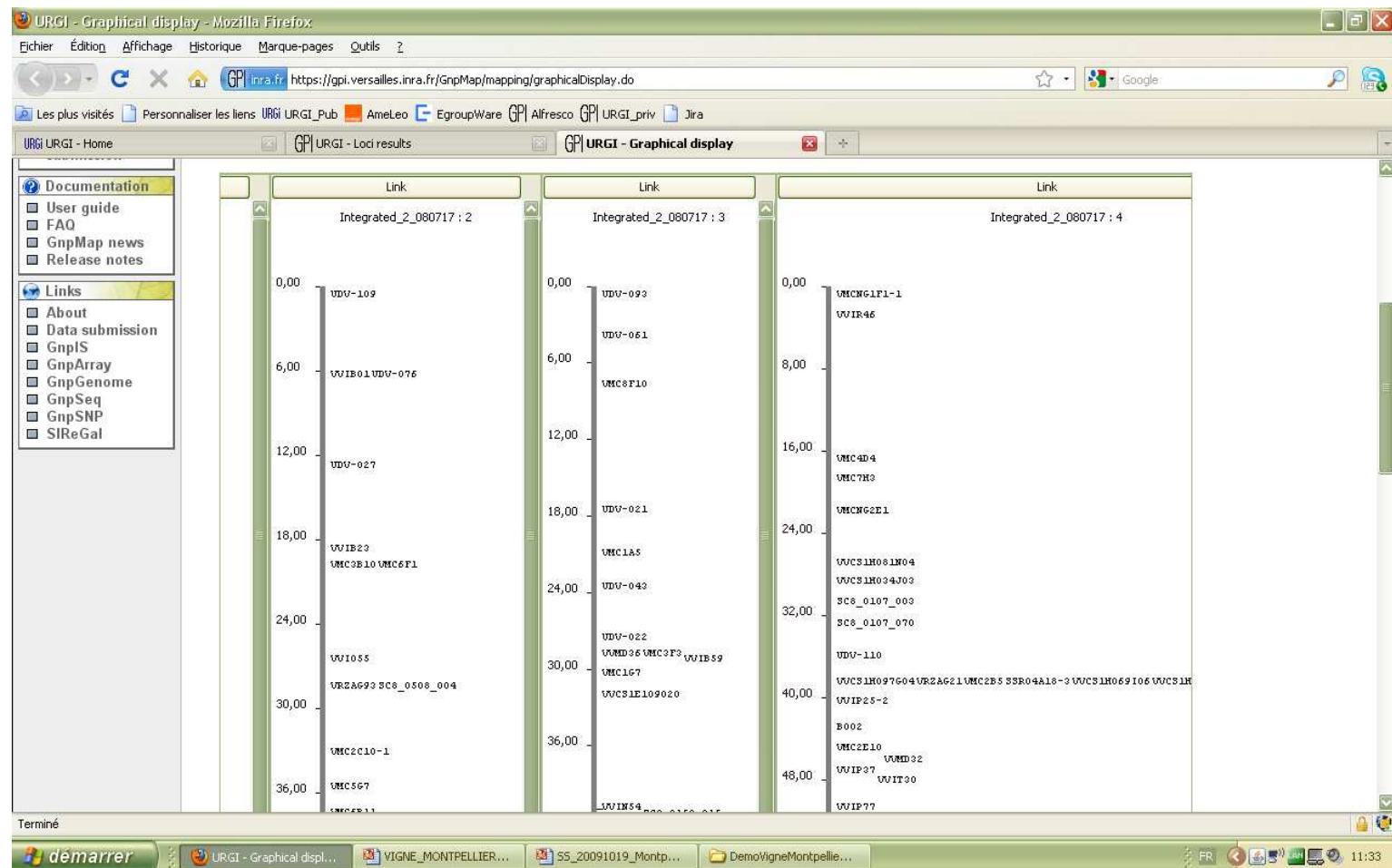
Measures	Nom du trait	Theme name	Number of QTL assignments
GY_ms.9.NI	grain_yield	Quality	1
GPC_ms.9.NI	Prot%	Kernel filling	2
AD_ms.9.NI	days_to_flowering	Earliness	4
AGN92_ms.9.NI	QN Harvest	Seed nitrogen accumulation	1
ONSEN_ms.9.NI	ONSEN	Senescence	4
durTot_ms.9.NI	durTot	Senescence	3

### ASSOCIATED PLACES

Place: 1

Place	Description	Climatic conditions	Date
Estrees-Mons	-	-	2009

# Draw QTLs maps by MapComparator tool soon: by BioMercator tool



# From QTL to loci

## GnpMap / QTL results

### RESULTS



2 items trouvés, affichage de 1 à 2 | Afficher  résultats par page

#	QTL name	Theme	Trait	Trait description	Map	Groupe de liaison	LOD	R2	Distance	From	to	Fiabilité(nom de la carte d'origine)	Link to loci	Link to loci large
1	ONSEN_ms.9.NI_1B	Senescence	ONSEN	date of the onset of the senescing phase	TOR107_101010	1B	4	4	0	0	8	unprojected	8	8
2	ONSEN_ms.9.Np_1B	Senescence	ONSEN	date of the onset of the senescing phase	TOR107_101010	1B	5	8	0	0	10	unprojected	8	8



Select loci

# Loci list around QTLs

## GnpMap / Loci

### RESULTS



8 items trouvés, affichage de 1 à 8 | Afficher  résultats par page

#	Nom	Nom du locus	Nom du marqueur	Protocole	Type de marqueur	Origine du marqueur	But	Fonction du gène (annotation manuelle)	Fiabilité/nom de la carte d'origine	Groupe de liaison	Bin	Distance	Extr prox du loc
1	TOR107_101010	XwPt-1973-1B	wPt1973	-	DArT	genomic DNA	-	-	-	1B	-	0.0	
2	TOR107_101010	XtPt-6091-1B	tPt6091	-	DArT	genomic DNA	-	-	-	1B	-	0.8	
3	TOR107_101010	XwPt-1786-1B	wPt1786	-	DArT	genomic DNA	-	-	-	1B	-	0.8	
4	TOR107_101010	XwPt-1672-1B	wPt1672	-	DArT	genomic DNA	-	-	-	1B	-	0.8	
5	TOR107_101010	XwPt-1770-1B	wPt1770	-	DArT	genomic DNA	-	-	-	1B	-	7.0	
6	TOR107_101010	XwPt-8245-1B	wPt8245	-	DArT	genomic DNA	-	-	-	1B	-	7.0	
7	TOR107_101010	XwPt-1313-1B	wPt1313	-	DArT	genomic DNA	-	-	-	1B	-	7.0	
8	TOR107_101010	XwPt-5577-1B	wPt5577	-	DArT	genomic DNA	-	-	-	1B	-	7.0	



Select QTL

# Details on one locus:

## XwPt-1973-1B

### GnpMap / Locus

#### DÉTAILS SUR LE LOCUS

Nom du locus : XwPt-1973-1B

Nom du marqueur : wPt1973

Type de marqueur : DArT

Fonction du gène (annotation manuelle) :

#### ASSIGNATIONS

Nombre d'assignations : 2

Nom de la carte	Fiabilité/(nom de la carte source)	Groupe de liaison	Bin	Distance	Limite proximale du locus	Limite distale du locus	Dist. %	Intervalle(s)	Locus proximal	LOD	Locus distal	Lien vers les QTL	Lien vers les QTL élargis
CF9107xToisondorxQuebon	-	1B	-	0.0	-	-	-	-	-	-	-	-	-
TOR107_101010	-	1B	-	0.0	-	-	-	-	-	-	-	2	2

# Locus is found on a another map: CF107xToisondorXQuebon

## GnpMap / Carte

### DÉTAILS SUR LA CARTE

Nom : CF9107xToisondorxQuebon

Type de carte : genetic

Date : 25/03/2011

Taxon : Triticum aestivum

Population : CFQUE-TORQUE-TOR107

Soumise par : BOGARD Matthieu

Fichier de génotype :

Fichier image :

Nombre de groupes de liaison : 34

Nombre de loci : 695

Nombre de QTL : 141

Nombre de QTL non projetés : 141

Nombre de MetaQTL : 15

# QTL meta-analysis

## GnpMap / Résultats

### RESULTS



1 2 ► ► | 15 items trouvés, affichage de 1 à 10 | Afficher 10 résultats par page

#	MetaQTL	Méta-analyse	Méta-trait	Trait(s)	Carte	Groupe de liaison	De	À	Position
1	MQTL7B_2	MQTL_CxQxT_7B	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7B	125.89	129.91	127.9
2	MQTL2D_2	MQTL_CxQxT_2D	Seed quality	GY 🔍	CF9107xToisondorxQuebon	2D	76.91	79.83	78.37
3	MQTL3A_2	MQTL_CxQxT_3A	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	3A	75.26	93.84	84.55
4	MQTL3A_3	MQTL_CxQxT_3A	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	3A	115.945	125.995	120.97
5	MQTL3B2_1	MQTL_CxQxT_3B2	Seed quality	GY 🔍	CF9107xToisondorxQuebon	3B2	38.825	45.095	41.96
6	MQTL5D1_1	MQTL_CxQxT_5D1	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	5D1	1.7	45.3	23.5
7	MQTL3A_4	MQTL_CxQxT_3A	Seed quality	GY 🔍	CF9107xToisondorxQuebon	3A	138.605	188.975	163.79
8	MQTL7D	MQTL_CxQxT_7D	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7D	71.3	72.44	71.87
9	MQTL5D1_2	MQTL_CxQxT_5D1	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	5D1	95.805	96.815	96.31
10	MQTL7B_1	MQTL_CxQxT_7B	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7B	48.36	56.42	52.39

# QTL meta-analysis

## GnpMap / Méta-analyse : MQTL\_CxQxT\_7B

### DÉTAILS DE LA MÉTA-ANALYSE

Méta-analyse	MQTL_CxQxT_7B
Méthode	Goffinet B.
Carte support	CF9107xToisondorxQuebon
Contact	Jacques LE GOUIS
Logiciel	MetaQTL

### METAQTLS IDENTIFIÉS

Nombre de MetaQTLs : 3

MetaQTL
MQTL7B_1
MQTL7B_2
MQTL7B_3

### CARTES UTILISÉES POUR LA MÉTA-ANALYSE

Nombre de cartes : 1

Carte génétique
CF9107xToisondorxQuebon

### QTLS UTILISÉS POUR LA MÉTA-ANALYSE



1 2 ► ► | 13 items trouvés, affichage de 1 à 10 | Afficher | 10 | résultats par page

#	QTL name	Trait	Carte(s)
1	nw.9.LN_GPD_7B_147.7	GPD	CF9107xToisondorxQuebon
2	mean_GPC_7B_53.6	GPC	CF9107xToisondorxQuebon
3	cf.9.HN_GY_7B_127.9	GY	CF9107xToisondorxQuebon
4	cf.9.HN_GY_7B_32.6	GY	CF9107xToisondorxQuebon
5	nw.9.HN_GPC_7B_53.6	GPC	CF9107xToisondorxQuebon
6	nw.9.HN_GY_7B_142.7	GY	CF9107xToisondorxQuebon

# Detail on Trait : GPD

## GnpMap / Trait card

### TRAIT DETAILS

Nom du trait	GPD
Trait description	Grain protein deviation
Unit	%
Short remark	
Theme	Quality
Genoplante classification	Agronomic
MetaQTLs	-

### ASSOCIATED MEASURES

Number of measures: 10

Measure	Description	Experimentation	Number of QTL assignments
cf.8.HN_GPD	Grain protein deviation	cf.8.HN	5
cf.9.LN_GPD	Grain protein deviation	cf.9.LN	3
cf.9.HN_GPD	Grain protein deviation	cf.9.HN	1
mean_GPD	Grain protein deviation	mean	8
LN_GPD	Grain protein deviation	LN	9
HN_GPD	Grain protein deviation	HN	9
nw.9.LN_GPD	Grain protein deviation	nw.9.LN	2
nw.9.HN_GPD	Grain protein deviation	nw.9.HN	7
sb.9.LN_GPD	Grain protein deviation	sb.9.LN	2
sb.9.HN_GPD	Grain protein deviation	sb.9.HN	6

### ASSOCIATED KEYWORDS

Number of keywords: 1

Keyword	Description	Short remark
yield	-	-

# Detail on experiment cf.8.HN

## GnpMap / Experiment card

### EXPERIMENT DETAILS

Experiment name : cf.8.HN

Synthesis method : mean

Vp Tc :

Population : TOR107

Culture conditions : high N supply

### ASSOCIATED MEASURES

Number of measures: 3

Measures	Nom du trait	Theme name	Number of QTL assignments
cf.8.HN_GPC	GPC	Quality	7
cf.8.HN_GPD	GPD	Quality	5
cf.8.HN_GY	GY	Quality	5

### ASSOCIATED PLACES

Place: 1

Place	Description	Climatic conditions	Date
Clermont-Ferrand	-	-	2009

# Detail on QTL assignments for the experiment cf.8.HN

## GnpMap / QTL results

### RESULTS



5 items trouvés, affichage de 1 à 5 | Afficher  résultats par page

#	QTL name	Theme	Trait	Trait description	Map	Groupe de liaison	LOD	R2	Distance	From	to
1	cf.8.HN_GPD_2D_73.8	Quality	GPD	Grain protein deviation	CF9107xToisondorxQuebon	2D	5	0.07	74	58	77
2	cf.8.HN_GPD_3A_134.3	Quality	GPD	Grain protein deviation	CF9107xToisondorxQuebon	3A	6	0.08	134	115	148
3	cf.8.HN_GPD_7D_71.7	Quality	GPD	Grain protein deviation	CF9107xToisondorxQuebon	7D	5	0.07	72	63	93
4	cf.8.HN_GPD_2A2_31.1	Quality	GPD	Grain protein deviation	CF9107xToisondorxQuebon	2A2	6	0.09	31	19	34
5	cf.8.HN_GPD_5A1_8.9	Quality	GPD	Grain protein deviation	CF9107xToisondorxQuebon	5A1	6	0.08	9	2	15



Select loci

# Get the theme card with associated traits

## GnpMap / Theme card

### THEME DETAILS

Theme name :	Quality
--------------	---------

Description :
---------------

### ASSOCIATED TRAITS

Number of traits: 14

Nom du trait	Trait description
GPC	grain protein content
Ha	Hardness
P/L	balance of the curve : parametre rehologique
PHS	pre-harvest sprouting
TKW	thousand grain weight
W	dough strength (W) : parametre rehologique
days_to_flowering	days to flowering
extensibility	dough extensibility (L) : parametre rehologique
grain_yield	grain yield
plant_height	plant height
tenacity	dough tenacity (P) : parametre rehologique
GPD	Grain protein deviation
GY	Grain yield
Seed quality	Seed quality

# Quality theme (ontology) and associated traits

## GnpMap / Theme card

### THEME DETAILS

Theme name : Quality

Description :

### ASSOCIATED TRAITS

Number of traits: 14

Nom du trait	Trait description
GPC	grain protein content
Ha	Hardness
P/L	balance of the curve : parametre rehologique
PHS	pre-harvest sprouting
TKW	thousand grain weight
W	dough strength (W) : parametre rehologique
days_to_flowering	days to flowering
extensibility	dough extensibility (L) : parametre rehologique
grain_yield	grain yield
plant_height	plant height
tenacity	dough tenacity (P) : parametre rehologique
GPD	Grain protein deviation
GY	Grain yield
Seed quality	Seed quality

# Trait Classification (Genoplante ontology)

## GnpMap / Genoplante classification card

### GENOPLANTE CLASSIFICATION DETAILS

Genoplante classification : Agronomic

### ASSOCIATED TRAITS

Number of traits: 39

Nom du trait	Trait description
oil_K	kernel oil content
GPC	grain protein content
Ha	Hardness
P/L	balance of the curve : parametre rehologique
PHS	pre-harvest sprouting
TKW	thousand grain weight
W	dough strength (W) : parametre rehologique
days_to_flowering	days to flowering
extensibility	dough extensibility (L) : parametre rehologique
grain_yield	grain yield
plant_height	plant height
tenacity	dough tenacity (P) : parametre rehologique
QN_Harvest	QN Straws + QN Seeds
ADM	aerial dry matter at maturity
LA	leaf area
LA_NTOT	ratio N conversion in LA efficiency
LRL	root lateral length
LRL_LRNL	root lateral mean length
LRL_PRL	root lateral length per cm of primary root
LRL_TRL	root lateral length per cm of total root
LRN_PRL	root branching rate
NTOT	N : total plant nitrogen
NUR	N : specific N uptake
RDM	root dry matter
RDM_TDM	ratio root total dry matter

# Quick search with theme name : Seed quality

All  seed quality

General information Botrytis (B0510) functional Botrytis (T4) functional Botrytis (T4) genome  
Leptosphaeria genome Leptosphaeria functional Poplar genome Sclerotinia functional  
Vitis (12X) genome **Genetic mapping** Polymorphism

---

**Themes (2)** **Traits (1)**

Seed nitrogen accumu...	★★★★★	Seed quality	★★★★★
Quality	★★★★★	-	-
-	-	-	-
-	-	-	-
-	-	-	-
-	-	-	-
-	-	-	-
-	-	-	-
-	-	-	-

---

2 items found, displaying 1 to 2 | Display  results per page

All  seed quality

# Quicksearch by : cf.8.HN (name autocomplete), or with: GPC\_1D

All  cf.8.HN

**Genetic mapping**

Measures (3)	Qtlis (17)
cf.8.HN_GPD ★★★★☆	cf.8.HN_GPC_2A2_23.8... ★★★★☆
cf.8.HN_GPC ★★★★☆	cf.8.HN_GPC_3A_119.9... ★★★★☆
cf.8.HN_GY ★★★★☆	cf.8.HN_GPC_2D_73.8 ★★★★☆
-	cf.8.HN_GPC_5D1_90.3... ★★★★☆
-	cf.8.HN_GPC_7D_71.7 ★★★★☆
-	cf.8.HN_GPC_5A1_8.9 ★★★★☆
-	cf.8.HN_GPC_5D1_23.5... ★★★★☆
-	cf.8.HN_GPD_3A_134.3... ★★★★☆
-	cf.8.HN_GPD_5A1_8.9 ★★★★☆
-	cf.8.HN_GPD_2A2_31.1... ★★★★☆

1 2 ► ► | 17 items found, displaying 1 to 10 | Display   results per page

All  cf.8.HN



# NEW: METAQTL QUERY BUILDER (steps 1,2)

## GnpMap / Recherche de MetaQTLs

### QUERY PARAMETERS



Taxons

All  
Triticum aestivum

Cartes

All  
ARE\_050606  
AXO\_050428  
CF9107xToisondorxQuebon

Nom du MetaQTL

Suite de la recherche

MetaQTL

Marqueur proximal

Marqueur distal

Suite de la recherche

MetaTrait

QTL

# METAQTL QUERY BUILDER

## (step 3a): MetaTrait selection

Suite de la recherche **MetaTrait** **QTL**

**Méta-trait**

- All
- ADM
- days\_to\_flowering
- days\_to\_flowering

**Méta-analyse**

- All

**Contacts**

- All
- LE GOUIS Jacques

**QTLs utilisés**

- All
- AD\_cf.8.Np\_2D
- AD\_cf.8.Np\_7D
- AD\_cf.9.NI\_2A2

**Groupes de liaison**

- All
- 1
- 1A
- 1AS

**Résultats**

# METAQTL QUERY BUILDER

## OR (step 3b): QTL selection

Suite de la recherche **MetaQTL**

**Cartes**

All  
ARE\_050606  
AXO\_050428  
CF9107xToisondorxQuebon

**Nom du MetaQTL**

**Marqueur proximal**

**Marqueur distal**

Suite de la recherche **MetaTrait** **QTL**

**QTL name**

MetaQTL belonging (between 0.0 and 1.0)

[Between] : [And]

Résultats

# Result: GET metaQTLs according filters set in step 1 to 3

## GnpMap / Résultats

### RESULTS



1 2 ► ► | 19 items trouvés, affichage de 1 à 10 | Afficher 10 résultats par page

#	MetaQTL	Méta-analyse	Méta-trait	Trait(s)	Carte	Groupe de liaison	De	À	Position
1	MQTL7B_2	MQTL_CxQxT_7B	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7B	125.89	129.91	127.9
2	MQTL-TOR107-2A	MQTL_TOR107_240811_2A	days_to_flowering	ONSEN 🔍	TOR107_101010	2A2	-0.1	3.3	1.6
3	MQTL2D_2	MQTL_CxQxT_2D	Seed quality	GY 🔍	CF9107xToisondorxQuebon	2D	76.91	79.83	78.37
4	MQTL3A_2	MQTL_CxQxT_3A	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	3A	75.26	93.84	84.55
5	MQTL3A_3	MQTL_CxQxT_3A	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	3A	115.945	125.995	120.97
6	MQTL3B2_1	MQTL_CxQxT_3B2	Seed quality	GY 🔍	CF9107xToisondorxQuebon	3B2	38.825	45.095	41.96
7	MQTL5D1_1	MQTL_CxQxT_5D1	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	5D1	1.7	45.3	23.5
8	MQTL-TOR107-7D	MQTL_TOR107_240811_7D	days_to_flowering	grain_yield 🔍	TOR107_101010	7D	16.4	26.7	21.6
9	MQTL3A_4	MQTL_CxQxT_3A	Seed quality	GY 🔍	CF9107xToisondorxQuebon	3A	138.605	188.975	163.79
10	MQTL7D	MQTL_CxQxT_7D	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7D	71.3	72.44	71.87

# New in next version: link GnpIS – Biomercator (graphical viewer)

## GnpMap / Results

### RESULTS

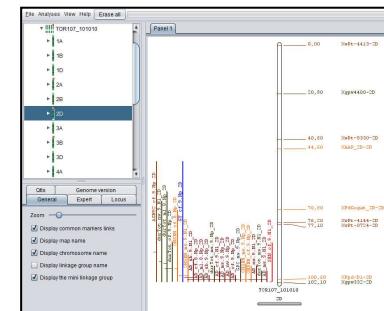


4 items found, displaying 1 to 4 | Display  results per page

#	MetaQTL	Meta-analysis	Meta-trait	Trait(s)	Map	Linkage group	From	To	Position	
1	MQTL-TOR107-2A	MQTL_TOR107_240811_2A	days_to_flowering	ONSEN		 TOR107_101010	2A2	-0.1	3.3	1.6
2	MQTL-TOR107-7D	MQTL_TOR107_240811_7D	days_to_flowering	grain_yield		 TOR107_101010	7D	16.4	26.7	21.6
3	MQTL-TOR107-3B	MQTL_TOR107_240811_3B	Prot%	grain_yield		 TOR107_101010	3B2	132.1	142.0	137.0
4	MQTL-TOR107-2D	MQTL_TOR107_240811_2D	days_to_flowering	grain_yield		 TOR107_101010	2D	98.1	103.4	100.7



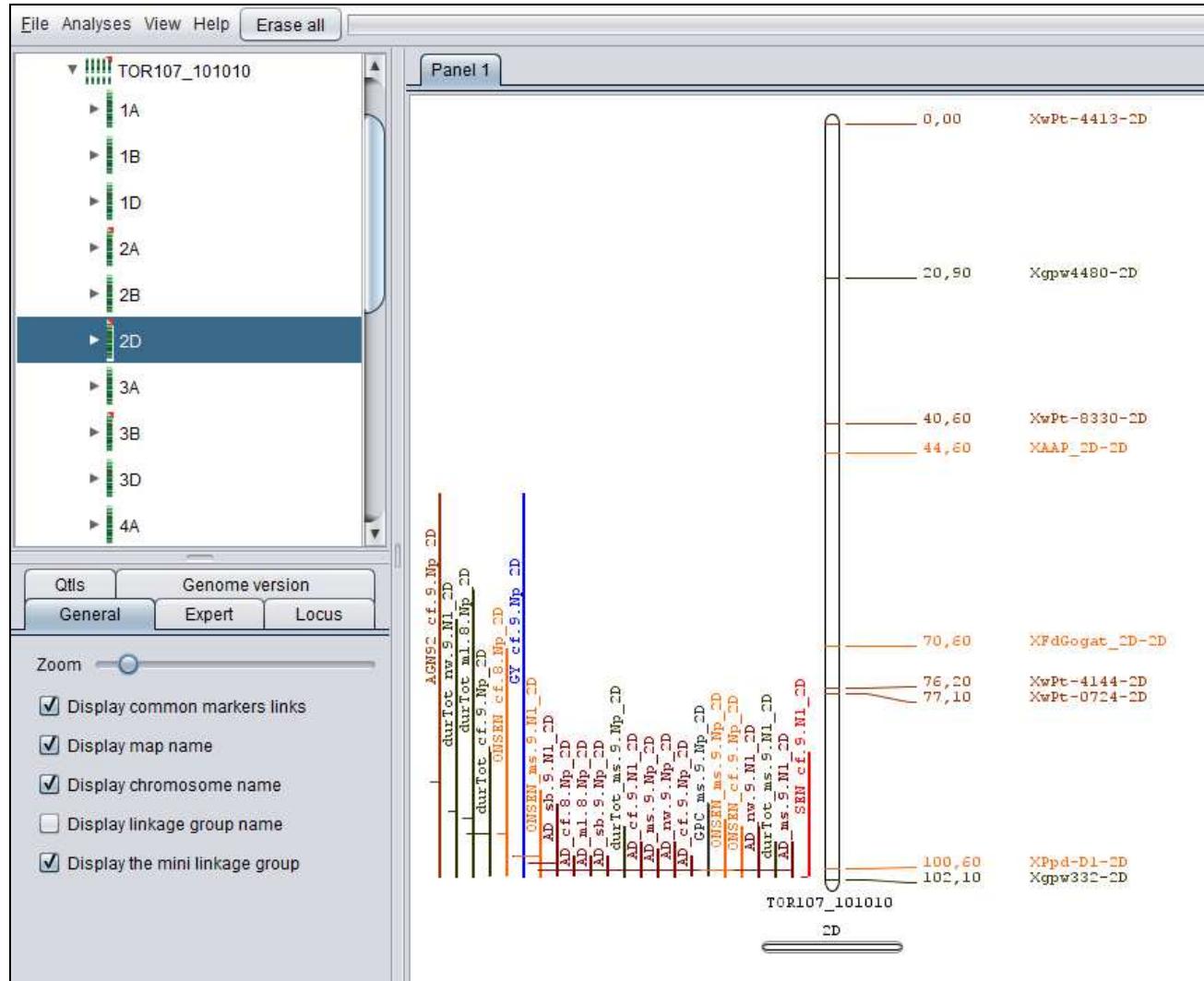
Launch: Biomercator (Java web start), analysis and display tool



# Biomercator V3, V4

O.Sosnovski  
J. Joets

*Paper in prep.*



# Loci Query BUILDER : (Step 1) : Species selection

## GnpMap / Recherche de loci

### QUERY PARAMETERS

---

**[Aide] Taxons**

- |                   |                                     |
|-------------------|-------------------------------------|
| Brassica napus L. | <input type="checkbox"/>            |
| Hordeum vulgare   | <input type="checkbox"/>            |
| Oryza sativa      | <input type="checkbox"/>            |
| Sorghum bicolor   | <input type="checkbox"/>            |
| Triticum aestivum | <input checked="" type="checkbox"/> |
| Vitis vinifera L. | <input type="checkbox"/>            |
| Zea mays L.       | <input type="checkbox"/>            |
| All               | <input type="checkbox"/>            |

# Loci Query Builder (step 2) : Map selection

Select map(s)

Map(s) :

all

ARE\_050606  
AXO\_050428  
CF9107xToisondorxQuebon

Sélectionner

Requêtes

Recherche par loci/région



Recherche par marqueur/séquence



# Loci Query Builder (step 3) : loci, distance, or between 2 loci, between 2

[Aide] Recherche par loci/région

Nom du locus

Xgpw2067-1B

Groupe de liaison :

All  
1A.1  
1A.2  
**1B**

Fiabilité :

All  
non\_framework

But :

[OPTIONS]

a. Sélection de la région autour des loci

Distance :

0  
10

in cM before the locus  
in cM after the locus

[OU]

b. Entre deux loci (prise en compte de l'intervalle de confiance des résultats)

Noms du locus (\*)

Locus de départ :

Locus de fin :

[OU]

c. Entre deux positions (prise en compte de l'intervalle de confiance des résultats)

de

à

Ensemble limité de colonnes :

yes

# Result: Get Loci on 1B between 0 and 20 cM

## GnpMap / Loci

### RESULTS



2 items trouvés, affichage de 1 à 2 | Afficher  résultats par page.

#	Nom	Nom du locus	Nom du marqueur	But	Fonction du gène (annotation manuelle)	Fiabilité/(nom de la carte d'origine)	Groupe de liaison	Bin	Distance	Lien vers le QTL	Lien vers le QTL élargi
1	ARE_050606	Xgpw2067-1B	GPW2067	Mapping	-	non_framework	1B	-	0.0	1	1
2	ARE_050606	Xgwm413-1B	GWM413	Mapping	UNKNOWN	non_framework	1B	-	12.3	1	1



Select QTL



# QTL QUERY BUILDER : (steps 1, 2)

## GnpMap / Recherche de QTLs

### QUERY PARAMETERS

#### [Aide] Taxons

*Brassica napus L.*

*Triticum aestivum*

All

#### Select map(s)

Map(s) :

- all
- ARE\_050606
- CF9107xToisondorxQuebon
- RER\_040618

Sélectionner

#### Requêtes

Recherche par trait et par expérimentation

Recherche par loci

Sélectionner

# QTL QUERY BUILDER :

## (Step 3) : by trait, Lod, R2, Linkage group

[Aide] Recherche par trait et par expérimentation

QTL name

Theme :

Trait :

All  
ADM  
days\_to\_flowering  
days\_to\_flowering

Genoplante classification :

All  
Agronomic  
Biochemical

Keyword :

All  
content  
flowering stage  
Fusarium Head Blight (FHB)

Lod >=

R2 :

>

Detection threshold :

>

Experiment name

Groupe de liaison :

All  
1  
1A  
1A.1

Pour les champs texte, la recherche est insensible à la casse. Utiliser le caractère '%' pour les recherches utilisant des caractères jokers.

Results

# Results: Get all QTLS for trait : days of flowering and EXPORT file

## GnpMap / QTL results

### RESULTS



1 2 | 12 items trouvés, affichage de 1 à 10 | Afficher |  résultats par page

#	QTL name	Theme	Trait	Trait description	Map	Groupe de liaison	LOD	R2	Distance	From	to	Fiabilité/nom de la carte d'origine)	Link to loci
1	QTL_DF_RER-F7_MO_99-1A	Quality	days_to_flowering	days to flowering	RER_040618	1A	-	42.2	55.5	38.4	59.6	unprojected	2
2	QTL_DF_RER-F7_LM_99-1A	Quality	days_to_flowering	days to flowering	RER_040618	1A	-	40.8	59.5	59.6	61.1	unprojected	2
3	QTL_DF_RER-F7_RN_99-1A	Quality	days_to_flowering	days to flowering	RER_040618	1A	-	30.6	59.8	59.6	61.1	unprojected	2
4	QTL_DF_RER-F7_MO_99-5A	Quality	days_to_flowering	days to flowering	RER_040618	5A	-	42.2	40	35.5	41.2	unprojected	2
5	QTL_DF_RER-F7_CF_99-2B	Quality	days_to_flowering	days to flowering	RER_040618	2B.2	-	33	58.3	48.1	58.4	unprojected	2
6	QTL_DF_RER-F7_MO_99-2B	Quality	days_to_flowering	days to flowering	RER_040618	2B.2	-	42.2	60.4	58.4	63.1	unprojected	2
7	QTL_DF_RER-F7_RN_99-2B	Quality	days_to_flowering	days to flowering	RER_040618	2B.2	-	30.6	60.8	58.4	63.1	unprojected	2
8	QTL_DF_RER-F7_LM_99-2B	Quality	days_to_flowering	days to flowering	RER_040618	2B.2	-	40.8	61.5	58.4	63.1	unprojected	2
9	QTL_DF_RER-F7_MO_99-2D	Quality	days_to_flowering	days to flowering	RER_040618	2D.1	-	42.2	77.2	75.9	84.8	unprojected	2
10	QTL_DF_RER-F7_CF_99-2D	Quality	days_to_flowering	days to flowering	RER_040618	2D.1	-	33	82.8	75.9	84.8	unprojected	2



Select loci



# NEW: METAQTL QUERY BUILDER: (steps 1,2)

## GnpMap / Recherche de MetaQTLs

### QUERY PARAMETERS



Taxons

All  
Triticum aestivum

Suite de la recherche

MetaQTL

Cartes

All  
ARE\_050606  
AXO\_050428  
CF9107xToisondorxQuebon

Nom du MetaQTL

Marqueur proximal

Marqueur distal

Suite de la recherche:

MetaTrait

QTL



# METAQTL QUERY BUILDER: (steps 1,2)

Cartes

All  
ARE\_050606  
AXO\_050428  
CF9107xToisondorxQuebon

Nom du MetaQTL

Marqueur proximal

Marqueur distal

Suite de la recherche

MetaTrait

QTL

Méta-traits

All  
Seed quality

Méta-analyse

Contacts

All  
LE GOUIS Jacques

QTLs utilisés

All  
cf.8.HN\_GPC\_2A2\_23.8  
cf.8.HN\_GPC\_2D\_73.8  
cf.8.HN\_GPC\_3A\_119.9

Groupes de liaison

All  
1A1  
1A2  
1B

# Results: Get MetaQTLs according filters settings

## GnpMap / Résultats

### RESULTS



1 2 ► ► | 15 items trouvés, affichage de 1 à 10 | Afficher 10 résultats par page

#	MetaQTL	Méta-analyse	Méta-trait	Trait(s)	Carte	Groupe de liaison	De	À	Position
1	MQTL7B_2	MQTL_CxQxT_7B	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7B	125.89	129.91	127.9
2	MQTL2D_2	MQTL_CxQxT_2D	Seed quality	GY 🔍	CF9107xToisondorxQuebon	2D	76.91	79.83	78.37
3	MQTL3A_2	MQTL_CxQxT_3A	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	3A	75.26	93.84	84.55
4	MQTL3A_3	MQTL_CxQxT_3A	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	3A	115.945	125.995	120.97
5	MQTL3B2_1	MQTL_CxQxT_3B2	Seed quality	GY 🔍	CF9107xToisondorxQuebon	3B2	38.825	45.095	41.96
6	MQTL5D1_1	MQTL_CxQxT_5D1	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	5D1	1.7	45.3	23.5
7	MQTL3A_4	MQTL_CxQxT_3A	Seed quality	GY 🔍	CF9107xToisondorxQuebon	3A	138.605	188.975	163.79
8	MQTL7D	MQTL_CxQxT_7D	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7D	71.3	72.44	71.87
9	MQTL5D1_2	MQTL_CxQxT_5D1	Seed quality	GPC 🔍	CF9107xToisondorxQuebon	5D1	95.805	96.815	96.31
10	MQTL7B_1	MQTL_CxQxT_7B	Seed quality	GY 🔍	CF9107xToisondorxQuebon	7B	48.36	56.42	52.39

# GnplS – Genetic resources collections module

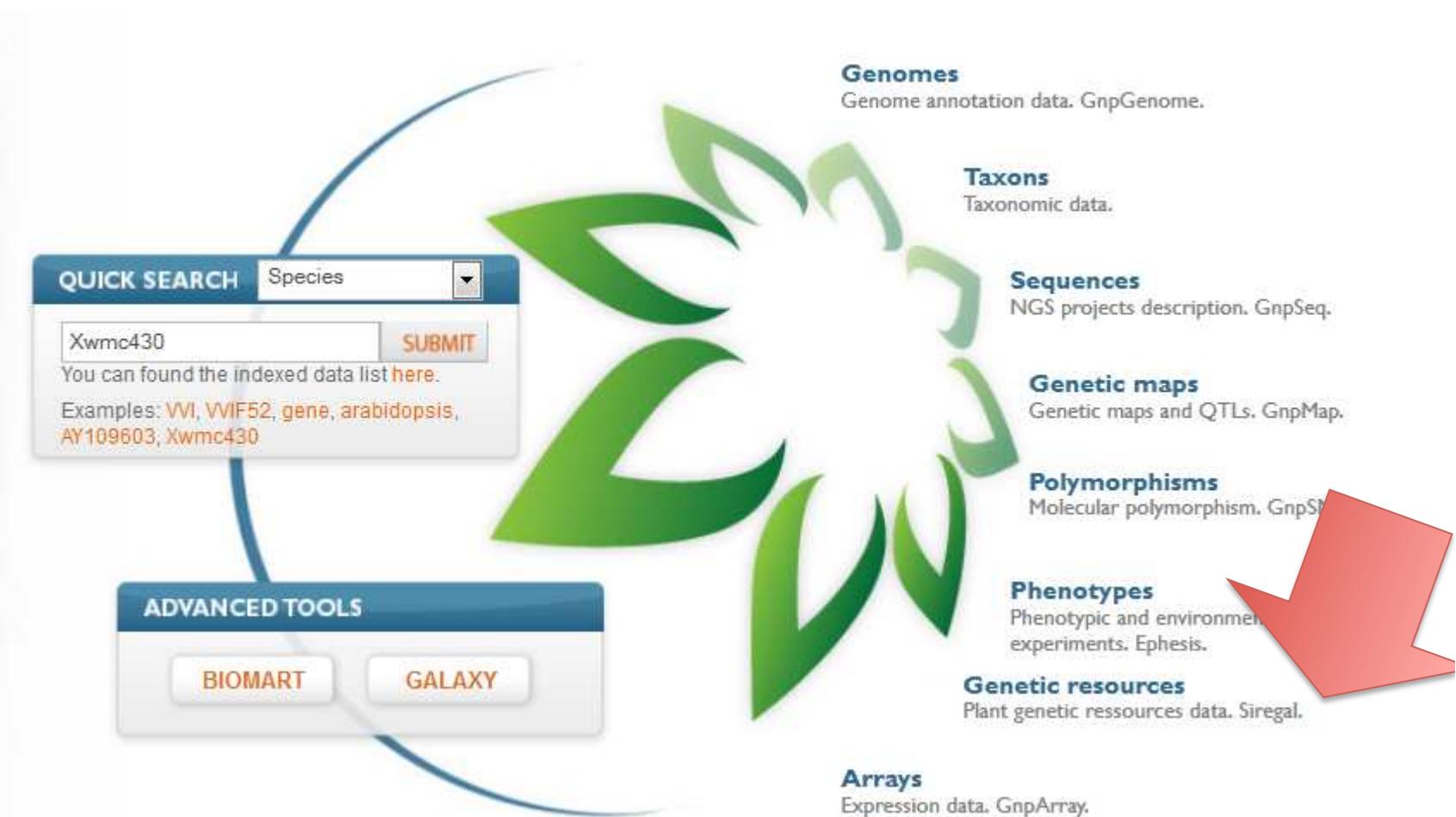
## INRA *Siregal project*



# GnplS – INRA resource genetic collections

Fruit species	Model species	Vegetable species	Crop species
			
			
			
			

# GnplS – Genetic mapping data dedicated module



# Quick search with accession name

Species  abundance

[General information](#) [Genetic resources](#)

**Accessions (1)**

ABONDANCE LEPEUPLE, ... 

1 items found, displaying 1 to 1 | Display  results per page

Species  abundance



# GnplS: accession QUERY

## Siregal / Recherche d'accessions

### PARAMÈTRES DE RECHERCHE

La recherche sera restreinte sur: CEREALS  [Aide]

Nom ou numéro d'accession (\*)

Variété ou espèce (\*)

(\*) Insensible à la casse, correspondance dans toute la chaîne, jokers autorisés. 

**Annuler**

**Résultats**

# Result : details on accession

## Siregal / Accession: ABONDANCE LEPEUPLE

### IDENTIFICATION



Numéro d'accession	773
Nom	ABONDANCE LEPEUPLE
Synonymes	BLE D'ABONDANCE [Français] ABUNDANCE [Français] BROAD LEAF CAPE [English] ABONDANCE [Français]
subspecies	<i>Triticum aestivum aestivum</i>
Pedigree	HYBRIDE DU JONCQUOIS/GARNET
Statut biologique	Cultivar traditionnel ou variété locale
Commentaire	-

### ORIGINE

Origine géographique : France

Sélectionnée

#### Site de sélection

Institution de sélection Maison Fernand Le Peuple

#### Date de création

-

#### Numéro original

-

#### Année d'enregistrement au catalogue français

1950

#### Année de retrait du catalogue français

-

#### Donnée

Institution donatrice UMR Génétique et Écophysiologie des Légumineuses à Graines, INRA-Dijon

#### Date de donation

-

#### Numéro original

-

Institution dépositaire UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont

### DONNÉES D'ÉVALUATION

-	Type de développement	Hiver - Winter
-	Précocité d'épaison (date en nombre de jours depuis le 01 janvier)	150,812
-	Classe de précocité d'épaison	8
-	Hauteur de la plante (cm)	121
-	Classe de hauteur de la plante	7
-	Sensibilité à <i>Puccinia recondita</i> (Rouille brune ou rouille des feuilles) - Année 2001	5

# Result : evaluation data

## DONNÉES D'ÉVALUATION

-	Type de développement	Hiver - Winter
-	Précocité d'épiaison (date en nombre de jours depuis le 01 janvier)	150,812
-	Classe de précocité d'épiaison	8
-	Hauteur de la plante (cm)	121
-	Classe de hauteur de la plante	7
-	Sensibilité à <i>Puccinia recondita</i> (Rouille brune ou rouille des feuilles) - Année 2001	5
-	Sensibilité à <i>Puccinia striiformis</i> f. sp. <i>hordei</i> (Rouille jaune) - Année 2001	2
-	Classe de poids de milles grains	5
-	Aristation du blé	3

## DISTRIBUTION

Statut de présence	Maintenu
Disponible	 Oui
Distributeur(s)	UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont

## COLLECTIONS

Appartient à	SOFT_WHEAT_FAO_COL
--------------	--------------------

# Result: detail on institution

## Siregal / Institution: UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont

### DÉTAILS SUR L'INSTITUTION

Code :	FRA040
Nom :	 UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont
Acronyme :	INRA GDEC Clermont
Organisation :	INRA
Type :	Organisme de recherche
Site internet :	<a href="http://www.clermont.inra.fr/umr1095/">http://www.clermont.inra.fr/umr1095/</a>
CRG gérés :	Céréales à paille 

### ADRESSE DE L'INSTITUTION

Adresse :	Site de Crouël, 234 avenue du Brézet
Code postal :	63100
Ville :	Clermont-Ferrand
Pays :	FRANCE

### CONTACT DE L'INSTITUTION

Coordinateur :	
Email :	F BALFOURIER
Téléphone :	+33 (0) 4.73.62.43.46
Fax :	+33 (0) 4.73.62.44.53
Gestionnaire des ressources :	
Email :	A DIDIER
Téléphone :	+33 (0) 4.73.62.43.90



# Result : select accession to order

## Siregal / Contenu du panier

### LISTE DES ARTICLES SÉLECTIONNÉS

[LISTE DES ACCESSIONS](#)[CONTENU DU PANIER](#)[COMMANDE](#)[RÉSUMÉ](#)[Retour aux résultats](#)

X	Accessions	Supprimer
1	773:ABONDANCE LEPEUPLE	

[Vider](#)[Commander](#)



# GnpIS : Passport Query Builder

## Siregal / Recherche d'acccessions

### PARAMÈTRES DE RECHERCHE

La recherche sera restreinte sur: CEREALS [\[Aide\]](#)

[Voir tout] | [Cacher tout]

#### Identification

Numéro d'accesion (+)

 [?](#)

Nom d'accesion (+)

 [?](#)

#### Taxinomie

Nom scientifique (+)

 [?](#) (Liste)

Nom commun :

 Tous [?](#)

#### Institution dépositaire

Institutions dépositaires :

Tous  
INRA GDEC Clermont – UMR Génétique, Diver:

[?](#)

#### Origine géographique

Pays :

 Tous [?](#)

#### Origine de collecte

Région de collecte (+)

 [?](#) (Liste)

Institutions de collecte :



Type d'environnement :



Altitude (mètres)

 [Et]  [?](#)

Latitude (degrés décimaux)

 [Et]  [?](#)

Longitude (degrés décimaux)

 [Et]  [?](#)

Année de collecte

 [Et]  [?](#)



# GnpIS : Passport Query Builder

## Sélection

Pays :



Institutions de sélection :

Tous

INRA SGAP Versailles – Station de Génétique e  
INRA UMR-SVQV Colmar – UMR Santé de la Vi  
BREUN – Saatzauchwirtschaft u. Breun  
ANZELEM – N.V. Clovis Matton Plant Breeding  
SCANEBC – Ste Coopérative Agricole du Nord-E



Année de sélection

 [Et] 

[Entre] :

[Entre] :

## Donateurs

Pays :

Tous

INRA SGAP Versailles – Station de Génétique e  
INRA UMR-SVQV Colmar – UMR Santé de la Vi  
VILAND – Vilmorin S.A.  
KLATOVY – RICP Praha-Ruzyně Agricultural Ri  
INRA LGAP LILLE – Laboratoire de Génétique e



Année de donation

 [Et] 

## Distributeurs

Pays :

Tous

INRA GDEC Clermont – UMR Génétique, Diver



## Phénotype

Descripteurs :

Tous

Nombre de rangs  
Hauteur de la plante (cm)  
Classe de précocité d'épiaison  
Sensibilité à Puccinia striiformis f. sp. hordei (



## Généalogie

Relation de parenté avec (\*)





# GnplS : Passport Query Builder

Année de donation  
[Entre] : [Et] ?

Distributeurs  
Pays : Tous ?  
Institutions distributrices : Tous  
INRA GDEC Clermont – UMR Génétique, Diver?

Phénotype  
Descripteurs : Tous  
Nombre de rangs  
Hauteur de la plante (cm)  
Classe de précocité d'épiaison  
Sensibilité à Puccinia striiformis f. sp. hordei ( )  
Sensibilité à Puccinia striiformis f. sp. hordei ( ) ?

Généalogie  
Relation de parenté avec (\*) ?

Collection  
Collection : SOFT\_WHEAT\_FAO\_COL ?

Année d'introduction  
[Entre] : [Et] ?

Divers  
Statut biologique : Tous  
Cultivar avancé ou variété améliorée  
Matériel de sélection ou de recherche  
Cultivar traditionnel ou variété locale  
Matériel de sélectionneur ?

Avec image :  ?

Disponible :  ?

(\*) Insensible à la casse, correspondance dans toute la chaîne, jokers autorisés. ?

Annuler

Résultats

(+) Insensible à la casse, jokers autorisés. ?

# Result: Accessions list

## Siregal / Accessions

LISTE DES ACCESIONS

CONTENU DU PANIER

COMMANDE

RÉSUMÉ

La recherche a été restreinte sur: CEREALS  [Aide]

1 2 3 4 5 6 7 8 9 10 ► ► | 119 items trouvés, affichage de 1 à 10 | Afficher 10 résultats par page

#	Numéro d'accession	Nom	Taxon	Statut biologique	Pays	Hauteur de la plante (cm)	Classe de précocité d'épiaison	Panier
1	773	ABONDANCE LEPEUPLE	<i>Triticum aestivum aestivum</i>	Cultivar traditionnel ou variété locale	FRA	121	8	
2	787	ADAMANT	<i>Triticum aestivum aestivum</i>	Cultivar avancé ou variété améliorée	FRA	91	8	
3	859	ALEX	<i>Triticum aestivum aestivum</i>	Cultivar traditionnel ou variété locale	FRA	86	5	
4	868	ALLIES	<i>Triticum aestivum aestivum</i>	Cultivar traditionnel ou variété locale	FRA	145	8	
5	871	ALMA	<i>Triticum aestivum aestivum</i>	Cultivar traditionnel ou variété locale	FRA	121	8	
6	934	APEXAL	<i>Triticum aestivum aestivum</i>	Cultivar avancé ou variété améliorée	FRA	90	7	
7	1015	ARMUR	<i>Triticum aestivum aestivum</i>	Cultivar avancé ou variété améliorée	FRA	85	6	
8	1019	ARONDE	<i>Triticum aestivum aestivum</i>	Cultivar avancé ou variété améliorée	FRA	125	7	
9	1064	ASTRON	<i>Triticum aestivum aestivum</i>	Cultivar avancé ou variété améliorée	DEU	100	8	
10	1076	ATOU	<i>Triticum aestivum aestivum</i>	Cultivar avancé ou variété améliorée	FRA	100	8	

1 2 3 4 5 6 7 8 9 10 ► ►

# GnplS – Genotype X Environment Phenotyping data *INRA EPHESIS project*



Integration of :

- trials
- variables
- ontologies of var.
- multisites
- environment: GXE



# GnplS: Trial QUERY

## Ephesis Beta / Trial query

### QUERY PARAMETERS

Trial name (+)

Trial comments (+)

Phenotypes names (+)

Accessions names (+)

Phenotyping Campaign Name

Trial's begin date after (mm-yyyy)



Trial's end date before (mm-yyyy)



(+) Case insensitive, wildcards allowed. 

[Cancel](#)

[Results](#)



# NEW (DEV) : GnpIS: Trial QUERY

## Ephesis Beta / Experimental data query

### QUERY PARAMETERS

 Trials Genotype Variables

Trial name

Phenotyping campaign

Experimental sites

- All
- Bergheim
- Bordeaux
- IPGPAS

(+) Case insensitive, wildcards allowed. 



# Result: list of trials

## *pilot data (grapevine)*

### Ephesis Beta / Essais

#### RESULTS



3 items found, displaying 1 to 3 | Display  results per page

#	Nom	Site	Date	Commentaire
1	RIGW section I	Bergheim	De : 01/01/2003 à : 01/01/2013	Essai pérenne
2	Prunier Collection nationale	Bordeaux	De : 01/01/2003 à : 31/12/2008	
3	IGR_2010_1	IPGPAS		IPGPAS public

# Result: trial detail

## Ephesis Beta / Essai RIGW section I

Nom de l'essai

RIGW section I

Date

De 01/01/2003 à 01/01/2013

Accessions utilisées dans  
RIGW section I :

0036E  
0072E  
0001E  
0058D  
0014E  
0048E  
0014D  
0022E  
0206E  
4082G

Nom  
d'accession

0036E

Numéro  
d'accession

41207Col0036E

Taxon

Vitis L.

[Plus d'informations dans Siregal](#)

Phénotypes utilisées dans  
RIGW section I :

NbRaml  
NbCours  
NbRamll  
NbGrmnds  
NbInfl  
NbInfcours  
NbInfill  
NbInfGrmnds  
NbRamTot  
NbInftot

Code de la  
variable

NbRaml

Nom de la  
variable

Nb prim. shoots

Détails de la  
variable

Nb prim. shoots (English)

Commentaires

Essai pérenne

Contact

Eric DUCHÈNE

Exporter

Récupérer le format d'échange avec l'en-tête uniquement  
Récupérer le format d'échange avec les données d'exemple





# GnplS: experimental data query

## Ephesis Beta / Experimental data query

### QUERY PARAMETERS

Please choose the experimental elements (micro parcel, whole plant, bloc, ...) and the available variables you wish to visualize and export.

Trial name : RIGW section I

#### Experimental Element #1

- Bloc complet  Bloc incomplet  Parcelle  Rang  Souche

#### variable

- Primary fertility  
 Nb shoots tot./m<sup>2</sup>  
 Nb prim. shoots  
 Nb shoots tot.  
 Nb shoots on spurs  
 Nb inflo. spurs  
 Nb inflo. tot.  
 Spurs fertility  
 Fertility non-count pos.  
 Total Nb inflo./nb prim. shoots  
 Nb shoots l/m<sup>2</sup>



Results

# Result : Get list of trials with phenotyping values

## Ephesis Beta / Experimental data

### RESULTS



Trial name : RIGW section I

1 2 3 4 5 6 7 8 9 10 ► ► | 751 items found, displaying 1 to 10 | Display 10 ↴ results per page

#	lotNumber	trialName	trialSite	BlocComplet	BlocIncomplet	Parcelle	Rang	Souche	Fertl	NbRamTotm2	NbRaml	NbRamTot
1	0005E	RIGW section I	Bergheim	1	6	26210	12	2	1.7142857	8.242424	14	17
2	0005E	RIGW section I	Bergheim	1	6	26210	12	3	2	7.757576	14	16
3	0071E	RIGW section I	Bergheim	1	6	26211	12	4	1.5714285	8.727273	14	18
4	0071E	RIGW section I	Bergheim	1	6	26211	12	5	2.2142856	7.757576	14	16
5	0051E	RIGW section I	Bergheim	1	6	26212	12	6	1.5384616	7.2727275	13	15
6	0051E	RIGW section I	Bergheim	1	6	26212	12	7	1.6	8.242424	15	17
7	0072E	RIGW section I	Bergheim	1	12	26213	12	8	2.357143	16.484848	14	34
8	0072E	RIGW section I	Bergheim	1	12	26213	12	9	2.2666667	12.121212	15	25
9	0001E	RIGW section I	Bergheim	1	12	26214	12	10	1.8571428	9.212121	14	19
10	0001E	RIGW section I	Bergheim	1	12	26214	12	11	2	7.757576	14	16

# Export trials results

## Ephesis Beta / Export data

### QUERY PARAMETERS



This query could take time.  
Please complete the form below in order to get your results by mail.

---

File name

Email (\*\*)



(\*\*) Mandatory field.

# EPHESIS Status

- EPHESIS data submission file:
  - done according EPHESIS, BREEDWHEAT and TRANSPLANT (Pawel & al)
- New query interface for selecting on trials, genotypes and variables
- Trait ontology: an ontology for Grapevine and \*\*\* Wheat \*\*\* is now set up in [cropontology.org](http://cropontology.org)
  - in agreement with Trait ontologies and Plant ontologies initiatives (mapping between these set of ontologies)
  - Cf. Wheat initiative



# GnpIS

## Polymorphism, Genotyping data

### *INRA GnpSNP project*



# GnpIS – polymorphism variation module



# GnpIS : polymorphism data (SNP, in-del...)

## GnpSNP

Bienvenue sur l'interface web de la base de données de polymorphisme de l'URGI. GnpSNP fait partie de la plateforme [GnpIS](#) au même titre que [GnpSeq](#), [GnpMap](#) et [GnpArray](#).

Cette application offre la possibilité de naviguer au sein des données de polymorphisme (comme les haplotypes ou les génotypes) stockées dans la base de données de l'URGI.

Différents formulaires de requête permettent de rechercher précisément de l'information.

Toutes les pages de résultats offrent des liens vers des informations supplémentaires (dans certains cas vers des ressources externes comme [dbSNP](#)), afin d'étendre la recherche de départ.

### APERÇU DU CONTENU DE LA BASE DE DONNÉES

<a href="#">Projets</a>	12
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### Nouveautés

#### 04 APRIL 2012

GnpSNP 2.0.3 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

Changements:

- Affichage de tous les génotypes appartenant à un taxon dans le formulaire simplifié de recherche de variants (GWT).
- Amélioration du formulaire de recherche de variants génomiques NGS (struts).
- Correction de bugs.

#### 06 MARCH 2012

GnpSNP 2.0.2 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

Changements:

- Migration de chromosome dans aster.
- Création d'un formulaire simplifié de recherche de variants (composants taxon et lignées) avec gwt.
- Correction de bugs.

#### 12 JANUARY 2012

GnpSNP 2.0.1 est maintenant disponible. Voir les [notes de version](#) pour plus d'informations sur les changements.

Changements:

- Amélioration de la lisibilité des principaux termes de l'application
- Corrections de bugs

# Several QUERY BUILDERS

- **QUERY by CONTENT**
- Or **QUERY by:**
  - Project
  - Genotypes
  - Experiments
  - Loci
  - Sequence Variation
  - Sequence Variation (NGS)

# GnpIS : NEW: VARIATION QUERY BUILDER (NGS reads)

## GnpSNP / Recherche de Variation de Séquence (NGS)

### PARAMÈTRES DE RECHERCHE



Par défaut la recherche accepte les caractères jokers et est sensible à la casse. Voir le guide de l'utilisateur pour plus d'informations.

Nom du génotype

Run

Séquence de référence

Chromosome

- chrUn
- chr1
- chr1\_random
- chr10

Position de mapping (pb)

[Entre] :

 [Et] 

Résultats

# Result: Get variations corresponding to selection

## GnpSNP / Variation de Séquence (NGS)

### RÉSULTATS



2 items trouvés, affichage de 1 à 2 | Afficher 10 résultats par page

#	Nom	Chromosome	Position de mapping	Séquence de référence	Run	Nom du génotype
1	<a href="#">PN40024 heterozygous SNPs chr10 93540</a>	chr10	93540	Vitis vinifera 12X	<a href="#">61EW6AAXX</a>	<a href="#">PN40024</a>
2	<a href="#">PN40024 heterozygous SNPs chr10 93560</a>	chr10	93560	Vitis vinifera 12X	<a href="#">61EW6AAXX</a>	<a href="#">PN40024</a>

# Details concerning variation

## GnpSNP / Sequence variation (NGS)PN40024\_heterozygous\_SNPs\_chr10\_93540

### DETAILS

Name PN40024\_heterozygous\_SNPs\_chr10\_93540

Type SNP

Localisation Vitis vinifera 12X

Chromosome chr10

Position 93540

Allelic variation C/A

### COMPLEMENTS

Run 61EW6AAXX

Line PN40024

Ref. allele C

Source MAPHITS pipeline

### QUALITY INDICATORS

Frequency of variant allele 54.55

Mapping quality mean of bases supporting Ref allele 65

Mapping quality mean of bases supporting Variant allele 65

PValue 1.8198952092469373E-14

### SEQUENCES

Seq. 5' flank unknown

Seq. 3' flank unknown

# Details on RUN

## GnpSNP / Run :61EW6AAXX

[GnpSNP](#)[GnpSeq NGS](#)

### RUN DETAILS

Name	61EW6AAXX
Run Date	13/04/2010
Description	PN40024 / Regale 114 pb

### SUB-RUN(S) DETAILS

61EW6AAXX\_s\_2\_PN40024

Sub-run name

Sub-run name 61EW6AAXX\_s\_2\_PN40024

Sub-run type lane

Reads number 69152078

Average reads length 114

Description PN40024

File(s) 61EW6AAXX\_s\_2\_PN40024\_114nt\_1.fasta  
61EW6AAXX\_s\_2\_PN40024\_114nt\_2.fasta  
README\_EPGV\_DataTransfer\_Illumina\_Sequencing.pdf

### COMPLEMENTS: SNP CALLING

Protocol [Illumina GA2 sequencing protocol](#)

Release genome version Vitis vinifera 12X

Genome Variants [\[Voir\]](#)Lines [\[Voir\]](#)

# Details on Line

## GnpSNP / Genotype: PN40024

### DETAILS

Name :	PN40024
Description :	Pinot Noir 40024

### COMPLEMENTS

Experiments :	VVC2985A-batch1	
NGS runs :	61EW6AAXX	
Polymorphic loci :	<a href="#">[Voir]</a>	
Sequence variations :	<a href="#">[Voir]</a>	
Taxon :	<a href="#">Vitis vinifera L.</a>	

# Details on polymorphic loci

## GnpSNP / Loci polymorphes

### RÉSULTATS



1 2 3 4 5 6 7 8 9 10 ► ► | 1968 items trouvés, affichage de 1 à 10 | Afficher 10 résultats par page

#	Nom	Source	Expériences
1	<a href="#">Vv_1272412</a>	GnpSNP	VV05786A-batch2
2	<a href="#">Vv_1272403</a>	GnpSNP	VV05788A-batch1
3	<a href="#">Vv_1272392</a>	GnpSNP	VV05793A-batch1
4	<a href="#">Vv_1272381</a>	GnpSNP	VV05796A-batch1
5	<a href="#">Vv_1272375</a>	GnpSNP	VV05796A-batch1
6	<a href="#">Vv_1272357</a>	GnpSNP	VVC2942AR-batch1
7	<a href="#">Vv_1272525</a>	GnpSNP	VV05776A-batch2
8	<a href="#">Vv_1272516</a>	GnpSNP	VV05778A-batch2
9	<a href="#">Vv_1272509</a>	GnpSNP	VV05778A-batch2
10	<a href="#">Vv_1272505</a>	GnpSNP	VV05778A-batch2

1 2 3 4 5 6 7 8 9 10 ► ►

# Details on one polymorphic locus

## GnpSNP / Locus polymorphe

### DÉTAILS SUR LE LOCUS POLYMORPHIQUE

Nom :	Vv_1272412
Source :	GnpSNP

### COMPLÉMENTS

Type :	SNP
Variation de séquence :	A/G
Linked with variations :	VV05786A_432_19 <a href="#">View list</a> 
Linked with lines :	2082Mtp1 <a href="#">View list</a> 

### INTERNAL REFERENCES

Base de données	Nom de la référence	Valeur de la référence
Vitis vinifera 12x Genome Browser	name	SNP_Vv_1272412

### SÉQUENCES

Fianquant 5' sur la séq. de réf. :	>Vv_1272412-5' TAGTTCTTACTTTGAAACCTAGAACATTTGCTTGGGCTTGATTGTTGAAAGATTGATCATTATATGCTGTTGA GTCTGGAGCTTCGCTAGAAAAGATGTGAATCTTTGCAGTTGGATACTAAAAAAACCTGATGTTAACCTTCTTAGTC TGGAGAAATACTCATTGTTCCAGATTGCTCTGGTAATGTCATTACTGTTGGCCAGAAAACCTCTA TTGACTCTG	
Fianquant 3' sur la séq. de réf. :	>Vv_1272412-3' AAAATGTTGAAGGTGCCTTATGTATCAAAGGATGGAGTCACAGTGGATCAAAGAAAACCACAGTATTCTGTTG ACGCCAAATCTGGAACAATTAAACACTTTAGATCAGATGCTCTCCTTGATAGGAGGTTCAAACTGATGAAGAA AACCTATCTATCTAGGAAAGAGATTGAAGAATTGATAGAGCCTGGTATGTTGAGAAGTTGAGCTGCCACT TTACATCATG	
Contexte génomique sur la séq. de réf. :	>Vv_1272412-genomic_context TAGTTCTTACTTTGAAACCTAGAACATTTGCTTGGGCTTGATTGTTGAAAGATTGATCATTATATGCTGTTGA GTCTGGAGCTTCGCTAGAAAAGATGTGAATCTTTGCAGTTGGATACTAAAAAAACCTGATGTTAACCTTCTTAGTC TGGAGAAATACTCATTGTTCCAGATTGCTCTGGTAATGTCATTACTGTTGGCCAGAAAACCTCTA TTGACTCTG[A/G]AAAATGTTGAAGGTGCCTTATGTATCAAAGGATGGAGTCACAGTGGATCAAAGAAAACCA CACTATTCTGTTGACCCAATTGGAACAATTAAACACTTTAGATCAGATGCTCTCCTTGATAGGAGGTT CAAAGTGTGAAGAAAACCTATTCTATCTAGGAAAGAGATTGAAGAATTGATAGAGCCTGGTATGTTGAGA AGTTGAGCTGCCACTTACATCATG	

# Get all genotypes

## GnpSNP / Genotype results

### AVAILABLE GENOTYPES



32 items trouvés, affichage de 1 à 32 | Afficher 40  résultats par page

#	Genotype name	Taxon
1	<a href="#">2082Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Mehdik</i>
2	<a href="#">0Mtp567</a>	<i>Vitis vinifera</i> L.
3	<a href="#">225Mtp2</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>César</i>
4	<a href="#">0Mtp1323</a>	<i>Vitis vinifera</i> L.
5	<a href="#">8500Mtp23</a>	<i>Vitis vinifera</i> L.
6	<a href="#">0Mtp636</a>	<i>Vitis vinifera</i> L.
7	<a href="#">1498Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Espadeiro tinto</i>
8	<a href="#">324Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Cabernet franc</i>
9	<a href="#">0Mtp697</a>	<i>Vitis vinifera</i> L.
10	<a href="#">1186Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Chirai</i>
11	<a href="#">192Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Chouchillon</i>
12	<a href="#">2471Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Tita Caprei</i>
13	<a href="#">0Mtp1150</a>	<i>Vitis vinifera</i> L.
14	<a href="#">0Mtp1557</a>	<i>Vitis vinifera</i> L.
15	<a href="#">2158Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Lambrusque E</i>
16	<a href="#">2651Mtp2</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Pervenetz praskovelsky</i>
17	<a href="#">2505Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Assul kara</i>
18	<a href="#">8500Mtp31</a>	<i>Vitis vinifera</i> L.
19	<a href="#">0Mtp224</a>	<i>Vitis vinifera</i> L.
20	<a href="#">2461Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Orlovi nogti</i>
21	<a href="#">0Mtp1583</a>	<i>Vitis vinifera</i> L.
22	<a href="#">1566Mtp2</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Sultanine</i>
23	<a href="#">0Mtp715</a>	<i>Vitis vinifera</i> L.
24	<a href="#">PN40024</a>	<i>Vitis vinifera</i> L.
25	<a href="#">150Mtp3</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Syrah</i>
26	<a href="#">2897Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Ak ouzolum tagapskii</i>
27	<a href="#">294Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Orbois = Arbois</i>
28	<a href="#">0Mtp583</a>	<i>Vitis vinifera</i> L.
29	<a href="#">1805Mtp1</a>	<i>Vitis vinifera</i> subsp <i>vinifera</i> cv. <i>Araklinos</i>
30	<a href="#">8500Mtp124</a>	<i>Vitis vinifera</i> L.
31	<a href="#">A500Mtn113</a>	<i>Vitis vinifera</i> L.



# See variation on reference genomic sequence

## GnpSNP / DB card

### DETAILS

Name :	Vitis vinifera 12x Genome Browser
Version :	2
Installed on :	01/01/2011
Url :	<a href="#">Σ<sub>W</sub> [Voir]</a>
External DB :	No

# GnplS: Vitis 12X grape genome and annotation

**Vitis vinifera (12x) Genome Browser: 20 kbp from chr17:12,971,413..12,991,412**

To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.  
To switch to another organism, use the Data Source menu.

New names of gene in 12X version according to the genome release at EMBL : GSVIVG00 to GSVIVG01  
New track available : Raw data of Genoscope automatic annotation (Gaze without filters) : 36738 gene predictions  
New tracks available : Gene prediction (named V1) produced by CRIBI on the 12X sequence assembly. This V1 annotation is divided in V1\_NR (non repetitive sequences) and V1\_R (repetitive sequences)

**Browser** Select Tracks Custom Tracks Preferences

**Search**

Landmark or Region:  
chr17:12,971,413..12,991,412 Search

Examples: chr15:5282664..5322663, GSVIVG01032605001, EGT00018252001, SNAPVvG00016689001, GWSUNIT02500482001, VV1I52, VV40024H100E01, Vv\_10003495, Vv0s0116g00040, GSVIVG01001153001, NEW20, VVTGPS65, SNP\_Vv\_1272338, indel\_Vv\_1272543, SNP\_Vv\_1273469, PN40024\_heterozygous\_SNPs\_chr1\_4012677, PN40024\_seqErr\_SNPs\_chr1\_1252920, SNP\_ENSVVV100100380.

Annotate Restriction Sites ▾ Configure... Go

**Data Source** Vitis vinifera (12x) Genome Browser

Scroll/Zoom: << < > >> Show 20 kbp ▾ + - ▾ Flip

**Overview**

chr17  
0M 1M 2M 3M 4M 5M 6M 7M 8M 9M 10M 11M 12M 13M 14M 15M 16M 17M

Marker

**Region**

12890k 12900k 12910k 12920k 12930k 12940k 12950k 12960k 12970k 12980k 12990k 13000k 13010k 13020k 13030k 13040k 13050k 13060k 13070k 13080k

5 kbp

Marker

Transcript phases (Gaze without filters)

V1\_R transcript

# GnpIS : NEW : GnpSeqNGS

## GnpSeq / Run :61EW6AAXX

[GnpSNP](#)[GnpSeq NGS](#)

### DÉTAILS SUR LE RUN

Nom	61EW6AAXX
Date du run	13/04/2010
Description	PN40024 / Regale 114 pb

### DÉTAILS SUR LE(S) SUB-RUN(S)

61EW6AAXX\_s\_2\_PN40024

#### Nom du sub-run

Nom du sub-run

Type de sub-run

Nombre de reads

Taille moyenne des reads

Description

Echantillon

Expérience(s)

Analyse(s)

Fichier(s)



# GnplS : NGS

## GnpSeq / Expérience : PN40024 resequencing

### DÉTAILS SUR L'EXPÉRIENCE

Nom	PN40024 resequencing
Projet	PN40024

### DÉTAILS SUR LE SÉQUENÇAGE

Type d'étude	resequencing
Séquenceur	Illumina GA II
Type de séquençage	paired end
Centre de séquençage	CNG-EPGV
Echantillon	PN40024
Runs	[Voir]



# GnplS : NGS : RUNS

## GnpSeq / Runs

### RÉSULTATS



2 items trouvés, affichage de 1 à 2 | Afficher 10 | 1 résultats par page

#	Nom	Date
1	61EW4AAXX	31/03/2010
2	61EW6AAXX	13/04/2010

# GnplS : NGS details

## GnpSeq / Project: PN40024

### PROJECT DETAILS

[GnpArray](#)[GnpMap](#)[GnpSNP](#)[GnpSeq NGS](#)[Siregal](#)

Project code :	PN40024
Project name :	PN40024 public data
Status :	open
Title :	PN40024 public data
Creation date :	01/01/2009
Remarques :	PN40024 NGS data produced for Muscares and GrapeReSeq projects

### ASSOCIATED CONTACTS

Coordinator(s) :	CHOISNE	<a href="#">Details</a>
Bioinformatic(s) :	CHOISNE	<a href="#">Details</a>
Partenaire(s) :	ADAM-BLONDON	<a href="#">Details</a>

### INFORMATION ASSOCIÉE

[Accès aux expériences](#)  
[Accès aux analyses](#)

# GnplS : NGS reads analysis details

## GnpSeq / Analysis results

### RÉSULTATS



1 items trouvés, affichage de 1 à 1 | Afficher 10 résultats par page

#	Name	Type	Taxon	Project
1	PN40024 polymorphism detection	SNP detection	Vitis vinifera L.	PN40024



# GnplS : NGS

## GnpSeq / Analyses : PN40024 polymorphism detection

### DÉTAILS SUR L'ANALYSE

Nom	PN40024 polymorphism detection
Type d'analyse	SNP detection
Logiciel	MapHits
Génome de référence	Vitis vinifera 12X
Commentaires	Allele differences between sanger reference sequence and illumina reads: residual heterozygosity and potential sanger sequencing errors.

### DÉTAILS SUR L'EXÉCUTION

Ligne de commande	Bwa with -n=0.01 & VarScan with Min coverage10, Min variant read=4, Min variant allele frequency=30%, Max P-Value=1e-3
Runs	[Voir]
Fichier de résultat	<a href="#">PN40024_114nt_SNPs.tab</a> <a href="#">PN40024_76nt_SNPs.tab</a> <a href="#">PN40024_all_SNPs.tab</a>

### INFORMATIONS COMPLÉMENTAIRES

Projet	PN40024
Contact	Nacer MOHELLIBI

# GnplS : files available in GALAXY analysis tool

Galaxy | Published History | PN40024 public data  
urgi.versailles.inra.fr/galaxy/u/nchoisne/h/pn40024-public-data

Galaxy Analyze Data Workflow Shared Data Visualization Help Using 0%

Published Histories | nchoisne | F User public data + Import history

Galaxy History 'PN40024 public data'

Dataset Annotation

1: 61EW4AAXX s 1 PN40024 76nt 1.fastq

2: 61EW4AAXX s 1 PN40024 76nt 2.fastq

3: 61EW6AAXX s 2 PN40024 114nt 1.fastq

4: 61EW6AAXX s 2 PN40024 114nt 2.fastq

5: PN40024 114nt SNPs.tab

6: PN40024 76nt SNPs.tab

7: PN40024 all SNPs.tab

About this History

Author nchoisne 

Related Histories [All published histories](#) [Published histories by nchoisne](#)

Rating Community (0 ratings, 0.0 average) 

Tags Community: none

# GnpSeqNGS

## GnpSeq / Experiment query

### PARAMÈTRES DE RECHERCHE



Experiment name

Taxons

Tous  
Triticum aestivum  
Vitis vinifera L.

Projects

Tous  
PN40024  
3BSEQ

Experiment types

Tous  
resequencing  
sequencing

Sequencers

Tous  
Illumina GA II  
454 Titanium

Trier les résultats par :

Experiment name

Résultats

# Wheat: GnpSeqNGS

## GnpSeq / Experiment : 3B Reference Sequence

### EXPERIMENT DETAILS

Name	3B Reference Sequence
Description	Sequence repository : <a href="http://urgi.versailles.inra.fr/Species/Wheat/Chr3B">http://urgi.versailles.inra.fr/Species/Wheat/Chr3B</a>
Project	3BSEQ

### SEQUENCING DETAILS

Study type	sequencing
Sequencer	454 Titanium
Sequencing type	paired end
Sequencing center	Genoscope
Sample	Chinese Spring
Runs	[Voir]

# Wheat : GnpSeqNGS

## GnpSeq / Sample : Chinese Spring

### SAMPLE DETAILS

Name	Chinese Spring
Type	gDNA
Taxon	<i>Triticum aestivum</i>
Projet	3BSEQ
Contact	Catherine FEUILLET

### LIBRARY DETAILS

Name	Chinese Spring sample
Obtention strategy	BAC pool sequencing
Protocol	pools of 10 BACs
Insert length (bp)	8000

# GnplS : POLYMORPHISM LOCI QUERY BUILDER

## GnpSNP / Recherche de loci polymorphes

### PARAMÈTRES DE RECHERCHE



Par défaut la recherche accepte les caractères jokers et est sensible à la casse. Voir le guide de l'utilisateur pour plus d'informations.

**Nom****Source****Taxons**

Tous  
Arabidopsis thaliana  
Oryza sativa  
**Triticum aestivum**

**Projets**

Tous  
AIP\_P00272  
BerrySize  
CM2006-var4

**Expériences**

Tous  
BIB\_CF-11  
BIB\_CF-12  
BIB\_CF-13

**Génotypes**

Tous  
ad10  
ad12  
ad13

**Nom de la variation de séquence****Résultats**

# Get variations for triticum (sequencing of several genes)

## GnpSNP / Loci polymorphes

### RÉSULTATS



1 2 3 ► ► | 95 items trouvés, affichage de 1 à 40 | Afficher 40 résultats par page

#	Nom	Source	Expériences
1	<a href="#">Tae_1272243</a>	GnpSNP	INRA_CF_ASP-55
2	<a href="#">Tae_1272247</a>	GnpSNP	INRA_CF_ASP-51
3	<a href="#">Tae_1272254</a>	GnpSNP	INRA_CF_ASP-55
4	<a href="#">Tae_1272260</a>	GnpSNP	INRA_CF_ASP-56
5	<a href="#">Tae_1272269</a>	GnpSNP	INRA_CF_ASP-56
6	<a href="#">Tae_1272273</a>	GnpSNP	INRA_CF_ASP-51
7	<a href="#">Tae_1272297</a>	GnpSNP	INRA_CF_ASP-56
8	<a href="#">Tae_1272303</a>	GnpSNP	INRA_CF_ASP-55
9	<a href="#">Tae_1272311</a>	GnpSNP	INRA_CF_ASP-55
10	<a href="#">Tae_1272315</a>	GnpSNP	INRA_CF_ASP-51
11	<a href="#">Tae_1272320</a>	GnpSNP	INRA_CF_ASP-55
12	<a href="#">Tae_1272328</a>	GnpSNP	INRA_CF_ASP-55
13	<a href="#">Tae_1272248</a>	GnpSNP	INRA_CF_ASP-53
14	<a href="#">Tae_1272251</a>	GnpSNP	INRA_CF_ASP-55
15	<a href="#">Tae_1272280</a>	GnpSNP	INRA_CF_ASP-55
16	<a href="#">Tae_1272307</a>	GnpSNP	INRA_CF_ASP-55
17	<a href="#">Tae_1272319</a>	GnpSNP	INRA_CF_ASP-56
18	<a href="#">Tae_1272321</a>	GnpSNP	INRA_CF_ASP-56
19	<a href="#">Tae_1272332</a>	GnpSNP	INRA_CF_ASP-51

# Detail on one locus

## GnpSNP / Locus polymorphe

## DÉTAILS SUR LE LOCUS POLYMORPHE

<b>Nom :</b>	Tae_1272243
<b>Source :</b>	GnpSNP

COMPLÉMENTS

Type :	SNP
Variation de séquence :	G/A
Linked with variations :	<input type="text" value="INRA_CF_AS..._BT001"/> <a href="#">[View list]</a>  
Linked with lines :	<input type="text" value="A4"/> <a href="#">[View list]</a>  

## INTERNAL REFERENCES

Base de données	Nom de la référence	Valeur de la référence
Wheat 3B annotation (FHB)	SNP name	Taa_1272243

SÉQUENCES

Flanquant 5' sur la séq. de réf. :	>Tae_1272243-5' CtctccatgnncanntcaccgccttcggcgagacctactccctgcgcgcgcgcgtCccatcagcctnacnaanaaa caagacgacggccggcgttgacacannaanaanaagaagCncngcgtatgtctgtnacggggccactacccgaagc tcgtcaactcgccggagatcGtnaaggccgengagaaggccgggttcgaggtgacnatagccggaccggccgggttcangtg Cggctca.
Flanquant 3' sur la séq. de réf. :	>Tae_1272243-3' gagctggcccttcggtaactcggtcgactcggtgtctgtctggcgtgcacggcGccggcctnaccaactcgggttctggc ccgggggggggggtcatccagggttgtccnTaaggcaactggggatggggcagagganttcggngacccgggg nnacatggggCtccggtaacctcgagtacagcatcncgggtggaggagagacgcgtctgganacgcgtggggCengaccac ccggccatca
Contexte génomique sur la séq. de réf. :	>Tae_1272243-genomic_context CtctccatgnncanntcaccgccttcggcgagacctactccctgcgcgcgcgcgtCccatcagcctnacnaanaaa caagacgacggccggcgttgacacannaanaanaagaagCncngcgtatgtctgtnacggggccactacccgaagc tcgtcaactcgccggagatcGtnaaggccgengagaaggccgggttcgaggtgacnatagccggaccggccgggttcangtg Cggctca[G/A]gagctggcccttcggtaactcggtcgactcggtgtctgtctggcgtgcacggcGccggcctnaccaact cgggatcttcgtcgenggggggtgttgtcatccagggttgtccnTaaggcaactggggatggggcagagganttcggngacccgggg ggggCengaccacccggccatca



# View locus on genomic reference sequence

## GnpSNP / DB card

### DETAILS

Name :	Wheat 3B annotation (FHB)
Version :	3
Installed on :	30/11/2009
Url :	<a href="#"> [Voir]</a>
External DB :	No



# Wheat 3B genome annotation (region)

Wheat annotation viewer v2: 0 pbp from ctg0954b.1:1,793,808..1,793,808

ctg0005b.1 ctg0011b.1 ctg0079b.1 ctg0091b.1 ctg0382b.1 ctg0464b.1 ctg0528b.1 ctg0616b.1 ctg0661b.1 ctg0954b.1 ctg1030b.1 ctg1035b.1 TaaCsp3BFhA\_

**Browser** Select Tracks Custom Tracks Preferences

Search

Landmark or Region: ctg0954b.1:1,793,808..1,793,808 Search Download Decorated FASTA File Configure... Go

Examples: TAA\_ctg0954b.00250.1, Xsts80-3B, ctgD\_rep\_0033, Tae\_1272250, cfp5001, pg4in2F1-ex3R1, cfb6001, QTL\_FHB\_SumStoa\_BLW\_3B.

Data Source: Wheat annotation viewer v2

Scroll/Zoom: << < = Show 1 bp > >> + - □ Flip

Overview

Region

Details

ctg0954b.1

0M 1M 2M 3M

1700k 1710k 1720k 1730k 1740k 1750k 1760k 1770k 1780k 1790k 1800k 1810k 1820k 1830k 1840k 1850k 1860k 1870k 1880k 1890k

ctg0954b.1: 1 bp 10 cbp

SNP (GnpSNP) Tae\_1272260

SNP allele Tower (GnpSNP) Tae\_1272260 G C

QTL

mRNA

SNP

Contig ctg954

ISBP

SSR

STS

Repeats (Repeats Unit or Repeat Regions)

Select Tracks Clear highlighting

# View SNP mapped one genome, with link to SNP card

**Wheat annotation viewer v2: 0 pbp from ctg0954b.1:1,793,808..1,793,808**

ctg0005b.1 ctg0011b.1 ctg0079b.1 ctg0091b.1 ctg0382b.1 ctg0464b.1 ctg0528b.1 ctg0616b.1 ctg0661b.1 ctg0954b.1 ctg1030b.1 ctg1035b.1 TaaCsp3BFhA\_0

---

rowser [Select Tracks](#) [Custom Tracks](#) [Preferences](#)

Search

Landmark or Region:  [Search](#) [Download Decorated FASTA File](#) [Configure...](#) [Go](#)

Examples: TAA\_ctg0954b.00250.1, Xsts80-3B, ctgD\_rep\_0033, Tae\_1272250, cfp5001, pg4in2F1-ex3R1, cfb6001, QTL\_FHB\_SumStoa\_BLW\_3B.

Data Source: Wheat annotation viewer v2

Overview

Region

Details

ctg0954b.1

Tae\_1272260

DIP : Tae\_1272260  
Db Source : GnpSNP  
GnpSNP ID : Tae\_1272260  
Position : 1793808 .. 1793808

Zoom to this feature  
Link to GnpSNP

10 cbp

SNP (GnpSNP)  
Tae\_1272260

SNP allele\_tower (GnpSNP)  
Tae\_1272260  
G  
C

QTL

mRNA

SNP

Contig  
ctg954

ISBP

SSR

STS

Repeats (Repeats Unit or Repeat Regions)

Select Tracks [Clear highlighting](#)

# View details on SNP

## GnpSNP / Locus polymorphe

### DÉTAILS SUR LE LOCUS POLYMORPHIQUE

Nom :	Tae_1272260
Source :	GnpSNP

### COMPLÉMENTS

Type :	SNP
Variation de séquence :	G/C
Linked with variations :	INRA_CF_ASP_842_BT001 <a href="#">[View list]</a>
Linked with lines :	A4 <a href="#">[View list]</a>

### INTERNAL REFERENCES

Base de données	Nom de la référence	Valeur de la référence
Wheat 3B annotation (FHB)	SNP name	Tae_1272260

### SÉQUENCES

Flanquant 5' sur la séq. de réf. :	>Tae_1272260-5' cgatgcggccggccatggcggtgcctccagctctcgctgtttactgggtcgacgcaatccgtgacactga ctgggttattttttttaatntcccggttccttcncttagttgttgcacgacgtcgctggggacacagaaga aagatgacacccatttgcaggacggcgtgtgtcgccgttgaggccgtggaggcccaaggacgtgacgacgcggccggcc cttctccctc	
Flanquant 3' sur la séq. de réf. :	>Tae_1272260-3' cctgtcgccaaacggcacgcaggaaagacaaggatggcgaggatccagtcgaccaaccgatttagtttagataagatgc ggcttggcataatctttttgttctggggaaaaggngatgtggatgttgcacagctgagcttgcgggtgttgc ttgggttgttgcaggatgttgcaggacaggatgtctgtgcggatgcctcgatgcggccaaatctccaaacaagac ggcaacaatg	
Contexte génomique sur la séq. de réf. :	>Tae_1272260-genomic_context cgatgcggccggccggccatggcggtgcctccagctctcgctgtttactgggtcgacgcaatccgtgacactga ctgggttattttttttaatntcccggttccttcncttagttgttgcacgacgtcgctggggacacagaaga aagatgacacccatttgcaggacggcgtgtgtcgccgttgaggccgtggaggcccaaggacgtgacgacgcggccggcc cttctccctc[G/C]cctgtcgccaaacggcacgcaggaaagacaaggatgtggatgttgcggatgcctcgatgcggccaaat tagtagataagatgcggcttgtgcataatctttttgttctggggaaaaggngatgtggatgttgcggatgcctcgatgcggcc gtttgcgggttgttgcaggatgttgcggatgcctcgatgcggccaaat	

# Get list of all SNPs found

## GnpSNP / Variations (SubSNPs)

### RÉSULTATS



1 2 3 4 5 | 41 items trouvés, affichage de 1 à 10 | Afficher  résultats par page

#	Nom	Type	Projet	Expérience	Génotype	Séquence de réf.	Position sur la séq. de réf.	Nom du gène/marqueur
1	<a href="#">INRA CF ASP 842 BT001</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">A4</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
2	<a href="#">INRA CF ASP 842 BT003</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">ARCHE</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
3	<a href="#">INRA CF ASP 842 BT004</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">AURORE</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
4	<a href="#">INRA CF ASP 842 BT005</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">Balkan</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
5	<a href="#">INRA CF ASP 842 BT006</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">BARBU DU FINISTERE</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
6	<a href="#">INRA CF ASP 842 BT007</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">BELLIEI 590</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
7	<a href="#">INRA CF ASP 842 BT008</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">CHINESE SPRING</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
8	<a href="#">INRA CF ASP 842 BT009</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">CHORTANDINKA</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
9	<a href="#">INRA CF ASP 842 BT010</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">CHYAMTANG</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1
10	<a href="#">INRA CF ASP 842 BT011</a>	SNP	<a href="#">EXEGESE-BLE</a>	<a href="#">INRA CF ASP-56</a>	<a href="#">COPPADRA</a>	<a href="#">consensus_hga3_includingSTARTcodon</a>	842	hga1



# Get details on experiment

## GnpSNP / Expérience

### DÉTAILS SUR L'EXPÉRIENCE

Nom :	INRA_CF_ASP-56
Description :	Polymorphisms in hga3 (partial sequence including start codon).
Nom du gène/marqueur :	hga1

### COMPLÉMENTS À PROPOS DE L'EXPÉRIENCE

Projet :	<a href="#">EXEGESE-BLE</a>
Tableau des génotypes : 	<a href="#">[Voir]</a>
Protocole :	<a href="#">Amplification Protocol</a>
Variations :	<a href="#">[Voir]</a>
Polymorphic loci :	<a href="#">[Voir]</a>
Liste des génotypes :	<a href="#">[Voir]</a>
Séq. de réf. :	<a href="#">consensus_hga3_includingSTARTcodon</a>

# GnpIS : polymorphism data (SNP, in-del...)

## GnpSNP / Genotype table

### RÉSULTATS



1 2 ► | 42 items trouvés, affichage de 1 à 40 | Afficher 40 résultats par page

The experiment INRA\_CF ASP-56 contains 19 marker(s).

Positions		217	218	381	680	693	709	842	960	1146	1283	1322	1326	1409	1529	1606	1683	1692	2064	2313	
Ref. Sequence	consensus_hga3_includingSTARTcodon	DEL	IN	n	DEL	n	n	n	n	DEL	DEL	n	n	n	n	n	n	DEL	n		
Genotype   Taxon	NABU EPI BLANC	Triticum aestivum	=	n/a	G	=	A	G	G	C	---	n/a	G	C	G	I	I	A	---	C	
Genotype   Taxon	NYU BAY	Triticum aestivum	n/a	C	G	N	C	G	G	A	---	n/a	C	C	G	C	I	G	n/a	I	
Genotype   Taxon	RENAN	Triticum aestivum	n/a	C	G	n/a	C	G	G	A	---	n/a	C	A	G	C	I	G	n/a	I	
Genotype   Taxon	OPATA 85	Triticum aestivum	=	n/a	G	=	A	G	G	G	C	---	n/a	G	C	G	I	I	A	---	C
Genotype   Taxon	A4	Triticum aestivum	=	n/a	G	=	A	G	G	G	A	---	n/a	G	C	G	C	I	A	---	I
Genotype   Taxon	CHYAMTANG	Triticum aestivum	=	n/a	G	=	A	G	G	G	C	---	n/a	G	C	G	I	I	A	---	C
Genotype   Taxon	MARS DE SUEDE ROUGE BARBU	Triticum aestivum	=	n/a	G	=	A	G	G	G	C	---	n/a	G	C	G	I	I	A	---	C
Genotype   Taxon	FRUH-WEIZEN	Triticum aestivum	n/a	C	G	n/a	C	G	G	A	A	---	n/a	C	A	G	C	I	G	n/a	I
Genotype   Taxon	ORNICAR	Triticum aestivum	=	n/a	G	=	A	G	G	G	N	NNNNN	N	N	N	N	I	I	A	---	C
Genotype   Taxon	SYNTETIQUE-W7984	Triticum aestivum	n/a	C	G	n/a	C	G	G	A	A	---	n/a	C	A	G	C	I	G	n/a	I
Genotype   Taxon	M708//G25/N163	Triticum aestivum	=	n/a	G	=	A	G	G	G	C	---	n/a	G	C	G	I	I	A	---	C
Genotype   Taxon	AIFENG NO4	Triticum aestivum	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a								
Genotype   Taxon	AURORE	Triticum aestivum	=	n/a	G	=	A	G	G	G	C	---	n/a	G	C	G	I	I	A	---	C
Genotype   Taxon	CHINESE SPRING	Triticum aestivum	=	n/a	G	=	A	G	G	G	C	---	n/a	G	C	G	I	I	A	---	C

# GnplS : polymorphism data (SNP, in-del...)

## GnpSNP / Variation de séquence : INRA\_CF\_ASP\_381\_BT026

### DÉTAILS

Nom :	INRA_CF_ASP_381_BT026
Type :	SNP
Variation de séquence :	G
Position sur la séq. de réf. :	381
Flanquant 5' sur la séq. de réf. :	<input checked="" type="checkbox"/>
Flanquant 3' sur la séq. de réf. :	<input checked="" type="checkbox"/>
Contexte génomique sur la séq. de réf. :	<input checked="" type="checkbox"/>
Longueur :	1
Génotype :	<u>NABU EPI BLANC</u>

### COMPLÉMENTS

Indice de confiance :	A 
Primers :	Hga3Ex2F1  
Expérience :	<u>INRA CF ASP-56</u>
Nom du gène/marqueur :	hga1
Séquence de réf. :	<u>consensus_hga3_includingSTARTcodon</u>
Polymorphic locus :	<u>Tae_1272271</u>
Projet :	<u>EXEGESE-BLE</u>

# GnpIS : Get SNPs for RENAN line

## GnpSNP / Recherche de variations de séquence

### PARAMÈTRES DE RECHERCHE



Par défaut la recherche accepte les caractères jokers et est sensible à la casse. Voir le guide de l'utilisateur pour plus d'informations.

Nom de la variation de séquence

Taxons :

Tous  
Arabidopsis thaliana  
Brassica napus L.  
Pinus pinaster  
Quercus petraea  
**Triticum aestivum**

Projets :

Tous  
AIP\_P00272  
BerrySize  
CM2006-var4

Expériences :

Tous  
BIB\_CF-11  
BIB\_CF-12  
BIB\_CF-13

Génotypes :

Renan  
Resseguié-1  
Rouge de Bordeaux  
R9403

Résultats

# Results: SNPs found for RENAN line

## GnpSNP / Variations (SubSNPs)

### RÉSULTATS



86 items trouvés, affichage de 1 à 86 | Afficher | 10 résultats par page

#	Nom	Type	Projet	Expérience	Génotype	Séquence de réf.	Position sur la séq. de réf.	Nom du gène/marqueur
1	<a href="#">INRA CF ASP_gluB1-1_1002_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1002	Glu-B1-1
2	<a href="#">INRA CF ASP_gluB1-1_1126_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1126	Glu-B1-1
3	<a href="#">INRA CF ASP_gluB1-1_1127_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1127	Glu-B1-1
4	<a href="#">INRA CF ASP_gluB1-1_1133_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1133	Glu-B1-1
5	<a href="#">INRA CF ASP_gluB1-1_1135_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1135	Glu-B1-1
6	<a href="#">INRA CF ASP_gluB1-1_1162_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1162	Glu-B1-1
7	<a href="#">INRA CF ASP_gluB1-1_1173_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1173	Glu-B1-1
8	<a href="#">INRA CF ASP_gluB1-1_1174_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1174	Glu-B1-1
9	<a href="#">INRA CF ASP_gluB1-1_1180_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1180	Glu-B1-1
10	<a href="#">INRA CF ASP_gluB1-1_1206_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1206	Glu-B1-1
11	<a href="#">INRA CF ASP_gluB1-1_1217_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1217	Glu-B1-1
12	<a href="#">INRA CF ASP_gluB1-1_1375_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1375	Glu-B1-1
13	<a href="#">INRA CF ASP_gluB1-1_1416_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1416	Glu-B1-1
14	<a href="#">INRA CF ASP_gluB1-1_1460_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1460	Glu-B1-1
15	<a href="#">INRA CF ASP_gluB1-1_1481_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1481	Glu-B1-1
16	<a href="#">INRA CF ASP_gluB1-1_1499_14</a>	DELETION	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1499	Glu-B1-1
17	<a href="#">INRA CF ASP_gluB1-1_1558_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1558	Glu-B1-1
18	<a href="#">INRA CF ASP_gluB1-1_1603_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1603	Glu-B1-1
19	<a href="#">INRA CF ASP_gluB1-1_1672_14</a>	SNP	CP1p5	<a href="#">INRA CF ASP-g</a>	Renan	<a href="#">consensus_glu_B1_1</a>	1672	Glu-B1-1

# GnplS : polymorphism data

## GnpSNP / Ref. sequence card

### REF. SEQUENCE DETAILS

Name : consensus\_glu\_B1\_1

Taxon : Triticum aestivum

Experiments : INRA\_CF\_ASPI-9 

FASTA : 

### SEQUENCE

5'  
CCAAAGGTTT CAGTTAGTTTC ATTGTCAAG GAAAGGTGTT TTCATAAGTC CAAAACCTTA  
CCAACCTTTT TGCACTGCAT AGCATAGATA GATGTTGTGA GTCAATTGGAT AGATATTGTG  
AGTCAGCATG GATTGTTGTG GCCTGGAAAT CCAACTAAAT GACAAGCAAC AAAACCTGAA  
ATGGGCTTGA GGAGAGATGG TTATCAATT TACATGTTCC ATGCAGGCTA CCTTCCACTA  
CTCGACATGG TTAGGAAGTT TGAGTGCCTC ATATTTGCCG AAGCAATGGC ACTACTCGAC  
ATGTTAGAA GTTTGAGTG CCCATATTT GCRGAAGCAA TGGCTAACAG ATACATATT  
TGGCAAACCC CAAGAAGGAT AATCACTCCT CTTAGATAAA RAGAACAGAC CAATGTACAA  
ACATCCACAC TTCTGCAAAC AACTACCCAG AACTAGGATT AAGCCCCATT CGTGGCTTTA  
GCAGACCGTC CAAAATCTG TTTTCAAGC AYCAATTGCT CTTTACTTAT CCAGCTTYTT  
TTGTGTTGGC AACTGCCCCTT TTCCAACCGA TTTTGTCTT CTCACCTTTT CTTCAAGGC  
TAAACTAACC TCRGCRTGCA CACAACCAGT TCTGAACTC TCACCTcGTC CCTATAAAAG  
CCCATCCAAAC CTCACAATC TCATCATCAG CCACAACACC GAGCACCCCCA ATCTACAGAT  
CAATTCACTG ACAGTTCACY GAGATGGCTA AGCGCCTGGT CCTCTTTGGG GCAGTAGTCG  
TCGCCCTCGT GGCTCTCACCC GCGGCTGAAG GTGAGGCCCTC TGGACAACTA CAATGTGAGC  
RCGAGCTCCG GAAGCGCGAG CTCGAGGCAT GCCAACAGGT GGTGGACCG CAACTYCAG  
ACGTAGCCC CGGGTCCCGC CCCATCACCG TCAGCCCCGG CACGAGRCAAC TACGAGCRGC  
AACCTGTGGT GCGCTCCAAG CCGGGATCCT TCTACCCAG CRAGACTACC CCTTCGCAGC  
AACTCCAACA ATAGATAATT TGCGGAATAC CTGCACTACT AAGAAGGTAT TACCCAAGTG  
TAACTCTTC GCAGCAGGGG TCATACTATC CAGGCCAAGC TTCTCMSCAA CARTYAGGAC  
AAGGACAGCA GCGCAGGACAA GRACAGCAAC CARRACAAGR GCAACAAAGAT CAGCAGCCAG  
GACAARGACA ACAAGGRTAC TACCCAACCTT CTCCGCAACA GCCAGGACAA GGGCAACAAAC  
TGGGACAAGG GCAACCAAGG TACTACCCAA CTTCACAGCA GCCAGGACAA AACGAGCAGG  
CAGGACAAGG GCAACAATCA GGACAAGGAC AACAAAGGTA CTACCCAACT TCCCYGAAC  
AGTCAGGACA AGGGCAACAA CGGGGACAAG GGCAASCAGG gTACTACCCAA ACTTCTCCGC  
AGCAGTCAGG ACAATGCAK CAAACAGGAC AACGGCAACA RCCAGGACAA GGGCAGCAAT  
CAGGACAAGG GCAACAAGGG CAGCAATCAG GACAAGGGCA ACAAGGTCAG CAGCCAGRAC  
AAGGCAACG ACCAGGACAAG GCAACAAGG gTACTACCC AAATTCCTCC CAACAGCCGG  
GACAAGGGCA ACAATCAGGA CAAGGGCAAC CAGGGTACTA CCCAACTCT TYGCGGCAGC  
CAGGACAATG GCAGCAACCA GGACAAGRC AGCAACCCAGG ACAAGGGCAA CAAGGTGAGC  
AGCCAGGACA AGGACAACAA YCAGGACAAG GACAACAAGG ATACTACCCAA ACTTCTCTGC  
AACAGCYAGG ACAAGGGCAA CAACYGGGAC AACGGCAACC AGGGTACTAC CCCA

3'

# GnplS : polymorphism

## GnpSNP / Genotype: Renan

### DETAILS

Name : Renan

Description : cultivar

### COMPLEMENTS

Experiments : BIB\_CF-12



Sequence variations : [\[Voir\]](#)

Taxon : [Triticum aestivum](#)

# GnplS : polymorphism

## GnpSNP / Genotype: Renan

### DETAILS

Name : Renan

Description : cultivar

### COMPLEMENTS

Experiments : BIB\_CF-12



Sequence variations : [\[Voir\]](#)

Taxon : [Triticum aestivum](#)

# GnpIS : polymorphism

## GnpSNP / Variations (SubSNPs)

### RÉSULTATS



1 2 3 4 5 ► | 86 items trouvés, affichage de 1 à 10 | Afficher | 10 résultats par page

#	Nom	Type	Projet	Expérience	Génotype	Séquence de réf.	Position sur la séq. de réf.	Nom du gène/marqueur
1	<a href="#">INRA_CF_ASPIpinA_14</a>	INSERTION	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -1	<a href="#">Renan</a>	<a href="#">Consensus_pinA</a>	1	pinA
2	<a href="#">INRA_CF_ASPIgluD1-1_31_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -3	<a href="#">Renan</a>	<a href="#">consepromglu-D1-1</a>	31	Glu-D1-1
3	<a href="#">INRA_CF_ASPIputativeisomerase5D_41_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -8	<a href="#">Renan</a>	<a href="#">consensus_epimerase_5D</a>	41	wPPbf_B
4	<a href="#">INRA_CF_ASPIgluD1-1_111_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -3	<a href="#">Renan</a>	<a href="#">consepromglu-D1-1</a>	111	Glu-D1-1
5	<a href="#">INRA_CF_ASPIPbfD_129_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -7	<a href="#">Renan</a>	<a href="#">consensus_PBF_D</a>	129	wPPbf_D
6	<a href="#">INRA_CF_ASPIgluB1-1_236_14</a>	INSERTION	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -9	<a href="#">Renan</a>	<a href="#">consensus_glu_B1_1</a>	236	Glu-B1-1
7	<a href="#">INRA_CF_ASPIspaA_248_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -10	<a href="#">Renan</a>	<a href="#">consensus_spaAexon1</a>	248	Spa_A
8	<a href="#">INRA_CF_ASPIgluD1-1_311_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -3	<a href="#">Renan</a>	<a href="#">consepromglu-D1-1</a>	311	Glu-D1-1
9	<a href="#">INRA_CF_ASPIgluB1-1_333_14</a>	SNP	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -9	<a href="#">Renan</a>	<a href="#">consensus_glu_B1_1</a>	333	Glu-B1-1
10	<a href="#">INRA_CF_ASPIPbfA_343_14</a>	DELETION	<a href="#">CP1p5</a>	<a href="#">INRA_CF_ASPI</a> -5	<a href="#">Renan</a>	<a href="#">consensus_PBF_A</a>	343	wPPbf_A



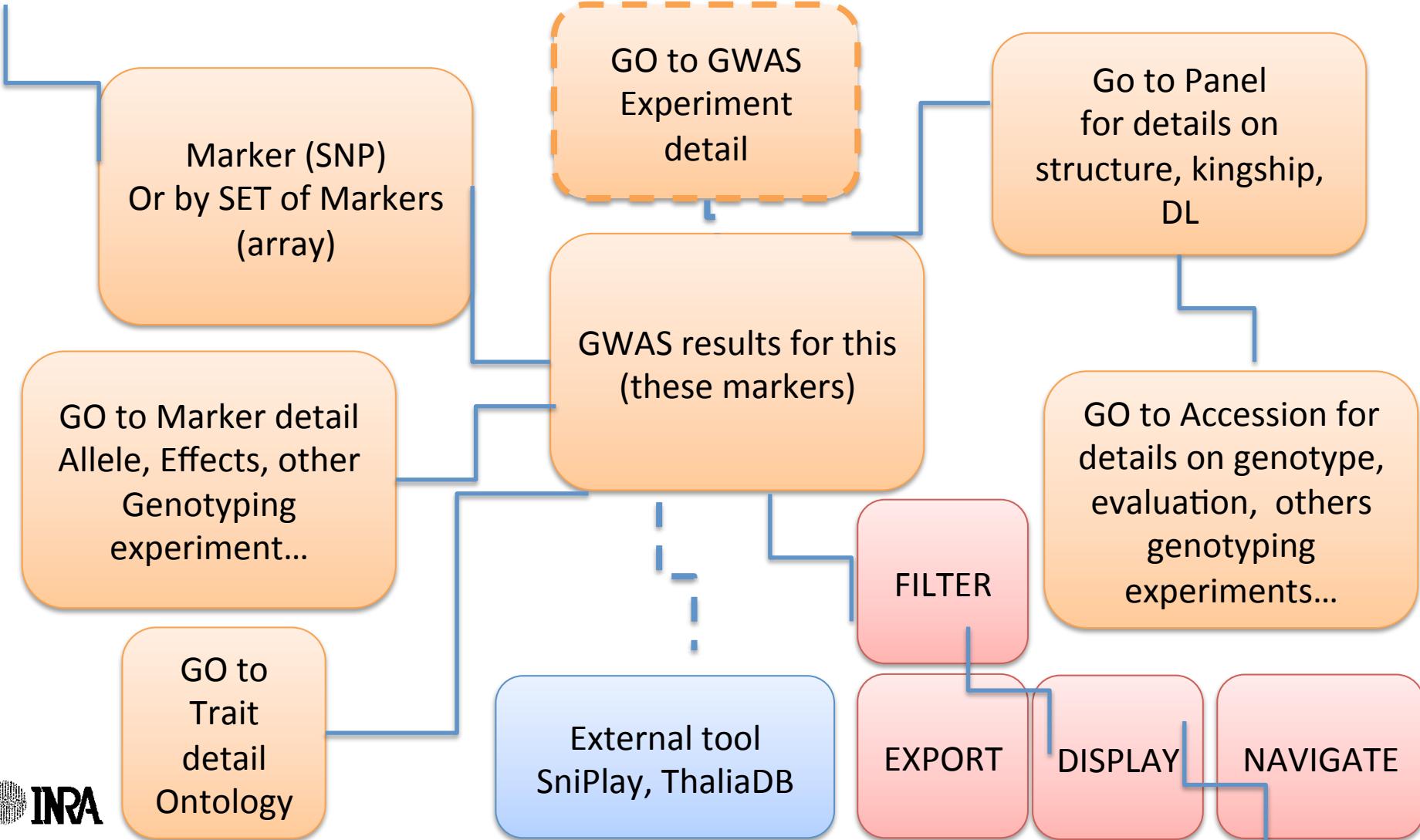
# GnpIS – Association studies results

## *ANR GnpAsso project*



# User Query (*in progress*)

Query by Marker (SNP) in GnpAsso query tool (or via the google index) :



# GnpIS – GWAS – *in DEV only*

## GnpAsso Beta / Association form

[Search by taxon](#) [Search by trait](#) [Search by marker](#)

Select set of markers:

Selected items

X

Select a marker:

Selected items

X

# Get association results

## GnpAsso Beta / Association results

### DETAILS

Number of associated traits: 60  
 Number of associated markers: 4824

### ASSOCIATION RESULTS

◀ ▶ 1-10 of 49,318 ⏪ ⏩ | Display 10  results per page

Experiment name	# of lots	Panel name	Trait name	Marker name	pval	-log(pval)	r2
ASSO_1	164		trait1	snp_LVH_00669	1.22E-5	4.91E0	1.1E-1
ASSO_1	165		trait1	snp_LVH_01071	7.44E-4	3.13E0	6.66E-2
ASSO_1	165		trait1	snp_LVH_01107	8.9E-4	3.05E0	6.47E-2
ASSO_1	165		trait1	snp_LVH_01109	8.9E-4	3.05E0	6.47E-2
ASSO_1	165		trait1	snp_LVH_01202	4.41E-4	3.36E0	7.21E-2
ASSO_1	164		trait1	snp_LVH_01227	6.06E-4	3.22E0	6.92E-2
ASSO_1	158		trait1	snp_LVH_01458	4.15E-4	3.38E0	7.58E-2
ASSO_1	166		trait1	snp_LVH_01505	4.9E-4	3.31E0	7.06E-2
ASSO_1	166		trait1	snp_LVH_01837	7.74E-4	3.11E0	6.58E-2
ASSO_1	164		trait1	snp_LVH_02442	2.52E-4	3.6E0	7.84E-2



Filter results

pval

<

>

Add filter

# Get details on Panel

## GnpAsso Beta / Panel card

### DETAILS ON ITEM

Name	P1
Lot(s)	LVH_103
GWAS experiment(s)	ASSO_P1

### RELATED STRUCTURES

1-10 of 1,344 | Display 10 results per page

Panel	Structure	Structure type	Structured group	Lot	Value
P1	P1Structure	P structure	GRP1	LVH_001	3E-3
		P structure	GRP2	LVH_001	9.71E-1
		P structure	GRP3	LVH_001	9E-3
		P structure	GRP4	LVH_001	4E-3
		P structure	GRP5	LVH_001	6E-3
		P structure	GRP6	LVH_001	2E-3
		P structure	GRP7	LVH_001	3E-3
		P structure	GRP8	LVH_001	2E-3
		P structure	GRP1	LVH_002	3.4E-1
		P structure	GRP2	LVH_002	1.24E-1

# Linkage disequilibrium, Kingship

## RELATED LINKAGE DISEQUILIBRIUMS

1-10 of 68,160 | Display 10 results per page

Panel	First marker	Second marker	Distance	pValue	r2	dPrime	LOD	IC Low	IC High
P1	snp_LVH_42007	snp_LVH_42012	8.98E4	-	4.95E-1	-	-	-	-
	snp_LVH_42007	snp_LVH_42013	9.02E4	-	4.08E-1	-	-	-	-
	snp_LVH_42007	snp_LVH_46639	5.13E5	-	6.2E-2	-	-	-	-
	snp_LVH_42008	snp_LVH_42010	2.36E3	-	1E0	-	-	-	-
	snp_LVH_42008	snp_LVH_42011	2.48E3	-	1E0	-	-	-	-
	snp_LVH_42008	snp_LVH_42016	5.01E5	-	1E-3	-	-	-	-
	snp_LVH_42008	snp_LVH_56630	9.08E5	-	1.63E-1	-	-	-	-
	snp_LVH_42009	snp_LVH_42012	8.32E4	-	1.88E-1	-	-	-	-
	snp_LVH_42009	snp_LVH_42027	9.96E5	-	6E-3	-	-	-	-
	snp_LVH_42011	snp_LVH_42020	6.46E5	-	1.06E-1	-	-	-	-

## RELATED KINSHIPS

1-10 of 56,448 | Display 10 results per page

Panel	Estimator	First lot	Second lot	Value
P1	Loiselle	LVH_103	LVH_103	-
	Loiselle	LVH_103	LVH_096	4.88E-1
	Loiselle	LVH_103	LVH_153	5.34E-1
	Loiselle	LVH_103	LVH_105	5.22E-1
	Loiselle	LVH_103	LVH_104	5.1E-1
	Loiselle	LVH_103	LVH_091	4.47E-1
	Loiselle	LVH_103	LVH_101	5.6E-1
	Loiselle	LVH_103	LVH_097	5.24E-1
	Loiselle	LVH_103	LVH_090	5.67E-1
	Loiselle	LVH_103	LVH_092	5.18E-1

# Association studies

**GnpMap / Trait card**

TRAIT DETAILS	
Trait name	trait1
Trait description	
Unit	
Short remark	
Theme	unknown
Genoplante classification	-
MetaQTLs	-
Association (GWAS) number :	817

ASSOCIATED MEASURES	
Number of measures: 0	

ASSOCIATED KEYWORDS	
Number of keywords: 0	

ASSO	Expt
ASSO	165
ASSO	165
ASSO	164
ASSO	158
ASSO	166
ASSO	166
ASSO	164

**sociation results**

| Display
10
results per page

Panel name	Trait name	Marker name	pval	-log(pval)	r2
P1	trait1	snp_LVH_00669	1.22E-5	4.91E0	1.1E-1
	trait1	snp_LVH_01071	7.44E-4	3.13E0	6.66E-2
	trait1	snp_LVH_01107	8.9E-4	3.05E0	6.47E-2
	trait1	snp_LVH_01109	8.9E-4	3.05E0	6.47E-2
	trait1	snp_LVH_01202	4.41E-4	3.36E0	7.21E-2
	trait1	snp_LVH_01227	6.06E-4	3.22E0	6.92E-2
	trait1	snp_LVH_01458	4.15E-4	3.38E0	7.58E-2
	trait1	snp_LVH_01505	4.9E-4	3.31E0	7.06E-2
	trait1	snp_LVH_01837	7.74E-4	3.11E0	6.58E-2
	trait1	snp_LVH_02442	2.52E-4	3.6E0	7.84E-2

 Filter results

<

Add filter

# Filters results, Export, Display...

## GnpAsso Beta / Association results

### DETAILS

Number of associated traits: 60  
 Number of associated markers: 4824

### ASSOCIATION RESULTS

1-10 of 284 | Display 10 results per page

Experiment name	# of lots	Panel name	Trait name	Marker name	pval	-log(pval)	r2
ASSO_P1	P1	P1	trait1	snp_LVH_02442	2.52E-4	3.6E0	7.84E-2
ASSO_P1			trait1	snp_LVH_02723	1.54E-4	3.81E0	8.26E-2
ASSO_P1			trait1	snp_LVH_02724	2.14E-4	3.67E0	7.97E-2
ASSO_P1			trait1	snp_LVH_08020	1.9E-4	3.72E0	8.05E-2
ASSO_P1			trait1	snp_LVH_08136	1.42E-4	3.85E0	8.35E-2
ASSO_P1			trait1	snp_LVH_08137	1.42E-4	3.85E0	8.35E-2
ASSO_P1			trait1	snp_LVH_08138	1.42E-4	3.85E0	8.35E-2
ASSO_P1			trait1	snp_LVH_10319	1.47E-4	3.83E0	8.36E-2
ASSO_P1			trait1	snp_LVH_15142	2.59E-4	3.59E0	7.91E-2
ASSO_P1			trait1	snp_LVH_15406	1.57E-4	3.8E0	8.29E-2



EXPORT

Filter results

FILTERS

pval

Filtered fields	Filter type	Threshold value(s)	Delete filter
pval	<	0.0005	X
r2	<>	0.0784 - 0.0842	X





# GnplS – Advanced search BIOMART



# GnpIS – polymorphism variation module



The image shows a screenshot of the GnpIS web interface. On the left, there is a search bar with a 'QUICK SEARCH' button, a 'Species' dropdown menu set to 'Species', and a text input field containing 'Xwmc430'. Below the input field is a 'SUBMIT' button. A red arrow points from the text 'ADVANCED' to the 'BIOMART' button. To the right of the search bar is a large green graphic of a plant or flower. To the right of the graphic are several sections with links:

- 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.

# User Query: in Advanced search tool: BIOMART

Query by any type of 'feature', qualifiers... in Biomart dataset (s)

Select Feature,  
qualifiers  
+ filters + attributes  
for results

GO to GnpIS detailed  
feature (mapping,  
polymorphism...)

GO GnpIS  
Gbrowse

Get tabulated results

GO to External tool  
Java web start, SRS,  
Gene report system

Export results in  
Excel, XML..

Export results to  
GALAXY tools for  
further analysis

# Biomart Query: FILTERS + ATTRIBUTES: Get SignalPeptide

## Query

- By feature  
(gene name, snp,  
go term...)
- By localisation
- BY qualifier
- Combination of filters

## Flexible

*All data loaded  
into the database  
from GFF3 input file  
Format  
= configuration*

## Interface generated

New Count Results URL XML Perl Help

Please restrict your query using criteria below

Feature  
 Reference Feature (% for Wildcard). Example: BotuT4\_P0001%

Feature Type  
 match  
 polypeptide  
 polypeptide\_domain  
 signal\_peptide

Feature Name (% for wildcard). Example:BotuT4\_P009%

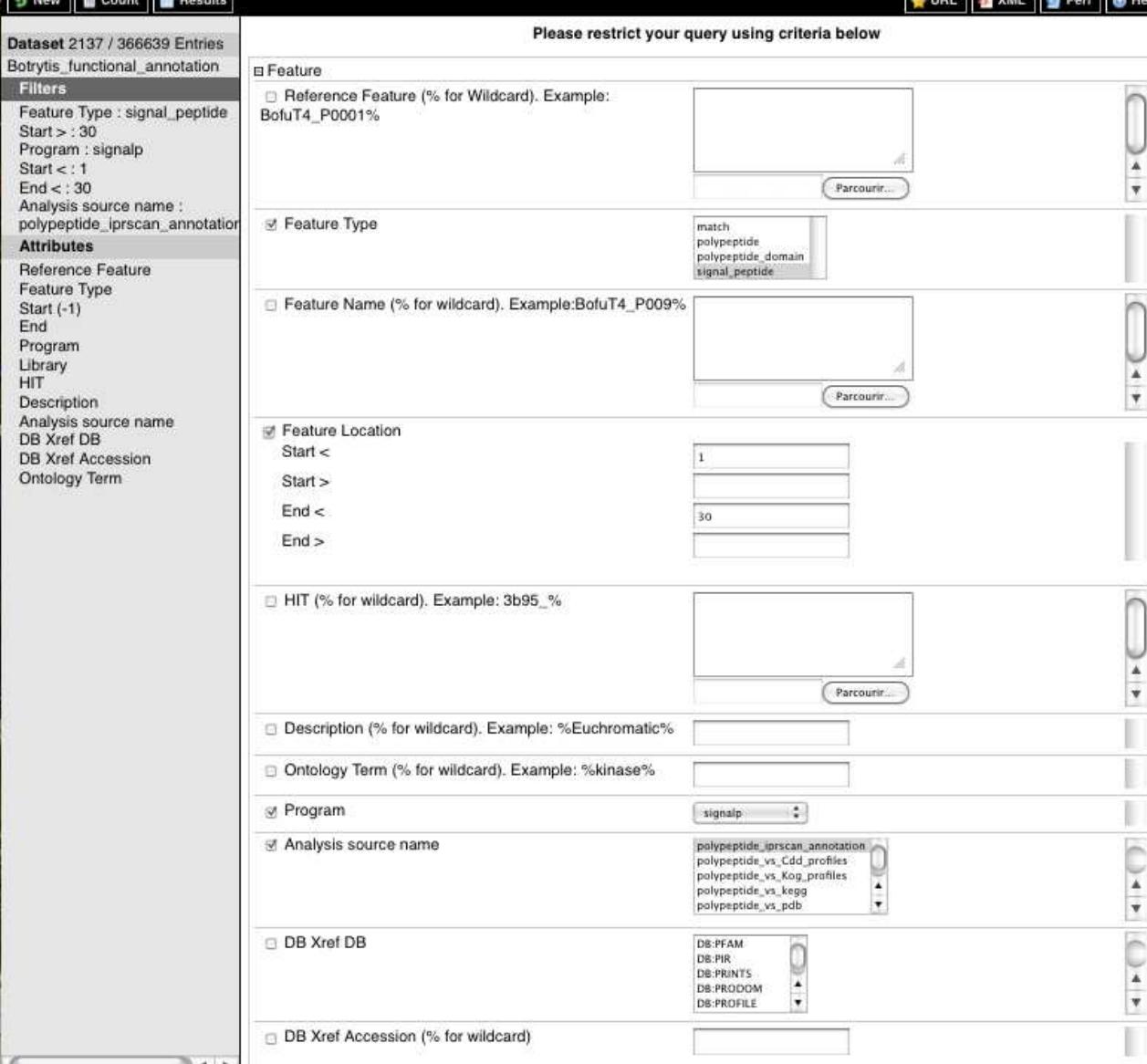
Feature Location  
 Start < 1  
 Start >  
 End < 30  
 End >

HIT (% for wildcard). Example: 3b95\_%

Description (% for wildcard). Example: %Euchromatic%  
 Ontology Term (% for wildcard). Example: %kinase%  
 Program signalp  
 Analysis source name  
 polypeptide\_iprscan\_annotation  
 polypeptide\_vs\_Cdd\_profiles  
 polypeptide\_vs\_Kog\_profiles  
 polypeptide\_vs\_kegg  
 polypeptide\_vs\_pdb

DB Xref DB  
 DB:PFAM  
 DB:PIR  
 DB:PRINTS  
 DB:PRODOM  
 DB:PROFILE

DB Xref Accession (% for wildcard)



# Another query on Wheat 3B datamart : select filters (Get SNPs)

GnpIS advanced search

New Count Results URL

Please restrict your query using criteria below

**Dataset**  
Wheat Annotation

**Filters**  
Feature Type : SNP

**Attributes**  
Common Name  
Feature Type  
Feature Name  
Start (-1)  
End

**Dataset**  
[None Selected]

**Qualifiers**

Feature Name (% for wildcard)

Feature Type   
region  
repeat\_region  
repeat\_unit  
**SNP**  
STS

Strand

Feature Location

Get QTL by :

Features mapped around QTL

# Select attributes for results

 *GnpIS advanced search*

[!\[\]\(0fb3f18c18ebf5ae9617c2bc39667b15\_img.jpg\) New](#) [!\[\]\(ae338e5958226f807cecfdc42faffb87\_img.jpg\) Count](#) [!\[\]\(80bf199b0b94df1deff1ff2b0932e636\_img.jpg\) Results](#) [!\[\]\(045e08dd7cbb42fd7cc00df9aff0cb07\_img.jpg\) URL](#) [!\[\]\(220d65e133f0643ad6ab85a2236f9f7e\_img.jpg\) Print](#)

**Dataset**  
Wheat Annotation

**Filters**  
Feature Type : SNP

**Attributes**

Common Name  
Feature Type  
Feature Name  
Start (-1)  
End  
Link to GnpSNP (ID)  
SNP Alleles  
Reference Name

---

**Dataset**  
[None Selected]

Please select columns to be included in the output and hit 'Results' when ready

ATTRIBUTES  QTL Features Query

Organism

Feature

**Feature**

Feature Type  Start (-1)  
 Feature Name  End  
 Feature Unique Name

**Qualifiers**

SNP Alleles  Product  
 Reference Name  Name Gene  
 Link to GnpSNP (ID)  Program  
 Genbank ID

# Result: Get list of SNPs mapped on wheat 3B genome

**GnpIS advanced search**

**New** **Count** **Results** **URL**

<b>Dataset</b>		Export all results to							
Wheat Annotation		File <input style="margin-left: 10px;" type="button" value="..."/> TSV <input style="margin-left: 10px;" type="button" value="..."/> <input type="checkbox"/> Unique results only							
<b>Filters</b>		Email notification to <input type="text"/>							
Feature Type : SNP		View <input style="margin-right: 10px;" type="button" value="10"/> rows as <input style="margin-right: 10px;" type="button" value="HTML"/> <input type="checkbox"/> Unique results only							
<b>Attributes</b>		Common Name	Feature Type	Feature Name	Start (-1)	End	Link to GnpSNP (ID)	SNP Alleles	Reference Name
Common Name	common wheat	SNP	<a href="#">pg1ex5F1-in5R1</a>	1209771	1210023				ctg0954b.1
Feature Type	common wheat	SNP	<a href="#">pg4in3F1-in4R1</a>	1538953	1539309				ctg0954b.1
Feature Name	common wheat	SNP	<a href="#">pg4in2F1-ex3R1</a>	1539450	1539724				ctg0954b.1
Start (-1)	common wheat	SNP	<a href="#">Hga3-int1del</a>	1793190	1793193				ctg0954b.1
End	common wheat	SNP	<a href="#">Hga3-int3-SNP1</a>	1793688	1793689				ctg0954b.1
Link to GnpSNP (ID)	common wheat	SNP	<a href="#">Hga3-int4-SNP1</a>	1793926	1793927				ctg0954b.1
SNP Alleles	common wheat	SNP	<a href="#">Hga3Ex5SNP</a>	1794112	1794113				ctg0954b.1
Reference Name	common wheat	SNP	<a href="#">Hga3Ex6del</a>	1795023	1795026				ctg0954b.1
	common wheat	SNP	<a href="#">Tae_1272243</a>	1571373	1571374	<a href="#">Tae_1272243</a>	G/A		ctg0954b.1
	common wheat	SNP	<a href="#">Tae_1272244</a>	1065312	1065313	<a href="#">Tae_1272244</a>	G/C		ctg0954b.1

**Dataset**  
[None Selected]



# Link to Gbrowse wheat browser (by feature name)

File Help

Wheat annotation viewer v2: 1.999 kbp from ctg0954b.1:1,208,898..1,210,897

ctg0005b.1 ctg0011b.1 ctg0079b.1 ctg0091b.1 ctg0382b.1 ctg0464b.1 ctg0528b.1 ctg0616b.1 ctg0661b.1 ctg0954b  
TaaCsp3BFhA\_0100L17.1

**Browser** Select Tracks Custom Tracks Preferences

Search

Landmark or Region: ctg0954b.1:1,208,898..1,210,897 Search Examples: TAA\_ctg0954b.00250.1, Xsts80-3B, ctgD\_rep\_0033, Tae\_1272250, cfp5001, pg4in2F1-ex3R1, cfb6001, QTL\_FHB\_SumStoa\_BLW\_3B. Download Decorated FASTA File Configure... Go

Data Source: Wheat annotation viewer v2 Scroll/Zoom: << < > >> Show 2 kbp

Overview

Region

Details

pg1ex5F1-in5R1  
Positions : 1209772 .. 1210023  
Length : 252  
[Zoom to this feature](#) [Detailed Report](#)

SNP

Contig

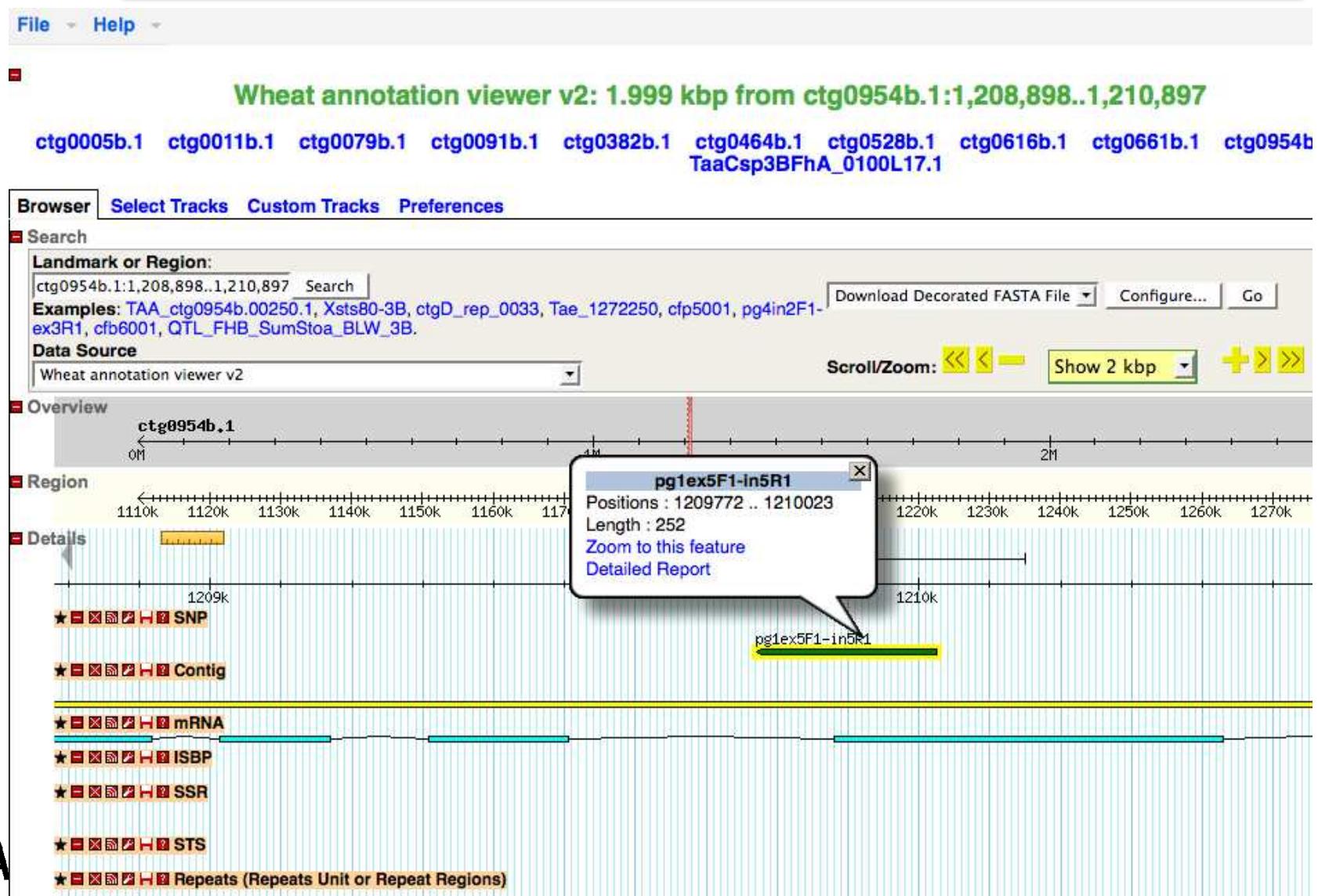
mRNA

ISBP

SSR

STS

Repeats (Repeats Unit or Repeat Regions)



# SNP detailed report

## pg1ex5F1-in5R1 Details

Name: pg1ex5F1-in5R1  
Type: SNP  
Description:  
Source: EMBL\_SNP  
Position: ctg0954b.1:1209772..1210023 (- strand)  
Length: 252  
dbxref: GFF\_source:EMBL\_SNP  
primary\_id: 7185  
gbrowse\_dbid: wheat3BRPH7:database

```
>pg1ex5F1-in5R1 class=Sequence position=ctg0954b.1:1209772..1210023 (- strand)
CCACAGGTCC TTAGCATGGT CAATGTAAG CCTTGCTCTC TGAGGGCCTG TCTATTGCCA CATTCCATCG AGGATCAAAA
TATGAGCTCC TGGACTCGCT TCGTGTATGA TTGTGGTACT GAACTCATTC GTCTTCAGAT AAGGTATTCT TTTTTCCGTG
GTATGAATCG ATACATATAT GTGAGGAACT GTACATTGAT TCTAGATAACG CATTGTTTG CTGATTAGTA AGTCCTGCAT
GATACTTAGT GG
```

# Link on SNP that exists in GnpIS polymorphic module (popup)



File Help

Wheat annotation viewer v2: 0 pbp from ctg0954b.1:1,571,374..1,571,374

ctg0005b.1 ctg0011b.1 ctg0079b.1 ctg0091b.1 ctg0382b.1 ctg0464b.1 ctg0528b.1 ctg0616b.1 ctg0661b.1 ctg0954b.1 ctg1030b.1 ctg1035b.1 TaaCsp3BFhA\_0100L17.1

Browser Select Tracks Custom Tracks Preferences

Search Landmark or Region: ctg0954b.1:1,571,374..1,571,374 Search Examples: TAA\_ctg0954b.00250.1, Xsts80-3B, ctgD\_rep\_0033, Tae\_1272250, cfp5001, pg4in2F1-ex3R1, cfb6001, QTL\_FHB\_SumStoa\_BLW\_3B.

Data Source: Wheat annotation viewer v2 Scroll/Zoom: << < > >> Show 1 bp + - □ Flip

Overview ctg0954b.1 0M 1M 2M 3M

Region 1480k 1530k 1540k 1550k 1560k 1570k 1580k 1590k 1600k 1610k 1620k 1630k 1640k 1650k 1660k 1670k

Details 10 ctp 1571374 .. 1571374

Tae\_1272243 DIP : Tae\_1272243 Db Source : GnpSNP GnpSNP ID : Tae\_1272243 Position : 1571374 .. 1571374 Zoom to this feature Link to GnpSNP

SNP (G) Tae\_1272243

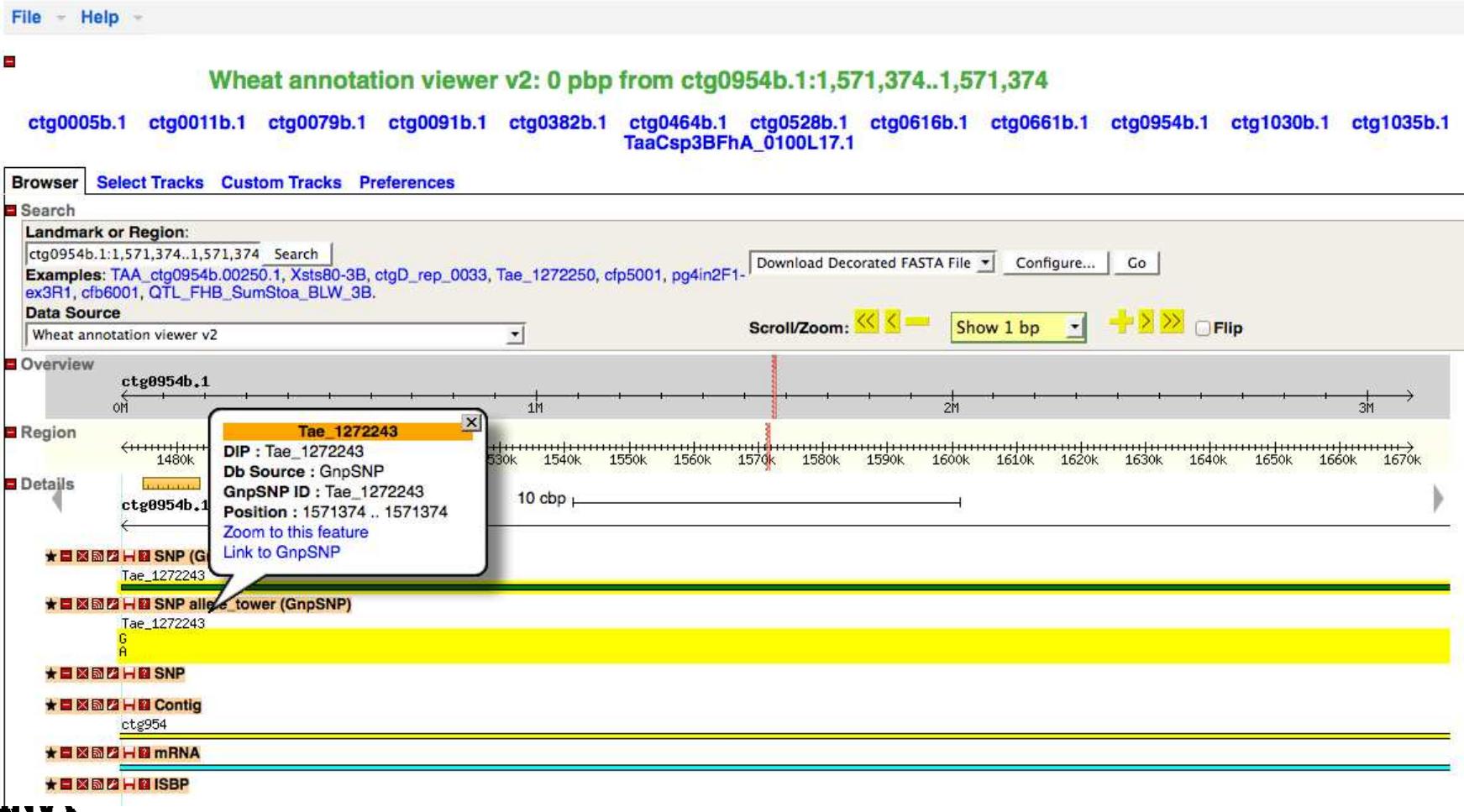
SNP allele tower (GnpSNP) Tae\_1272243 G A

SNP

Contig ctg954

mRNA

ISBP



# Details on SNP in Card

## GnpSNP / Locus polymorphe

### DÉTAILS SUR LE LOCUS POLYMPORHE

Nom :	Tae_1272243
Source :	GnpSNP

### COMPLÉMENTS

Type :	SNP
Variation de séquence :	G/A
Lié avec les variations de séquence :	<input type="text" value="INRA_CF_ASP_249_BT001"/>   <a href="#">Voir la liste</a>
Lié avec les Génotypes :	<input type="text" value="A4"/>   <a href="#">Voir la liste</a>

### RÉFÉRENCES INTERNES

Base de données	Nom de la référence	Valeur de la référence
<a href="#">Wheat 3B annotation (FHB)</a>	SNP name	<a href="#">Tae_1272243</a>

### SÉQUENCES

Flanquant 5' sur la séq. de réf. :	>Tae_1272243-5' CtccatgncaanttcaccgccttcccgagacctaactccctgcgcgcgcgtCccatcagcctnacnaanaaa caaggcagccgcgggtggacacannaanaagaagCncgctgtgtctngacggggcactaccggaaac tgcgcaactgcggagatcGtnaaggccgcngagaaggccgggtcgaggtgacnatagcggaccgcgggtcaangtg Cgcgtcaa	
Flanquant 3' sur la séq. de réf. :	>Tae_1272243-3' gagctggcccttcgtgaactcgtaactcgacgtgtctnggcgtgcacggcGccggctinaccaactcgccgttccgtcc gcggggggcggtgtcatccagggtggtgccnTacgcaagctggagccatggcgacaggganttcggngaccccgogg nnaacatggggCtcggtagactcgtagacatcnccgtggaggagacgcgtctgganacgtggggCngaccac ccggccatca	
Contexte génomique sur la séq. de réf. :	>Tae_1272243-genomic_context CtccatgncaanttcaccgccttcccgagacctaactccctgcgcgcgcgcgtCccatcagcctnacnaanaaa caaggcagccgcgggtggacacannaanaagaagCncgctgtgtctngacggggcactaccggaaac tgcgcaactgcggagatcGtnaaggccgcngagaaggccgggtcgaggtgacnatagcggaccgcgggtcaangtg Cgcgtcaa[G/A]gactggcccttcgtgaactcgtaactcgacgtgtctnggcgtgcacggcGccggctnaccaact cgccgttctgcgcggngggcggtgtcatccagggtggtgccnTacgcaagctggagccatggcgacaggganttc ggngaccccggnnaacatggggCtcggtagactcgtagacatcnccgtggaggagacgcgtctgganacgtggggCngaccac ggggCngaccaccccccata	

# Biomart : Get list of signal peptides found by a special (filtered) software in a special (filtered) analysis

**GnpIS advanced search**

[New](#) [Count](#) [Results](#) [URL](#) [XML](#) [Perl](#) [Help](#)

**Dataset 2137 / 366639 Entries**  
**Botrytis\_functional\_annotation**

**Filters**

Feature Type : signal\_peptide  
Start > : 30  
Program : signalp  
Start < : 1  
End < : 30  
Analysis source name : polypeptide\_iprscan\_annotation

**Attributes**

Reference Feature  
Feature Type  
Start (-1)  
End  
Program  
Library  
HIT  
Description  
Analysis source name  
DB Xref DB  
DB Xref Accession  
Ontology Term

Export all results to [File](#) [TSV](#)  Unique results only [Go](#)

Email notification to

View 10 rows as [HTML](#)  Unique results only

Reference Feature	Feature Type	Start (-1)	End	Program	Library	HIT	Description	Analysis source name	DB Xref DB	DB Xref Accession
<a href="#">BotuT4_P000030.1</a>	signal_peptide	0	25	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BotuT4_P000070.1</a>	signal_peptide	0	18	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BotuT4_P000200.1</a>	signal							polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BotuT4_P000210.1</a>	signal							polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BotuT4_P000260.1</a>	signal							polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BotuT4_P000270.1</a>	signal							polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BotuT4_P000590.1</a>	signal							polypeptide_iprscan_annotation	GFF_source	signalp

**Botrytis cinerea T4 GRS**

**Functional annotation**

BotuT4\_P000210.1

[Link to GRS](#)

[Gene Identifier](#)

[+ Domain/Motif \(Interproscan results\)](#)

[+ Localization / Targeting](#)

Analysis	Start	End	Length	Location	Reliability class	Signal Peptide CutOff	Mitochondrion CutOff
targetp	1	19	19	Secretory pathway	3	0.820	0.301
signalp	1	19	18	immm	Not result		

[+ Blast based analysis](#)

[+ Other analysis](#)

[+ Functional Browse](#)

[+ Structural Browse](#)

[+ Genome Mapping at gene locus](#)

[+ Current manual annotation](#)

# Link to GnpIS-Gbrowse

The figure displays the GnpArray Genome Report System interface. On the left, a navigation sidebar lists various data sources and analysis tools. A central feature is a detailed gene report for **BofuT4\_T146270.1**, showing its length (2381 bp), reference coordinates (bt4\_SupSuperContig\_110r\_56\_1: 219664..222044), and quality (regular). Below this, a 'GnpArray Gene Report' section provides links to 'Gene Report', 'Gene Domain Browser', 'Zoom to this feature', and 'Detailed Report'. To the right, a 'Gene - BofuT4\_P014290.1' card shows gene details, associated gene lists, normalized data, and a heatmap. The bottom right corner features a 'Gbrowse: functional domains' tool.



# GnplS – Advanced search GALAXY



# GnpIS – polymorphism variation module





# GALAXY URGI SERVER

GnPLS  
datamarts

The screenshot shows the Galaxy URGI Server interface. At the top, there is a navigation bar with links for Analyze Data, Workflow, Shared Data, Visualization, Help, and User. Below the navigation bar, the main content area features the URGI logo and the INRA logo. A text block states: "The Galaxy team is a part of BX at Penn State. This project is supported in part by NSF, NHGRI, and the Huck Institutes of the Life Sciences." On the left side, there is a sidebar titled "Tools" which lists various genomic analysis tools. A red arrow points from the "GnPLS datamarts" text to the "Tools" menu.

- Tools
- Options ▾
- search tools
- [Get Data](#)
- [Send Data](#)
- [ENCODE Tools](#)
- [Lift-Over](#)
- [Text Manipulation](#)
- [Filter and Sort](#)
- [Join, Subtract and Group](#)
- [Convert Formats](#)
- [Extract Features](#)
- [Fetch Sequences](#)
- [Fetch Alignments](#)
- [Get Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Wavelet Analysis](#)
- [Graph/Display Data](#)
- [Regional Variation](#)
- [Multiple regression](#)
- [Multivariate Analysis](#)
- [Evolution](#)
- [Motif Tools](#)
- [Multiple Alignments](#)
- [Metagenomic analyses](#)
- [FASTA manipulation](#)
- [NCBI BLAST+](#)
- [NGS: QC and manipulation](#)
- [NGS: Picard \(beta\)](#)
- [NGS: Mapping](#)
- [NGS: Indel Analysis](#)
- [NGS: RNA Analysis](#)
- [NGS: SAM Tools](#)
- [NGS: GATK Tools \(beta\)](#)





# GALAXY URGI SERVER

**Galaxy**

Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools Options

**URGI TOOLS**

- [URGI: Get Data for grapevine](#)
- [URGI: BAC analysis](#)
- [URGI: MAPHITS – PreProcess Tools](#)
- [URGI: MAPHITS – Tools](#)
- [URGI: MAPHITS – PostProcess Tools](#)
- [URGI: MAPHITS – SNPs Chip Tools](#)
- [URGI: S-MART](#)

**APLIBIO TOOLS**

- [colorGff Parses a DOOR report file and writes the information in a gff3 out file.](#)
- [coverageGff Computes reads coverage from a "nbElements" tag and writes the calculated coverage in a gff3 out file.](#)
- [strictlyIncludeGff Prints the elements which are strictly included in the template.](#)
- [sortGff Sorts a gff file.](#)
- [seedGff Creates the seed from -15 to -25 bp before ATG](#)
- [prepareAnnotationFile Prepares Annotation file -> clusterizes, filters exon and sorts annotations.](#)
- [listAnnotation Shows the information of Annotation file -> Number of genes, rRNA, tRNA.](#)
- [interElementGff Creates a new Gff output, which corresponds to the region of two successive Elements.](#)
- [removeExonLines Removes the lines containing Exon.](#)
- [countNumber Calculate the number of reads\(annotations\) overlapping for each transcript.](#)
- [listinputs Give a list of input files from different conditions/groups](#)

History Options

0 bytes

**INRA**

The Galaxy team is a part of BX at Penn State. This project is supported in part by NSF, NHGRI, and the Huck Institutes of the Life Sciences.



# GnplS – Biomart – Galaxy

## interoperability between 3 tools

**QUICK SEARCH** Species

Xwmc430  
You can found the indexed data list [here](#).  
Examples: VII, VVIF52, gene, arabidopsis, AT109603, 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. Epheats.

**Genetic resources**  
Plant genetic resources data. Siregal.

**Arrays**  
Expression data. GnpArray.

**EURLi** [GnpT advanced search](#)

**Dataset** 2137 / 366639 Entries

**Botrytis\_fungus\_annotation**

**Filters**

Feature Type : signal\_peptide

Start > -30

Program : signal

Start = 1

End < 30

Analysis source name : peptide\_iprscan\_annotation

**Attributes**

Reference Feature

Feature Type

Start (-1)

End

Program

Library

HIT

Description

Analysis source name

DB Xref DB

DB Xref Accession

Ontology Term

View  rows as [HTML](#)  Unique results only

Email notification to

File   Unique results only

Reference	Feature	Feature Type	Start (-1)	End	Program	Library	HIT	Description	Analysis source name	DB Xref DB	DB Xref Accession
Sd4/T1	P00000000.1	signal_peptide	0	25	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000001.1	signal_peptide	0	18	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000002.1	signal_peptide	0	18	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000003.1	signal_peptide	0	19	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000004.1	signal_peptide	0	19	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000005.1	signal_peptide	0	19	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000006.1	signal_peptide	0	19	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000007.1	signal_peptide	0	17	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000008.1	signal_peptide	0	17	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000009.1	signal_peptide	0	19	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt
Sd4/T1	P00000010.1	signal_peptide	0	3	signalt	model	SignaP		polypeptide_prascan_annotation	GFF source	signalt

The Galaxy team is a part of [BX](#) at Penn State.  
 This project is supported in part by [NSF](#), [NHGRI](#), and [the Huck Institutes of the Life Sciences](#).




- [Upload File](#) from your computer
- [UCSC Main](#) table browser
- [UCSC Test](#) table browser
- [UCSC Archaea](#) table browser
- [BX main](#) browser
- [Get Microbial Data](#)
- [BioMart](#) Central server
- [BioMart INRA URGI Gnpis](#)



# Conclusion





# GnpIS : an information system: databases + query interfaces + analysis tools linked together

Species	<input type="text" value="Xwmc430"/>	<b>SUBMIT</b>
<a href="#">Wheat physical map: 3B v1</a> <span style="margin: 0 20px;"> </span> <a href="#">Wheat physical map: 3B v2</a> <span style="margin: 0 20px;"> </span> <a href="#">Genetic mapping</a>		
<h3>Features (1)</h3> <hr/> <p>Xwmc430-3B ★★★★☆</p> <hr/> <p>-</p> <hr/> <p>1 items found, displaying 1 to 1   Display <b>10</b> <input type="button" value="▼"/> results per page</p>		



GnpMap / MetaQTL: MQTL2D_2				
METAQTL DETAILS				
MetaQTL	MQTL2D_2			
Meta analysis	MQTL_CxQTL_2D			
Number of MetaQTL(s)	2			
Taxon	Triticum aestivum			
Meta-trait	Seed quality			
QTL DETAILS				
QTL	MetaQTL belonging			Trait
c8 HN_GPC_2D_73.8	0.97			GPC
c8 HN_GY_2D_76.8	1.0			GY
HN_GPC_2D_73.8	0.93			GPC
HN_GY_2D_93.7	1.0			GY
LN_GPC_2D_73.8	0.89			GPC
LN_GY_2D_76.8	0.89			GY
mean_GPC_2D_73.8	0.89			GPC
mean_GY_2D_78.8	0.97			GY
nw9 HN_GY_2D_85.8	1.0			GY
nw9 LN_GY_2D_85.8	1.0			GY
ASSOCIATED ASSIGNMENTS				
Map	Linkage group		Distance	From
CPH107xTosonidorXquebon	2D		78.37	76.91
	To			79.83

# GnpAsso Beta / Association results

---

## DETAILS

Number of associated traits:	60
Number of associated markers:	4824

---

## ASSOCIATION RESULTS

1-10 of 49,318 | Display 10  results per page

Experiment name	# of lots	Panel name	Trait name	Marker name	pval	-log(pval)	r2
trait1			snp_LVH_00669		1.22E-5	4.91E0	1.1E-1
trait1			snp_LVH_01071		7.44E-4	3.13E0	6.66E-2
trait1			snp_LVH_01107		8.9E-4	3.05E0	6.47E-2
trait1			snp_LVH_01109		8.9E-4	3.05E0	6.47E-2
trait1			snp_LVH_01202		4.41E-4	3.36E0	7.21E-2
trait1			snp_LVH_01227		6.06E-4	3.22E0	6.92E-2
trait1			snp_LVH_01459		4.15E-4	3.38E0	7.58E-2
trait1			snp_LVH_01509		4.9E-4	3.31E0	7.06E-2
trait1			snp_LVH_01837		7.74E-4	3.11E0	6.50E-2
trait1			snp_LVH_02442		2.52E-4	3.6E0	7.84E-2

---

## 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 ressources data. Siregal.

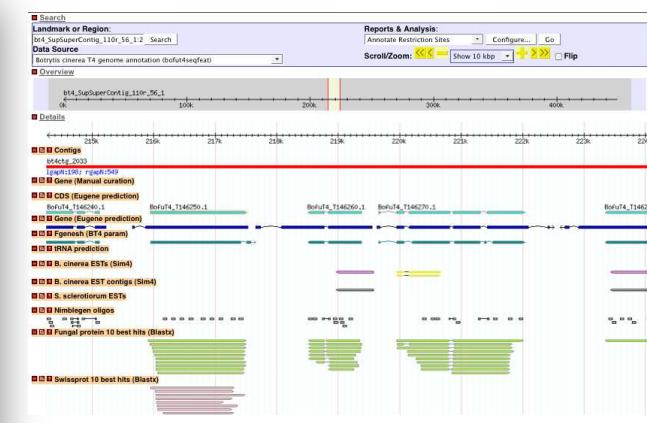
---

## data. GnpArray.

Add filter
 




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# Thank you for your attention



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