



User Training Workshop: GnplS tool training session

**Survey sequence, physical map
integrated to GnplS**

Michael Alaux

Wheat website @ URGI



Wheat website

Wheat

Sequence Repository

Projects

Data

Tools

Triannot Pipeline

Deletion Bins

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PLANT AND FUNGI DATA INTEGRATION

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Platform | Research | Projects | Data | Tools | Species | SEARCH OK

 CJW Newsletter Article     ?

Species

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Botrytis

Leptosphaeria

Microbotryum

Venturia

Arabidopsis

Oryza

Populus

Maize

Medicago

Pisum

Flax

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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 website

Wheat

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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 website

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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 | | |

Wheat website

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Public data

| | |
|--------------------------------|--------|
| Genetic maps | 26 |
| Physical maps | 3 |
| Reference sequence chromosomes | 1 |
| Survey sequence chromosomes | 21 |
| QTL | 324 |
| Markers | 19029 |
| Accessions | 2245 |
| SNP | 10819 |
| EST | 544529 |

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

Wheat website

Wheat

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free access tool



registered access tool

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

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

Wheat website

Wheat

Sequence Repository

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Data

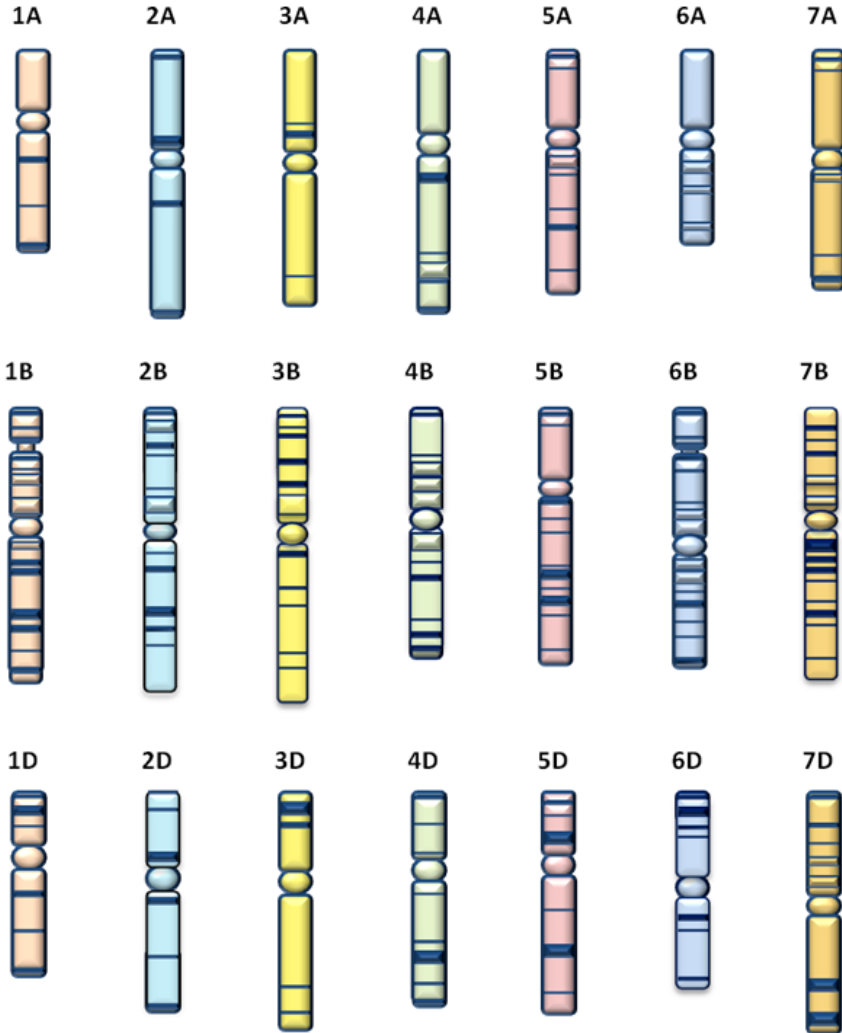
Tools

Triannot Pipeline

Deletion Bins

Publications

Links



Survey Sequence & Physical maps



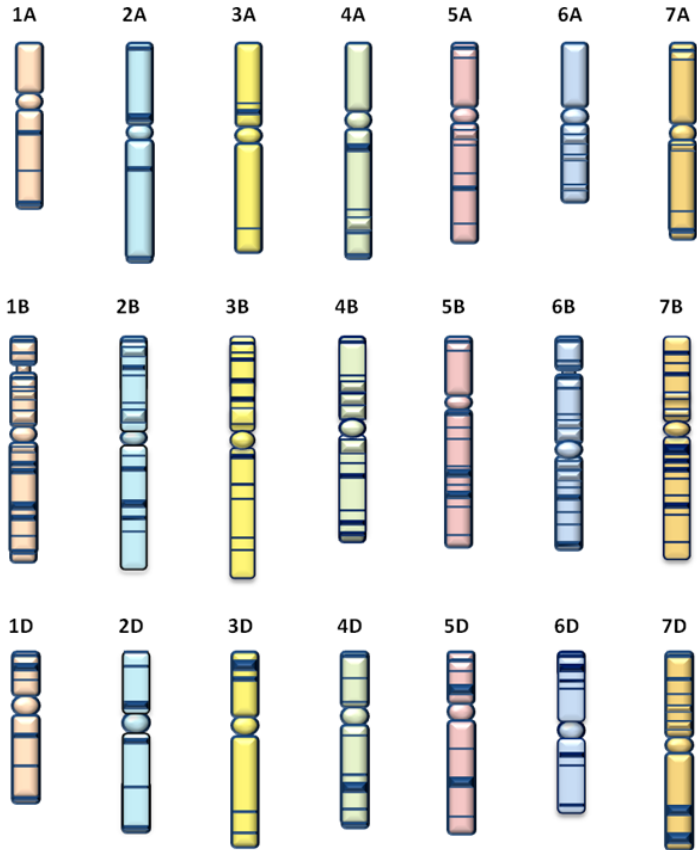
Survey Sequence Repository



International
Wheat Genome
Sequencing
Consortium

Click on a chromosome to access the survey sequence and the viewers.

- **Process** to create an account to access the download and BLAST.
- **BLAST** direct link (registered access).
- **FAQ** section.
- **News:** All chromosomes are now available for download and BLAST.



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

- **BLAST** search (*Blast agreement*)
- **Download** (*Data agreement*)
- **Viewers:** physical map, annotations when available

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

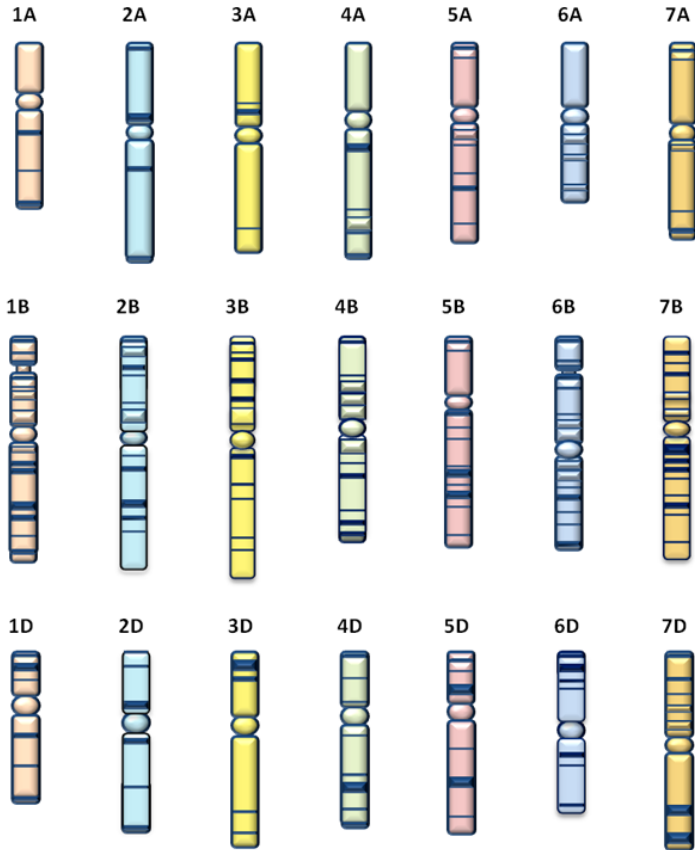
Survey Sequence Repository



International
Wheat Genome
Sequencing
Consortium

Click on a chromosome to access the survey sequence and the viewers.

- **Process** to create an account to access the download and BLAST.
- **BLAST** direct link (registered access).
- **FAQ** section.
- **News:** All chromosomes are now available for download and BLAST.



News:

- It is possible to **download contigs** from a BLAST result.

<http://urgi.versailles.inra.fr/srs83/displayTool.do?toolName=BlastN>

- **FAQ** section

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

- Download preliminary genome **zipper** (MIPS)

- **BLAST Demo Video**

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

Survey Sequence Repository

Account creation process is detailed on the IWGSC website:

<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.

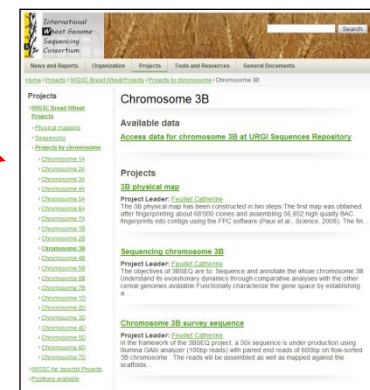
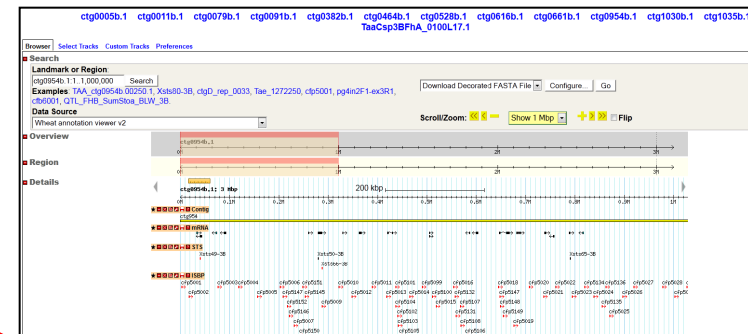
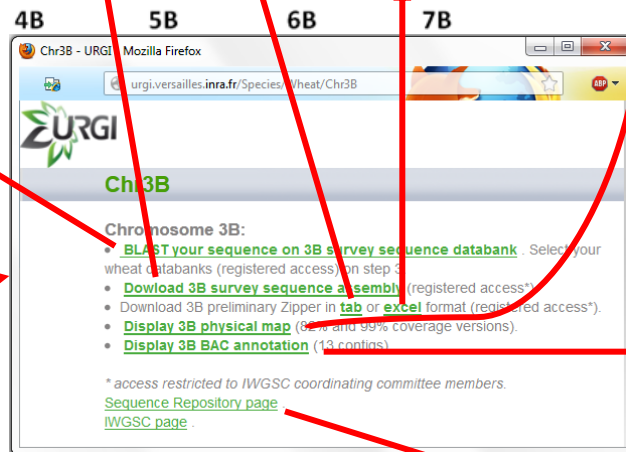
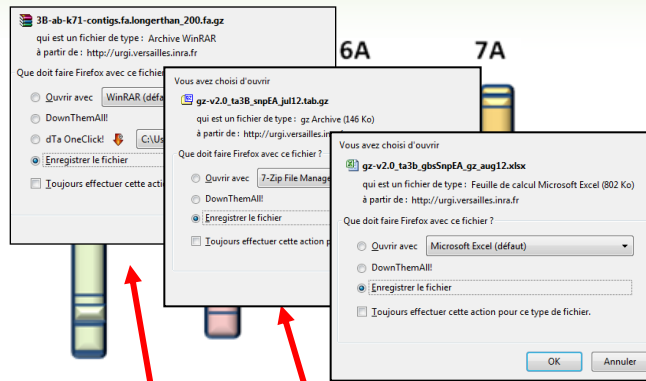
For Coordinating Committee members and their team members to gain full access, please sign-in to your IWGSC account and then agree to the [IWGSC Data Release Statement of Agreement](#). If you are not already a member of the IWGSC, you may register by clicking the "register" link at the top of any page 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](#).



[illegible]

Survey Sequence Repository

Step 1 : Data Source ?

☒ Upload from file :

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

Step 2 : Launch Options

Views:

Parameter Sets:

☐ Save my settings as a parameter set

You may continue tool settings below

Step 3 : Tool Settings

? Database to search:

Currently Selected : None, please select database from below

☒ WHEAT sequence survey databases (restricted to IWGSC)

| | | |
|-------------------------------------|----------------------------------|----------------------------------|
| <input type="checkbox"/> chr 1AL_v2 | <input type="checkbox"/> chr 1AS | <input type="checkbox"/> chr 1BL |
| <input type="checkbox"/> chr 1BS | <input type="checkbox"/> chr 1DL | <input type="checkbox"/> chr 1DS |
| <input type="checkbox"/> chr 2AL | <input type="checkbox"/> chr 2AS | <input type="checkbox"/> chr 2BL |
| <input type="checkbox"/> chr 2BS | <input type="checkbox"/> chr 2DL | <input type="checkbox"/> chr 2DS |
| <input type="checkbox"/> chr 3AL | <input type="checkbox"/> chr 3AS | <input 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 4BL | <input type="checkbox"/> chr 4BS |
| <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 5BL | <input type="checkbox"/> chr 5BS |
| <input type="checkbox"/> chr 5DL | <input type="checkbox"/> chr 5DS | <input type="checkbox"/> chr 6AL |
| <input type="checkbox"/> chr 6AS | <input type="checkbox"/> chr 6BL | <input type="checkbox"/> chr 6BS |
| <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 | |

Step 4 : (Optional) Advanced Settings

☐ Search Parameters

☒ Options to limit the number of results

| | |
|---|--|
| ? The E value | <input type="text" value="10.000000"/> |
| ? Number of hits and alignments to show | <input type="text" value="50"/> |
| ? Use Best-Hits filtering algorithm: | <input type="checkbox"/> |
| ? Best Hits algorithm overhang value: | <input type="text" value="0.100000"/> |
| ? Best Hits algorithm score edge: | <input type="text" value="0.100000"/> |
| ? Culling Limit: | <input type="text"/> |
| ? Minimum identity percentage: | <input type="text"/> |

☐ Advanced HSP Extension Options

☐ Query Filtering Options

☐ Save my settings as a parameter set

Survey Sequence Repository

Step 1 : Data Source ?

☒ Upload from file : C:\Users\malaux\Downloads\bac Parcourir...

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

Step 2 : Launch Options

Views: HomologyView

Parameter Sets: Default

☐ Save my settings as a parameter set

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

Step 3 : Tool Settings

Database to search:

Currently Selected : chr 1AS
chr 1BL

☒ WHEAT sequence survey databases (restricted to IWGSC)

| | | |
|-------------------------------------|---|---|
| <input type="checkbox"/> chr 1AL_v2 | <input checked="" type="checkbox"/> chr 1AS | <input checked="" type="checkbox"/> chr 1BL |
| <input type="checkbox"/> chr 1BS | <input type="checkbox"/> chr 1DL | <input type="checkbox"/> chr 1DS |
| <input type="checkbox"/> chr 2AL | <input type="checkbox"/> chr 2AS | <input type="checkbox"/> chr 2BL |
| <input type="checkbox"/> chr 2BS | <input type="checkbox"/> chr 2DL | <input type="checkbox"/> chr 2DS |
| <input type="checkbox"/> chr 3AL | <input type="checkbox"/> chr 3AS | <input 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 4BL | <input type="checkbox"/> chr 4BS |
| <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 5BL | <input type="checkbox"/> chr 5BS |
| <input type="checkbox"/> chr 5DL | <input type="checkbox"/> chr 5DS | <input type="checkbox"/> chr 6AL |
| <input type="checkbox"/> chr 6AS | <input type="checkbox"/> chr 6BL | <input type="checkbox"/> chr 6BS |
| <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 | |

Survey Sequence Repository

To speed up your Blast

Step 4 : (Optional) Advanced Settings ⊕ Expand All ⊖ Collapse All

⊕ Search Parameters

⊖ Options to limit the number of results

| | |
|---|--------------------------|
| ⓘ The E value | 0.001000 |
| ⓘ Number of hits and alignments to show | 25 |
| ⓘ Use Best-Hits filtering algorithm: | <input type="checkbox"/> |
| ⓘ Best Hits algorithm overhang value: | 0.100000 |
| ⓘ Best Hits algorithm score edge: | 0.100000 |
| ⓘ Culling Limit: | |
| ⓘ Minimum identity percentage: | |

⊕ Advanced HSP Extension Options

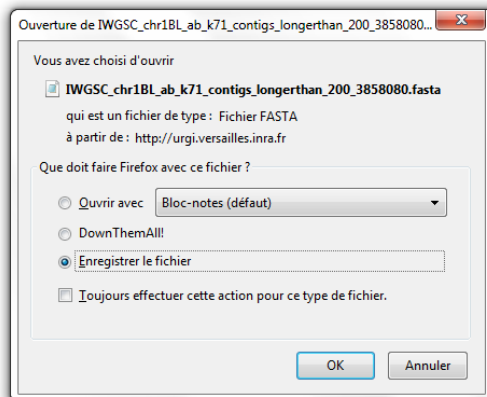
⊕ Query Filtering Options

☐ Save my settings as a parameter set

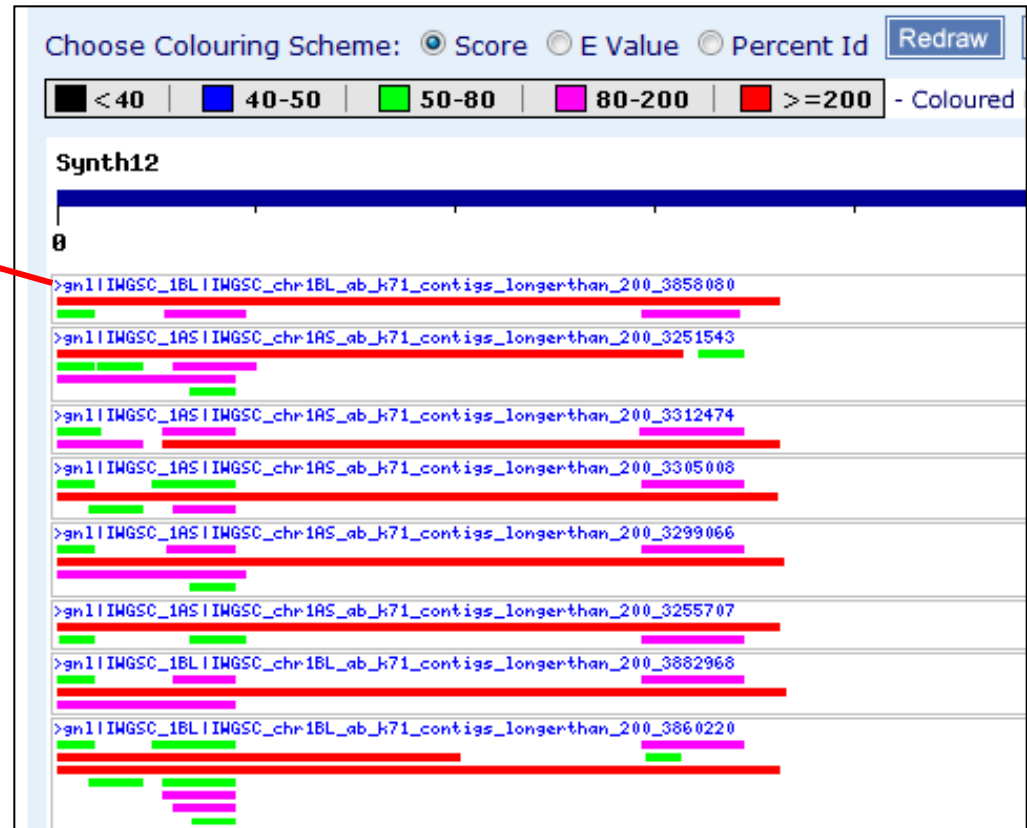
<http://urgi.versailles.inra.fr/Species/Wheat/Sequence-Repository>

Survey Sequence Repository

To download the contigs



Homology View (default view)

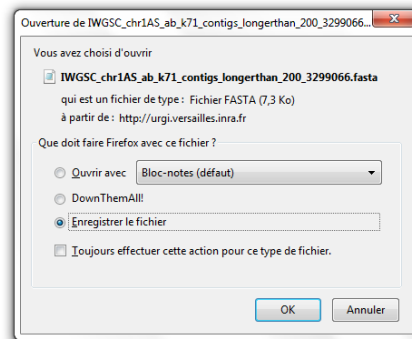


Survey Sequence Repository

To download the contigs

Blast View

| Primary Search | Query | Database | Hit | Description | Top Score | E value | Percentage Identity | Match Length |
|-------------------------------------|---------|-----------|--|-------------|-----------|---------|---------------------|--------------|
| BLASTN:temp_job19_1 | Synth12 | IWGSC_1BL | >gnl IWGSC_1BL IWGSC chr1BL_ab k71 contigs longerthan 200 3858080 | | 769 | 0.0 | 84 | 722 |
| BLASTN:temp_job19_2 | Synth12 | IWGSC_1AS | >gnl IWGSC_1AS IWGSC chr1AS_ab k71 contigs longerthan 200 3251543 | | 762 | 0.0 | 87 | 624 |
| BLASTN:temp_job19_3 | Synth12 | IWGSC_1AS | >gnl IWGSC_1AS IWGSC chr1AS_ab k71 contigs longerthan 200 3312474 | | 733 | 0.0 | 87 | 616 |
| BLASTN:temp_job19_4 | Synth12 | IWGSC_1AS | >gnl IWGSC_1AS IWGSC chr1AS_ab k71 contigs longerthan 200 3305008 | | 708 | 0.0 | 83 | 720 |
| BLASTN:temp_job19_5 | Synth12 | IWGSC_1AS | >gnl IWGSC_1AS IWGSC chr1AS_ab k71 contigs longerthan 200 3299066 | | 700 | 0.0 | 80 | 726 |



Survey Sequence Repository

To launch TBlastX or other tools

The screenshot displays the Biowisdom SRS web interface. At the top left is the 'biowisdom SRS' logo. A search bar with the text 'Find' and a 'Go' button is located at the top right. Below the search bar, the text 'malaux logged in | Start permanent session' is visible. A 'my SRS' button is also present. The main content area is titled 'Tool Launch : BlastN'. Underneath, 'Step 1 : Data Source' is shown with two options: 'Upload from file : C:\Users\malaux\Doc...' and 'Paste/Create your own sequence(s) or t...'. A central 'Analysis Tools' dropdown menu is open, showing a list of tools. The 'Quick Launch' tab is selected. The list of tools includes: TBlastX, SpitterN, SplitterP, StretcherN, StretcherP, SupermatcherN, SupermatcherP, Syco, TBlastN, TBlastX (highlighted), TFastA, TFastX, TFastY, Tcode, Tfscan, Tmap, Transeq, Trimest, TrimseqN, TrimseqP, UnionN, and UnionP.

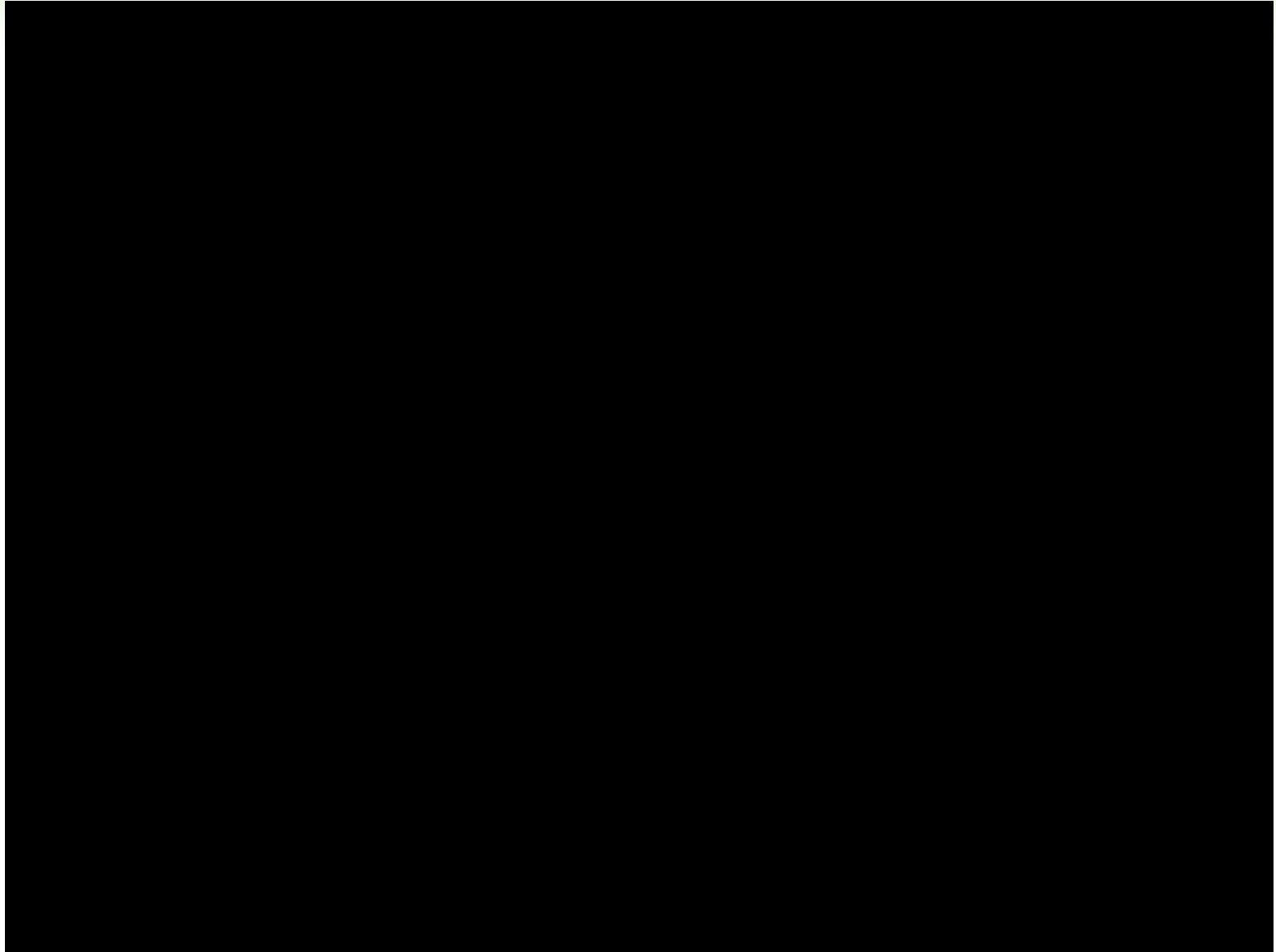
Analysis Tools

Quick Launch

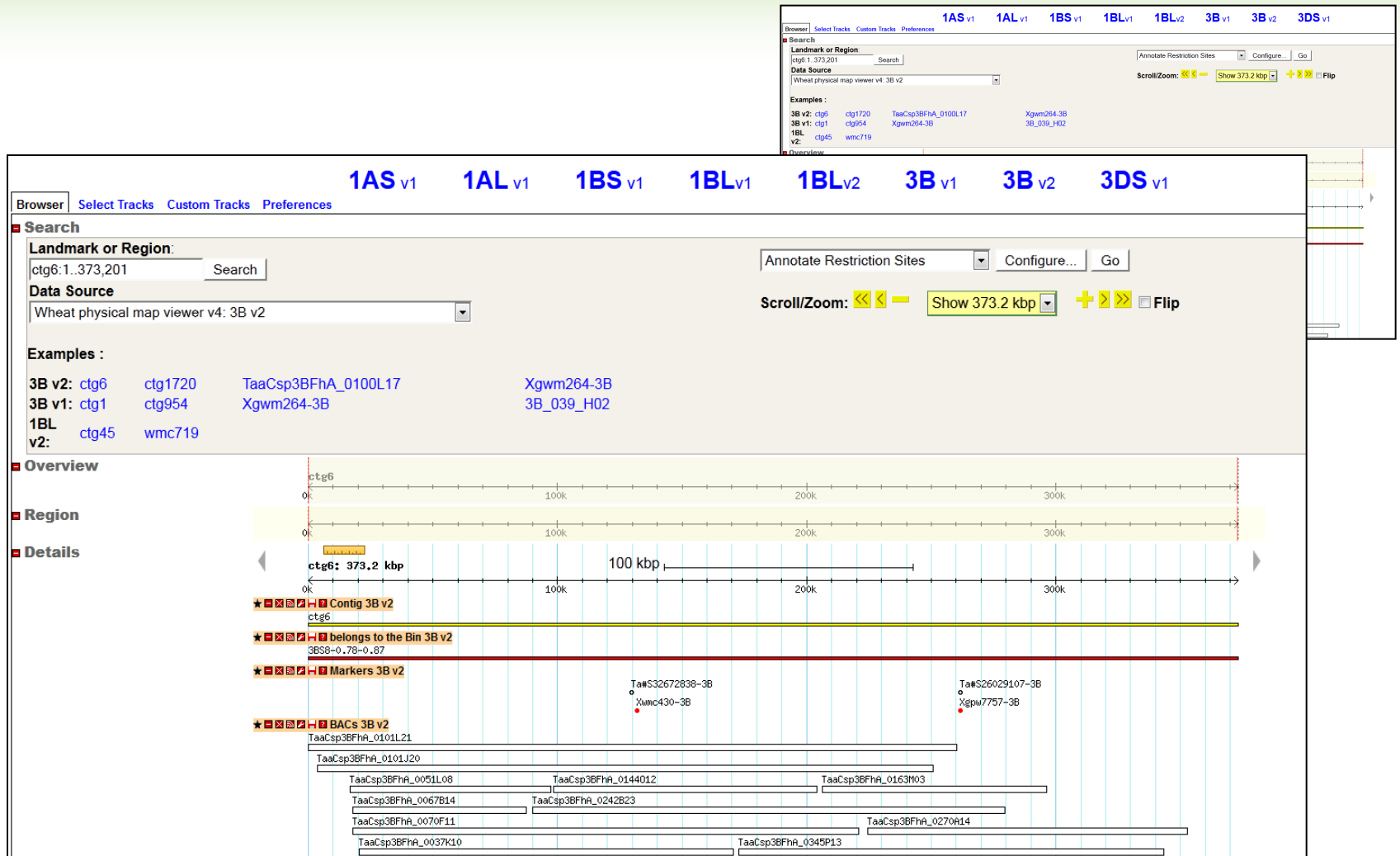
Launch analysis tool :

- TBlastX
- SpitterN
- SplitterP
- StretcherN
- StretcherP
- SupermatcherN
- SupermatcherP
- Syco
- TBlastN
- TBlastX**
- TFastA
- TFastX
- TFastY
- Tcode
- Tfscan
- Tmap
- Transeq
- Trimest
- TrimseqN
- TrimseqP
- UnionN
- UnionP

Demo Video



Survey Sequence Repository



http://urgi.versailles.inra.fr/gb2/gbrowse/wheat_phys_pub/

Wheat Physical Map Viewer

H B Contig 3B (99%)

ctg6

H B belongs to the Bin 3B (99%)

3BS8-0.78-0.87

H B Markers3B (99%)

Ta#S32672838-3B

3BS8-0.78-0.87

Source: FPC

Reference: ctg6

[Link to Deletion Bins Image](#)

H B BA

TaaCsp

TaaCs

Ta

TaaCsp3BFhA_0067B14

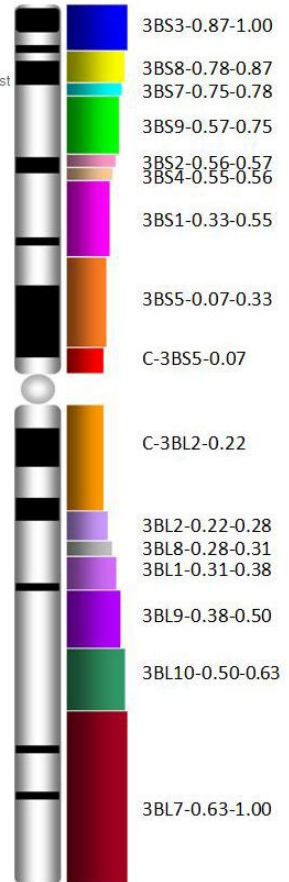
TaaCsp3BFhA_0232J05

TaaCsp3BFhA_0070F11

TaaCsp3

Deletion Bins

Click on a bin to display the contigs list in the physical map browser



Wheat Physical Map Viewer

H **3** Contig 3B (99%)

ctg6

H **3** belongs to the Bin 3B (99%)

3BS8-0.78-0.87

H **3** Markers3B (99%)

H **3** BACs 3B (99%)

TaaCsp3BFhA_0101L21

TaaCsp3BFhA_0101J20

TaaCsp3BFhA_0051L08

TaaCsp3BFhA_0067B14

TaaCsp3BFhA_0070F11

TaaCsp3BFhA

Position: 18001..2

Source: FPC

Reference: ctg6

Zoom to this feature

Detailed Report

| | |
|---------------|---------------------|
| Name: | TaaCsp3BFhA_0070F11 |
| Class: | BAC |
| Type: | BAC |
| Description: | |
| Source: | FPC |
| Position: | ctg6:18001..220801 |
| Length: | 202801 |
| Contig_hit: | "6" |
| Marker_hit: | Xwmc430-3B 0 0 |
| Name: | TaaCsp3BFhA_0070F11 |
| primary_id: | 24477 |
| gbrowse_dbid: | wheatFPC3B:database |

http://urgi.versailles.inra.fr/gb2/gbrowse/wheat_phys_pub/

Wheat Physical Map Viewer

MARKER DETAILS

| | |
|---------------------|----------------------|
| Marker name : | WMC430 |
| Taxon : | Triticum aestivum |
| Marker type : | SSR |
| Marker origin : | amplicon |
| Target : | WMC |
| Origin laboratory : | ITCF |
| Reverse primer : | TAGGGACCCCTTGACAAAAA |
| Forward primer : | TAGGGACCCCTTGACAAAAA |

MAPPED LOCI

Mapped loci: 4

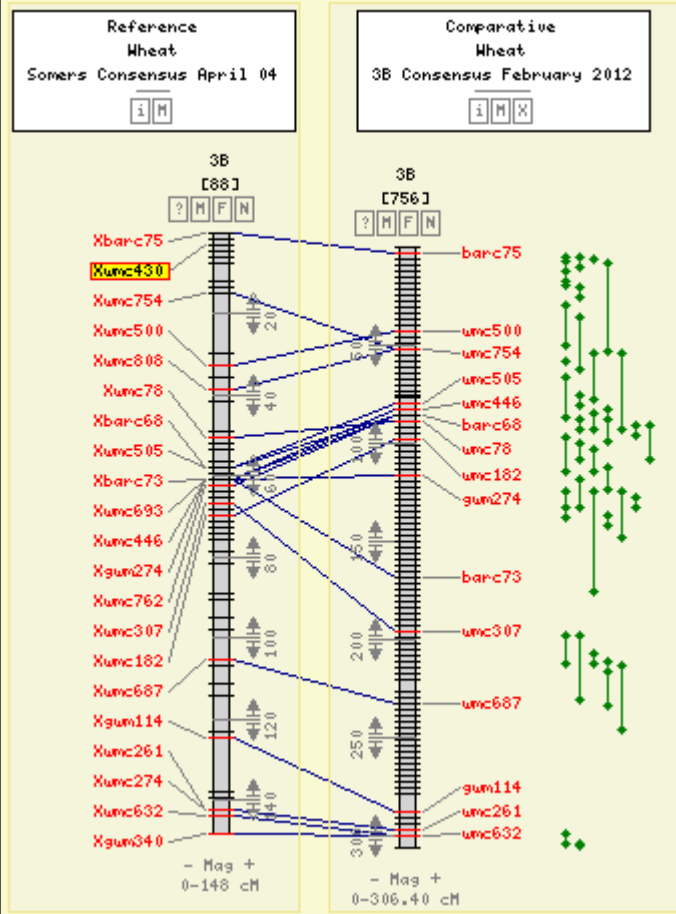
| Locus name | Map name | Taxon | Linkage group | Distance | Reliability / (source map name) |
|------------|-----------------------|-------------------|---------------|----------|---------------------------------|
| Xwmc430-5B | TaVirtualPop01_071219 | Triticum aestivum | 5B | 154.0 | non_framework |
| Xwmc430-5B | RLAc_071219 | Triticum aestivum | 5B | 162.6 | non_framework |
| Xwmc430-3B | SupBW_071212 | Triticum aestivum | 3B | 3.1 | non_framework |
| Xwmc430-3B | TaVirtualPop01_071219 | Triticum aestivum | 3B | 3.0 | non_framework |

CROSS REFERENCES

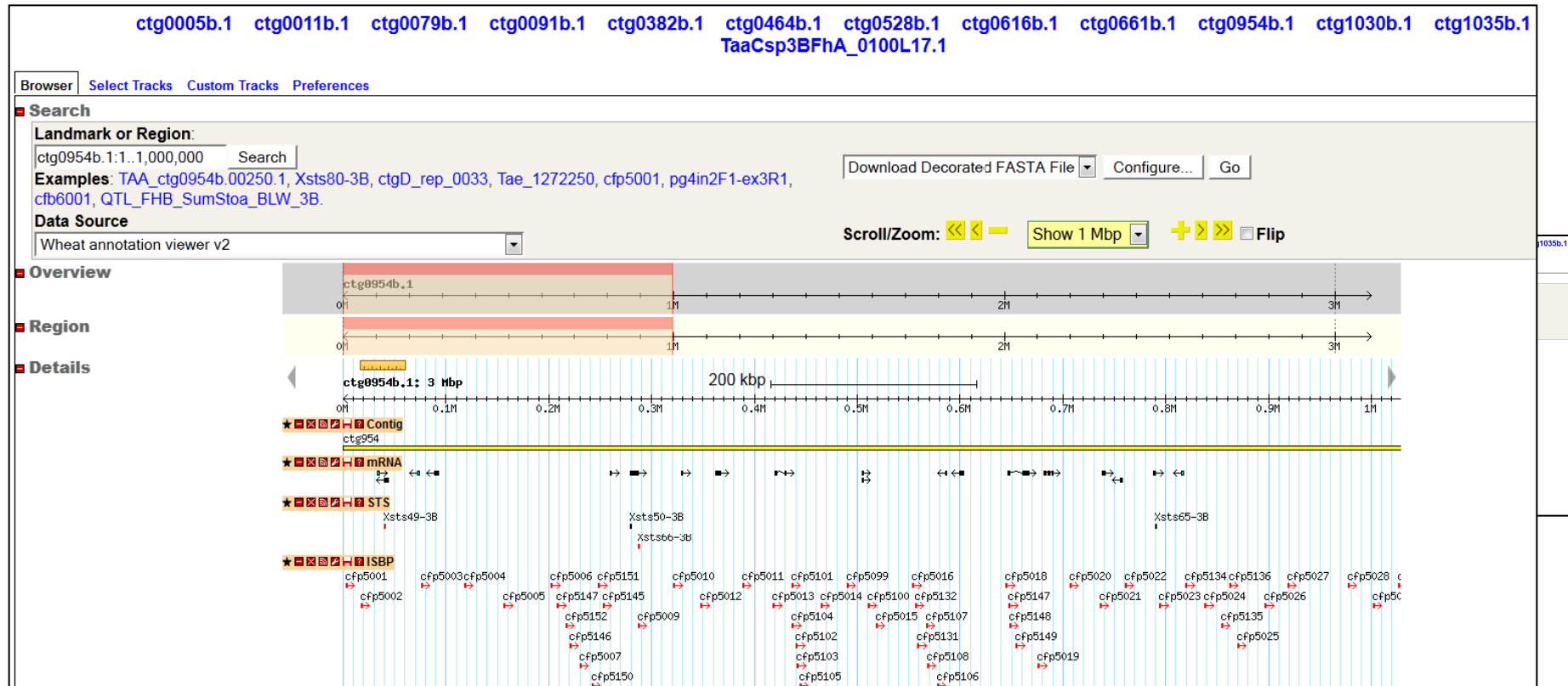
Cross references: 1

| Db name | Reference name | Reference value | Evidence |
|---------|----------------|-----------------|----------------------------------|
| WMC430 | SSR | Wheat | Framework Feb07 |
| Xwmc430 | SSR | Wheat | RL4452*AC Domain SO 05/08 |
| Xwmc430 | SSR | Wheat | Somers Consensus April 04 |
| Xwmc430 | SSR | Wheat | Somers Consensus April 04 |
| Xwmc430 | SSR | Wheat | Somers Grain Genes Consensus Map |
| Xwmc430 | SSR | Wheat | Somers Grain Genes Consensus Map |
| wmc430 | SSR | Wheat | 5B Consensus November 2011 |

Name: Xwmc430-3B
 Class: marker
 Type: marker
 Description:
 Source: FPC
 Position: ctg6:132001..132001



Survey Sequence Repository



http://urgi.versailles.inra.fr/gb2/gbrowse/wheat_3B_RPH7_pub/

Wheat Annotation Viewer

★ [icons] Contig

★ [icons] BAC

★ [icons] mRNA

★ [icons] STS

Xsts194-3B

★ [icons] SSR

★ [icons] ISBP

★ [icons] Repeats (Repeats Unit or Repeat Regions)

20

rph7_rep_0221

rph7_rep_02215

rph7_rep_0222

rph7_rep_0223

rph7_rep_0224

★ [icons] SNP allele_tower (GnpSNP)

Name: 3B_103_E15
Type: BAC
Description:
Source: EMBL
Position: ctg0954b.1:881492..1071583 (+ strand)
Length: 190092
dbxref: GFF_source:EMBL
primary_id: 1494
gbrowse_dbid:wheat3BRPH7:database

```
>3B_103_E15 class=Sequence position=ctg0954b.1:881492..1071583 (+ strand)
CCCCCCCCC CCGCGCTGCG AGCGCCCGCG ATCAGTCAGG CAGATGGCCT CCTCAAGCAT CTGGGCTTGC TTCTCCGCGT
CCATCTCTAG CTTCTCTCTT TGGATCTCCT TAAAGGCGTT CATTTGCTCC TCTTTAAACG CCGGCGCTCC TCCTCTCTTG
AGTCCTTCTT GTTCATCATG CCTTCCACGC TTGTGATCAA GCGGTTCAAT GCGGCATCCT GCTTGTCTCT CTTCITGGAG
TTGGTCTTCC CCGGTGCGCG AGCGGCTGCG CCGTCCCAAA CCCTCTCCAT GGCCTTCTTT CCGGCGGTGA CTGAGGCGCG
GCATATTGCG CTTTGAACCT CTCTCATCT TTGATGACCC TATAGCAATG GGAGAGGTTG AAGCACTTGC CGTTGTGTTG
GACATTGAAT GCCTCCAAAG CTTGAAATGC CTACAAATGT TTTGATGCAA GCATGTTGCG ACAAAATGGA TGCAAATGAA
CACGCAAGCA TGAACCTGAT GACACAAAAG AGGGCGGCTT ACTACCATAC CATGTCTTGC ATGTCAATGC CACTCACGGG
ACGGGCGCTT ACCTCTCTCA GAGTGCGACA AAACCTTGCG CACTCTTATT GGATCATCTT CCATCGCTTC GAAATGGACA
CCCAACCCAG CGTGCTCACA ATTTGTAAG GAGGAAACTT CTTGCGCTCA TGAAACTCCC GGTGGACATG AATCCAAAAA
GTTGAATGCT TTTGTTGCGC GCTGCTCTTG GGGTCTTGTC CAATGTCCCT TCAAACTCGC CAAAGAAGCT TGTCTCGAC
CGCCGTGTAT GCCTTCGTGC GCTTGTCTTT GCACCTCGGC TTCGGCCCGA GCGGCTTGGT GGCGAGCTCG TCCTCAAAAC
AAGCCTCCAC TTCGATGTC CACTCTCTTA CTTTCTTATA TTTTATCGT CGTTCGTTTT GATATCCCCC CTGTAGTGTG
TATTGTTTGA TCCCTGGGAA TCAAAATGCT AGTCTTAAAT CTCTAATAT TTCACAGAGG AGTACTTAAA TATCTGTGCA
GATTTCGTG TTTAATACTG TAAACCCATG CTAGTCGACC TTACATTTAG GAGAAACATT TCCTCTTGTC ACCCCTAATG
```

3B_103_E15

Positions

Length

Zoom to this feature

Detailed Report

Link to 3B Physical Map

C G
T C

Wheat Annotation Viewer

★ [icons] Contig

★ [icons] BAC

★ [icons] mRNA

★ [icons] STS

Xsts194-3B

★ [icons] TAA_ctg0954b.00200.1

Positions

1065073 ..
1068219

Length

3147

Gene Name

gad1

Function

glutamate
decarboxylase
putative
expressed
best blast hit in
Brachypodium
distachyon:
Bradi3g37830.1
87% identity
100%

Note 1

cfb6110
▶

rph7_rep_0224
▶

Wheat Annotation Viewer

★ [icons] Contig

★ [icons] BAC

★ [icons] mRNA

★ [icons] STS

Xsts194-3B

★ [icons] SSR

★ [icons] ISBP

★ [icons] Repeat

20

★ [icons] SNP allele_tower (GnpSNP)

MARKER DETAILS

| | |
|-----------------|-------------------|
| Marker name : | STS194 |
| Taxon : | Triticum aestivum |
| Marker type : | PCR |
| Marker origin : | amplicon |
| Target : | Public |

MAPPED LOCI

Mapped loci: 1

| Locus name | Map name | Taxon | Linkage group | Distance | Reliability / (source map name) |
|------------|--------------------|-------------------|---------------|----------|---------------------------------|
| Xsts194-3B | Neighbour3B_080407 | Triticum aestivum | 3B | 67.92 | non_framework |

Xsts194-3B

Positions

Length

626

[Zoom to this feature](#)

[Detailed Report](#)

[Link to GnpMap](#)

rph7_rep_0224

C T G C

Wheat Annotation Viewer

★       Contig

★       BAC







★       mRNA

★       STS

Xsts194-3B


★       SSR


★       ISBP

★       Repeats (Repeats Unit or Repeat Regions)

20







rph7_rep_0221

rph7_rep_02215

cfp5030


rph7_rep_022

rph7_rep_0223

★       SNP allele_tower (GnpSNP)

rph7_rep_0223

Positions 1062329 .. 1062934

Length 606

Note 1 retrotransposon:Copia

Note 2 RLC_Angela_3B_103_E15-2
partial element

[Zoom to this feature](#)

[Detailed Report](#)

C T
G C

Wheat Annotation Viewer

DETAILS

Name : Tae_1272250
Source : GnpSNP

COMPLEMENTS

Type : SNP
Sequence variation : C/T
Linked with variations : INRA_CF_ASP
[View list]
Linked with lines : ARCHE
[View list]

INTERNAL REFERENCES

| Database | Reference name | Reference value |
|---------------------------|----------------|-----------------|
| Wheat 3B annotation (FHB) | SNP name | Tae_1272250 |

SEQUENCES

5' flanker on ref.seq. :
>Tae_1272250-5'
cttgattcttgtataattattgtggaggggtgcgtatgtgaactgtcaagantgcctcctccgtatttgtacgtacgc
acgcggattgcactgtcacntgtataatcncatctgtttctttttaataaaggggtttcccccggctccagttttcggtg
atgaaaccaggcagcagagctcaaagctcccaggcataaccaaaggtagtcagccaggttaagacgttcaaccaaaccggt
gtcataaaga

3' flanker on ref.seq. :
>Tae_1272250-3'
ccatgagaataactcttttccaactggctactataatcaggtttgccta

Genomic context on ref. seq. :
>Tae_1272250-genomic_context
cttgattcttgtataattattgtggaggggtgcgtatgtgaactgtcaagantgcctcctccgtatttgtacgtacgc
acgcggattgcactgtcacntgtataatcncatctgtttctttttaataaaggggtttcccccggctccagttttcggtg
atgaaaccaggcagcagagctcaaagctcccaggcataaccaaaggtagtcagccaggttaagacgttcaaccaaaccggt
gtcataaaga [C/T] ccatgagaataactcttttccaactggctactataatcaggtttgccta

IDENTIFICATION

| | |
|-------------------|----------------------------|
| Accession number | 964 |
| Accession name | ARCHE |
| Synonyms | - |
| subspecies | Triticum aestivum aestivum |
| Pedigree | TRIBUTE/MM644-9-4-1 |
| Biological status | Advanced/improved cultivar |
| Comment | - |

ORIGIN

| | |
|------------------------------------|--|
| Geographical origin | France |
| Bred | - |
| Breeding site | - |
| Breeding institution | Nickerson |
| Creation year | - |
| Original number | - |
| French catalog registration year | 1989 |
| French catalog deregistration year | - |
| Donated | - |
| Donor institution | Unité expérimentale du Magneraud, GEVES |
| Donation date | 1989 |
| Original number | - |
| Holding institution | UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont |

value

0

ctgtacgtacgc
cagttttcggtg
aaccaaacggct

ctgtacgtacgc
cagttttcggtg
aaccaaacggct

ctgtacgtacgc
cagttttcggtg
aaccaaacggct

rep_0224

Michael Alaux

Wheat Annotation Viewer

IDENTIFICATION

| | |
|-------------------|----------------------------|
| Accession number | 964 |
| Accession name | ARCHE |
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| Pedigree | TRIBUTE/VM644-9-4-1 |
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ORIGIN

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| Breeding site | |
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| Donated | |
| Donor institution | Unite experimentale du Magneraud, GEVES |
| Donation date | 1989 |
| Original number | - |


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

Wheat Annotation Viewer

EVALUATION DATA

| | | |
|---|--|----------------|
| - | Growth class | Hiver - Winter |
| - | Days to heading (Counted as days from sowing to 50% of panicles fully emerged) | 141 |
| - | Scale of days to heading | 7 |
| - | Plant height (cm) | 85 |
| - | Scale of plant height | 5 |
| - | Scale of 1000 kernels weight | 5 |
| - | Wheat awnedness | 5 |

DISTRIBUTION

| | |
|-----------------|--|
| Presence status | Maintained |
| Available |  Yes, with restrictions |
| Distributor(s) | UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont |

COLLECTIONS

| | |
|---------|--|
| Part of | WHEAT_TRITIPOL_COL WHEAT_GENOPLANT_COL SOFT_WHEAT_CORE_COL WHEAT_INRA_COL |
|---------|--|

GENOTYPING

This accession has been genotyped: see **ARCHE** in GnpSNP.

Wheat dataflow overview

[illegible][illegible]

1BL 3B (95% coverage) 3B (82% coverage)

ScrollZoom: 100% Show 372.1 kbp + Map Flip

Wheat physical map viewer GBrowse

International
Wheat Genome
Sequencing
Consortium

Click on a chromosome to have access to the survey sequence and the viewers when available.

Survey sequences and related databanks are access restricted. To download or blast the sequence, you have to be member of the [IWGSC](#) coordinating committee.

The process to ask an account will be soon available.

Survey sequences progress is available at [IWGSC](#) for projects leader (access restricted), already informateurs.

Chromosomes 1B and 3B have no survey sequences.

Wheat survey sequence repository

Blast Download

1A 2A 3A 4A 5A 6A 7A

1B 2B 3B 4B 5B 6B 7B


[illegible]

Results

1234567891042 items found, displaying 1 to 10 | Display: 10 • results per page

The experiment [DRA_OF_ASP52](#) contains 46 marker(s).

| Positions | 24 | 68 | 83 | | | |
|---------------|-------------------|-----|----|---|---|---|
| Ref. Sequence | SNP | Ref | R | T | C | G |
| Line | SA | A | C | C | G | G |
| Line | ARFNO NDA | A | C | C | G | G |
| Line | ARCHE | A | C | C | G | G |
| Line | ALBROSE | A | C | C | G | G |
| Line | Bethan | A | C | C | G | G |
| Line | BABRU DU FINESTRE | A | C | C | G | G |
| Line | BELLER | A | C | C | G | G |
| Line | CHINESE_SPRING | A | C | C | G | G |
| Line | CHORINDONGA | A | C | C | G | G |
| Line | CHAMANTIA | A | C | C | G | G |



Accession: (210-13*M)-1-37

Identification

| | |
|------------------|-----------------------------------|
| Accession number | 27 |
| Accession name | (210-13*M)-37 |
| Synonyms | |
| subspecies | Tribulus aestivus aestivus |
| Pedigree | Fr. selection 'VICARATTO' MOISSON |
| Biological data | Breeder's material |
| Comment | |

Origin

- Genetic origin

| | |
|----------------------------------|--|
| Breeding site | |
| Breeding institution | UMR 1213 Horticulture Végétale, INRA-Orserre |
| Creation year | |
| Original number | |
| French catalog registration year | |
| French catalog designation year | |
- Derived

| | |
|-------------------|--|
| Donor institution | UMR 1213 Horticulture Végétale, INRA-Orserre |
| Donation date | 1984 |
| Original number | |
- Holding institution

UMR Génétique, Diversité et Ecophysiology des Céréales, INRA-Clermont

New Wheat website


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

Xwmc430

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

Examples: [gene](#), [Xwmc430](#)

EVENT & PUBLICATIONS

31 Jan 2012
TriAnnot: a versatile and high performance pipeline for the automated ...
 ACL (papers with reading committee)
 Frontiers in Plant Genetics and Genomics (2012) 3:1-14
 ...

12 Apr 2011
Breedwheat english press release
 Breedwheat project english press release in PRweb.
 ...

04 Mar 2011
Breedwheat and Amaizing approvals press release
 The 2 projects Breedwheat and Amaizing have been both approved by the french program ...

03 Aug 2011
Wheat annotation viewer v1.4
[Wheat_annotation_viewer_v1.4](#) is now available. The FHB QTL link to GnpMap is publicly available.
 ...

12 Jul 2011
New wheat data are now available on public site
[Neighbour1BL_110314](#) map and [FHB_QTL](#) are now available on public site.
 ...

24 Mar 2011
Wheat annotation viewer v1.3
[Wheat_annotation_viewer_v1.3](#) is now available. It displays 13 annotated contigs of the 3B chromosome.
 ...

24 Mar 2011
Wheat physical map viewer v3.0
[Wheat_physical_map_viewer_v3.0](#) is now available. It displays the two versions of the 3B FPC assembly (82% and 99% coverage) and the 1BL FPC assembly.
 ...

15 Dec 2010
GnpGenome Wheat Physical Map v2.4 available
[v2.4](#) : Add link to deletion bins image and external link to CMap composite maps (R. Appels) at GrainGenes.
 ...

06 Dec 2010
TriAnnot v2.1

- Important improvement of the NIAS-search module, much more efficient (Developed by H. Sakai, N. Amano from NIAS and P. Leroy from GDEC).
- Databanks :
 - New proteome databanks: CDS derived peptides from genome model and addition of EMBL proteomes for several plant species. Used within Block10 and Block17.
- Possibility to download best hit alignments from Block10.
- New Web interface for sequence submission:
 - Block10: addition of % of protein coverage and % of protein positive

New Wheat website

The collage displays four overlapping screenshots of the EURGI Wheat website interface, showcasing its layout and content:

- Top Screenshot (Homepage):** Features the EURGI logo, navigation links (Projects, Data, Tools, Seq Repository, About us), and a "REGISTER" button. The main content area includes a "Projects" sidebar with links to 3BSeq, BreedWheat, and TriticumGenome, and a main text area titled "Why develop Wheat?" discussing the importance of wheat in agriculture.
- Second Screenshot (Data Section):** Shows the "Data" section with a sidebar containing links to Map, Genome, Polymorphism, Genetic collections, EST, and Transcriptome. The main content area lists various data resources like Sequence survey, Physical maps, Annotations, and Genetic maps.
- Third Screenshot (Tools Section):** Displays the "Tools" section with a sidebar containing links to Help, Versions, Architecture, Usage, Softwares, Databanks, Defaults, List of users, Links, Presentation in congress, Run Pipeline, Acknowledgments, Quick search in Gnpis, Physical map viewer, Annotation viewer, Deletion bins, and dbWFA. The main content area features the "Triannot pipeline" section, which includes a detailed description of wheat genome structure and a figure showing the genome map.
- Bottom Screenshot (Genome Map):** Shows a detailed view of the wheat genome map, including a chromosome map, a sequence alignment plot, and a table of sequence data.

Acknowledgments



M. Alaux
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D. Steinbach
H. Quesneville

