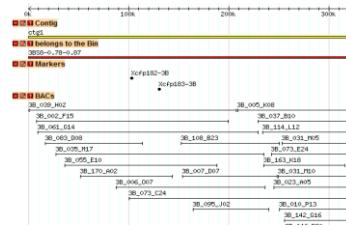
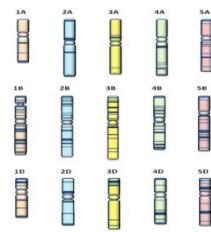


IWGSC - Standards and Protocols session

In-silico mapping of my favorite gene using the survey sequence of wheat

Michael Alaux



Wheat bioinformatics at URGI



Wheat Portal

Wheat

- [Sequence Repository](#)
- [Projects](#)
- [Data](#)
- [Tools](#)
- [Triannot Pipeline](#)
- [Deletion Bins](#)
- [Publications](#)
- [Links](#)

PLANT AND FUNGI DATA INTEGRATION

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Species

- [Vitis](#)
- [**Wheat**](#)
- [Sequence Repository](#)
- [Projects](#)
- [Data](#)
- [Tools](#)
- [Triannot Pipeline](#)
- [Deletion Bins](#)
- [Publications](#)
- [Links](#)
- [Botrytis](#)
- [Leptosphaeria](#)
- [Microbotryum](#)
- [Venturia](#)
- [Arabidopsis](#)
- [Oryza](#)
- [Populus](#)
- [Maize](#)
- [Medicago](#)
- [Pisum](#)
- [Flax](#)

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

Wheat

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

New [IWGSC Survey Sequence Repository](#) is available !



Why develop Wheat genomics?

Today, agriculture is facing one of its greatest challenges since it began 10 000 years ago, that of producing an ample supply of high quality food and feed for a growing world population in a sustainable and environment friendly manner. Bread wheat (*Triticum aestivum L.*) is the staple food for more than 35% of the people and is grown on over 95% of the wheat growing area. Its sequence holds the key to genetic improvements that will allow growers to meet the increasing demands for high quality food and feed produced in an environmentally sensitive, sustainable, and profitable manner. Further, because of its recent history, hexaploid wheat is a very good model to study polyploidy, a driving evolutionary force for more than 90% of all plants.

The [International Wheat Genome Sequencing Consortium \(IWGSC\)](#), was established by a group of plant scientists, breeders, and growers dedicated to sequencing the wheat genome to enhance our knowledge of the structure and function of the wheat genome. By gaining increased understanding of the biology of agronomically important traits and deploying state-of-the-art molecular tools, plant scientists and breeders will be able to accelerate wheat improvement to meet the challenges of the 21st century. The IWGSC is committed to ensuring that the sequence of the wheat genome and the resulting DNA-based tools are available for all to use without restriction.

The [European Triticeae Genomics Initiative \(ETGI\)](#) is a platform for the coordination and representation of Triticeae (Wheat, barley, rye) genomics research at the European level and serves as a link to the International research community represented by the International Triticeae Mapping Initiative (ITMI). ETGI consists of European scientists from public and private research institutes who are interested in developing complementary and coordinated research projects on Triticeae genomics to pave the way for a better understanding of crop plant systems biology and, thereby, enable substantial improvements of these essential crop species for the EU and world agriculture. ETGI partners coordinate applications for national and European research and training projects to assist in strengthening and structuring of the European Research Area (ERA). For three years beginning in 2007, ETGI networking activities are supported by the COST action "Tritigen" (FA0604).



<http://urgi.versailles.inra.fr/Species/Wheat>

Wheat Portal

Wheat

[Sequence Repository](#)[Projects](#)[Data](#)[Tools](#)[Triannot Pipeline](#)[Deletion Bins](#)[Publications](#)[Links](#)

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 ...

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 ...

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 ...

Wheat Initiative



Launch of the Wheat Initiative, 15 September 2011

The Wheat Initiative (International Research Initiative for Wheat Improvement) was officially launched on the 15th of September 2011 (see). The Wheat Initiative, proposed by research and funding organisations from several countries (see

Wheat Portal

Wheat
Sequence Repository
Projects
Data
Tools
Triannot Pipeline
Deletion Bins
Publications
Links

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

Sequence survey		
Physical maps : 3B (99% and 82% coverage) and 1BL		
Annotations : 13 contigs of 3B		
Deletion bins of 3B chromosome		
Genetic maps		
QTL		
Markers		
Genetic resources		
EST		
SNP		

Wheat Portal

Wheat
Sequence Repository
Projects
Data
Tools
Triannot Pipeline
Deletion Bins
Publications
Links

Data summary (November 2011)

Public data

Genetic maps	26
Physical maps	3
Reference sequence chromosomes	1
Survey sequence chromosomes	15
QTL	324
Markers	19029
Accessions	2245
SNP	10819
EST	544529

Total (public + registered) data

Genetic maps	26
Physical maps	5
Reference sequence chromosomes	1
Survey sequence chromosomes	15
QTL	608
Markers	21371
Accessions	2575
SNP	134904
EST	603672

Wheat Portal

Wheat
Sequence Repository
Projects
Data
Tools
Triannot Pipeline
Deletion Bins
Publications
Links

	free access tool		registered access tool
---	------------------	---	------------------------

TriAnnot Pipeline		
Quick search		
Taxon card		
Physical map viewer		
Annotation viewer		
dbWFA		

Wheat Portal

Wheat

Sequence Repository (circled in red)

Projects

Data

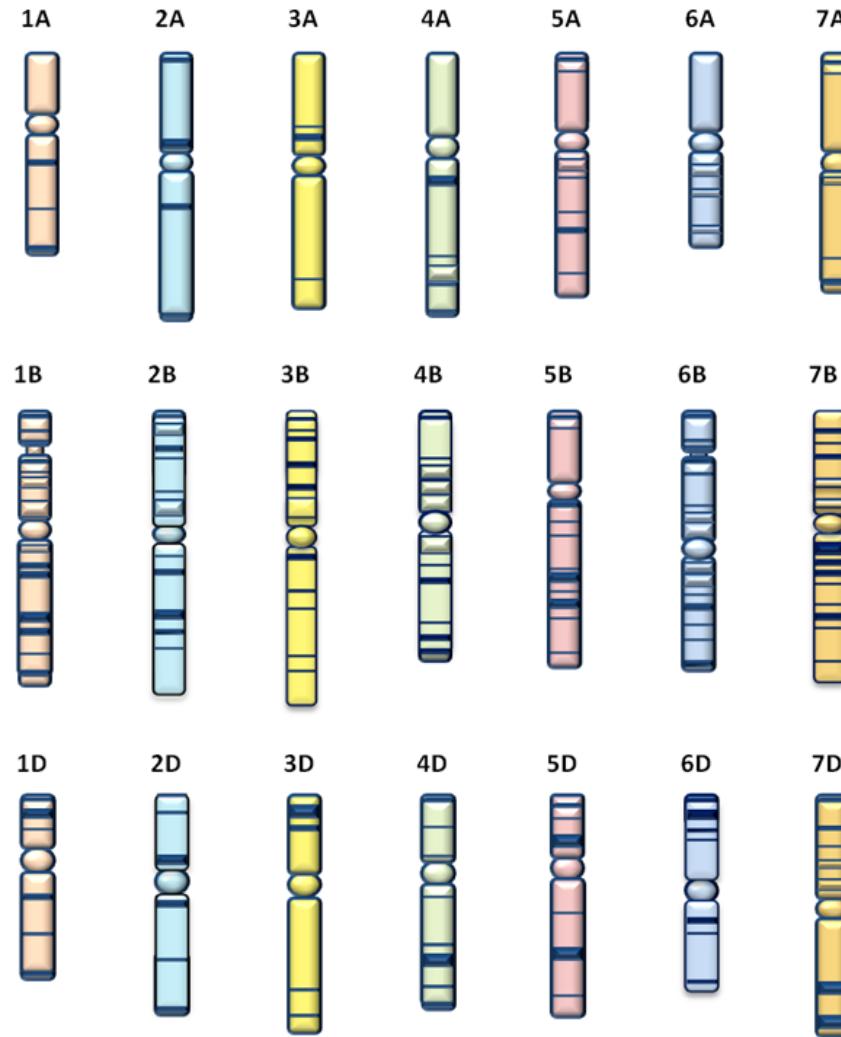
Tools

Triannot Pipeline

Deletion Bins

Publications

Links



IWGSC Survey Sequence



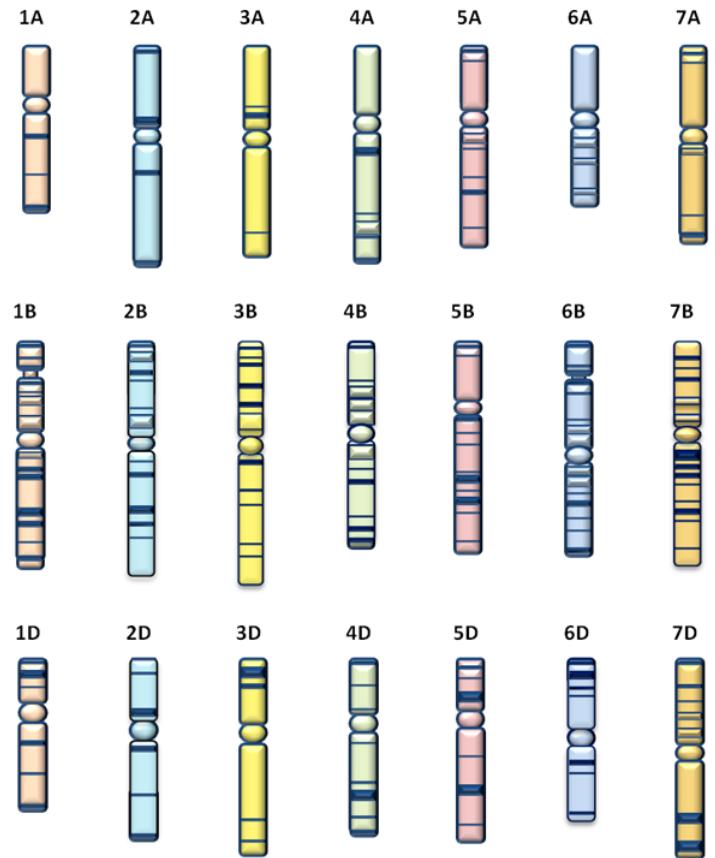
Survey Sequence Repository



Click on a chromosome to have access to the survey sequence and the viewers when available.
The process to have access to the download and blast is explained [here](#).
Survey sequence assemblies progress is available at [TGAC](#) (restricted access). About Blast, you could select one or multiple chromosomes arms on step 3 in the "WHEAT sequence survey databases (restricted to IWGSC)" section and set the search options (evaluate, max results) on step 4.

... BLAST is now available for BLAST ONLY account too.

[Talk at PAG XX](#) at the IWGSC Standard and protocol session Tuesday



Click on a chromosome to access to the survey sequence chromosome arm assemblies for:

- **BLAST** search
- **Download**
- **Viewers** (physical map, annotations)

<http://urgi.versailles.inra.fr/Species/Wheat/Sequence-Repository>

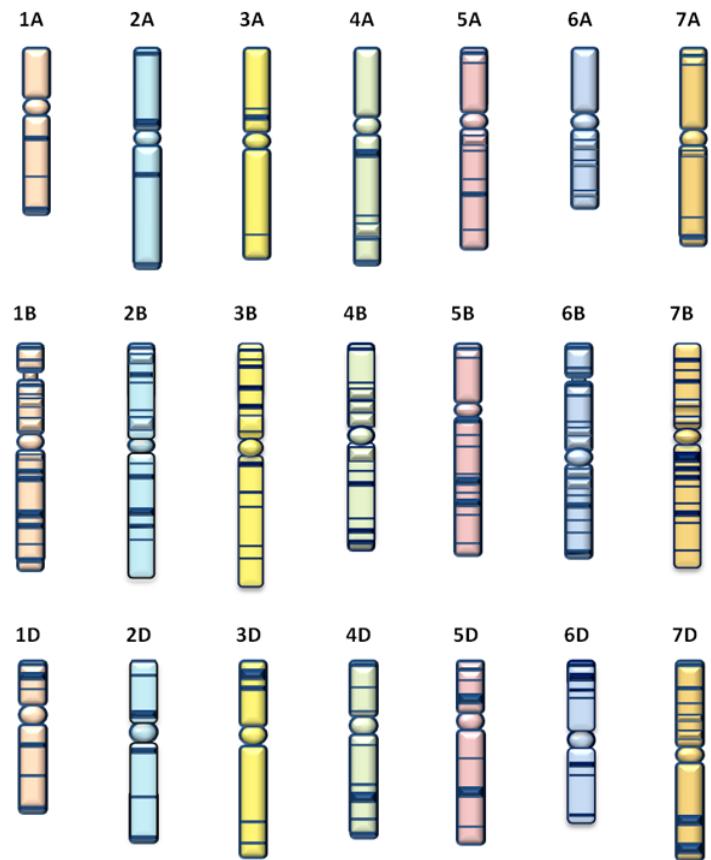
Survey Sequence Repository



Click on a chromosome to have access to the survey sequence and the viewers when available.
The process to have access to the download and blast is explained [here](#).
Survey sequence assemblies progress is available at [TGAC](#) (restricted access). About Blast, you could select one or multiple chromosomes arms on step 3 in the "WHEAT sequence survey databases (restricted to IWGSC)" section and set the search options (evaluate, max results) on step 4.

... BLAST is now available for BLAST ONLY account too.

[Talk at PAG XX](#) at the IWGSC Standard and protocol session Tuesday



More than 50% of the survey sequence assemblies are available in the repository:

1BS 1DL

2AS 2DL 2DS

3AL 3AS 3B 3DL 3DS

4AL 4AS 4DL 4DS

5AL 5AS

6AL 6AS 6DL 6DS

7AL 7AS 7BL 7BS 7DL 7DS

Last survey sequence assemblies are in progress at TGAC.

<http://urgi.versailles.inra.fr/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Account creation process is detailed on the IWGSC website:

IWGSC Coordinating Committee members -> Download

IWGSC members and non-members -> BLAST

<http://www.wheatgenome.org/Tools-and-Resources>

Tools and Resources

The IWGSC is developing a variety of tools and resources that are available first to members of the coordinating committee, second to general members of the consortium, and subsequently to the entire scientific community. On behalf of the IWGSC, a [central repository](#) for access to physical map data and sequences has been established by the [URGI](#) (France). Early, pre-publication access is provided to coordinating committee and individual scientists who agree to the data access statement. While scientists who agree to abide by the data access agreement will be able to BLAST the data in advance of publication, Coordinating Committee members and active members of their group will also be permitted to download the data. Data will be made available to the public upon publication, upon deposition into the public archives, or within one-year from the conclusion of the data generation. The IWGSC reserves the right to publish the first global analyses including:

- Whole chromosome or whole genome level analyses on genes, gene families, repetitive sequences; and
- Comparative analyses with other organisms.

For Coordinating Committee members and their team members to gain full access, please sign-in to your IWGSC account and then agree to the [IWGSC Data Release Statement of Agreement](#). If you are not already a member of the IWGSC, you may register by clicking the "register" link at the top of any page on the IWGSC website. If you are not actively in a team or group of a Coordinating Committee or a staff member of a sponsor, please do not claim that you are part of the group or team as this may delay your account validation.

For general members of the IWGSC and nonmembers, you can gain early access to BLAST data by signing the [BLAST Access Agreement](#). If you are a general member of the IWGSC, please sign-in to your IWGSC account and then agree to the BLAST Access Agreement. Nonmembers may gain access by [registering for an IWGSC user account](#) and signing the [BLAST Access Agreement](#).

Once the appropriate access agreement has been signed and your access or website account has been validated, an account will be established for you at the URGI to access the IWGSC repository and you will automatically receive an email regarding "Your INRA URGI account". If you already have a URGI account, this account will be upgraded to permit you to access the IWGSC repository and you will receive a confirmation email.

If you have any questions regarding account access, please contact [Kellye Eversole](#).

Survey Sequence Repository

1A



2A



5A



1B



2B



3B



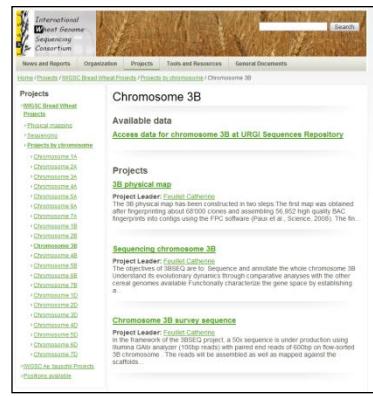
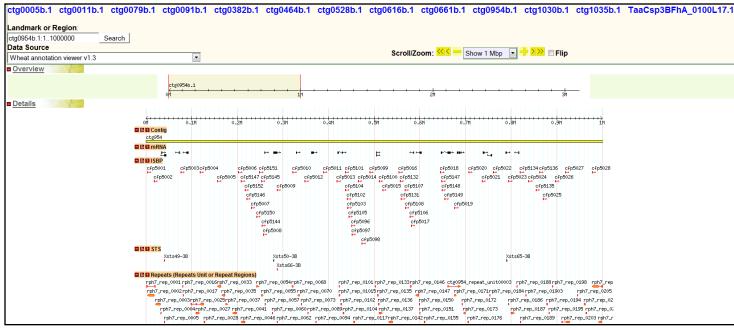
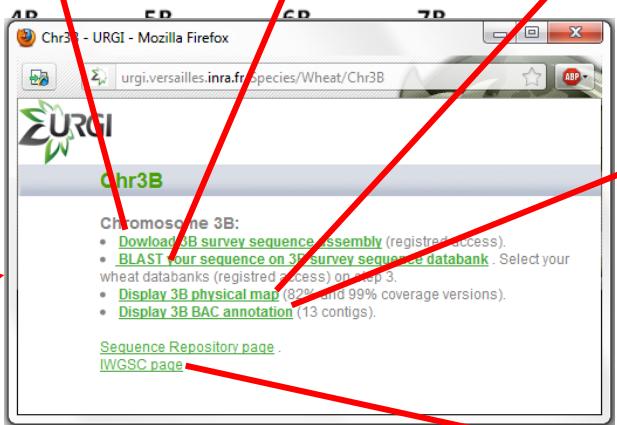
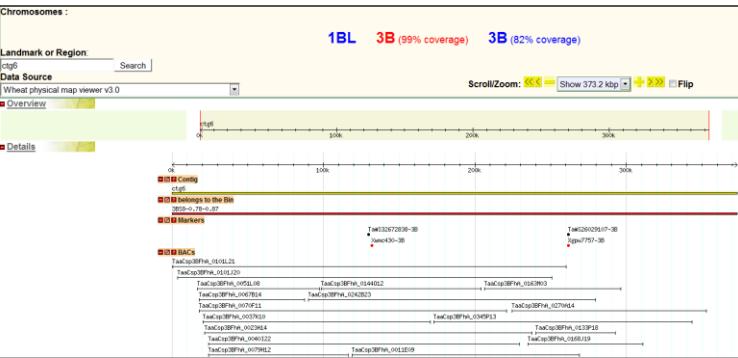
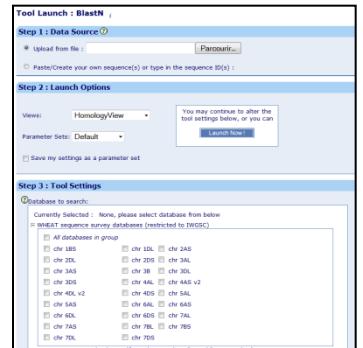
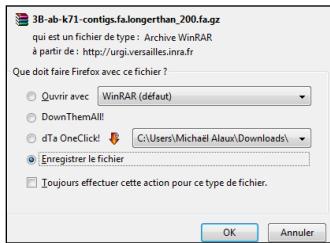
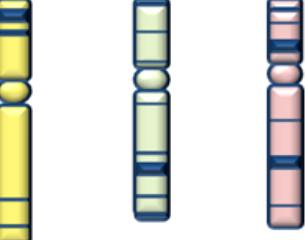
1D



2D



3D



<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Tool Launch : BlastN

Step 1 : Data Source

Upload from file :

Paste/Create your own sequence(s) or type in the sequence ID(s) :

Step 4 : (Optional) Advanced Settings

Minimum Options

Output Options

- Number of hits and alignments to show
- Number of best hits from a region to keep

Search Parameters

- Filter query sequence
- Penalty for a nucleotide mismatch
- Reward for a nucleotide match
- The E value
- Word size
- Perform gapped alignment
- Cost to open a gap
- Cost to extend a gap
- Use lowercase filtering of query sequence

Step 2 : Launch Options

Views:

Parameter Sets:

Save my settings as a parameter set

You may continue to alter the tool settings below, or you can

Step 3 : Tool Settings

Database to search:

Currently Selected : None, please select database from below

- WHEAT sequence survey databases (restricted to IWGSC)

- All databases in group
- chr 1BS
- chr 2DL
- chr 3AS
- chr 3DS
- chr 4DL v2
- chr 5AS
- chr 6DL
- chr 7AS
- chr 7DL
- chr 1DL
- chr 2AS
- chr 2DS
- chr 3AL
- chr 3B
- chr 3DL
- chr 4AL
- chr 4AS v2
- chr 4DS
- chr 5AL
- chr 6AL
- chr 6AS
- chr 6DS
- chr 7AL
- chr 7BL
- chr 7BS
- chr 7DS

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Step 1 : Data Source ?

Upload from file : C:\Users\Michaël Alaux\Documents \ Parcourir...

Paste/Create your own sequence(s) or type in the sequence ID(s) :

Step 2 : Launch Options

Views: HomologyView ▾

Parameter Sets: Default ▾

You may continue to alter the tool settings below, or you can

Save my settings as a parameter set

Step 3 : Tool Settings

Database to search:

Currently Selected : chr 3B

WHEAT sequence survey databases (restricted to IWGSC)

<input type="checkbox"/> All databases in group	<input type="checkbox"/> chr 1BS	<input type="checkbox"/> chr 1DL	<input type="checkbox"/> chr 2AS
	<input type="checkbox"/> chr 2DL	<input type="checkbox"/> chr 2DS	<input type="checkbox"/> chr 3AL
	<input type="checkbox"/> chr 3AS	<input checked="" type="checkbox"/> chr 3B	<input type="checkbox"/> chr 3DL
	<input type="checkbox"/> chr 3DS	<input type="checkbox"/> chr 4AL	<input type="checkbox"/> chr 4AS v2
	<input type="checkbox"/> chr 4DL v2	<input type="checkbox"/> chr 4DS	<input type="checkbox"/> chr 5AL
	<input type="checkbox"/> chr 5AS	<input type="checkbox"/> chr 6AL	<input type="checkbox"/> chr 6AS
	<input type="checkbox"/> chr 6DL	<input type="checkbox"/> chr 6DS	<input type="checkbox"/> chr 7AL
	<input type="checkbox"/> chr 7AS	<input type="checkbox"/> chr 7BL	<input type="checkbox"/> chr 7BS
	<input type="checkbox"/> chr 7DL	<input type="checkbox"/> chr 7DS	

If you select all the chromosomes,
your sequence have to be small !

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

To speed up your Blast

Step 4 : (Optional) Advanced Settings

[+ Expand All](#)[- Collapse All](#)

+ Minimum Options

- Output Options

(?) Number of hits and alignments to show

(?) Number of best hits from a region to keep

- Search Parameters

(?) Filter query sequence	<input checked="" type="checkbox"/>
(?) Penalty for a nucleotide mismatch	<input type="text" value="-3"/>
(?) Reward for a nucleotide match	<input type="text" value="1"/>
(?) The E value	<input type="text" value="0.001000"/>
(?) Word size	<input type="text" value="13"/>
(?) Perform gapped alignment	<input checked="" type="checkbox"/>
(?) Cost to open a gap	<input type="button" value="Default"/>
(?) Cost to extend a gap	<input type="button" value="Default"/>
(?) Use lowercase filtering of query sequence	<input type="checkbox"/>

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

HomologyView



<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

CompleteEntry

```
>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10567088 3505 62189
    4936946+,...,988109+
Length = 3505
```

```
Score = 2012 bits (1015), Expect = 0.0
Identities = 1022/1023 (99%), Gaps = 1/1023 (0%)
Strand = Plus / Plus
```

```
Query: 538 ttgttaccaaccgggactaaagggtggagctccagacagcggccgcgtggagggccttag 597
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 565 ttgttaccaaccgggactaaagggtggagctccagacagcggccgcgtggagggccttag 624
```

```
Query: 598 tccccgttctagaaccgggactaaagggtcggtattaaaggcccccttagtcctggtt 657
|||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 625 tccccgttctagaaccgggactaaagggtcggtattaaaggcccccttagtcctggtt 684
```

```
Query: 658 cttgtacgaaccgggatctaaaggccctctagaaccgggacaaatgagccttttctact 717
||||||||||||||| |||||||||||||||||||||||||||||
```

```
Sbjct: 685 cttgtacgaaccggg-ctaaaggccctctagaaccgggacaaatgagccttttctact 743
```

```
Query: 718 agtggtagctccgtcgtaacaactcacctcatctagatgaatgtgtgcataagcaatcct 777
|||||||||||||||||||||||||||||||||||
```

```
Sbjct: 744 agtggtagctccgtcgtaacaactcacctcatctagatgaatgtgtgcataagcaatcct 803
```

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Blast_View

Select: All, None	Primary Search	Query	Database	Hit	Description	Top Score	E value	Percentage Identity	Match Length
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_1	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10567088		2012	0.0	99	1023
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_2	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10502352		569	1e-160	91	437
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_3	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10552080		531	1e-149	93	359
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_4	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10575476		513	1e-143	93	342
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_5	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10670621		507	1e-141	88	458
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_6	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10758230		494	1e-137	93	328
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_7	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10447443		488	1e-135	92	341
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_8	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10620351		486	1e-135	92	360
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_9	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10588181		486	1e-135	88	458
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_10	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10422867		484	1e-134	92	355
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_11	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10434795		480	1e-133	92	341
<input type="checkbox"/> <input checked="" type="checkbox"/>	BLASTN:temp_job1_12	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10562484		478	1e-132	92	340

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Clic on Tool

To download the result

Primary Search ★ Refine Query Expression: [BLASTN-JobName:temp_job1]

Found 50 entries

Options: Selected Entries View Results/Page Page 1/2 >

Select: All, None

	Primary Search	Query	Database	Hit	Description	Top Score	E value	Percentage Identity	Match Length
<input checked="" type="checkbox"/>	BLASTN:temp_job1_1	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10567088		2012	0.0	99	1023
<input checked="" type="checkbox"/>	BLASTN:temp_job1_2	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10502352		569	1e-160	91	437
<input checked="" type="checkbox"/>	BLASTN:temp_job1_3	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10552080		531	1e-149	93	359
<input checked="" type="checkbox"/>	BLASTN:temp_job1_4	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10575476		513	1e-143	93	342
<input checked="" type="checkbox"/>	BLASTN:temp_job1_5	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10670621		507	1e-141	88	458
<input checked="" type="checkbox"/>	BLASTN:temp_job1_6	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10758230		494	1e-137	93	328
<input checked="" type="checkbox"/>	BLASTN:temp_job1_7	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10447443		488	1e-135	92	341
<input checked="" type="checkbox"/>	BLASTN:temp_job1_8	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10620351		486	1e-135	92	360
<input checked="" type="checkbox"/>	BLASTN:temp_job1_9	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10588181		486	1e-135	88	458
<input checked="" type="checkbox"/>	BLASTN:temp_job1_10	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10422867		484	1e-134	92	355
<input checked="" type="checkbox"/>	BLASTN:temp_job1_11	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10434795		480	1e-133	92	341
<input checked="" type="checkbox"/>	BLASTN:temp_job1_12	Synth12	IWGSC_3B	>IWGSC_chr3B_ab_k71_contigs_longerthan_200:10562484		478	1e-132	92	340

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Analysis Tools

Go to Tools Page
or Launch specific Tool:
ConsambigN ▾
Launch

Tools

Refine Query Expression: [BLASTN-JobName:temp_job1]

Page 1/2 >

Sequence

Add to My Nucleotide Sequences

Save/Export

XML or Text format 

Microsoft Excel 

Acrobat PDF

Link to Related Information

Link to...

Term Highlighting

Switch Off

BLASTN:temp_job1_1 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10567088

BLASTN:temp_job1_2 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10502352

BLASTN:temp_job1_3 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10552080

BLASTN:temp_job1_4 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10575476

BLASTN:temp_job1_5 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10670621

BLASTN:temp_job1_6 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10758230

BLASTN:temp_job1_7 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10447443

BLASTN:temp_job1_8 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10620351

BLASTN:temp_job1_9 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10588181

BLASTN:temp_job1_10 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10422867

BLASTN:temp_job1_11 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10434795

BLASTN:temp_job1_12 Synth12 IWGSC_3B >IWGSC_chr3B_ab_k71_contigs_longerthan_200:10562484

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

Saving 50 entries from the query:

[BLASTN-JobName:temp_job1]

Save Options:

ASCII text/table

Save with view: **CompleteEntry**

Field Separator: \t Record Separator: \n

Generic XML format

Using the loader: Blastv

application/octet-stream

text/plain

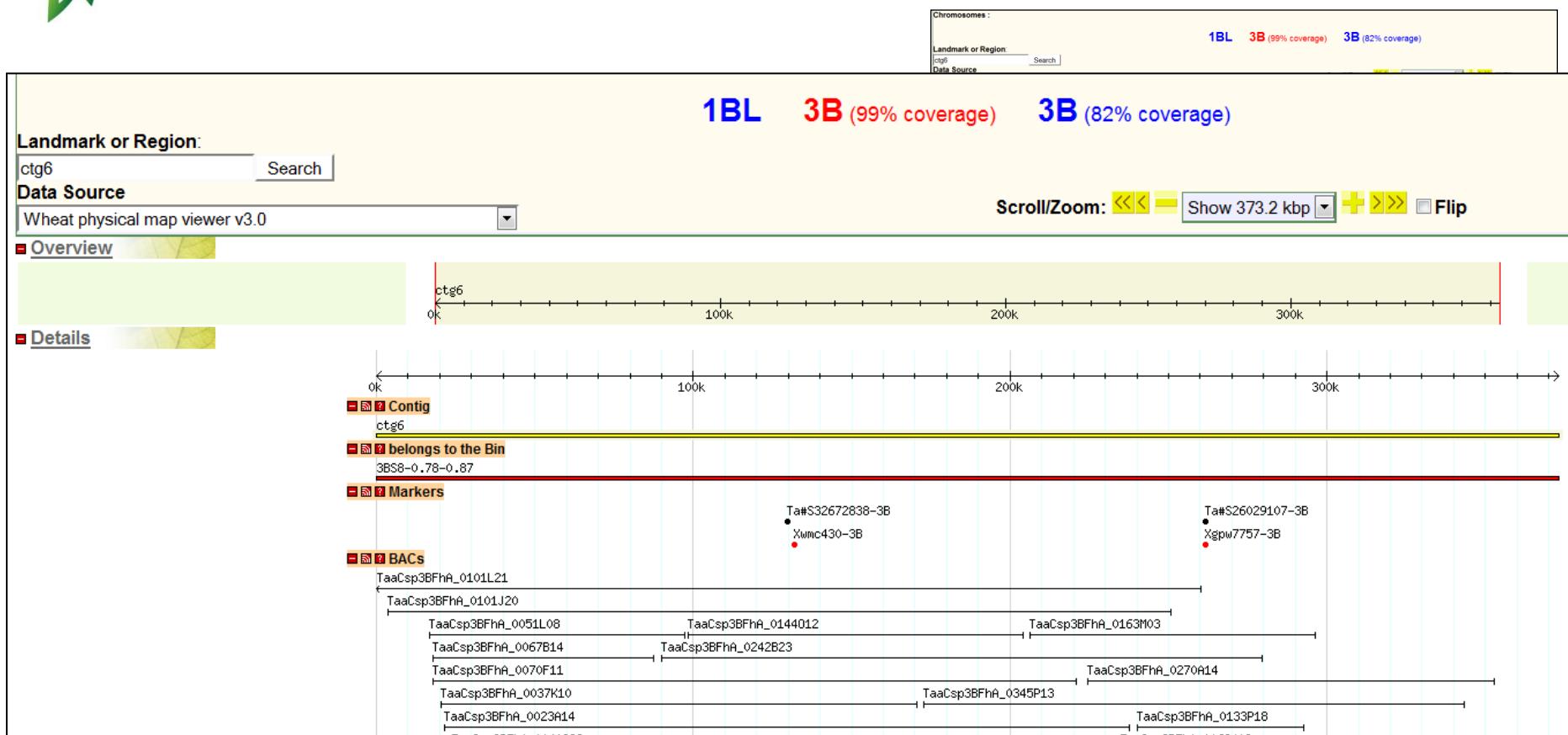
other:

Save

Close

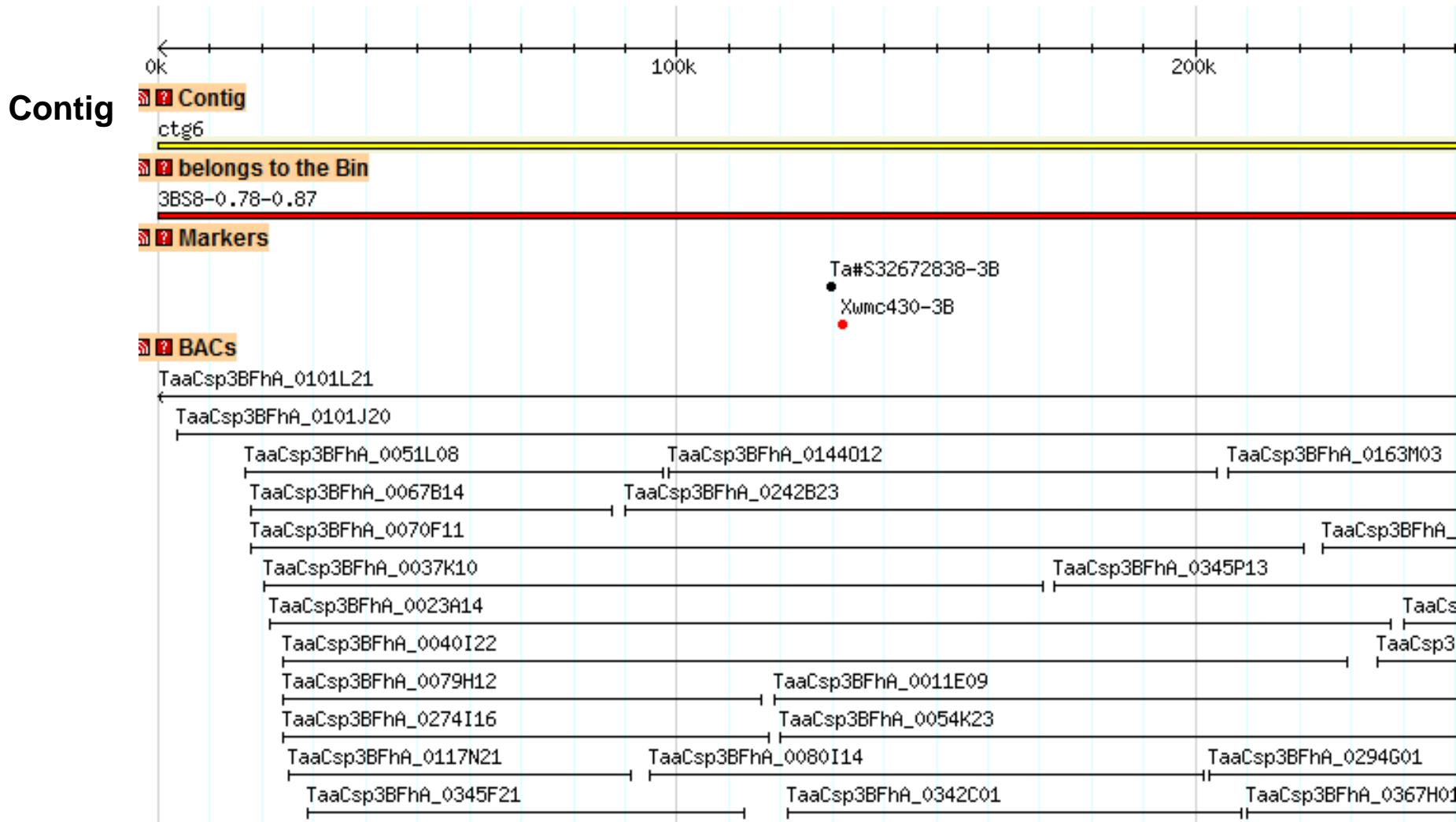
<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

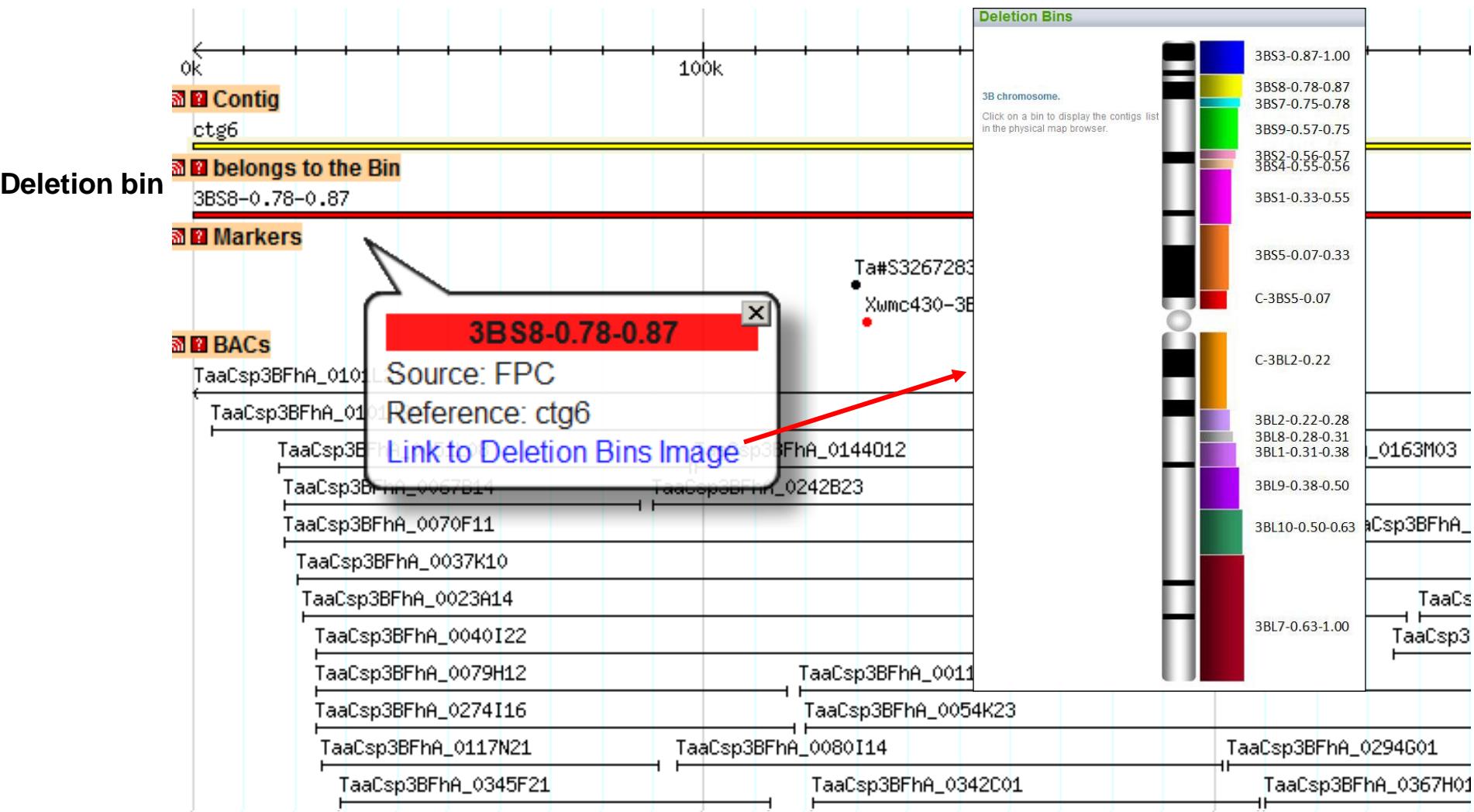


<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

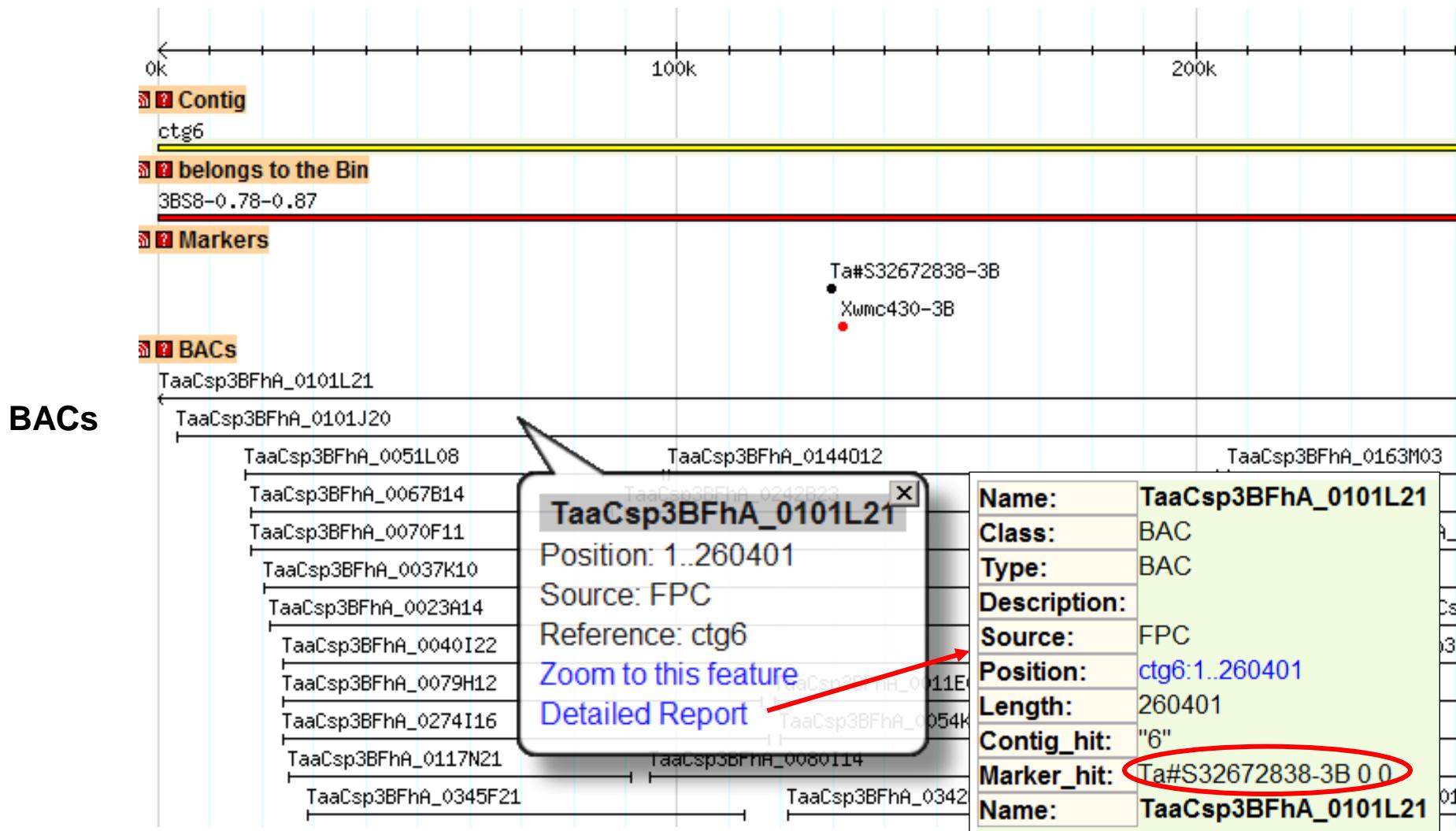
Wheat physical map viewer



Wheat physical map viewer

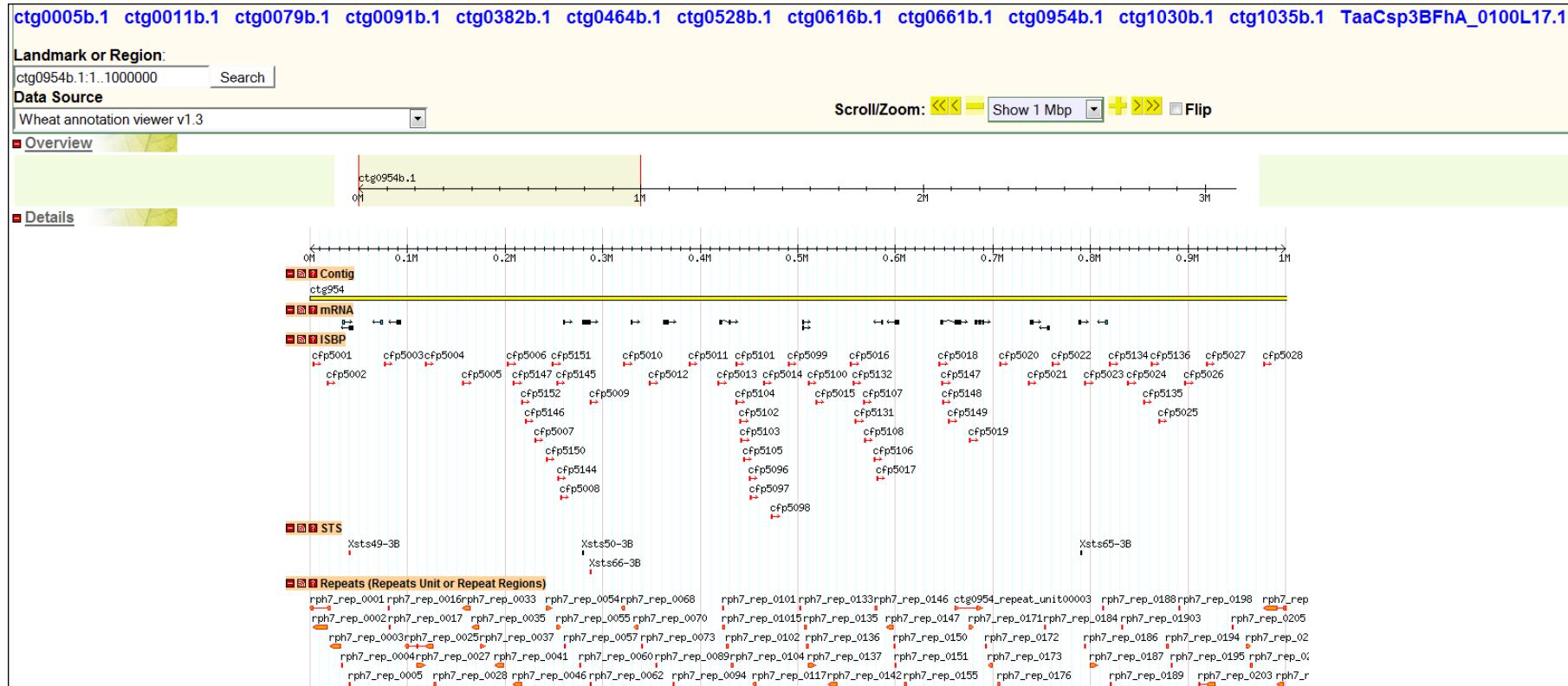


Wheat physical map viewer



Wheat physical map viewer

Survey Sequence Repository

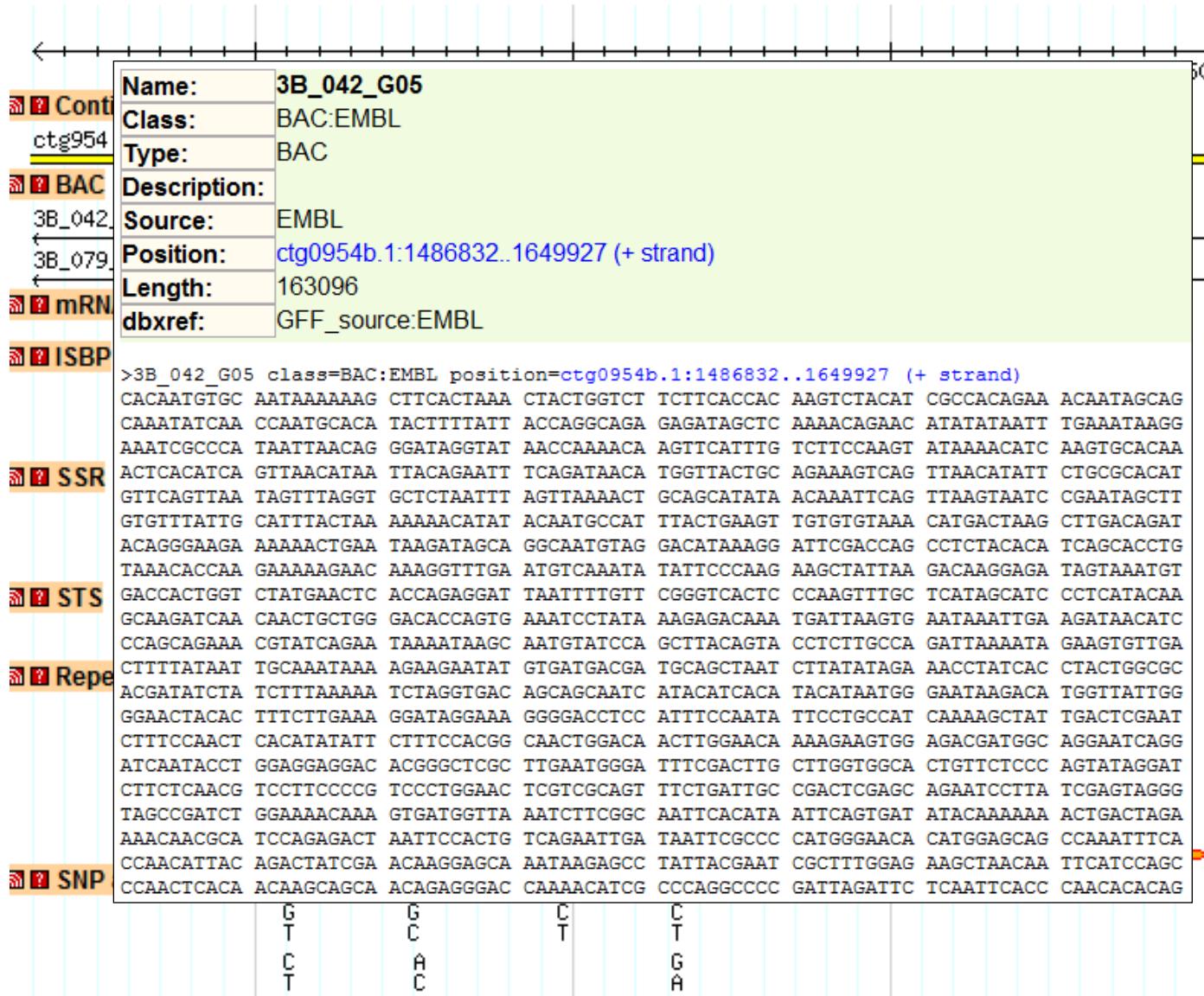


<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>

Wheat annotation viewer

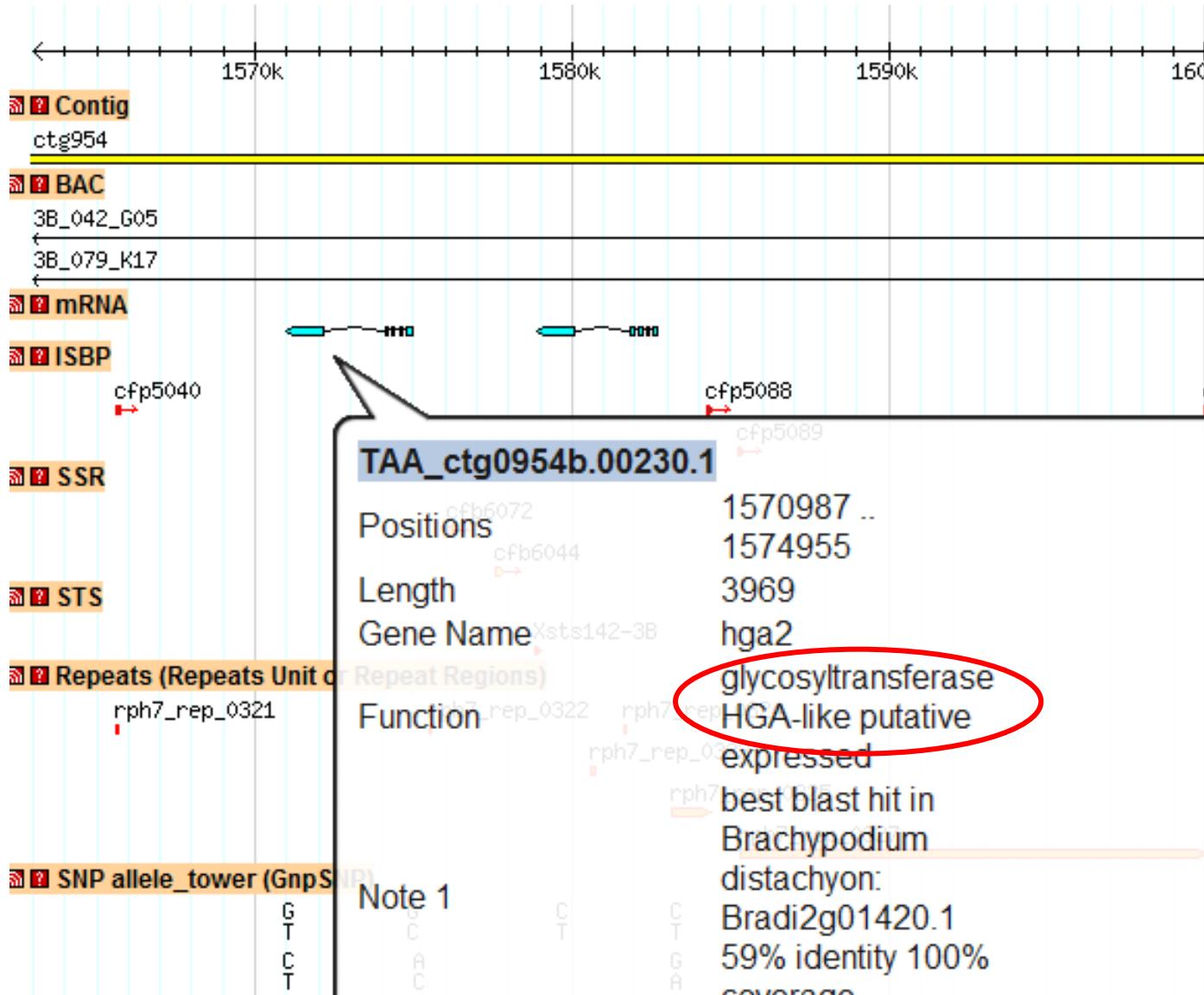
Contig

BAC



Wheat annotation viewer

mRNA



Wheat annotation viewer

Name:	TAA_ctg0954b.00230.1												
Class:	mRNA:EMBL												
Type:	mRNA												
Description:	best blast hit in Brachypodium distachyon: Bradi2g01420.1 59% identity 100% coverage; 57% identity 96% coverage												
Source:	EMBL												
Position:	ctg0954b.1:1570987..1574955 (- strand)												
Length:	3969												
Note:	best blast hit in Brachypodium distachyon: Bradi2g01420.1 59% identity 100% coverage best blast hit in Oryza sativa IRGSP: Os01g0119000 57% identity 96% coverage best blast hit in Oryza sativa TIGR: Os01g02930.1 57% identity 96% coverage												
dbxref:	GFF_source:EMBL												
genbankID:	Bradi2g01420.1 Os01g0119000 Os01g02930.1												
gene:	hga2												
product:	glycosyltransferase HGA-like putative expressed												
Parts:	<table border="1"> <tr><td>Type:</td><td>exon</td></tr> <tr><td>Description:</td><td></td></tr> <tr><td>Source:</td><td>EMBL</td></tr> <tr><td>Position:</td><td>ctg0954b.1:1570987..1572173 (- strand)</td></tr> <tr><td>Length:</td><td>1187</td></tr> <tr><td>dbxref:</td><td>GFF_source:EMBL</td></tr> </table>	Type:	exon	Description:		Source:	EMBL	Position:	ctg0954b.1:1570987..1572173 (- strand)	Length:	1187	dbxref:	GFF_source:EMBL
Type:	exon												
Description:													
Source:	EMBL												
Position:	ctg0954b.1:1570987..1572173 (- strand)												
Length:	1187												
dbxref:	GFF_source:EMBL												

cfp5041-cfp5090

cfp

```
>TAA_ctg0954b.00230.1 class=mRNA:EMBL position=ctg0954b.1:1570987..1574955 (- strand)
ATGGTCAGGG TCGACCGCAA GCAGCGGGGG CGGGGGAAAGGG GCTGTGCTG GGGGACTGTTG CGCAGAGGCA
CCTCAACCTG TGCTGCTCG CGGGTTCT CTCACCTAC TCGTGTCTC CCAGCAGTTC GCGGTCAACCT
CCCCCGCTGG TAGTACTAG TAGCGGGTTG ATTCGATCAC CCAACCAAAC TACACTCTCC TCCCTCCCTC CCTCACTCGC
CGCCCGCAC CGCTCATTC GTCACTGTTG ATCTGAGCT GTCCCCACGA CGACGACGCA CAGGAAGCAT CAGGCAGTCA
AGTCCCCCGG CGCCCGCGAA GCAGGTGAGC ACCCATCGCC ATCCCTGCC CTGCAATTCT CTGTCATT TCAACTACTC
TTCGACTTCG TTCTGTTCCAT CGACATTGAT GCCGCACTAC CCCGGCTTC GCCGGGGCCC GGCGCCGGGG TGGTGAAGAAG
AAAGAAAAAG AACACAATTAA AGTCAACCTG TTATTGGAA GCAGTGAGG GTGCTCTCT GACTCTGACT CATCGAATCA
TGACTAAATT GACTAGGT AGGATTAACG CAAGGGGATC GAGGAGGAGA GGGGAAGGGG GAGGCCAAT CAGCTCAAGA
GCAGCAGCAC GAGCAGCAC CGGGTAAGTA TAAACATCTT CTTTTTGCG CGCTAAATAT AAATACATCT CTCCTCTGT
CGGTGGCATG GTATGGACGG ATATGAGTGA CGAAAGGGCG CTGTTTTTT ACCAAAGCA GGCGCCCGGA AAGCAGAGGG
CGCGCGCGCG GGTGTGGGA AGAGAGACGA CGACGGTGC CGCAAGCCGT TCGGTATGTC CAATATTCT CCTCCCCCTA
ACTAAACTAC TCTAGTATA CGAGATTAA TGTGATGAGA TGACGCATT TATTCCTGCT ACTTTAGAA AATATATACA
```

0 100% identity 100%

coverage

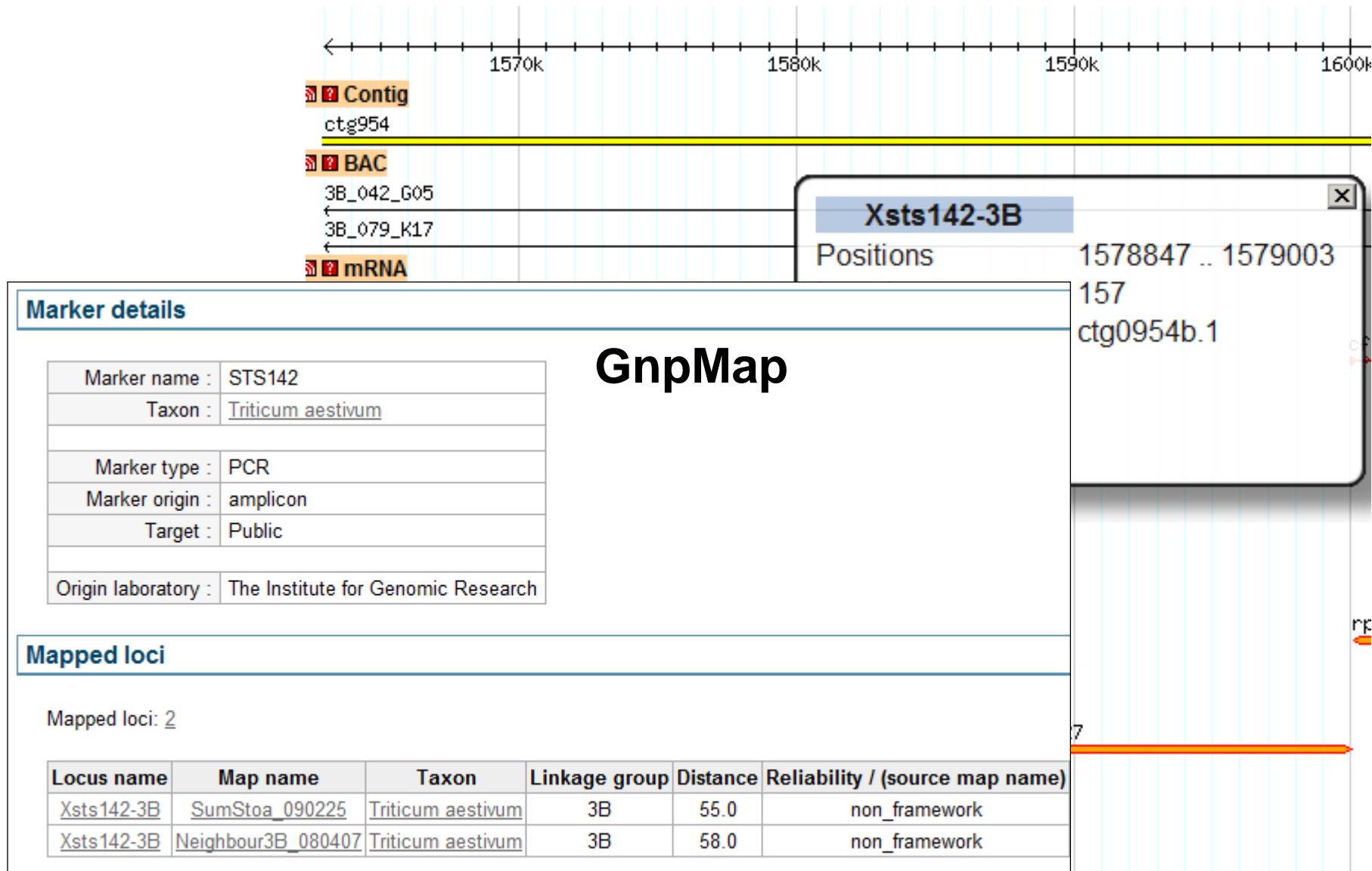
Bradi2g01420.1 Os01g0119000 Os01g02930.1

ctg0954b.1

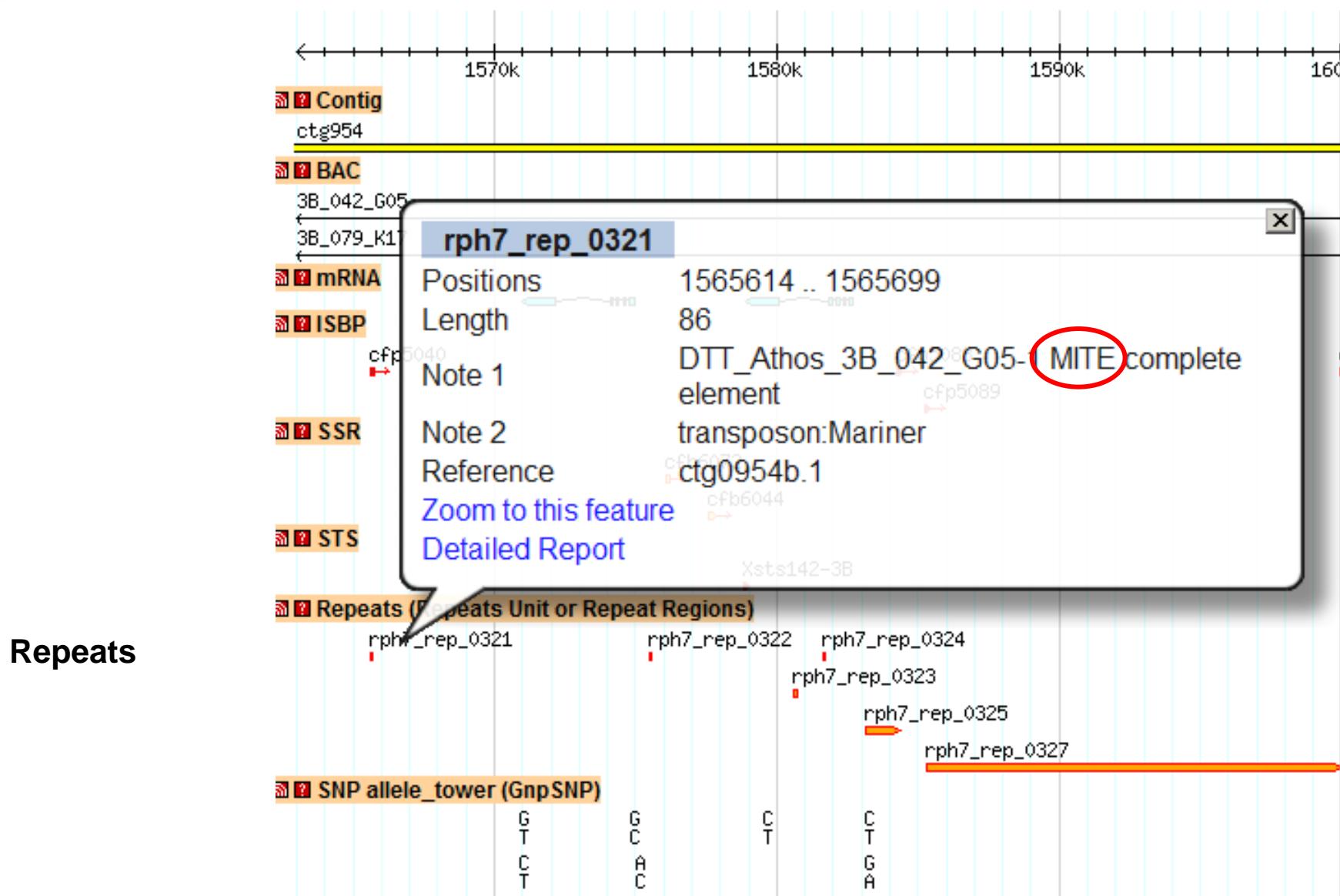
Zoom to this feature

Detailed Report

Wheat annotation viewer



Wheat annotation viewer



Repeats

Wheat annotation viewer

SNP details

Name : Tae_1272275
Source : GnpSNP

Internal references

Database : Wheat 3B annotation (FHB)	Reference name : SNP name	Reference value : Tae_1272275
--------------------------------------	---------------------------	-------------------------------

SNP complements

SNP type : SNP
Variation : G/T
Linked with variations : INRA_CF_AS_P_662_BT001
Linked with lines : A4

SNP sequences

5' flanker on ref.seq. : >Tae_1272275-5' aacatggggCtccggtaacctcgagttacagcatcncggtgaggagagcacgctgtgganacgcgtggggCcnngaccaccc cgccatcaaggancngattcngtccaccggagcggnntggacaaggtcGcngagtnctacctngcaagcagaacgtgc gcgtcgacgtcgaaagggttcgcgcgacgCtcgcgtngcgctnaccatctccggcgnnnantagttangttacatgc cngtgagggA
3' flanker on ref.seq. : >Tae_1272275-3' gacgacacagaccgttgtacatccgttagctgcaaaggagttcacatttccctttgagtatatata
Genomic context on ref. seq. : >Tae_1272275-genomic_context aacatggggCtccggtaacctcgagttacagcatcncggtgaggagagcacgctgtgganacgcgtggggCcnngaccaccc cgccatcaaggancngattcngtccaccggagcggnntggacaaggtcGcngagtnctacctngcaagcagaacgtgc gcgtcgacgtcgaaagggttcgcgcgacgCtcgcgtngcgctnaccatctccggcgnnnantagttangttacatgc cngtgagggA[G/T] gacgacacagaccgttgtacatccgttagctgcaaaggagttcacatttccctttgagtata tatga

GnpSNP

Internal references

Database : Wheat 3B annotation (FHB)	Reference name : SNP name	Reference value : Tae_1272275
--------------------------------------	---------------------------	-------------------------------

SNP complements

SNP type : SNP
Variation : G/T
Linked with variations : INRA_CF_AS_P_662_BT001
Linked with lines : A4

SNP sequences

5' flanker on ref.seq. : >Tae_1272275-5' aacatggggCtccggtaacctcgagttacagcatcncggtgaggagagcacgctgtgganacgcgtggggCcnngaccaccc cgccatcaaggancngattcngtccaccggagcggnntggacaaggtcGcngagtnctacctngcaagcagaacgtgc gcgtcgacgtcgaaagggttcgcgcgacgCtcgcgtngcgctnaccatctccggcgnnnantagttangttacatgc cngtgagggA
3' flanker on ref.seq. : >Tae_1272275-3' gacgacacagaccgttgtacatccgttagctgcaaaggagttcacatttccctttgagtatatata
Genomic context on ref. seq. : >Tae_1272275-genomic_context aacatggggCtccggtaacctcgagttacagcatcncggtgaggagagcacgctgtgganacgcgtggggCcnngaccaccc cgccatcaaggancngattcngtccaccggagcggnntggacaaggtcGcngagtnctacctngcaagcagaacgtgc gcgtcgacgtcgaaagggttcgcgcgacgCtcgcgtngcgctnaccatctccggcgnnnantagttangttacatgc cngtgagggA[G/T] gacgacacagaccgttgtacatccgttagctgcaaaggagttcacatttccctttgagtata tatga

SNP

Wheat annotation viewer

Identification

Accession number :	748
Accession name :	A.4
Synonyms :	-
subspecies :	<u>Triticum aestivum aestivum</u>
Pedigree :	-
Biological status :	Breeding/research material
Comment :	-

Distribution

Presence status : Maintained

Available :  Yes

Distributor(s) : UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont

Siregal

Origin

- Geographical origin : Afghanistan
- Donated :

Donor institution :	<u>Unité expérimentale du Magneraud, GEVES</u>
Donation date :	-
Original number :	-

- Holding institution : UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont

Collections

Part of : WHEAT TRITIPOL COL
SOFT WHEAT CORE COL
WHEAT INRA COL

Genotyping

This accession has been genotyped: see A4 in GnpSNP.



Evaluation data

-	Growth class	Hiver - Winter
- Days to heading (Counted as days from sowing to 50% of panicles fully emerged)	142,812	
- Scale of days to heading	7	
- Plant height (cm)	130,906	
- Scale of plant height	8	
- Susceptibility to Puccinia recondita (Leaf rust) - Year 2001	0	
- Susceptibility to Puccinia striiformis f. sp. hordei (Yellow rust) - Year 2001	2	
- Scale of 1000 kernels weight	7	
- Wheat awnedness	5	

Genomic context on ref. seq.

gatgtacagcatcnccgtggaggagagcacgctgtgganacgcgtggggCcnngaccaccc
 gtcccacccggagcggnntggacaagggtcGcngagtnctacctngcaagcagaacgtgc
 gncgacgCtcgcgctngcgtcnaccatctccggcgnnnantagttangttacatgc



ttccgcgttagtgc当地aaaggagttcacatttcccttttgagtatatatga



ontext
 gatgtacagcatcnccgtggaggagagcacgctgtgganacgcgtggggCcnngaccaccc



Survey Sequence Repository



International Wheat Genome Sequencing Consortium

News and Reports Organization Projects Tools and Resources General Documents

[Home](#) / [Projects](#) / [IWGSC Bread Wheat Projects](#) / [Projects by chromosome](#) / Chromosome 3B

Projects

- > [IWGSC Bread Wheat Projects](#)
- > [Physical mapping](#)
- > [Sequencing](#)
- > [Projects by chromosome](#)
 - > [Chromosome 1A](#)
 - > [Chromosome 2A](#)
 - > [Chromosome 3A](#)
 - > [Chromosome 4A](#)
 - > [Chromosome 5A](#)
 - > [Chromosome 6A](#)
 - > [Chromosome 7A](#)
 - > [Chromosome 1B](#)
 - > [Chromosome 2B](#)
 - > [Chromosome 3B](#)
 - > [Chromosome 4B](#)
 - > [Chromosome 5B](#)
 - > [Chromosome 6B](#)
 - > [Chromosome 7B](#)
 - > [Chromosome 1D](#)
 - > [Chromosome 2D](#)
 - > [Chromosome 3D](#)
 - > [Chromosome 4D](#)
 - > [Chromosome 5D](#)
 - > [Chromosome 6D](#)
 - > [Chromosome 7D](#)
- > [IWGSC Ae. tauschii Projects](#)
- > [Positions available](#)

Chromosome 3B

Available data

[Access data for chromosome 3B at URGI Sequences Repository](#)

Projects

3B physical map

Project Leader: [Feuillet Catherine](#)

The 3B physical map has been constructed in two steps: The first map was obtained after 68'000 clones and assembling 56,952 high quality BAC fingerprints into contigs using the al., Science, 2008). The fin...

Sequencing chromosome 3B

Project Leader: [Feuillet Catherine](#)

The objectives of 3BSEQ are to: Sequence and annotate the whole chromosome 3B Under dynamics through comparative analyses with the other cereal genomes available Function gene space by establishing a...

Chromosome 3B survey sequence

Project Leader: [Feuillet Catherine](#)

In the framework of the 3BSEQ project, a 50x sequence is under production using Illumina reads) with paired end reads of 600bp on flow-sorted 3B chromosome . The reads will be mapped against the scaffolds...

Chromosome 3B survey sequence

Project Leader: [Feuillet Catherine](#)

Targeted chromosomes



Click on a chromosome to access associated data (when available) at URGI Sequences Repository.

Project team

First name	Last name	Email	Institution	Country
Frederic	Choulet	frederic.choulet@clermont.inra.fr	INRA GDEC	France
Etienne	Paux	etienne.paux@sancy.clermont.inra.fr	INRA GDEC	France
Philippe	Leroy	leroy@sancy.clermont.inra.fr	INRA GDEC	France
Patrick	Wincker	pwincker@genoscope.cns.fr	Genoscope	France
Michael	Alaux	michael.alaux@versailles.inra.fr	INRA URG1	France
Hadi	Quesneville	Hadi.Quesneville@versailles.inra.fr	INRA URG1	France

Project collaborators

First name	Last name	Email	Institution	Country
Jaroslav	Dolezel	dolezel@ueb.cas.cz	IEB Olomouc	Czech Republic

Chromosome 3B Survey Sequence

Project Leader: [Feuillet Catherine](#)
 In the framework of the 3BSEQ project, a 50x sequence is under production using Illumina reads) with paired end reads of 600bp on flow-sorted 3B chromosome . The reads will be mapped against the scaffolds...

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat/Sequence-Repository>



URGI Wheat dataflow overview at URGI

Species

- Vitis
- Wheat**
- Sequence Repository
- Projects
- Data
- Tools
- Deletion Bins
- Publications
- Links

Botryos

- Lily
- Moss
- Yarrow
- Wormwood

Arabidopsis

Oryza

Populus

Maize

Medicago

Pisum

Flax

You are here : Home / Species / Wheat

Wheat Portal

Very develop Wheat genomics?

New portal currently in development

No one can be a statesman who is entirely ignorant of the problems of wheat (Desiderius, 470-398BC).

Today, agriculturists, facing one of the greatest challenges of our time, began 10 000 years ago, that of producing enough food to sustain a growing population. This is a task which requires a deep knowledge of the structure and function of the plant, and the ability to breed new varieties. By developing state-of-the-art molecular tools, plant breeders and breeders will be able to accelerate wheat improvement to meet the challenges of the 21st century. The INRA is committed to ensuring that the sequence of the wheat genome is available to all scientists and breeders around the world.

The European Union has allocated €100 million for the development of the first phase of the International Wheat Genome Sequencing Project. This is the largest international research project ever undertaken by the EU. The INRA is leading the work on wheat, and is working with other European partners to ensure that the results of the project are available to all scientists and breeders around the world.

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http://urgi.versailles.inra.fr/Species/Wheat

URGI

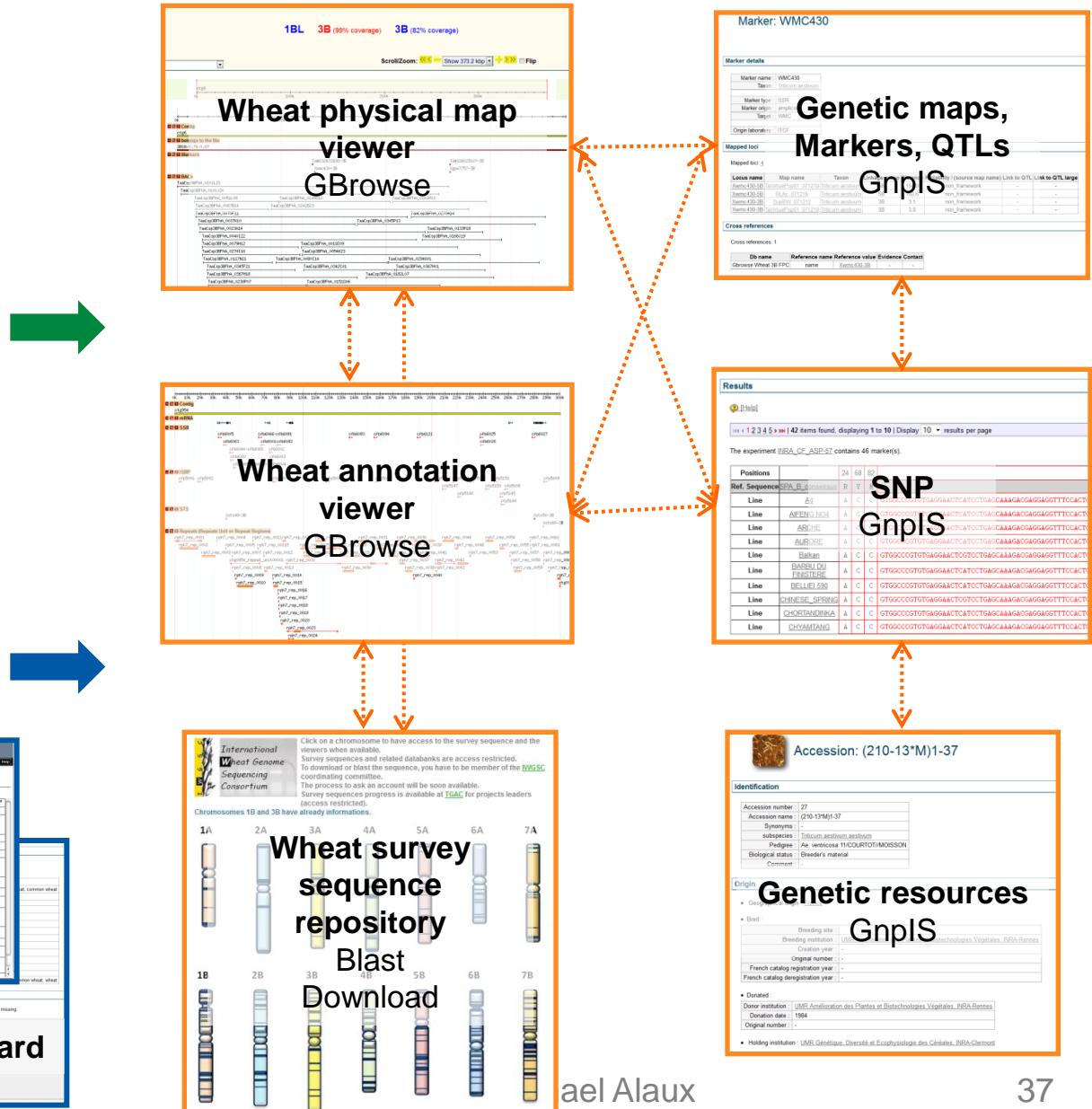
Wheat dataflow overview at URGI

Results

Quicksearch
Google-like

Advanced search
BioMart

Taxon card



Perspectives



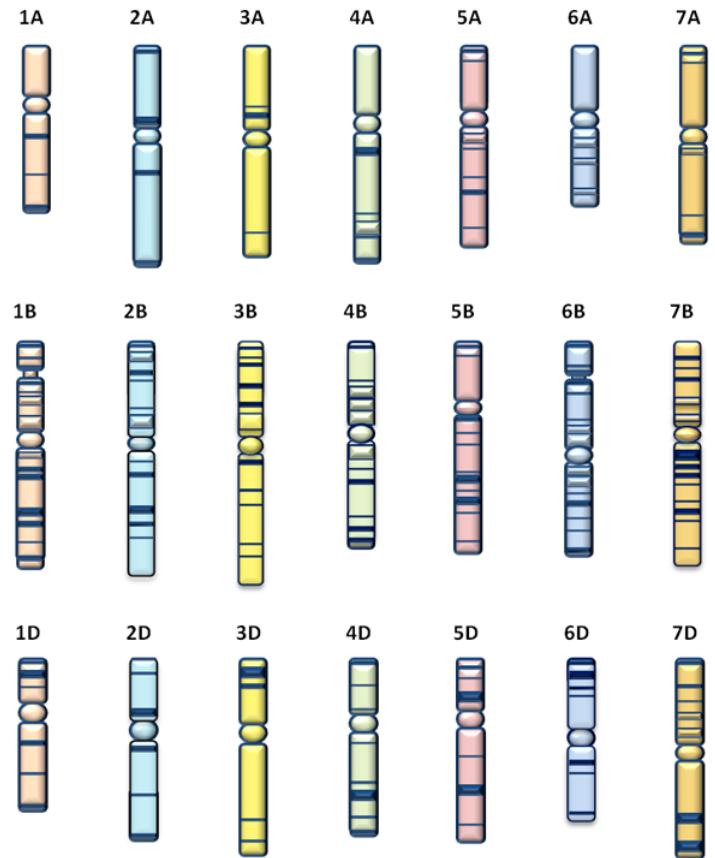
Survey Sequence Repository



Click on a chromosome to have access to the survey sequence and the viewers when available.
The process to have access to the download and blast is explained [here](#).
Survey sequence assemblies progress is available at [TGAC](#) (restricted access). About Blast, you could select one or multiple chromosomes arms on step 3 in the "WHEAT sequence survey databases (restricted to IWGSC)" section and set the search options (evaluate, max results) on step 4.

-- BLAST is now available for BLAST ONLY account too.

-- [Talk at PAG XX](#) at the IWGSC Standard and protocol session Tuesday



Last survey sequence assemblies will be available in few weeks.

FAQ will be added to help the people to perform their Blast analysis.

<http://urgi.versailles.inra.fr/Species/Wheat/Sequence-Repository>

Wheat physical map viewer v4

Wheat physical map viewer v4.0: 381.6 kbp from ctg6:1..381,601

Chromosomes :

1AS * **1BL** **3B** (99% coverage) **3B** (82% coverage) **3DS ***

* : Registered access

Browser Select Tracks Custom Tracks Preferences

■ Search

Landmark or Region:

ctg6:1..381,601

Data Source

Wheat physical map viewer v4.0

Scroll/Zoom: Show 381.6 kbp

Flip

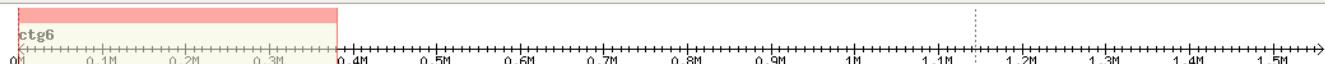
Examples :

For 3B (82% coverage): ctg1 ctg1:1..500000 ctg954 Xgwm264-3B 3B_039_H02

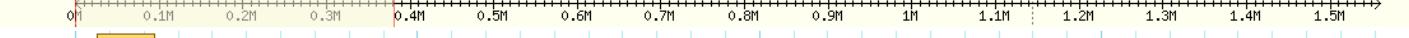
For 3B (99% coverage): ctg6 ctg1720 TaaCsp3BFhA_0100L17 Xwmc430-3B Xgwm264-3B

For 1BL : ctg2622 wmc419

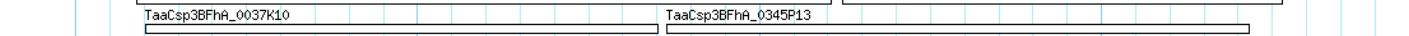
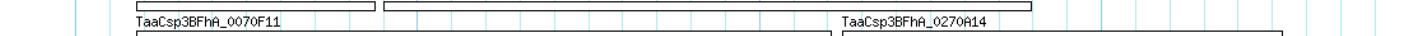
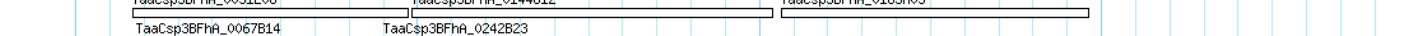
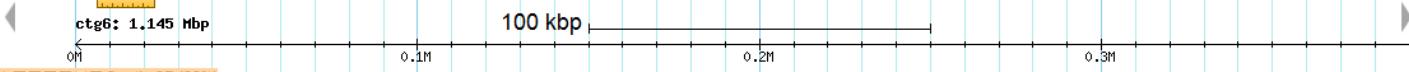
■ Overview



■ Region



■ Details

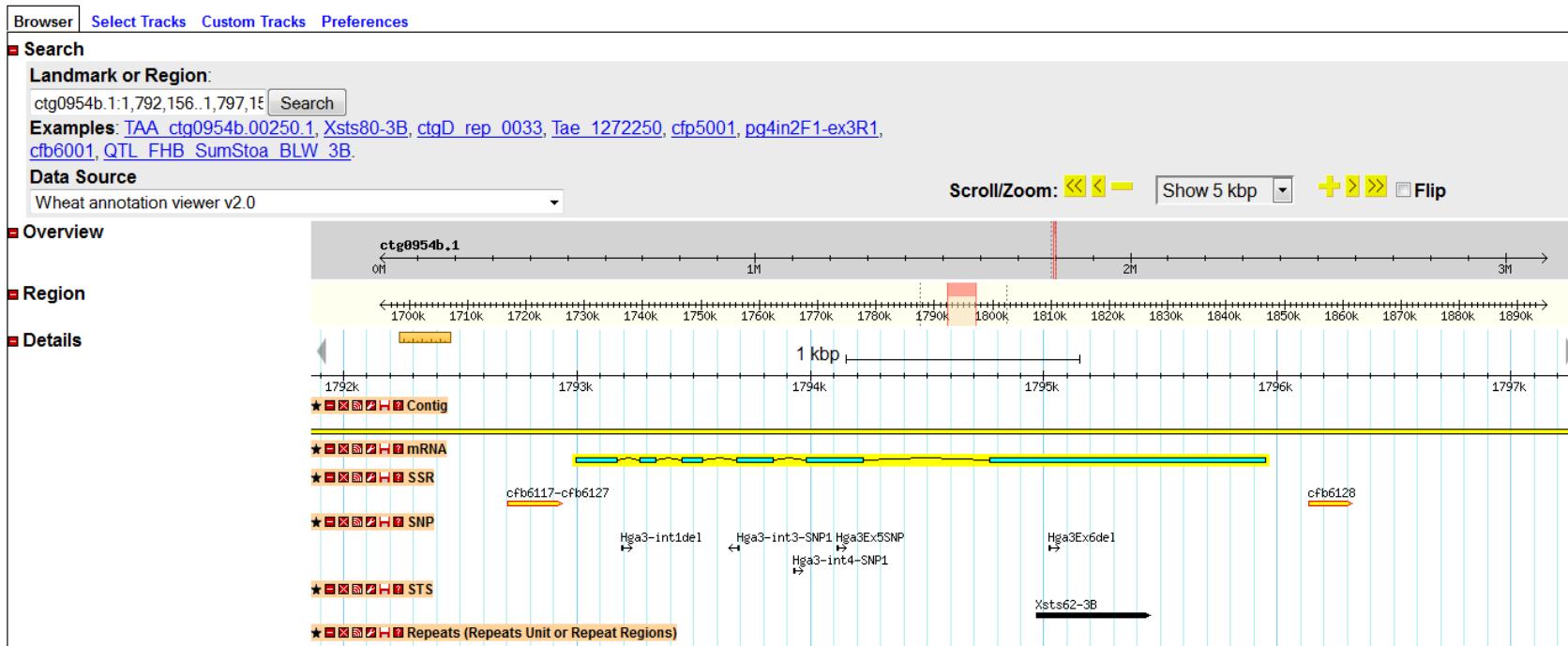


Wheat annotation viewer v2

- Use GBrowse 2: faster and smoother interface

Wheat annotation viewer v2.0: 4.999 kbp from ctg0954b.1:1,792,156..1,797,155

[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](#)



- 3B automatic annotations (Triannot pipeline) soon available

URGI New Wheat Portal in development

The screenshot shows the homepage of the URGI New Wheat Portal. At the top, there's a navigation bar with links for FEEDBACK, CONTACT, SITE MAP, REGISTER, PROJECTS, DATA, TOOLS, SEQ REPOSITORY, ABOUT US, and WHAT'S NEW?. A large orange header features the URGI logo and a wheat ear graphic. Below the header, a central feature is a circular diagram of a wheat ear with various genomic resources listed around it: Sequence survey, Physical maps, Annotations, Deletion bins, Genetic maps, QTL, Markers, SNP, EST, and Genetic resources. To the left, a "QUICK SEARCH" box contains a search field with "VVIF52" and a "SUBMIT" button. Below the search box, there's a note about indexed databases and examples like VV1*, VVIF52, gene, arabidopsis, AY109603, Xcfe107-3B. The bottom section is divided into EVENT & PUBLICATIONS and WHAT'S NEW? sections. The EVENT & PUBLICATIONS section lists events for June 30th, 16th, and 2nd. The WHAT'S NEW? section lists updates from May 19th, 19th, 15th, and 12th, along with an RSS feed link.

FEEDBACK | CONTACT | SITE MAP

REGISTER

PROJECTS DATA TOOLS SEQ REPOSITORY ABOUT US

WHAT'S NEW ? RSS

Sequence survey

Physical maps

Annotations

Deletion bins

Genetic maps

QTL

Markers

SNP

EST

Genetic resources

QUICK SEARCH

VVIF52

You can found the indexed databases list [here](#)
Examples : VV1*, VVIF52, [gene](#), [arabidopsis](#),
AY109603, [Xcfe107-3B](#)

EVENT & PUBLICATIONS RSS

June 30th 2009
Steering committee : The next steering committee for Siregal and Ephesis projects is organized at URGI

June 16th 2009
[Siregal project CSU](#) : The next CSU (Comité Scientifique des Utilisateurs) for Siregal project is organized at INRA Avignon center

June 2nd 2009
URGI platform CSU : The next CSU (Comité Scientifique des Utilisateurs) is organized at Ivry-sur-Seine. URGI will present to users (at least one person per species, thematic and main project in collaboration) the platform activity and its projects report..

May 19th and 29 2009
[Training to LabKey software](#) : Doriane company organize a training to LabKey software, opened to Siregal, Ephesis and CRB users.

May 12th 2009
[Ephesis project CSU](#) : The next CSU for Ephesis project is organized.

May 19th 2009
New poplar genetic maps : Available in [GnpMap](#) (restricted to Poplar community (INRA Evry, Orleans), Collab V. Jorge and for interoperability GnpIntegr project)

May 19th 2009
6 new grape genetic maps : Available in [GnpMap](#) (restricted to Grape community, collab N. Choisne & A.A. Blondin for GrapeSeq and interoperability projects)

May 19th 2009
[New tools list](#) : The new softwares list presents analysis tools on our public and secure servers

May 15th 2009
URGI activity : The GnpIS databases surveys sent to INRA DSPPV (Direction Scientifique Plantes et Produits du Végétal)

May 15th 2009
[GnpGenome](#) : The poplar genome release 1, developed in the framework of ANR GnpIntegr and interoperability projects, is available on our secure server, collab I. Bourgat & V. Jorge (INRA Orléans), P. Faivre-Rampant (INRA Evry) for ANR GnpIntegr and interoperability projects

[Training sessions](#) on URGI's tools
> EST
> SNP
> REPET *New*
> GMOD

[MORE... >](#) [MORE... >](#)

Take-Home Message

Survey Sequence Repository

<http://urgi.versailles.inra.fr/Species/Wheat/Sequence-Repository>

Ask an account

<http://www.wheatgenome.org/Tools-and-Resources>

New dedicated wheat portal in development at URGI

Contact me at michael.alaux@versailles.inra.fr

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URGI

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Questions

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