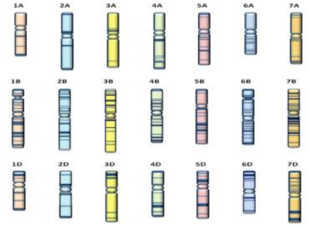
IWGSC

Survey sequence repository improvements.

How to map my favorite gene on the survey sequence of wheat?

Michael Alaux

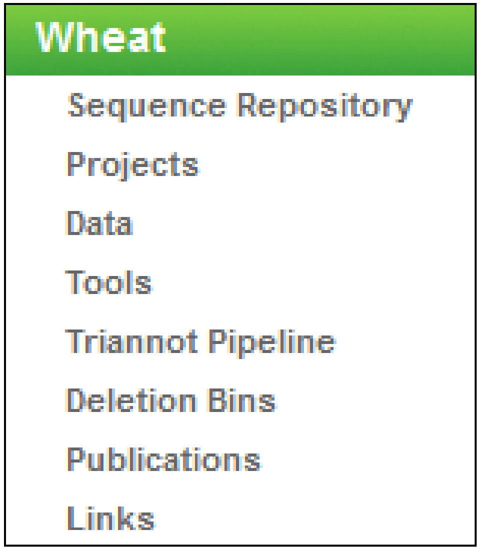




ITMI – IWGSC meeting June 2012 Fargo

Wheat bioinformatics at URGI

Michael Alaux

Wheat Portal



Wheat

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

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?

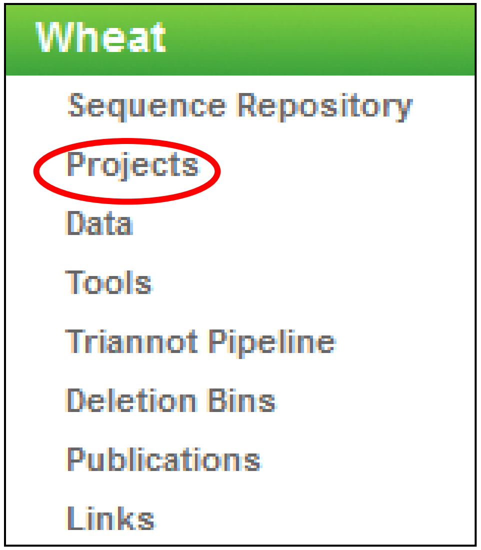
Today, agriculture is facing one of its greatest challenges since it began 10 000 years ago, that of producing an ample supply of high quality food and feed for a growing world population in a sustainable and environment friendly manner. Bread wheat (Triticum aestivum L.) is the staple food for more 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



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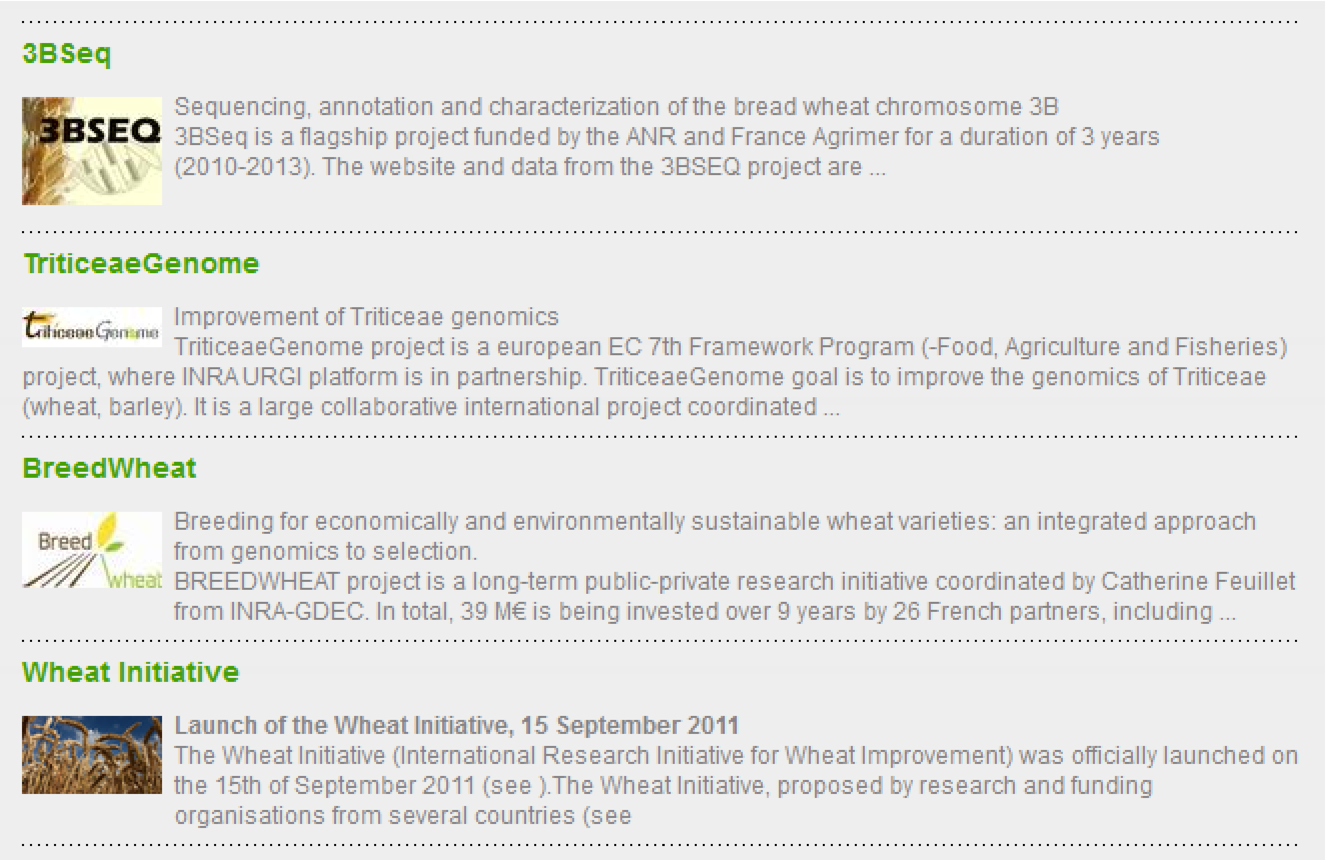


3BSeq

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

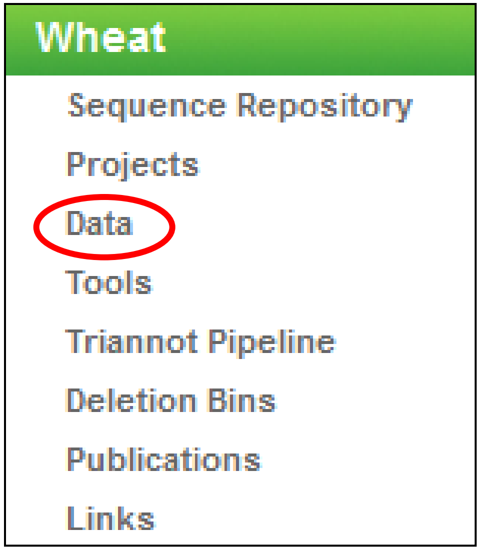
Breeding for economically and environmentally sustainable wheat varieties: an integrated approach from genomics to selection.
BREEDWHEAT project is a long-term public-private research initiative coordinated by Catherine Feuillet from INRA-GDEC. In total, 39 M€ is being invested over 9 years by 26 French 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

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

Wheat Portal



Wheat

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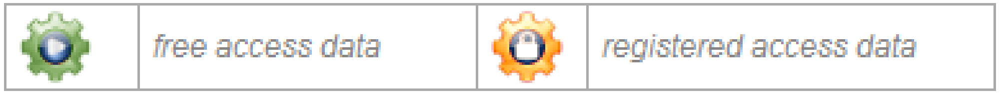
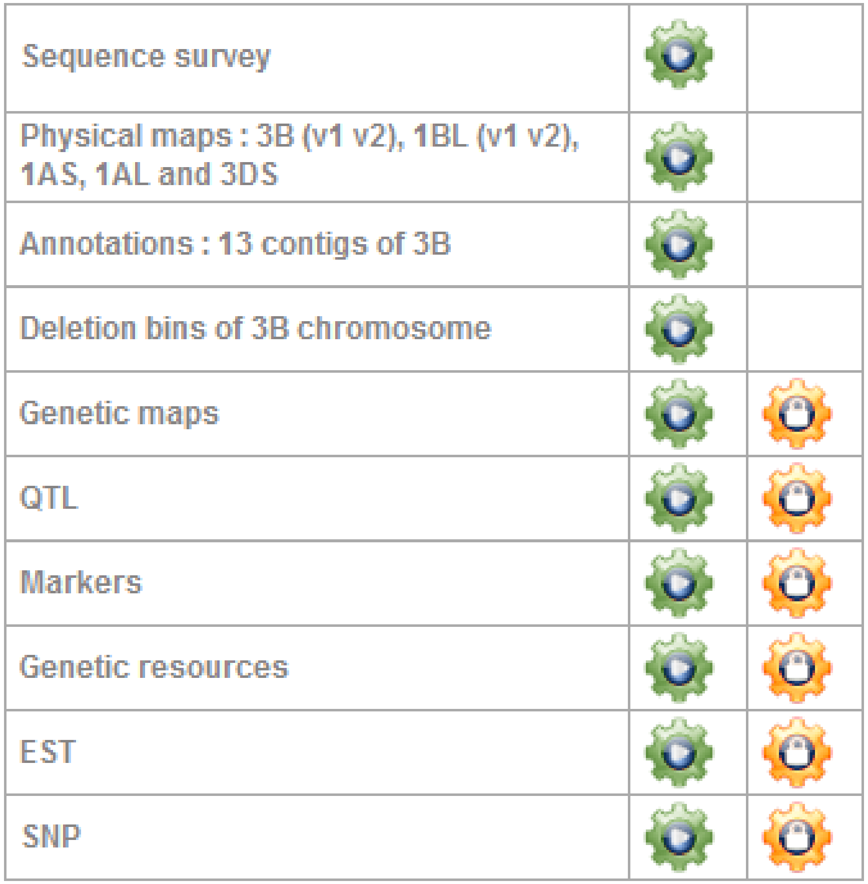


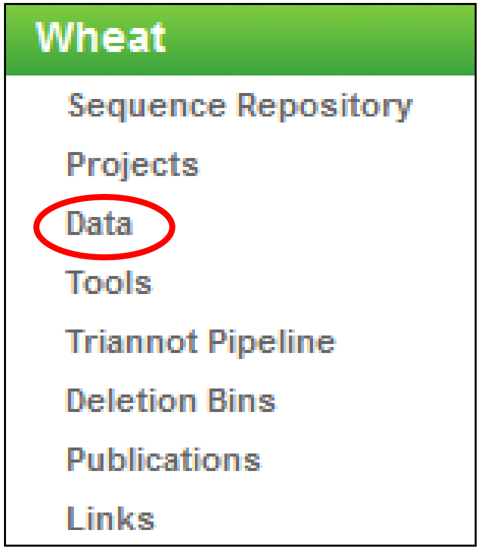
🟢	*free access data*	🟠	*registered access data*



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

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

Wheat Portal



Wheat

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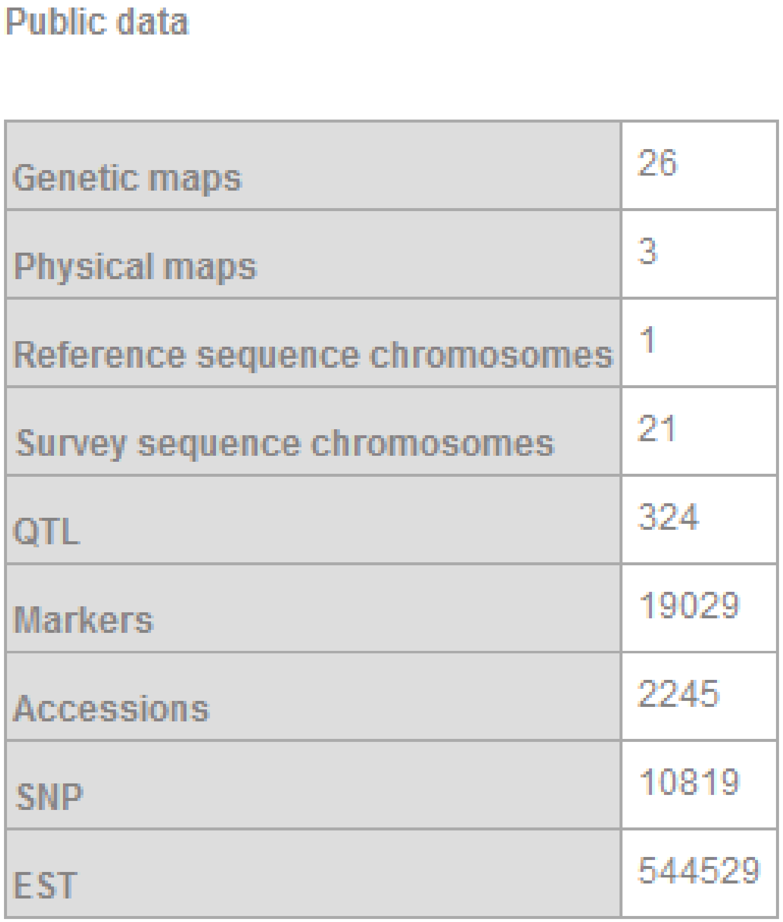
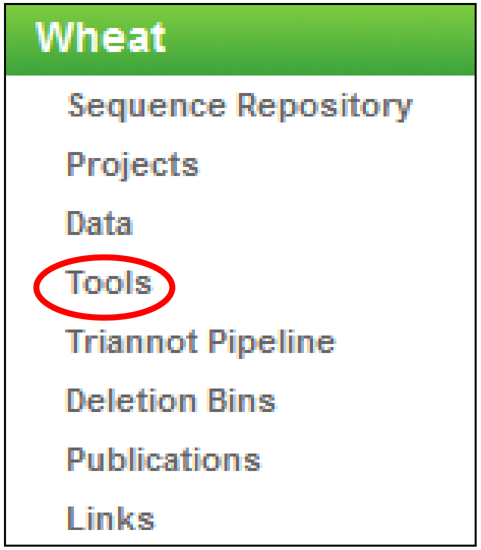


Public data

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 Portal



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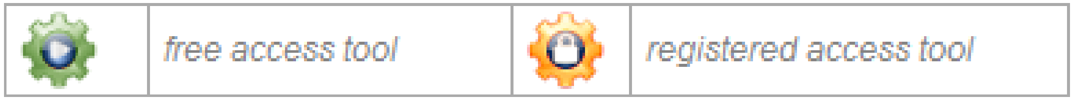
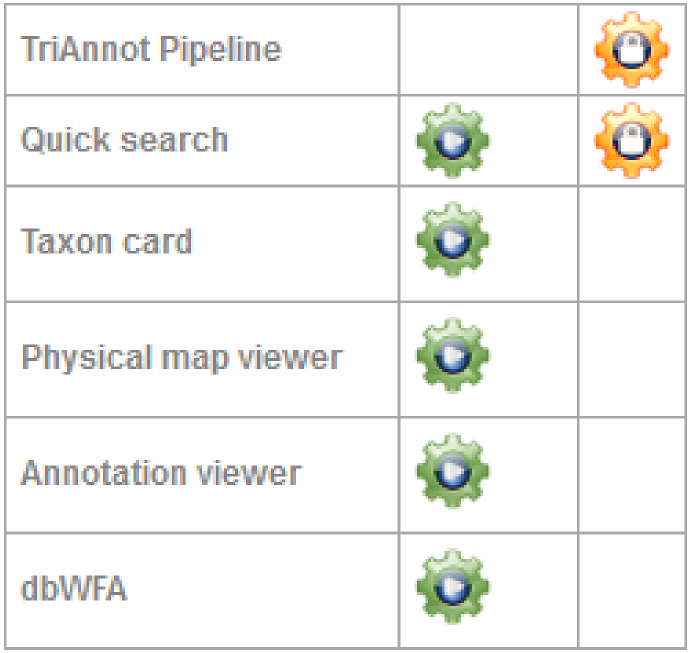


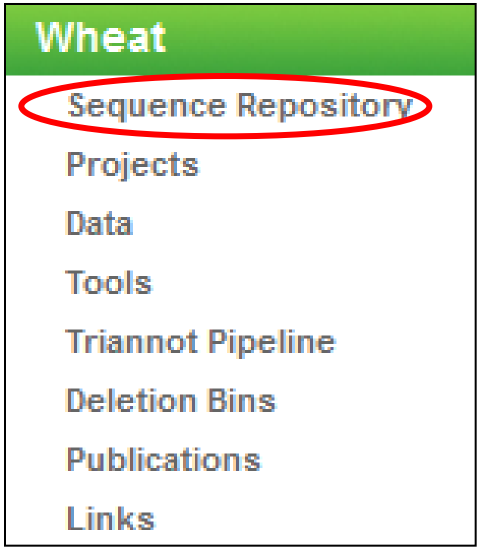
🟢	*free access tool*	🟠	*registered access tool*



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

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

Wheat Portal



Wheat

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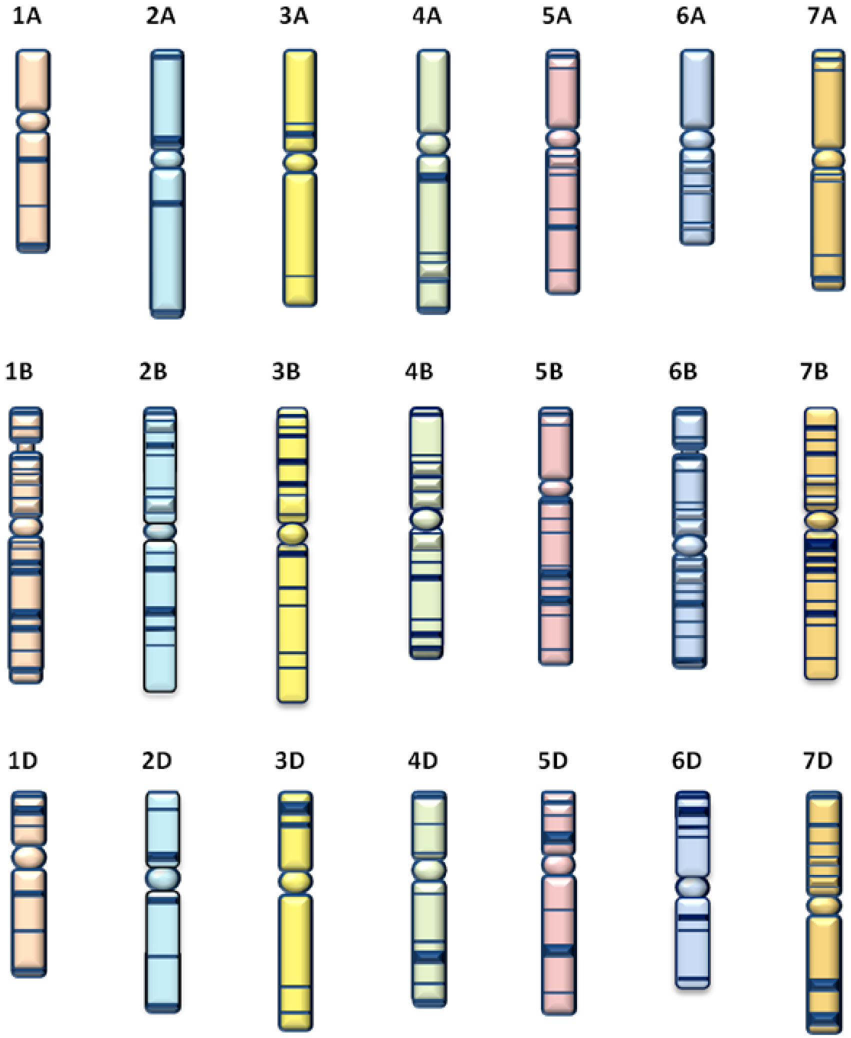
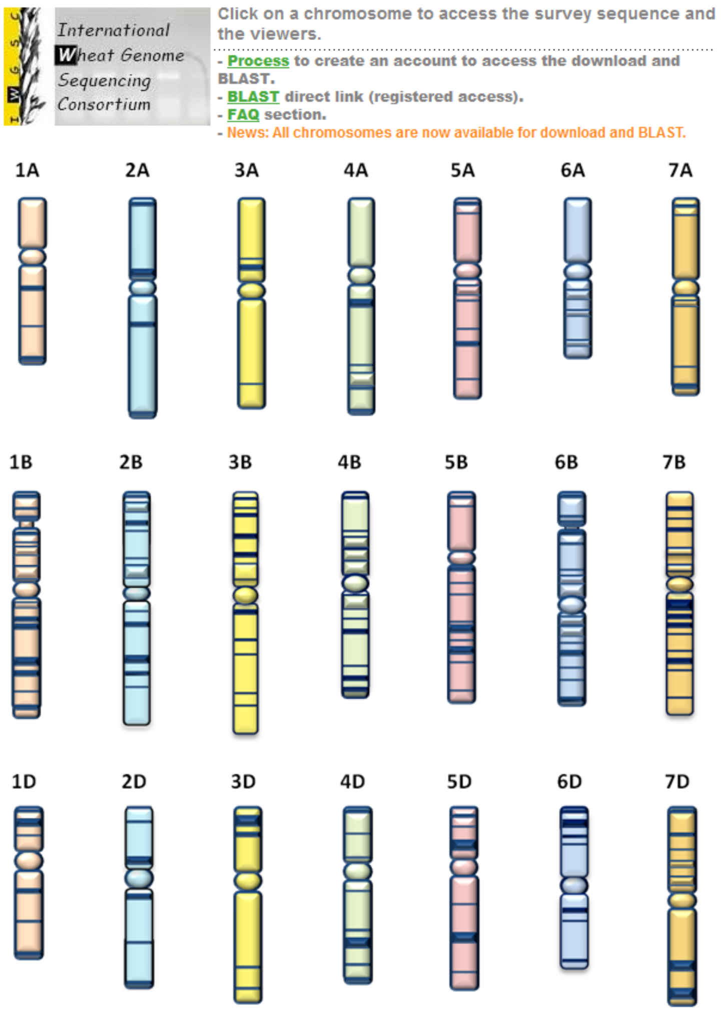


http://urgi.versailles.inra.fr/Species/Wheat

IWGSC Survey Sequence

Michael Alaux

Survey Sequence Repository



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:

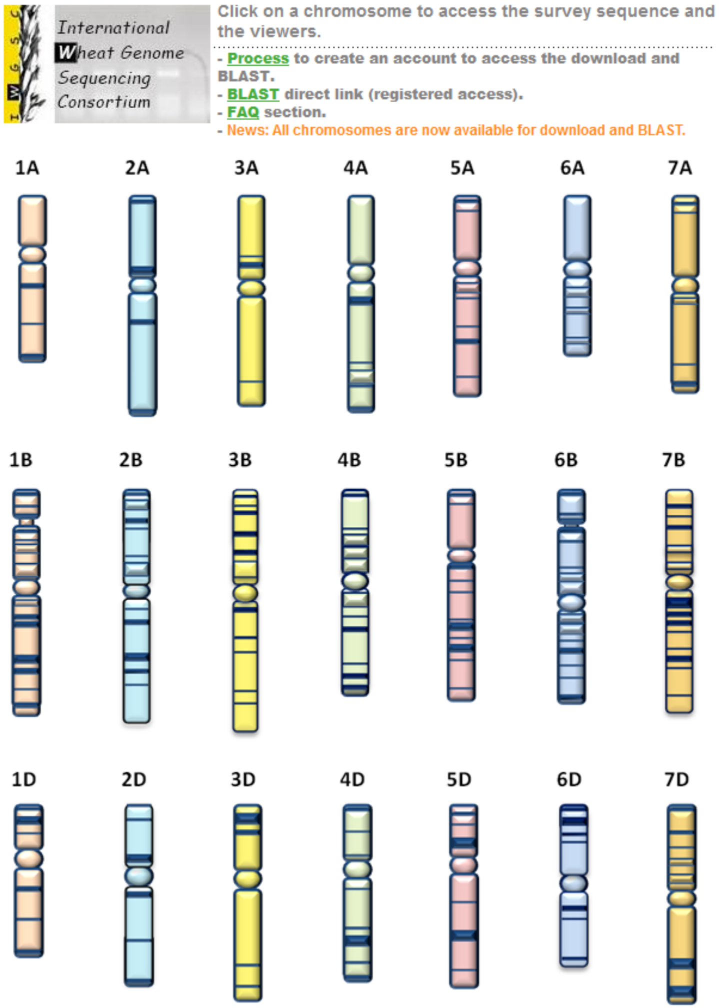
- **BLAST** search *(Blast agreement)*
- **Download** *(Data agreement)*

All the assemblies are now available!

- **Viewers**: physical map, annotations when available

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

Survey Sequence Repository



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

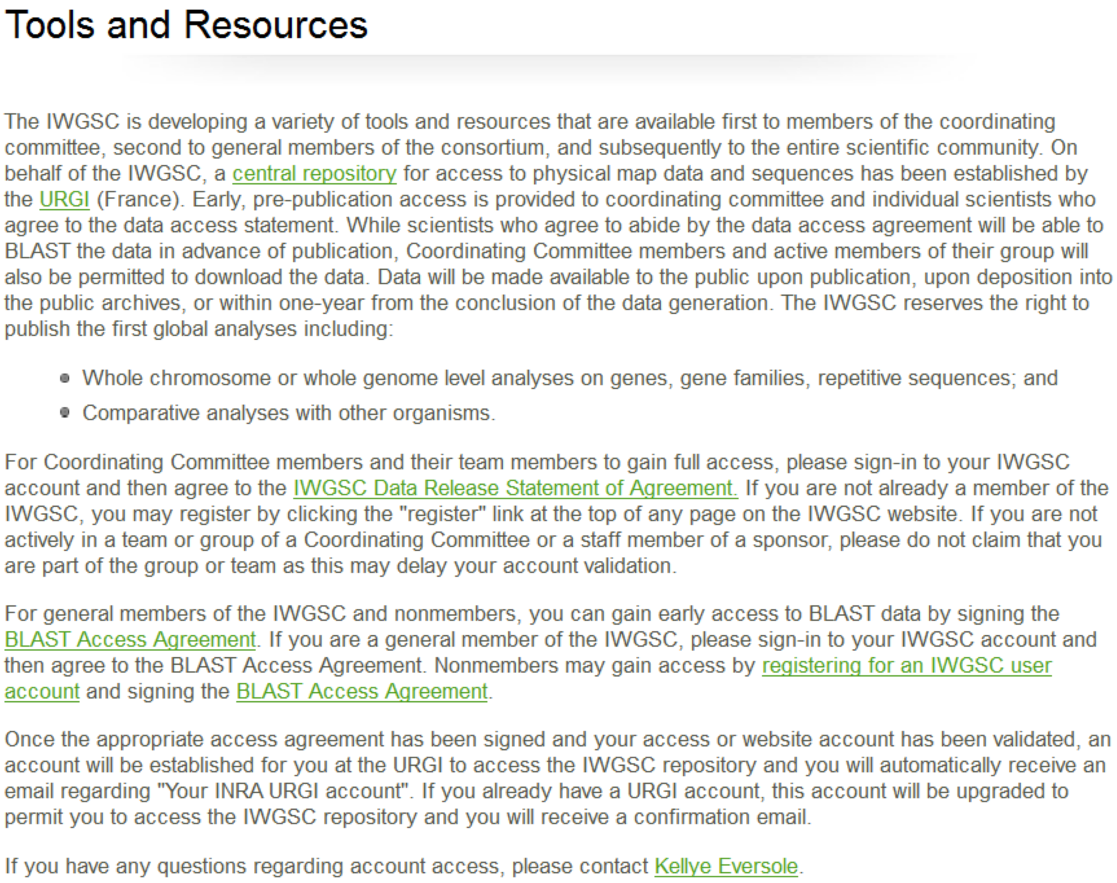
How do I access the survey sequence?
How do I launch a BLAST?
Can I BLAST multiple chromosome arms simultaneously?
Is there a way to speed up the BLAST?
What is the contig nomenclature?
How can I save the alignment of the analysis?
How can I download contigs from an analysis result?
How do I launch another kind of Blast (BlastP, BlastX, tBlastX, etc.) ?

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.

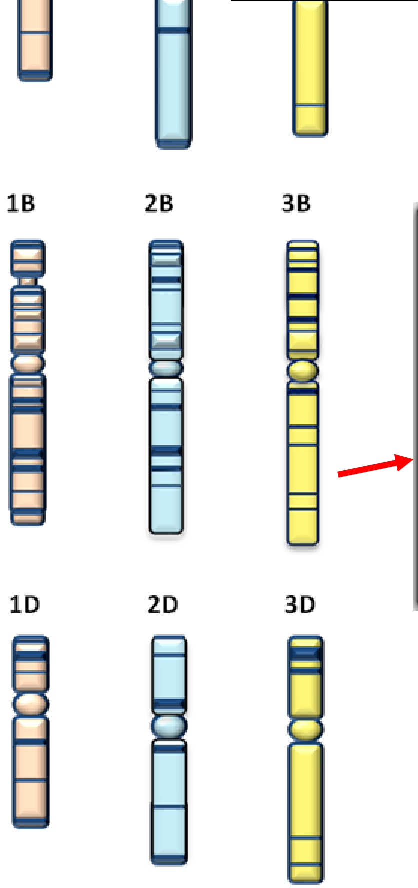
For Coordinating Committee members and their team members to gain full access, please sign-in to your IWGSC account and then agree to the IWGSC Data Release Statement of Agreement. If you are not already a member of the IWGSC, you may register by clicking the "register" link at the top of any page on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

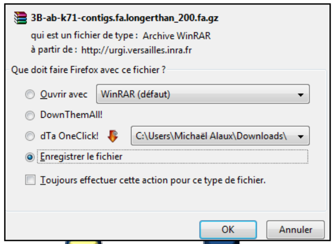
For general members of the IWGSC and nonmembers, you can gain early access to BLAST data by signing the BLAST Access Agreement. If you are a general member of the IWGSC, please sign-in to your IWGSC account and then agree to the BLAST Access Agreement. Nonmembers may gain access by registering for an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

Survey Sequence Repository





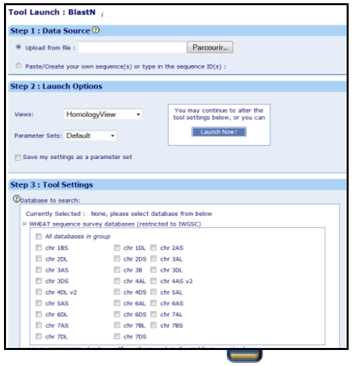
3B-ab-k71-contigs.fa.longerthan_200.fa.gz

qui est un fichier de type : Archive WinRAR

à partir de : http://urgi.versailles.inra.fr

Que doit faire Firefox avec ce fichier ?

- ○ Ouvrir avec: WinRAR (défaut)
- ○ DownThemAll!
- ○ dTa OneClick!: C:\Users\Michaël Alaux\Downloads\
- ● Enregistrer le fichier
- ☐ Toujours effectuer cette action pour ce type de fichier.



Tool Launch : BlastN

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: 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 : None, please select database from below

WHEAT sequence survey databases (restricted to IWGSC)

- ☐ *All databases in group*

☐ chr 1BS	☐ chr 1DL	☐ chr 2AS
☐ chr 2DL	☐ chr 2DS	☐ chr 3AL
☐ chr 3AS	☐ chr 3B	☐ chr 3DL
☐ chr 3DS	☐ chr 4AL	☐ chr 4AS v2
☐ chr 4DL v2	☐ chr 4DS	☐ chr 5AL
☐ chr 5AS	☐ chr 6AL	☐ chr 6AS
☐ chr 6DL	☐ chr 6DS	☐ chr 7AL
☐ chr 7AS	☐ chr 7BL	☐ chr 7BS
☐ chr 7DL	☐ chr 7DS	

1AS v1 **1AL** v1 **1BS** v1 **1BL**v1 **1BL**v2 **3B** v1 **3B** v2 **3DS** v1

Search

Landmark or Region: ctg6:1..373,201

Data Source: Wheat physical map viewer v4: 3B v2

Annotate Restriction Sites

Scroll/Zoom: Show 373.2 kbp ☐ **Flip**

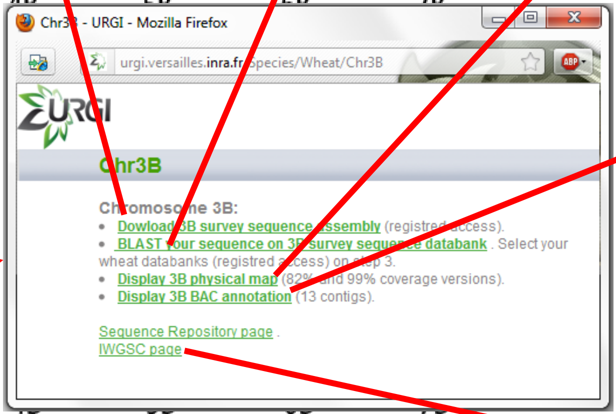
Examples :

3B v2:	ctg6	ctg1720	TaaCsp3BFhA_0100L17	Xgwm264-3B
3B v1:	ctg1	ctg954	Xgwm264-3B	3B_039_H02
1BL v2:	ctg45	wmc719		

Overview

Region

Details



Chr3B - URGI - Mozilla Firefox

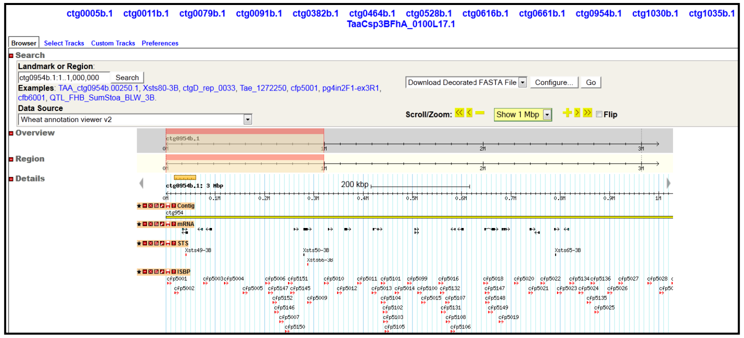
urgi.versailles.inra.fr/Species/Wheat/Chr3B

Chr3B

Chromosome 3B:

- Dowload 3B survey sequence assembly (registred access).
- BLAST your sequence on 3B survey sequence databank . Select your wheat databanks (registred access) on step 3.
- Display 3B physical map (82% and 99% coverage versions).
- Display 3B BAC annotation (13 contigs).

Sequence Repository page .
IWGSC page



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

Search

Landmark or Region: ctg0954b.1:1..1,000,000

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

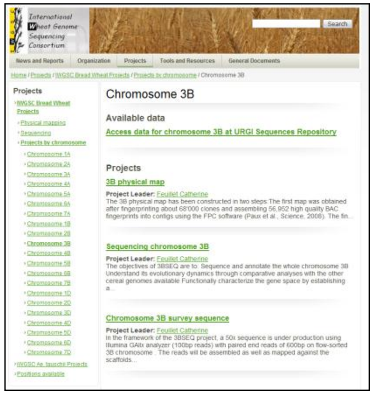
Download Decorated FASTA File

Scroll/Zoom: Show 1 Mbp ☐ **Flip**

Overview

Region

Details



International Wheat Genome Sequencing Consortium

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 fingerprinting about 68'000 clones and assembling 56,952 high quality BAC fingerprints into contigs using the FPC software (Paux et 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 Understand its evolutionary dynamics through comparative analyses with the other cereal genomes available Functionally characterize the gene space by establishing a...

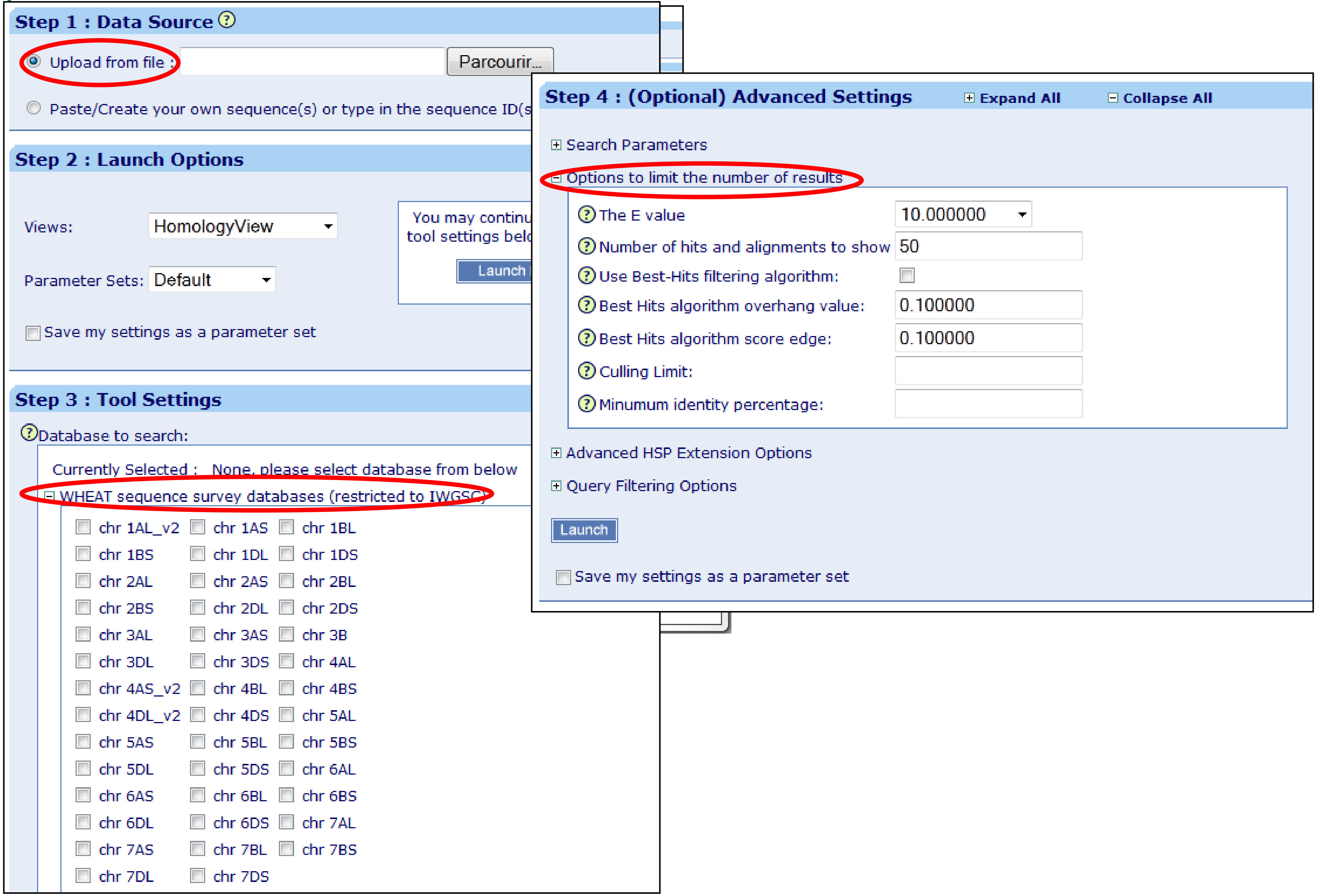
Chromosome 3B survey sequence

Project Leader: Feuillet Catherine
In the framework of the 3BSEQ project, a 50x sequence is under production using Illumina GAIIx analyzer (100bp reads) with paired end reads of 600bp on flow-sorted 3B chromosome . The reads will be assembled as well as mapped against the scaffolds...

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

Michael Alaux

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: HomologyView

Parameter Sets: Default

You may continu
tool settings bel

☐ Save my settings as a parameter set

Step 3 : Tool Settings

Database to search:

Currently Selected : None, please select database from below

⊟ WHEAT sequence survey databases (restricted to IWGSC)

☐ chr 1AL_v2 ☐ chr 1AS ☐ chr 1BL
☐ chr 1BS ☐ chr 1DL ☐ chr 1DS
☐ chr 2AL ☐ chr 2AS ☐ chr 2BL
☐ chr 2BS ☐ chr 2DL ☐ chr 2DS
☐ chr 3AL ☐ chr 3AS ☐ chr 3B
☐ chr 3DL ☐ chr 3DS ☐ chr 4AL
☐ chr 4AS_v2 ☐ chr 4BL ☐ chr 4BS
☐ chr 4DL_v2 ☐ chr 4DS ☐ chr 5AL
☐ chr 5AS ☐ chr 5BL ☐ chr 5BS
☐ chr 5DL ☐ chr 5DS ☐ chr 6AL
☐ chr 6AS ☐ chr 6BL ☐ chr 6BS
☐ chr 6DL ☐ chr 6DS ☐ chr 7AL
☐ chr 7AS ☐ chr 7BL ☐ chr 7BS
☐ chr 7DL ☐ chr 7DS

Step 4 : (Optional) Advanced Settings

⊞ Search Parameters

⊟ Options to limit the number of results

The E value	10.000000
Number of hits and alignments to show	50
Use Best-Hits filtering algorithm:	☐
Best Hits algorithm overhang value:	0.100000
Best Hits algorithm score edge:	0.100000
Culling Limit:	
Minumum identity percentage:	

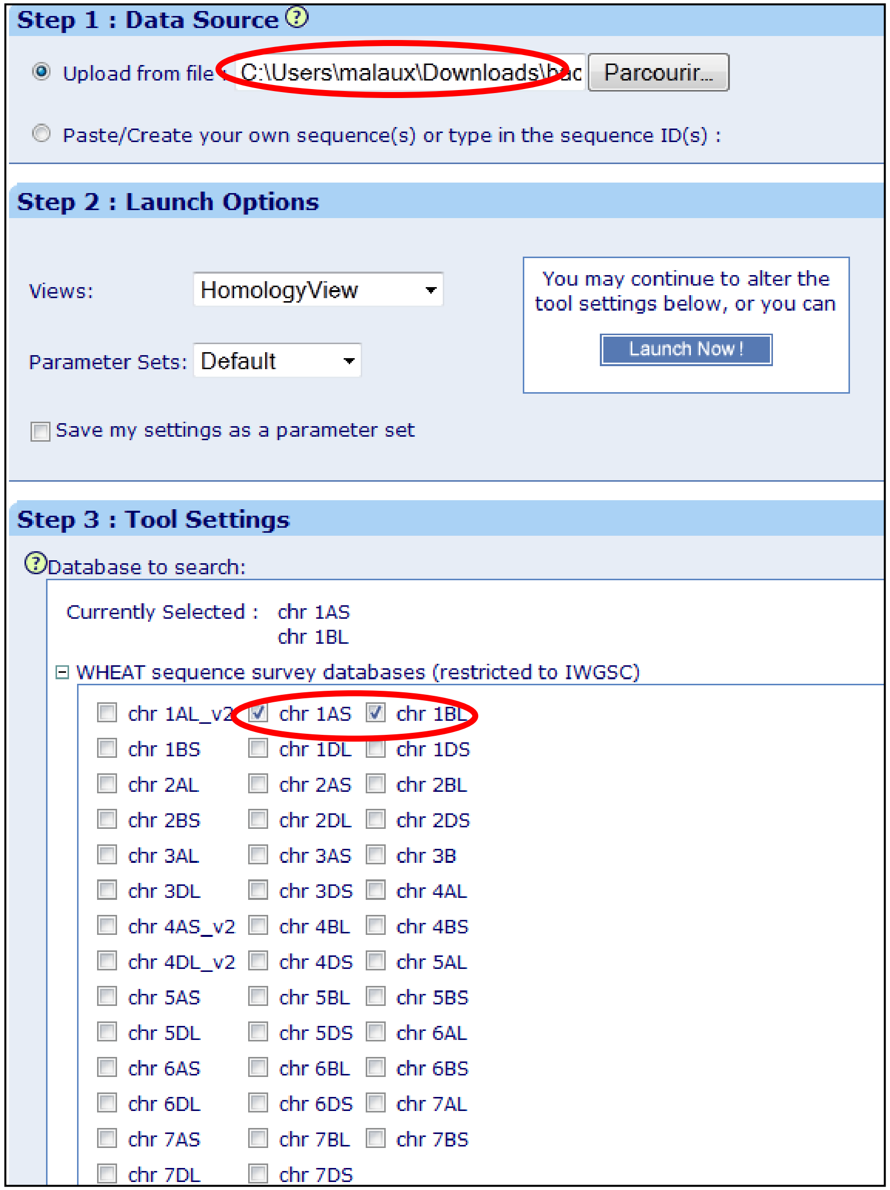
⊞ Advanced HSP Extension Options

⊞ Query Filtering Options

☐ Save my settings as a parameter set

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

Survey Sequence Repository



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

Step 3 : Tool Settings

Database to search:

Currently Selected : chr 1AS
chr 1BL

⊟ WHEAT sequence survey databases (restricted to IWGSC)

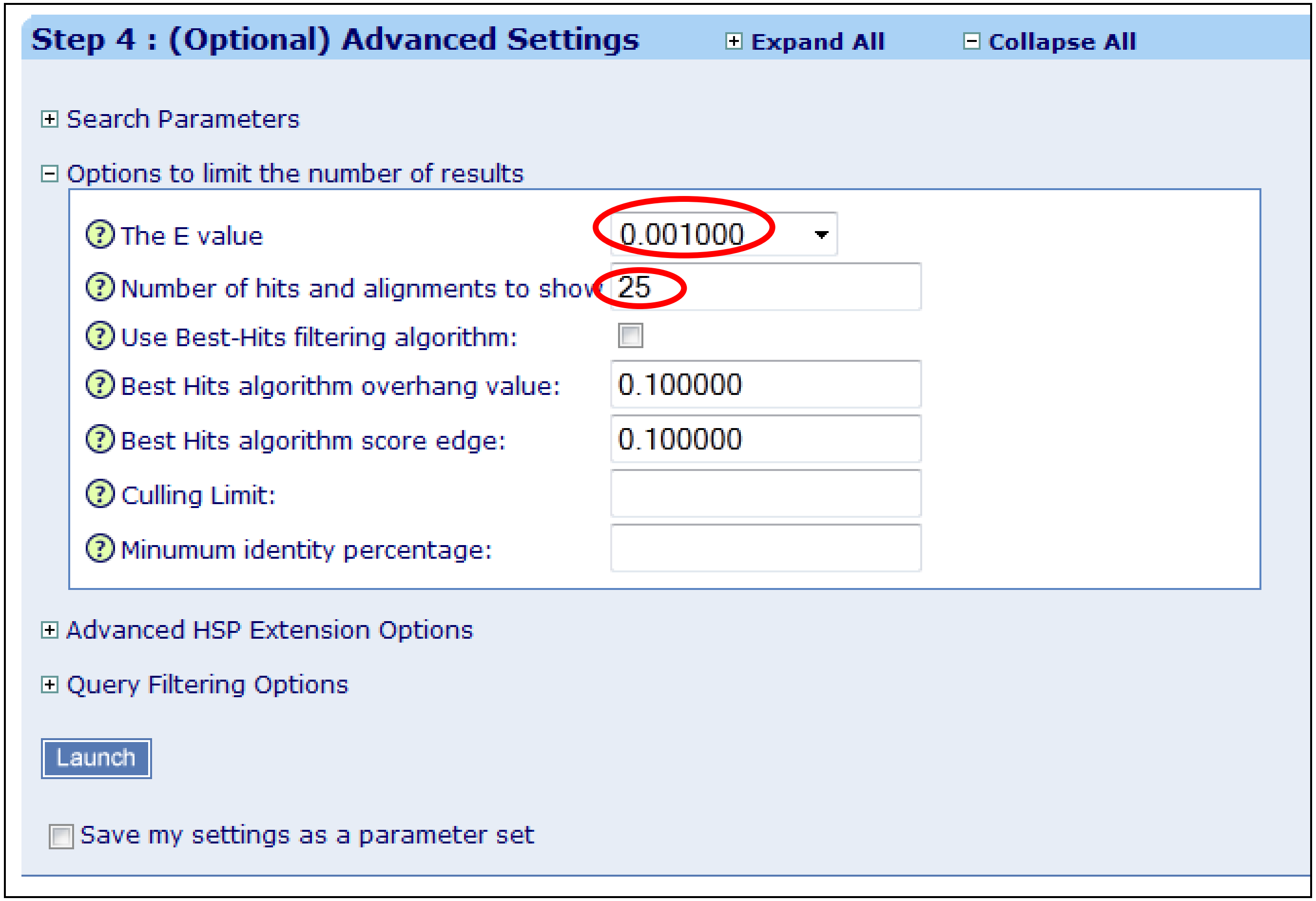
☐ chr 1AL_v2	☑ chr 1AS	☑ chr 1BL
☐ chr 1BS	☐ chr 1DL	☐ chr 1DS
☐ chr 2AL	☐ chr 2AS	☐ chr 2BL
☐ chr 2BS	☐ chr 2DL	☐ chr 2DS
☐ chr 3AL	☐ chr 3AS	☐ chr 3B
☐ chr 3DL	☐ chr 3DS	☐ chr 4AL
☐ chr 4AS_v2	☐ chr 4BL	☐ chr 4BS
☐ chr 4DL_v2	☐ chr 4DS	☐ chr 5AL
☐ chr 5AS	☐ chr 5BL	☐ chr 5BS
☐ chr 5DL	☐ chr 5DS	☐ chr 6AL
☐ chr 6AS	☐ chr 6BL	☐ chr 6BS
☐ chr 6DL	☐ chr 6DS	☐ chr 7AL
☐ chr 7AS	☐ chr 7BL	☐ chr 7BS
☐ chr 7DL	☐ chr 7DS	

If your select multiple chromosomes, please use a small query

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

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: ☐

Best Hits algorithm overhang value: 0.100000

Best Hits algorithm score edge: 0.100000

Culling Limit:

Minumum identity percentage:

⊞ Advanced HSP Extension Options

⊞ Query Filtering Options

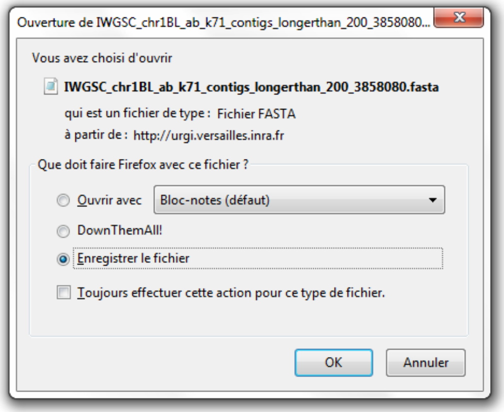
Launch

☐ Save my settings as a parameter set

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

Survey Sequence Repository

To download the contigs



Ouverture de IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3858080...

Vous avez choisi d'ouvrir

IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3858080.fasta

qui est un fichier de type : Fichier FASTA

à partir de : http://urgi.versailles.inra.fr

Que doit faire Firefox avec ce fichier ?

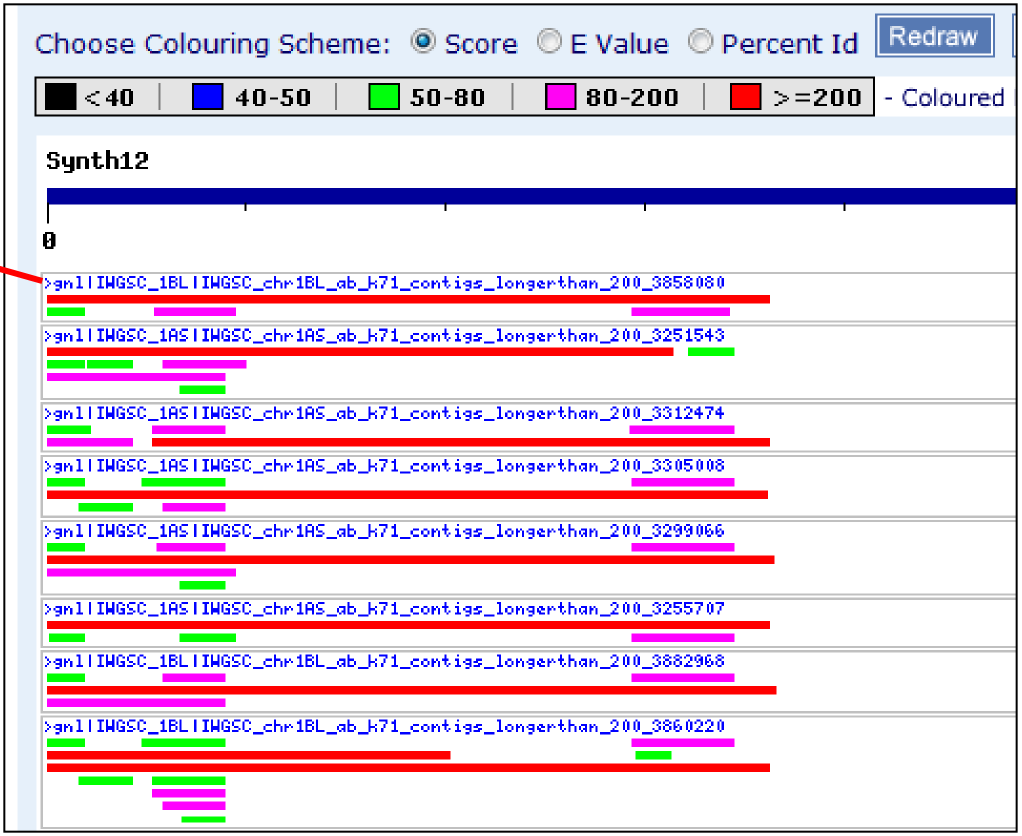
○ Ouvrir avec Bloc-notes (défaut)

○ DownThemAll!

● Enregistrer le fichier

☐ Toujours effectuer cette action pour ce type de fichier.

Homology View (default view)



Choose Colouring Scheme: ● Score ○ E Value ○ Percent Id

■ <40 | 🟦 40-50 | 🟩 50-80 | 🟪 80-200 | 🟥 >=200 - Coloured

Synth12

>gnl|IWGSC_1BL|IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3858080

>gnl|IWGSC_1AS|IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3251543

>gnl|IWGSC_1AS|IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3312474

>gnl|IWGSC_1AS|IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3305008

>gnl|IWGSC_1AS|IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3299066

>gnl|IWGSC_1AS|IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3255707

>gnl|IWGSC_1BL|IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3882968

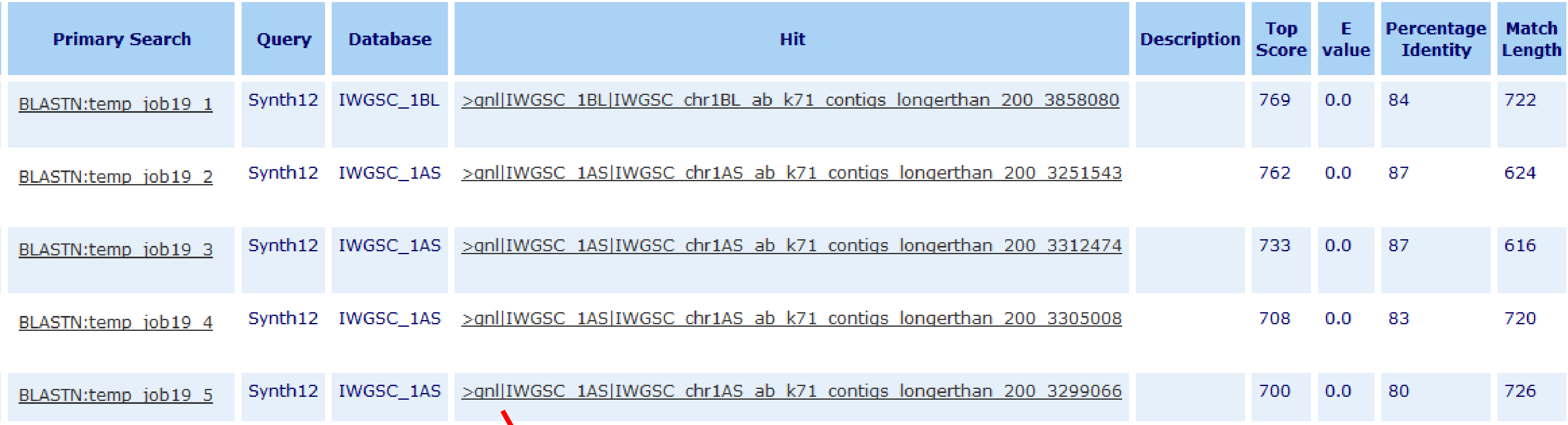
>gnl|IWGSC_1BL|IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3860220

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

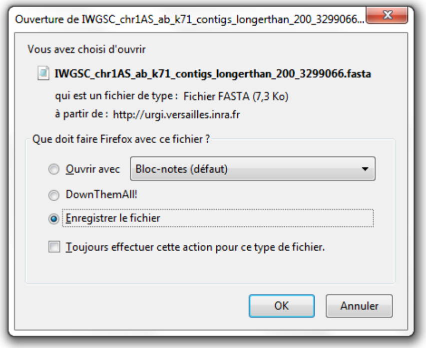
Survey Sequence Repository

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



Ouverture de IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3299066...

Vous avez choisi d'ouvrir

IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3299066.fasta

qui est un fichier de type : Fichier FASTA (7,3 Ko)

à partir de : http://urgi.versailles.inra.fr

Que doit faire Firefox avec ce fichier ?

○ Ouvrir avec Bloc-notes (défaut)

○ DownThemAll!

● Enregistrer le fichier

☐ Toujours effectuer cette action pour ce type de fichier.

Survey Sequence Repository

To download the contigs

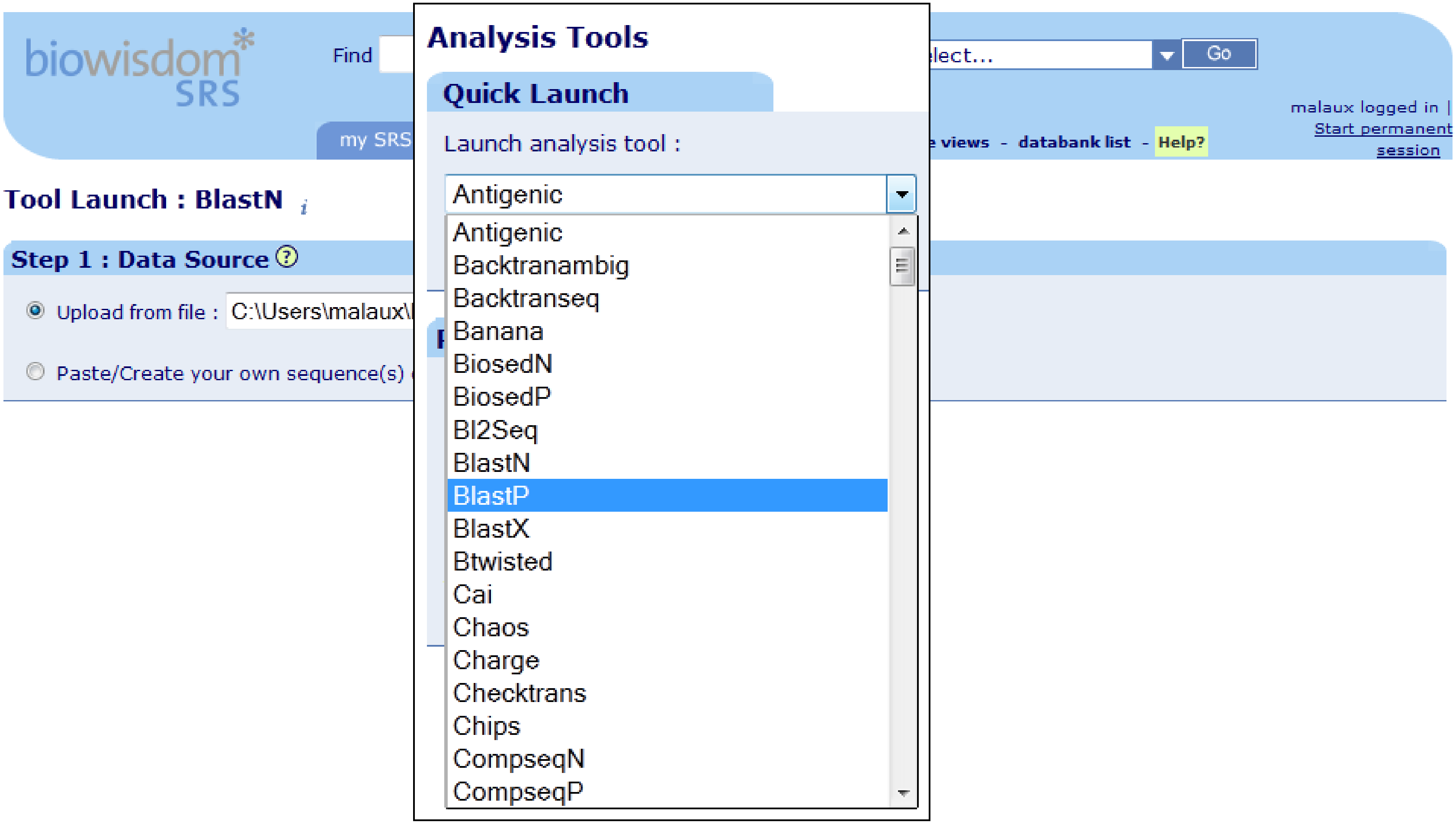
Limits to ensure data security and compliance with the IWGSC access agreement:

- Dowload one contig at a time
- 10 sec waiting period in between the download of each contig
- Maximum 500 contig downloads per day.

If you have a BLAST account and want to download an entire chromosome arm, please contact Kellye Eversole at eversole@eversoleassociates.com.

Survey Sequence Repository

To launch BlastP, BlastX, tBlastX…



Tool Launch : BlastN

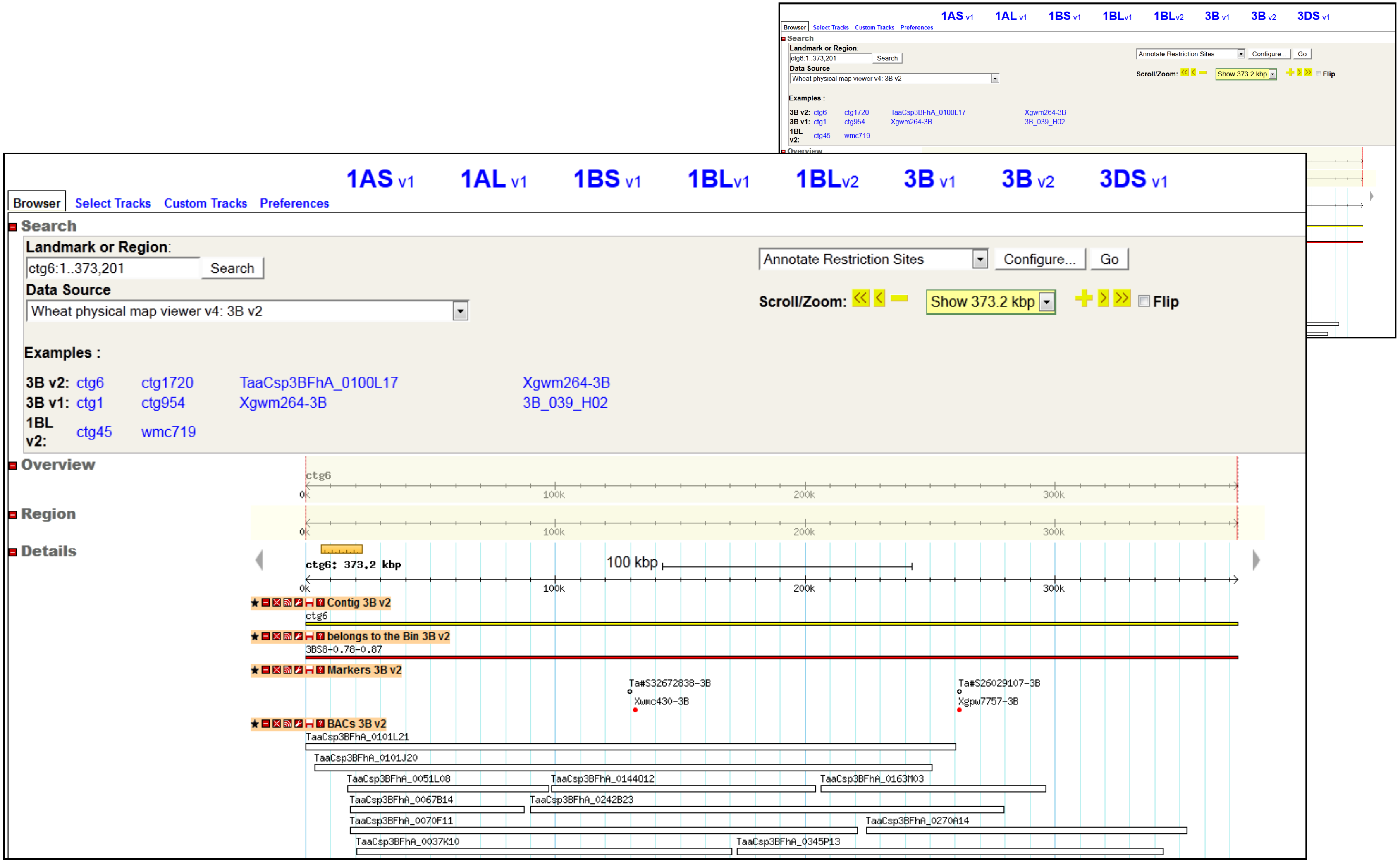
Step 1 : Data Source

● Upload from file : C:\Users\malaux\

○ Paste/Create your own sequence(s)

Launch analysis tool : Antigenic

Survey Sequence Repository



1AS v1 1AL v1 1BS v1 1BLv1 1BLv2 3B v1 3B v2 3DS v1

Browser | Select Tracks | Custom Tracks | Preferences

Search

Landmark or Region: ctg6:1..373,201 Search

Data Source: Wheat physical map viewer v4: 3B v2

Annotate Restriction Sites | Configure... | Go

Scroll/Zoom: Show 373.2 kbp ☐ **Flip**

Examples :

3B v2: ctg6	ctg1720	TaaCsp3BFhA_0100L17	Xgwm264-3B
3B v1: ctg1	ctg954	Xgwm264-3B	3B_039_H02
1BL v2: ctg45	wmc719		

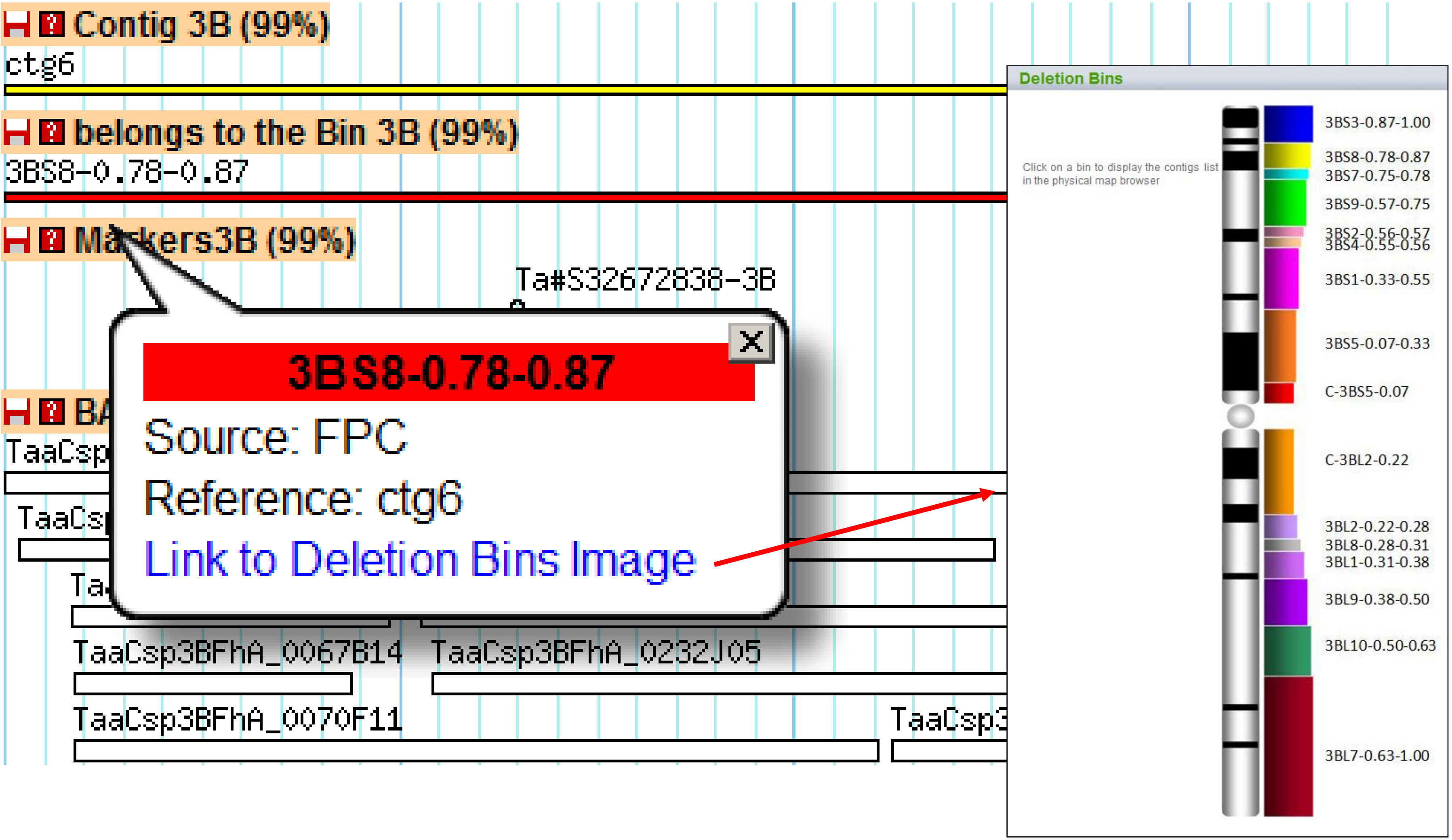
Overview

Region

Details

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

Wheat Physical Map Viewer



Contig 3B (99%)

ctg6

belongs to the Bin 3B (99%)

3BS8-0.78-0.87

Markers3B (99%)

Ta#S32672838-3B

BA

TaaCsp

TaaCsp

Ta

TaaCsp3BFhA_0067B14

TaaCsp3BFhA_0232J05

TaaCsp3BFhA_0070F11

TaaCsp3

3BS8-0.78-0.87

Source: FPC

Reference: ctg6

Link to Deletion Bins Image

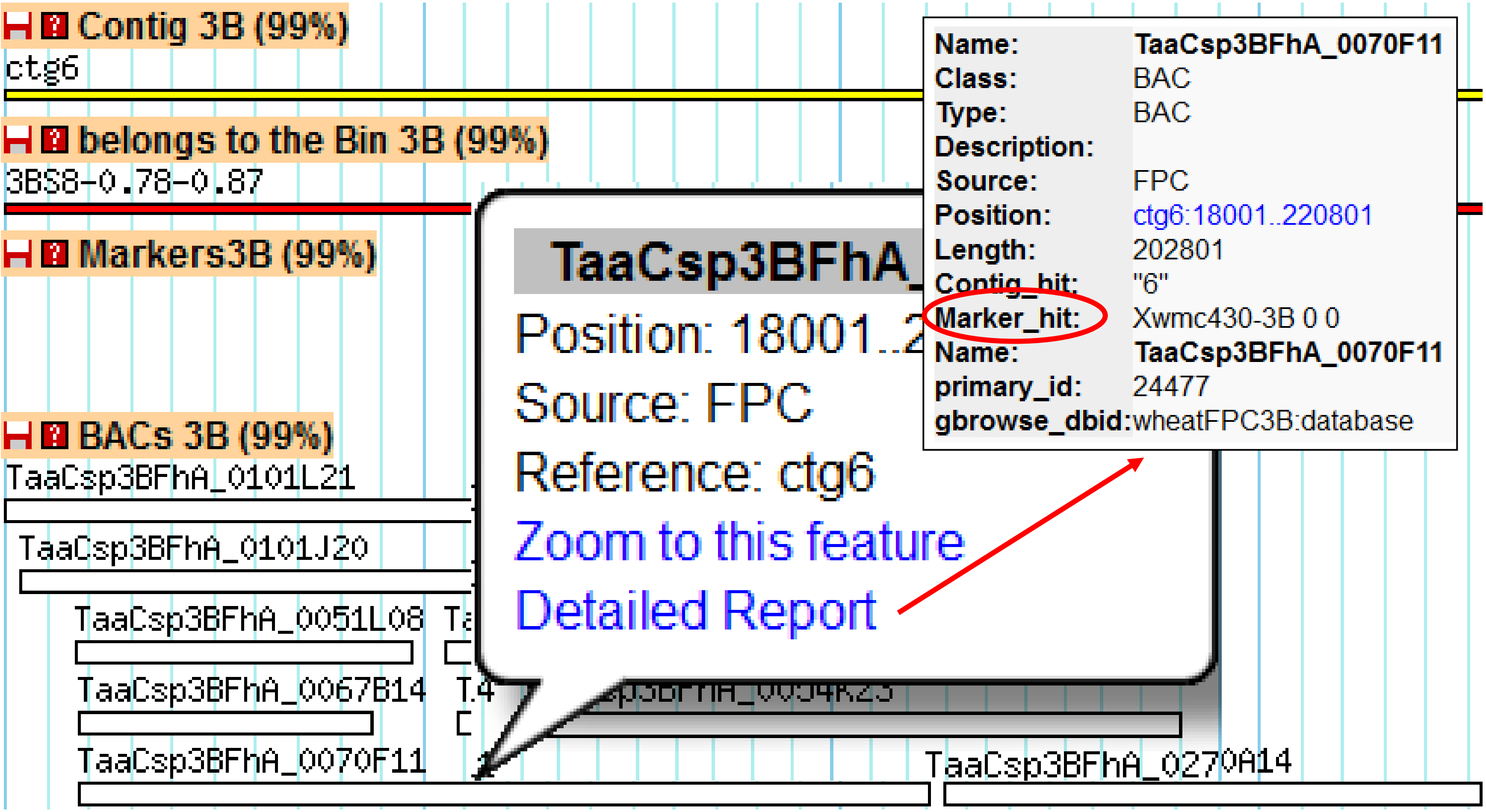
Deletion Bins

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

- 3BS3-0.87-1.00
- 3BS8-0.78-0.87
- 3BS7-0.75-0.78
- 3BS9-0.57-0.75
- 3BS2-0.56-0.57
- 3BS4-0.55-0.56
- 3BS1-0.33-0.55
- 3BS5-0.07-0.33
- C-3BS5-0.07
- C-3BL2-0.22
- 3BL2-0.22-0.28
- 3BL8-0.28-0.31
- 3BL1-0.31-0.38
- 3BL9-0.38-0.50
- 3BL10-0.50-0.63
- 3BL7-0.63-1.00

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

Wheat Physical Map Viewer



Contig 3B (99%)

ctg6

belongs to the Bin 3B (99%)

3BS8-0.78-0.87

Markers3B (99%)

BACs 3B (99%)

TaaCsp3BFhA_0101L21

TaaCsp3BFhA_0101J20

TaaCsp3BFhA_0051L08 Ta

TaaCsp3BFhA_0067B14 T.4

TaaCsp3BFhA_0070F11

TaaCsp3BFhA_0270A14

TaaCsp3BFhA_

Position: 18001..2

Source: FPC

Reference: ctg6

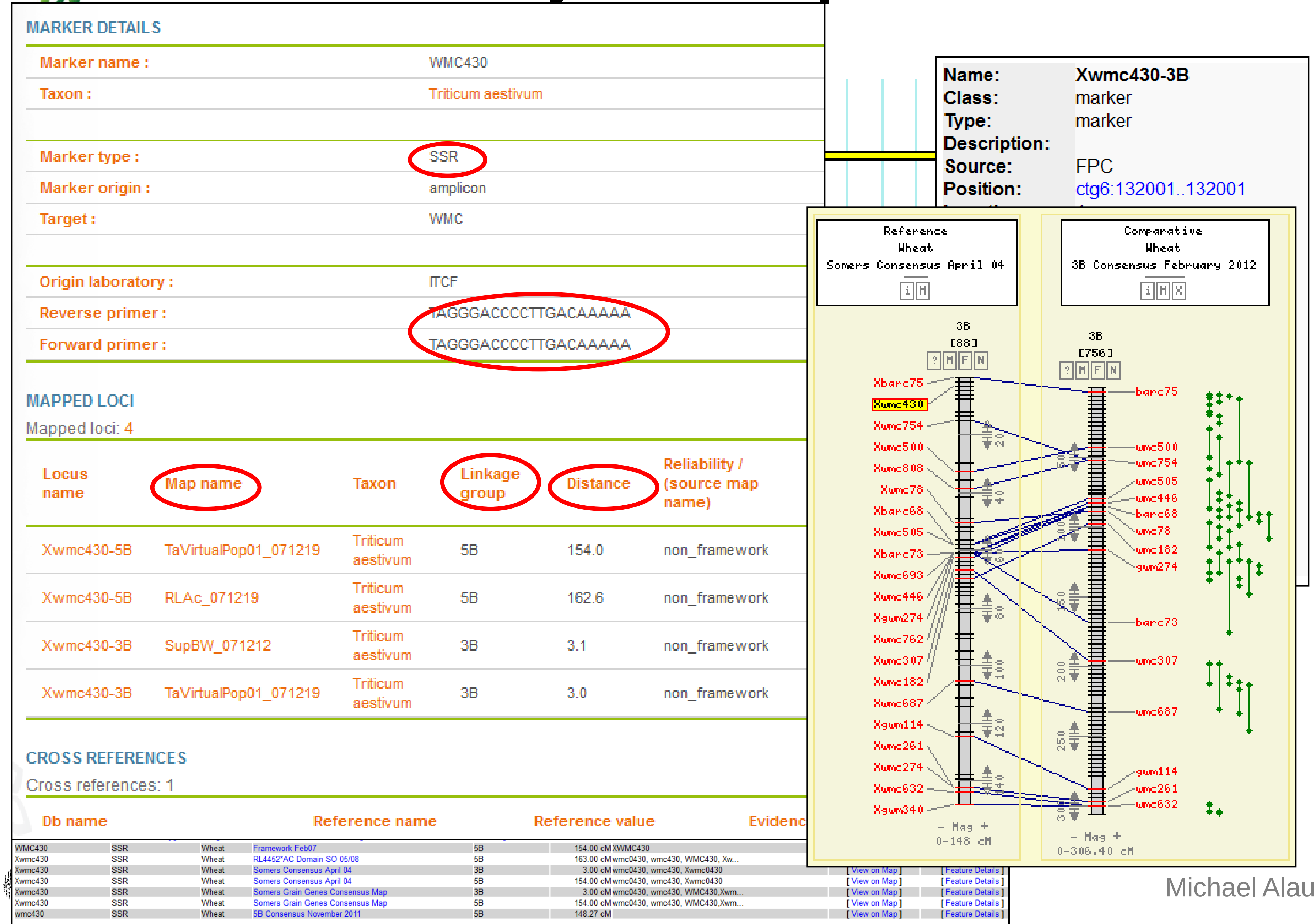
Zoom to this feature

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	Evidenc

WMC430	SSR	Wheat	Framework Feb07	5B	154.00 cM	XWMC430		
Xwmc430	SSR	Wheat	RL4452*AC Domain SO 05/08	5B	163.00 cM	wmc0430, wmc430, WMC430, Xw...		
Xwmc430	SSR	Wheat	Somers Consensus April 04	3B	3.00 cM	wmc0430, wmc430, Xwmc0430	[View on Map]	[Feature Details]
Xwmc430	SSR	Wheat	Somers Consensus April 04	5B	154.00 cM	wmc0430, wmc430, Xwmc0430	[View on Map]	[Feature Details]
Xwmc430	SSR	Wheat	Somers Grain Genes Consensus Map	3B	3.00 cM	wmc0430, wmc430, WMC430,Xwm...	[View on Map]	[Feature Details]
Xwmc430	SSR	Wheat	Somers Grain Genes Consensus Map	5B	154.00 cM	wmc0430, wmc430, WMC430,Xwm...	[View on Map]	[Feature Details]
wmc430	SSR	Wheat	5B Consensus November 2011	5B	148.27 cM		[View on Map]	[Feature Details]

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

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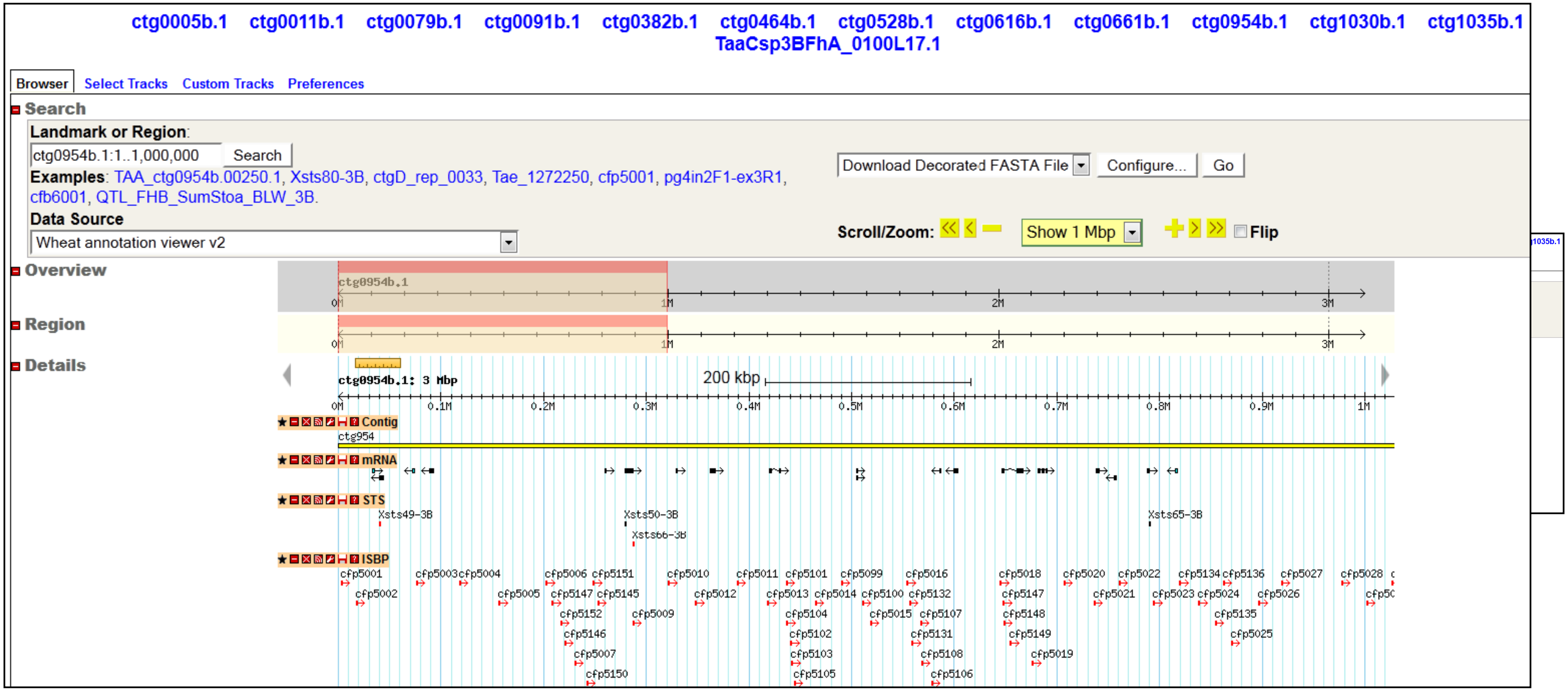
Survey Sequence Repository



Landmark or Region:

ctg0954b.1:1..1,000,000

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

ctg0954b.1: 3 Mbp

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

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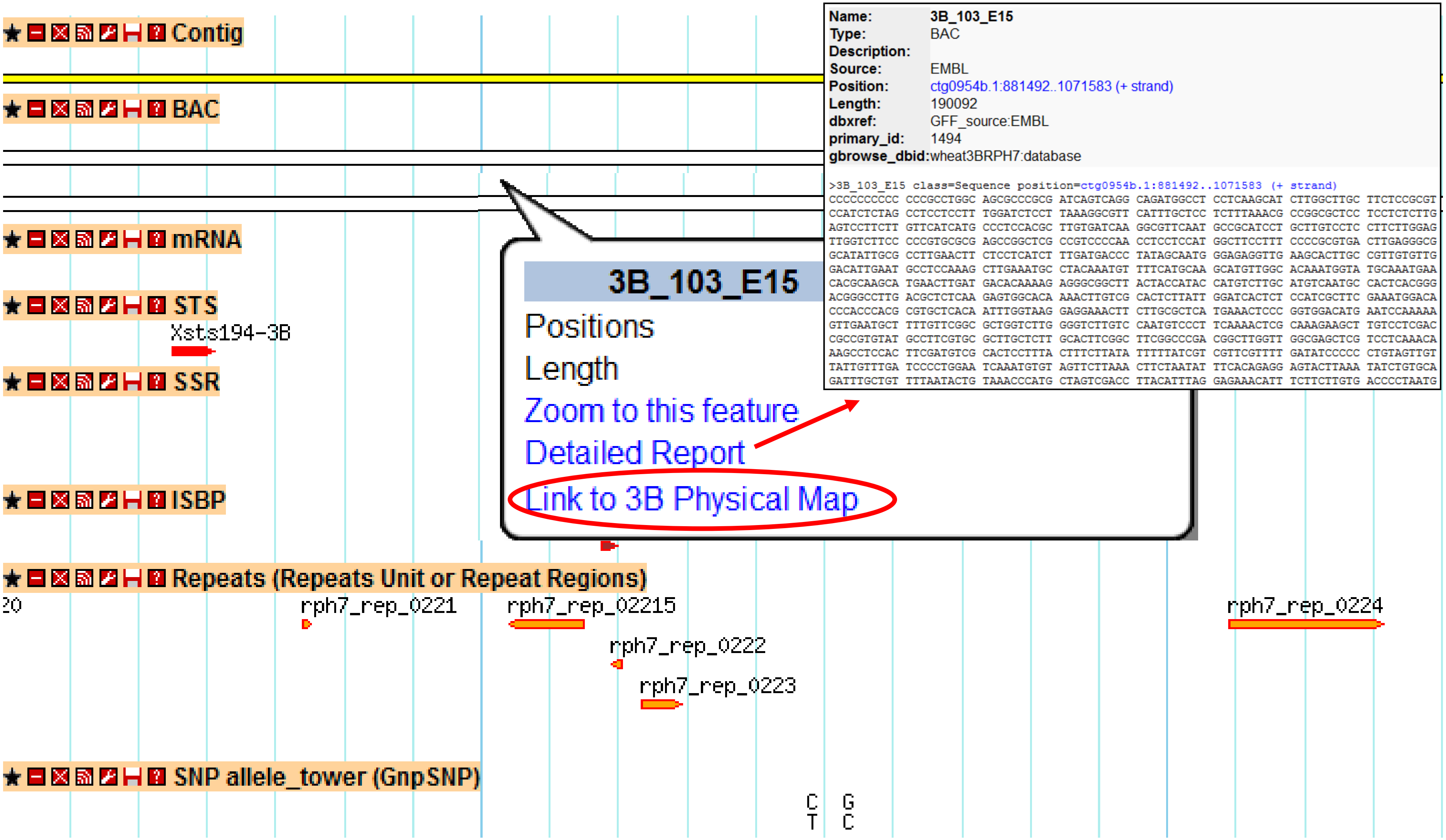
Wheat Annotation Viewer



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)
CCCCCCCCCC CCCGCCTGGC AGCGCCCGCG ATCAGTCAGG CAGATGGCCT CCTCAAGCAT CTTGGCTTGC TTCTCCGCGT
CCATCTCTAG CCTCCTCCTT TGGATCTCCT TAAAGGCGTT CATTTGCTCC TCTTTAAACG CCGGCGCTCC TCCTCTCTTG
AGTCCTTCTT GTTCATCATG CCCTCCACGC TTGTGATCAA GGCGTTCAAT GCCGCATCCT GCTTGTCCTC CTTCTTGGAG
TTGGTCTTCC CCCGTGCGCG AGCCGGCTCG CCGTCCCCAA CCTCCTCCAT GGCTTCCTTT CCCCGCGTGA CTTGAGGGCG
GCATATTGCG CCTTGAACTT CTCCTCATCT TTGATGACCC TATAGCAATG GGAGAGGTTG AAGCACTTGC CGTTGTGTTG
GACATTGAAT GCCTCCAAAG CTTGAAATGC CTACAAATGT TTTCATGCAA GCATGTTGGC ACAAATGGTA TGCAAATGAA
CACGCAAGCA TGAACTTGAT GACACAAAAG AGGGCGGCTT ACTACCATAC CATGTCTTGC ATGTCAATGC CACTCACGGG
ACGGGCCTTG ACGCTCTCAA GAGTGGCACA AAACTTGTCG CACTCTTATT GGATCACTCT CCATCGCTTC GAAATGGACA
CCCACCCACG CGTGCTCACA ATTTGGTAAG GAGGAAACTT CTTGCGCTCA TGAAACTCCC GGTGGACATG AATCCAAAAA
GTTGAATGCT TTTGTTCGGC GCTGGTCTTG GGGTCTTGTC CAATGTCCCT TCAAAACTCG CAAAGAAGCT TGTCCTCGAC
CGCCGTGTAT GCCTTCGTGC GCTTGCTCTT GCACTTCGGC TTCGGCCCGA CGGCTTGGTT GGCGAGCTCG TCCTCAAACA
AAGCCTCCAC TTCGATGTCG CACTCCTTTA CTTTCTTATA TTTTTATCGT CGTTCGTTTT GATATCCCCC CTGTAGTTGT
TATTGTTTGA TCCCCTGGAA TCAAATGTGT AGTTCTTAAA CTTCTAATAT TTCACAGAGG AGTACTTAAA TATCTGTGCA
GATTTGCTGT TTTAATACTG TAAACCCATG CTAGTCGACC TTACATTTAG GAGAAACATT TCTTCTTGTG ACCCCTAATG
```

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

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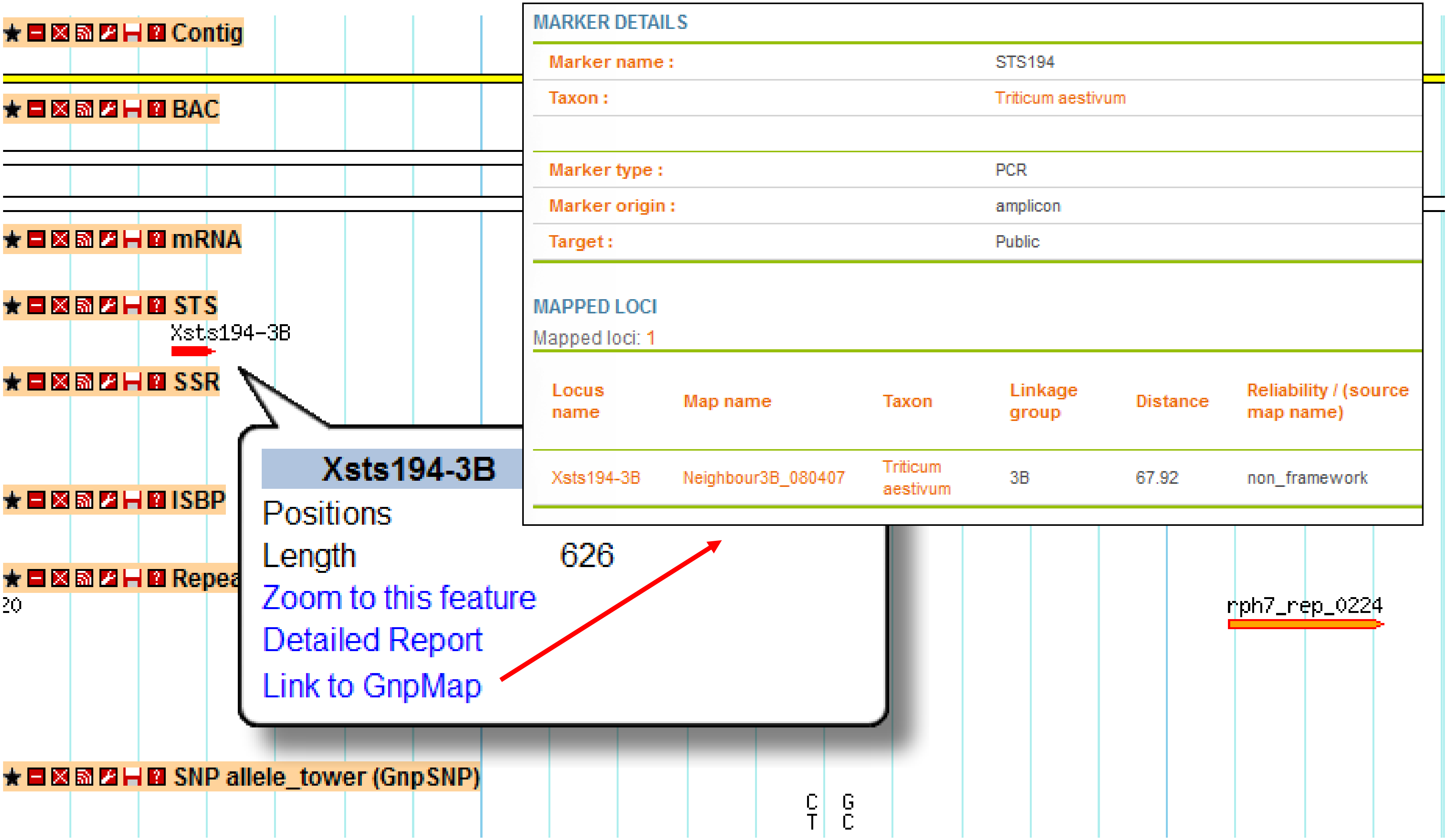
Wheat Annotation Viewer

TAA_ctg0954b.00200.1

Positions	1065073 .. 1068219
Length	3147
Gene Name	gad1
Function	glutamate decarboxylase putative expressed
Note 1	best blast hit in Brachypodium distachyon: Bradi3g37830.1 87% identity

Wheat Annotation Viewer



Xsts194-3B

Positions

Length 626

Zoom to this feature

Detailed Report

Link to GnpMap

MARKER DETAILS

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

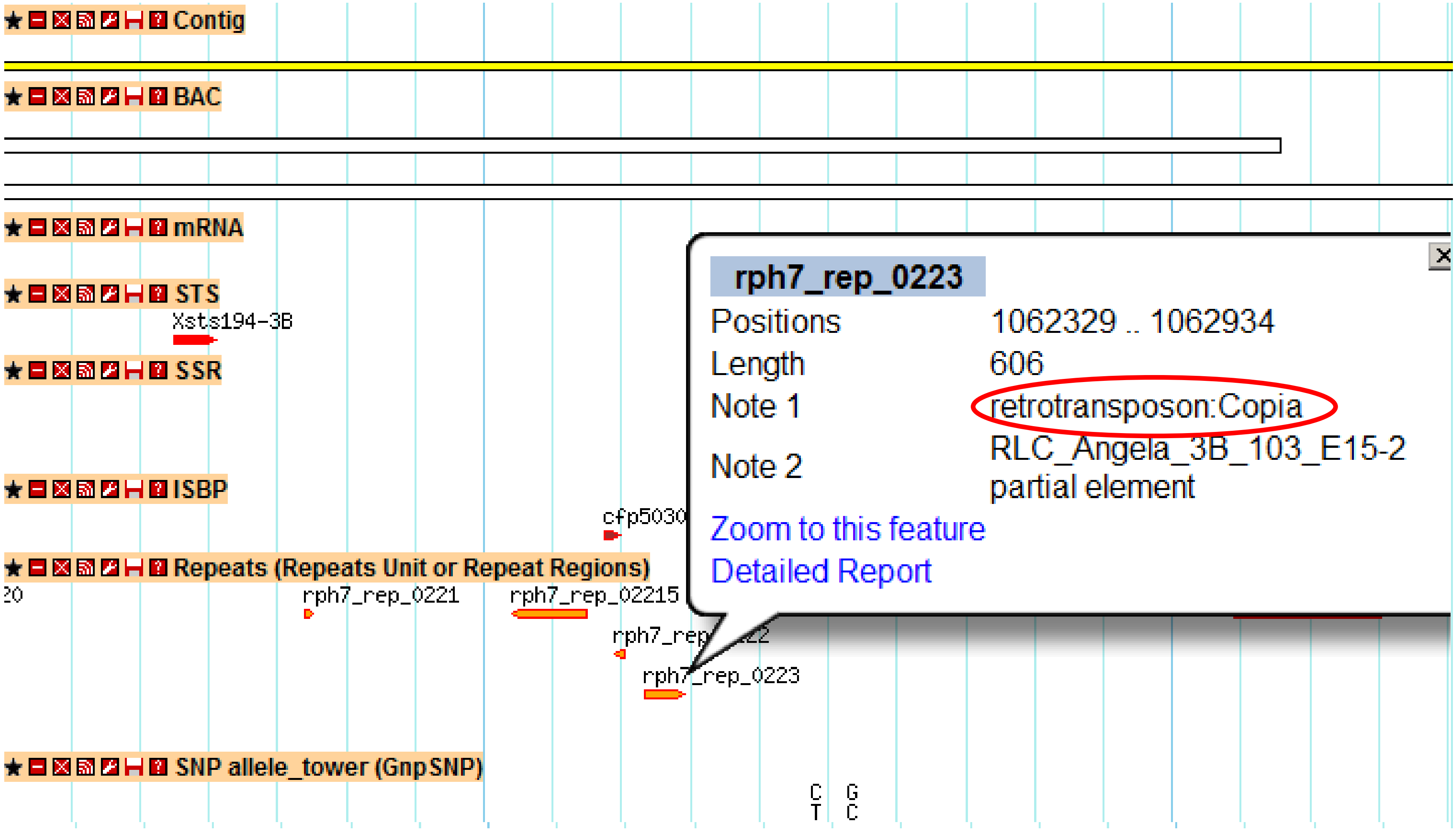
MAPPED LOCI

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

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

Wheat Annotation Viewer

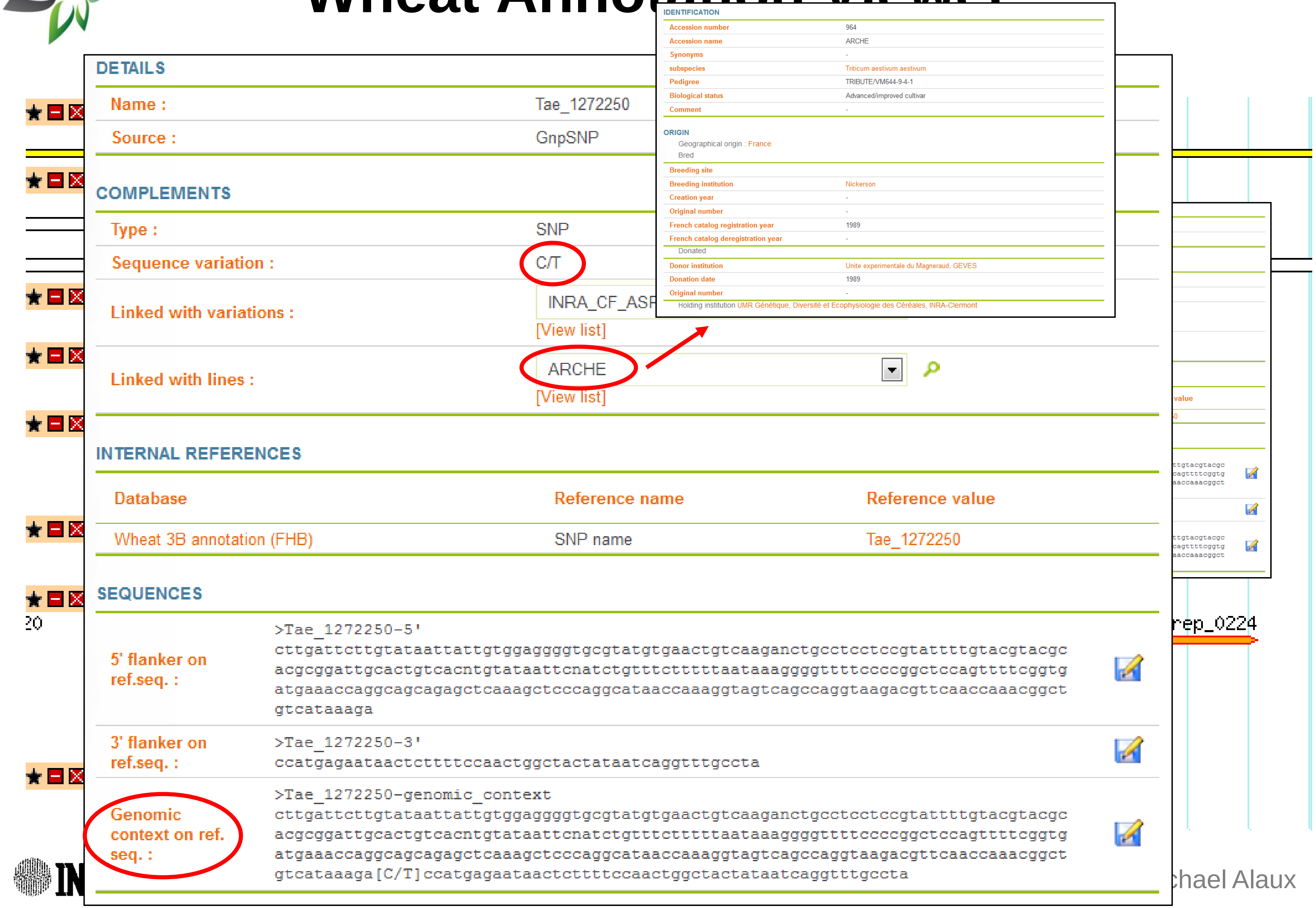


rph7_rep_0223

Positions	1062329 .. 1062934
Length	606
Note 1	retrotransposon:Copia
Note 2	RLC_Angela_3B_103_E15-2 partial element

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

Wheat Annotation Viewer



DETAILS

Name :	Tae_1272250
Source :	GnpSNP

COMPLEMENTS

Type :	SNP
Sequence variation :	C/T
Linked with variations :	INRA_CF_ASF [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'
cttgattcttgtataattattgtggaggggtgcgtatgtgaactgtcaaganctgcctcctccgtattttgtacgtacgc
acgcggattgcactgtcacntgtataattcnatctgtttctttttaataaaggggttttccccggctccagttttcggtg
atgaaaccaggcagcagagctcaaagctcccaggcataaccaaaggtagtcagccaggtaagacgttcaaccaaacggct
gtcataaaga
```

3' flanker on ref.seq. :

```
>Tae_1272250-3'
ccatgagaataactcttttccaactggctactataatcaggtttgccta
```

Genomic context on ref. seq. :

```
>Tae_1272250-genomic_context
cttgattcttgtataattattgtggaggggtgcgtatgtgaactgtcaaganctgcctcctccgtattttgtacgtacgc
acgcggattgcactgtcacntgtataattcnatctgtttctttttaataaaggggttttccccggctccagttttcggtg
atgaaaccaggcagcagagctcaaagctcccaggcataaccaaaggtagtcagccaggtaagacgttcaaccaaacggct
gtcataaaga[C/T]ccatgagaataactcttttccaactggctactataatcaggtttgccta
```

IDENTIFICATION

Accession number	964
Accession name	ARCHE
Synonyms	-
subspecies	Triticum aestivum aestivum
Pedigree	TRIBUTE/VM644-9-4-1
Biological status	Advanced/improved cultivar
Comment	-

ORIGIN

Geographical origin : France

Bred

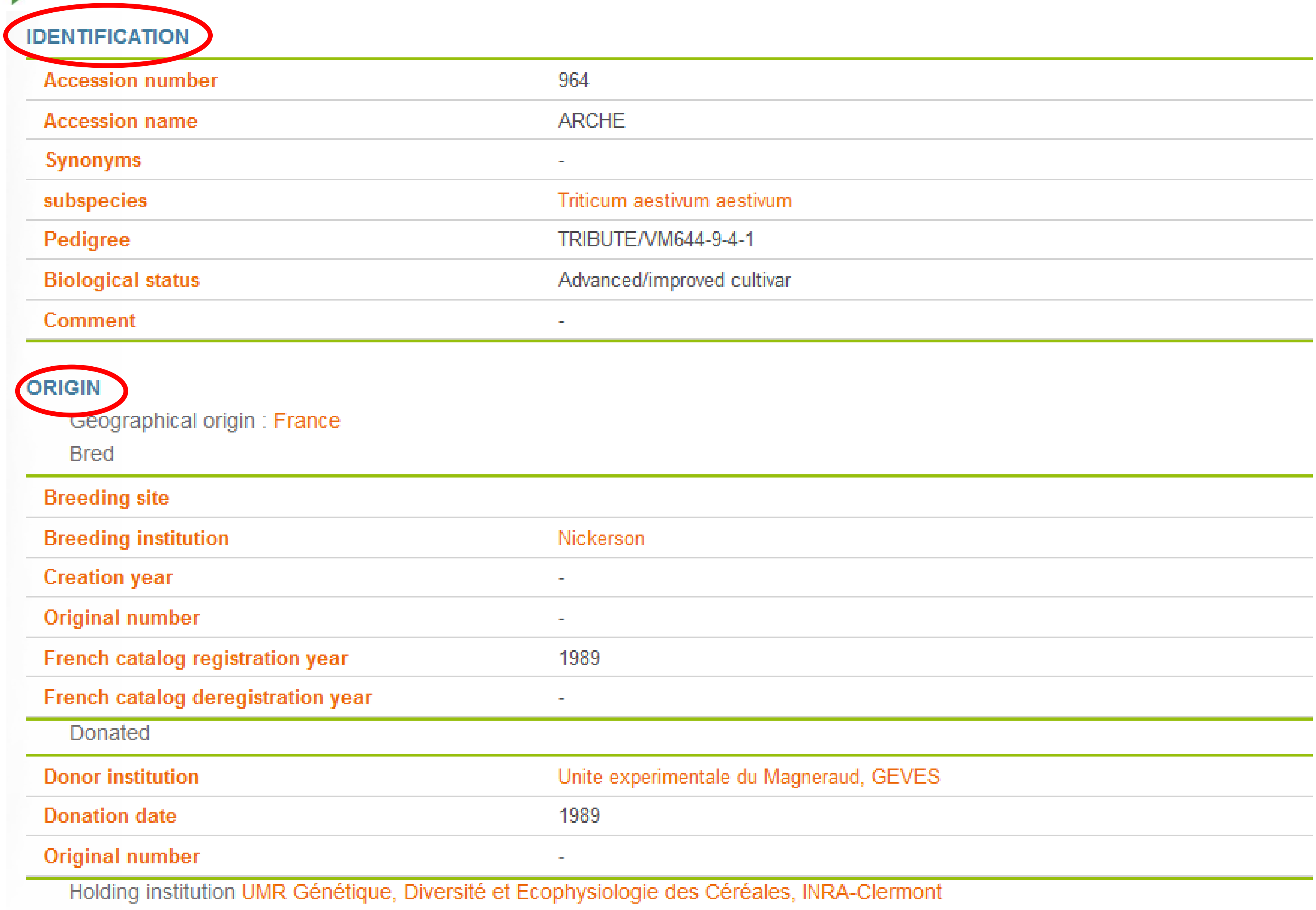
Breeding site	
Breeding institution	Nickerson
Creation year	-
Original number	-
French catalog registration year	1989
French catalog deregistration year	-

Donated

Donor institution	Unite experimentale du Magneraud, GEVES
Donation date	1989
Original number	-

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

Wheat Annotation Viewer



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

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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

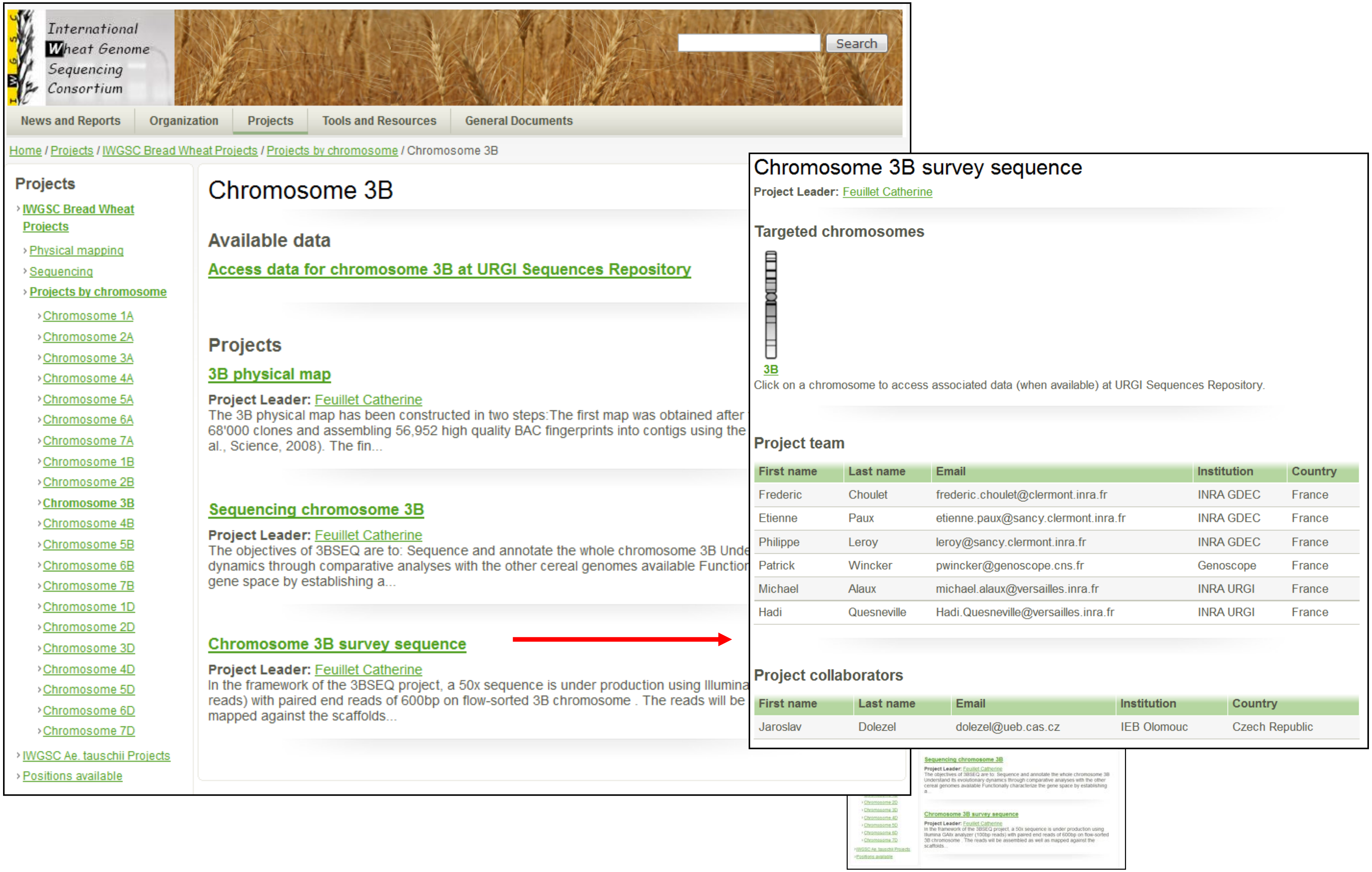
GENOTYPING

This accession has been genotyped: see ARCHE in GnpSNP.

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

Michael Alaux

Survey Sequence Repository



International Wheat Genome Sequencing Consortium

Search

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 Unde
dynamics through comparative analyses with the other cereal genomes available Functior
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
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Project collaborators

First name	Last name	Email	Institution	Country
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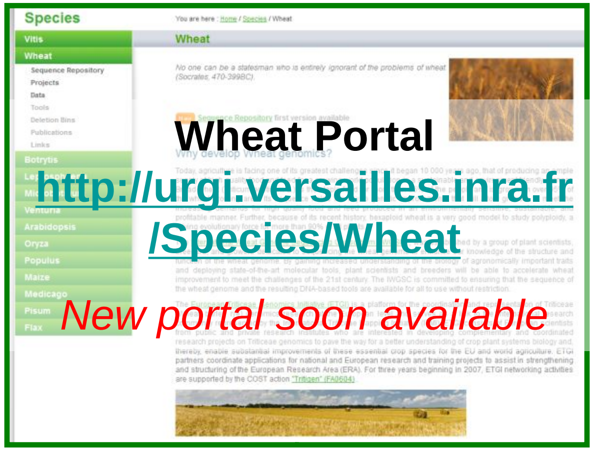
Sequencing chromosome 3B
Project Leader: Feuillet Catherine
The objectives of 3BSEQ are to: Sequence and annotate the whole chromosome 3B Understand its evolutionary dynamics through comparative analyses with the other cereal genomes available Functionally characterize the gene space by establishing a...

Chromosome 3B survey sequence
Project Leader: Feuillet Catherine
In the framework of the 3BSEQ project, a 50x sequence is under production using Illumina GAIIx analyzer (100bp reads) with paired end reads of 600bp on flow-sorted 3B chromosome . The reads will be assembled as well as mapped against the scaffolds...

Chromosome 2D
Chromosome 3D
Chromosome 4D
Chromosome 5D
Chromosome 6D
Chromosome 7D
IWGSC Ae. tauschii Projects
Positions available

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

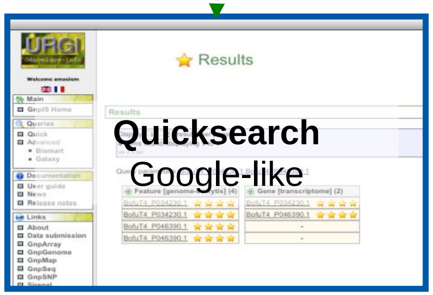
Wheat dataflow overview at URGI



Wheat Portal

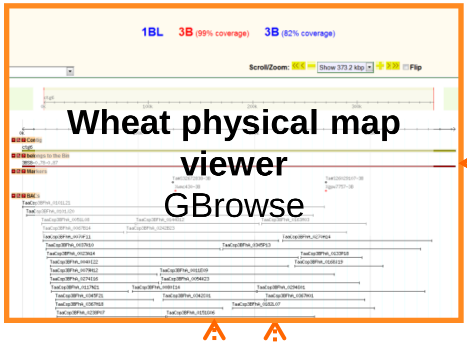
http://urgi.versailles.inra.fr/Species/Wheat

New portal soon available



Quicksearch

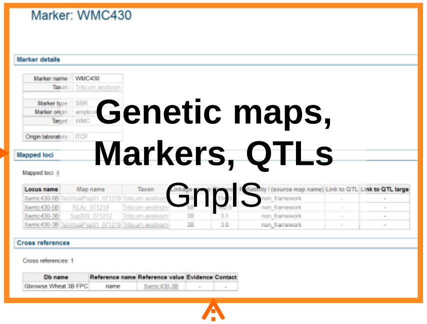
Google-like



1BL 3B (99% coverage) 3B (82% coverage)

Wheat physical map viewer

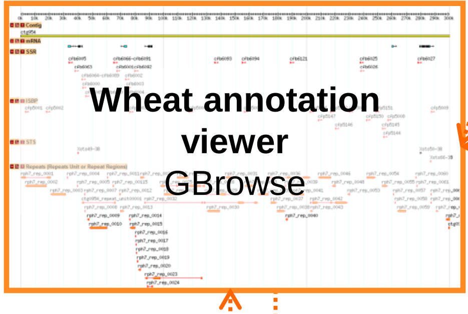
GBrowse



Marker: WMC430

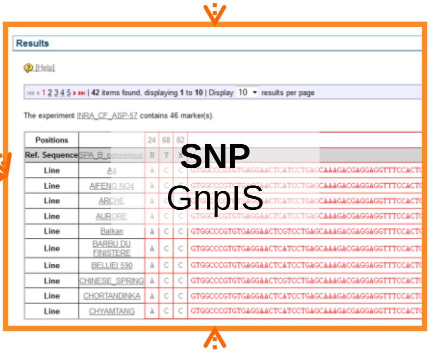
Genetic maps, Markers, QTLs

GnpIS



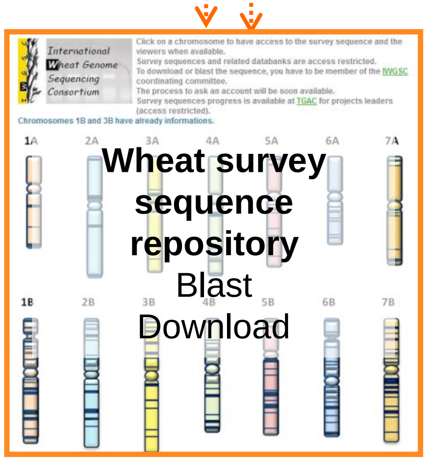
Wheat annotation viewer

GBrowse



SNP

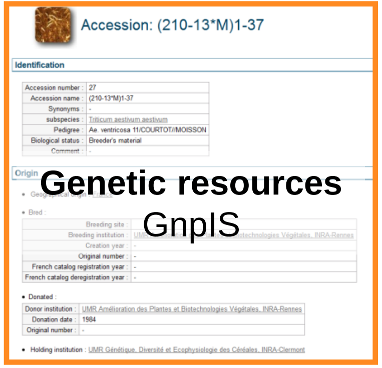
GnpIS



Wheat survey sequence repository

Blast

Download



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

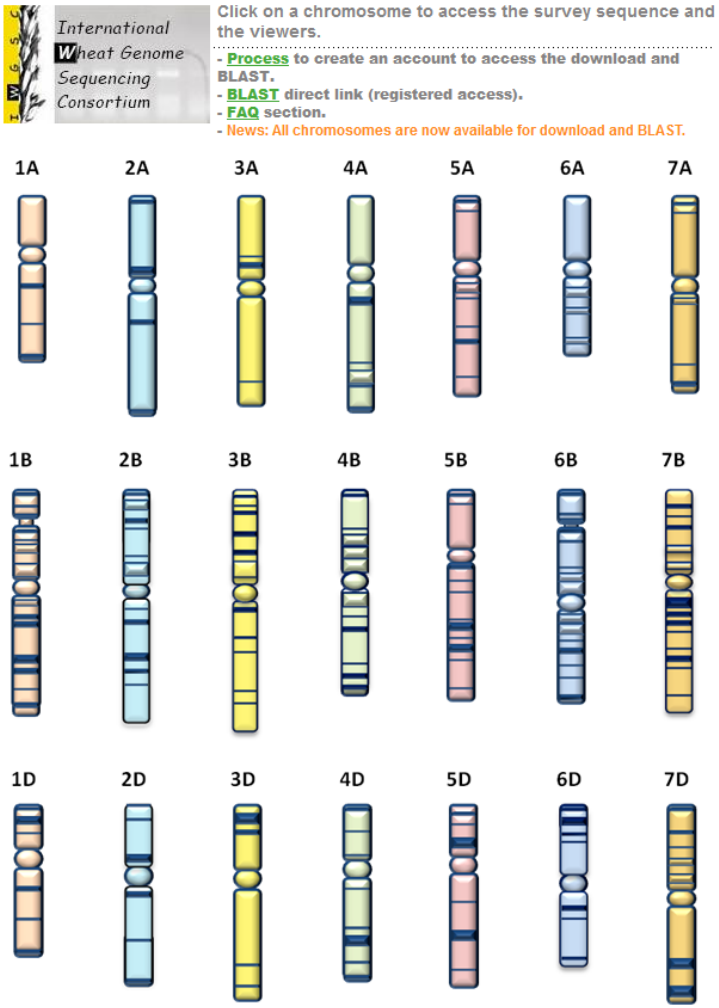
Genetic resources

GnpIS

Michael Alaux

Perspectives

Survey Sequence Repository



International Wheat Genome Sequencing Consortium

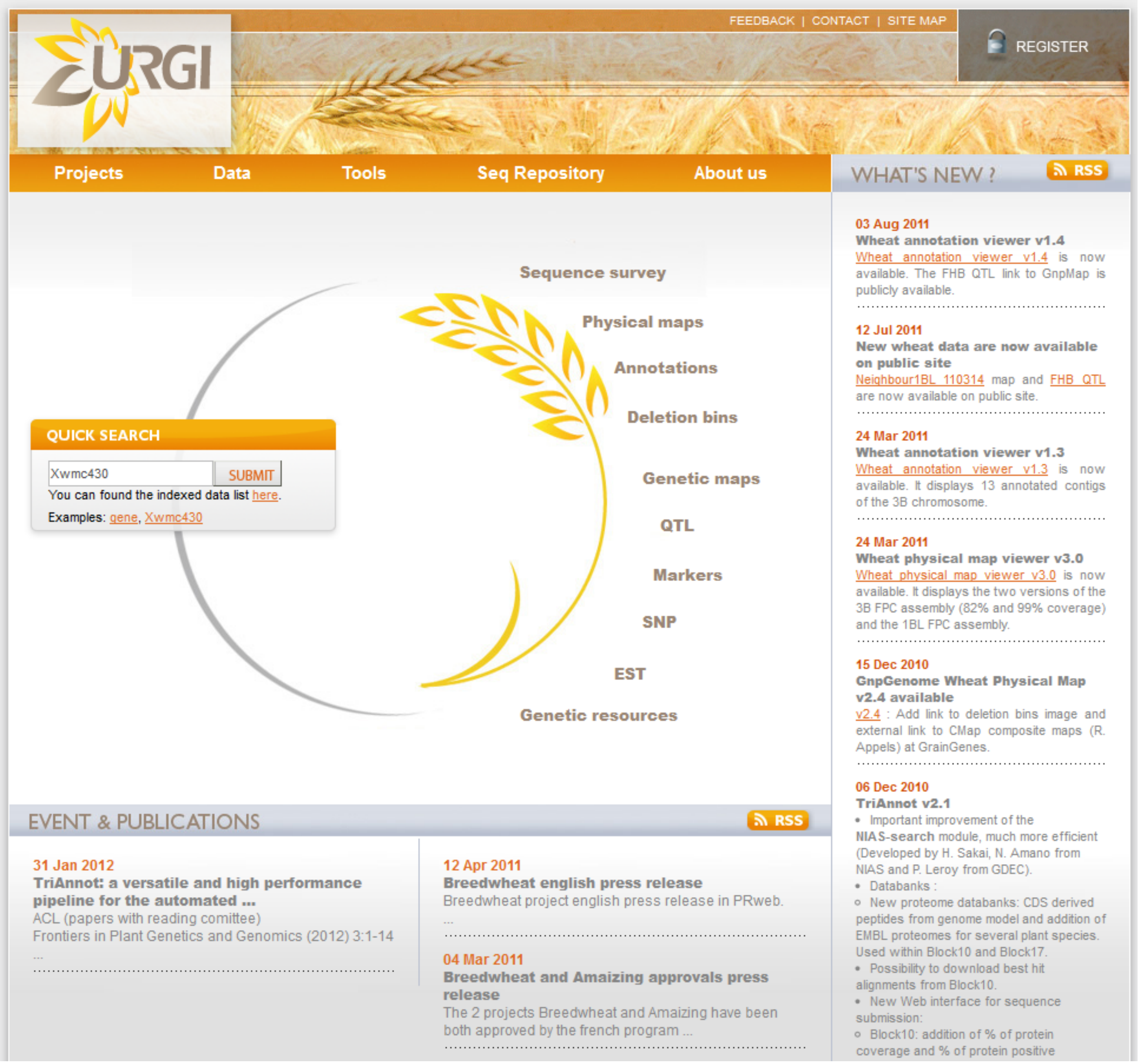
Click on a chromosome to access the survey sequence and the viewers.

- **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.

- Page to access easily the other kind of BLAST.
- Add 454 data

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

New Wheat Portal soon available



You can found the indexed data list here.

Examples: gene, Xwmc430

WHAT'S NEW ? RSS

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

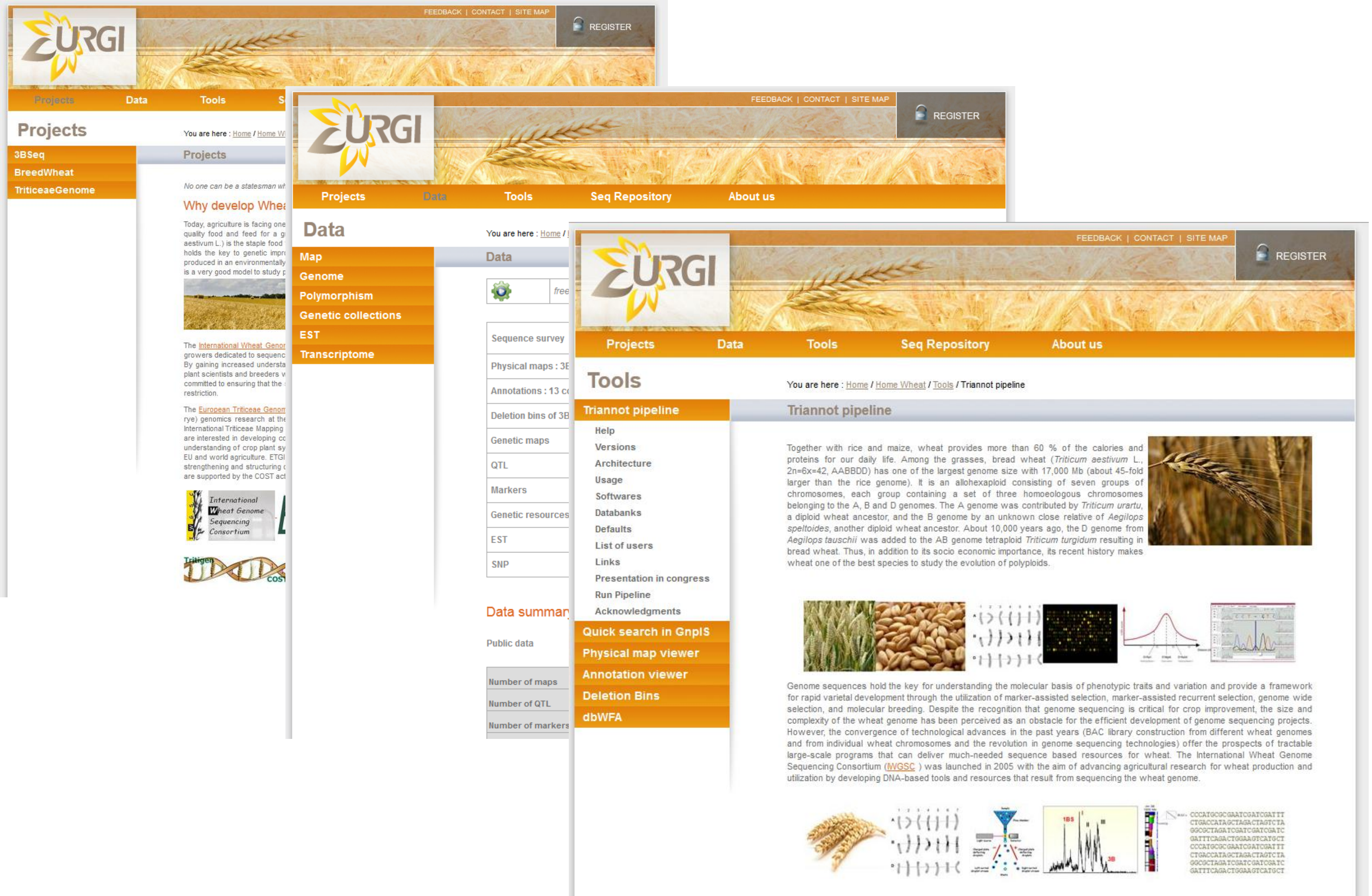
EVENT & PUBLICATIONS RSS

31 Jan 2012
TriAnnot: a versatile and high performance pipeline for the automated ...
ACL (papers with reading comitee)
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 ...

New Wheat Portal soon available



Projects

- 3BSeq
- BreedWheat
- TriticeaeGenome

Data

- Map
- Genome
- Polymorphism
- Genetic collections
- EST
- Transcriptome

Sequence survey

Genetic maps

QTL

Markers

Genetic resources

EST

SNP

Data summary

Public data

Number of maps

Number of QTL

Number of markers

Tools

You are here : Home / Home Wheat / Tools / Triannot pipeline

Triannot pipeline

- 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

dbWFA

Triannot pipeline

Together with rice and maize, wheat provides more than 60 % of the calories and proteins for our daily life. Among the grasses, bread wheat (*Triticum aestivum* L., 2n=6x=42, AABBDD) has one of the largest genome size with 17,000 Mb (about 45-fold larger than the rice genome). It is an allohexaploid consisting of seven groups of chromosomes, each group containing a set of three homoeologous chromosomes belonging to the A, B and D genomes. The A genome was contributed by *Triticum urartu*, a diploid wheat ancestor, and the B genome by an unknown close relative of *Aegilops speltoides*, another diploid wheat ancestor. About 10,000 years ago, the D genome from *Aegilops tauschii* was added to the AB genome tetraploid *Triticum turgidum* resulting in bread wheat. Thus, in addition to its socio economic importance, its recent history makes wheat one of the best species to study the evolution of polyploids.

Genome sequences hold the key for understanding the molecular basis of phenotypic traits and variation and provide a framework for rapid varietal development through the utilization of marker-assisted selection, marker-assisted recurrent selection, genome wide selection, and molecular breeding. Despite the recognition that genome sequencing is critical for crop improvement, the size and complexity of the wheat genome has been perceived as an obstacle for the efficient development of genome sequencing projects. However, the convergence of technological advances in the past years (BAC library construction from different wheat genomes and from individual wheat chromosomes and the revolution in genome sequencing technologies) offer the prospects of tractable large-scale programs that can deliver much-needed sequence based resources for wheat. The International Wheat Genome Sequencing Consortium (IWGSC) was launched in 2005 with the aim of advancing agricultural research for wheat production and utilization by developing DNA-based tools and resources that result from sequencing the wheat genome.

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 soon available at URGI

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

URGI

Acknowlegments

URGI

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International Wheat Genome Sequencing Consortium

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TGAC The Genome Analysis Centre™
BBSRC EEDA Greater Norwich Development Partnership

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3BSEQ

Triticeae Genome

Breed Wheat

GNPannot

GENOSCOPE
biogemma
INRA Transfert
Filiale de l'INRA

Agence Nationale de la Recherche ANR GIP
GENOPLANTE
SEVENTH FRAMEWORK PROGRAMME
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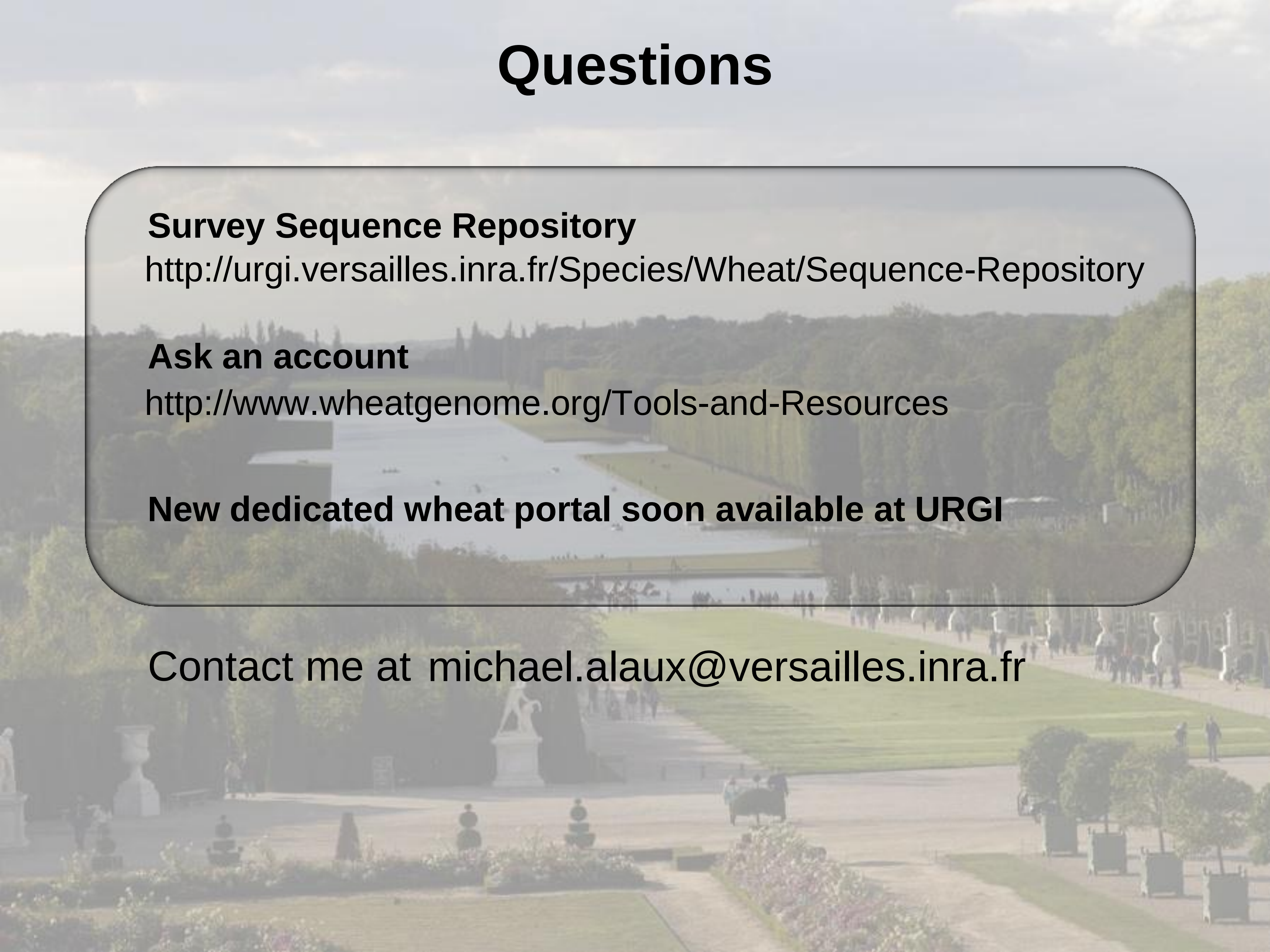

Questions

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