IWGSC Sequence Repository : new data and browsers

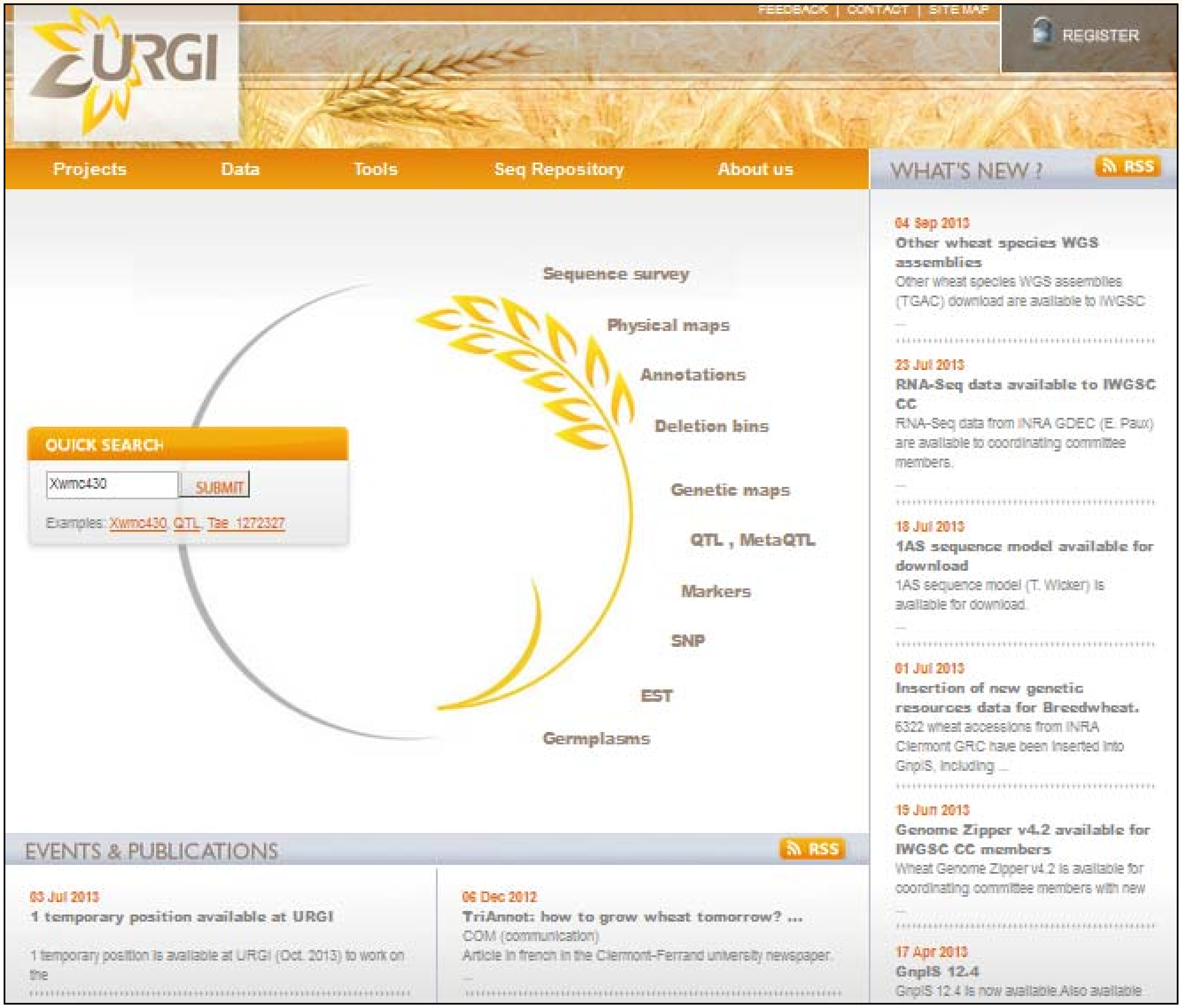
Michael Alaux

IWGS 2013 Yokohama – IWGSC workshop

Wheat@URGI website

Michael Alaux

Wheat@URGI



WHAT'S NEW ?

04 Sep 2013
Other wheat species WGS assemblies
Other wheat species WGS assemblies (TGAC) download are available to IWGSC
...

23 Jul 2013
RNA-Seq data available to IWGSC CC
RNA-Seq data from INRA GDEC (E. Paux) are available to coordinating committee members.
...

18 Jul 2013
1AS sequence model available for download
1AS sequence model (T. Wicker) is available for download.
...

01 Jul 2013
Insertion of new genetic resources data for Breedwheat.
6322 wheat accessions from INRA Clermont GRC have been inserted into GnpIS, including ...

19 Jun 2013
Genome Zipper v4.2 available for IWGSC CC members
Wheat Genome Zipper v4.2 is available for coordinating committee members with new
...

17 Apr 2013
GnpIS 12.4
GnpIS 12.4 is now available Also available

EVENTS & PUBLICATIONS

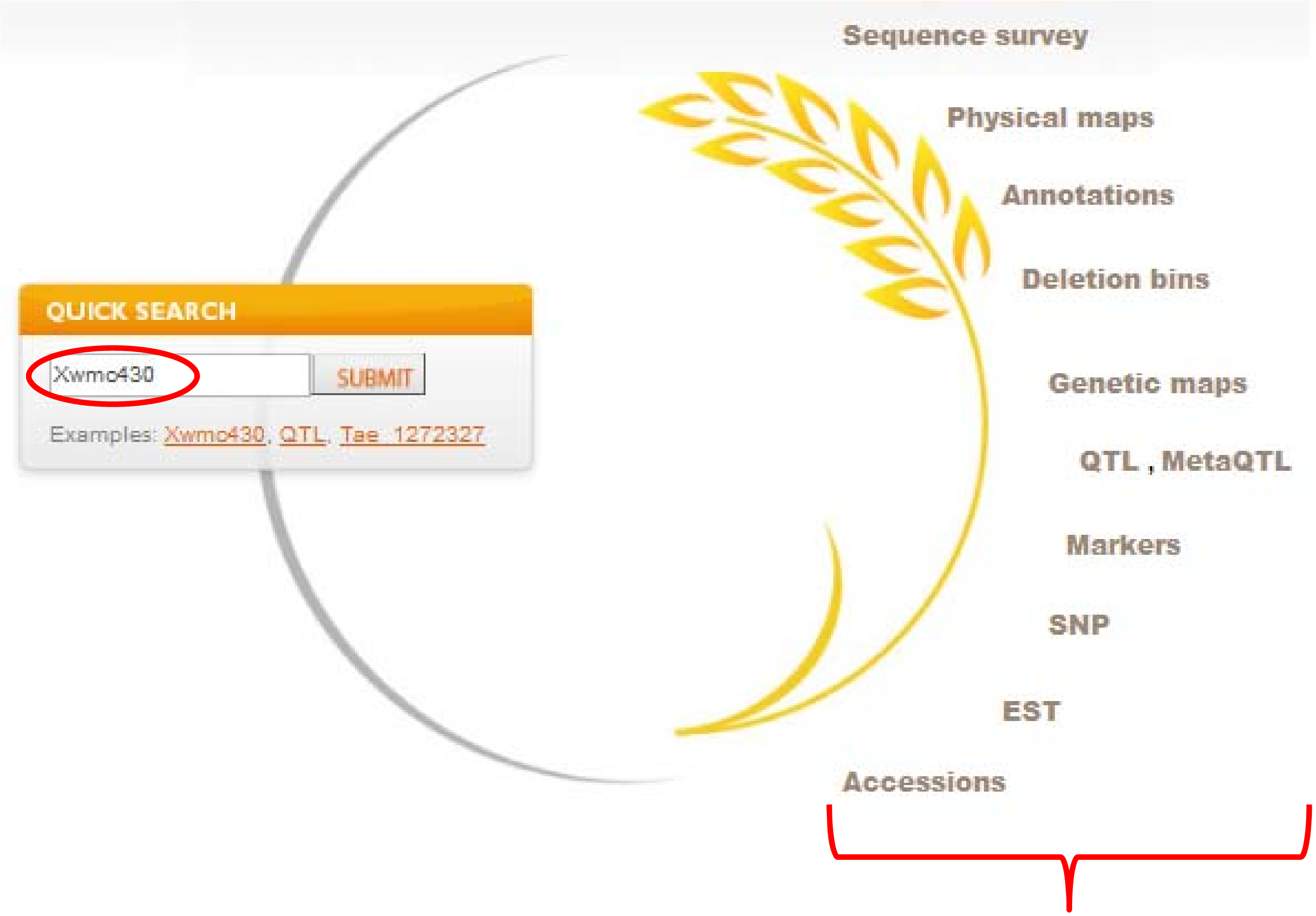
03 Jul 2013
1 temporary position available at URGI
1 temporary position is available at URGI (Oct. 2013) to work on the

06 Dec 2012
TriAnnot: how to grow wheat tomorrow? ...
COM (communication)
Article in french in the Clermont-Ferrand university newspaper.
...

http://wheat-urgi.versailles.inra.fr

Wheat@URGI

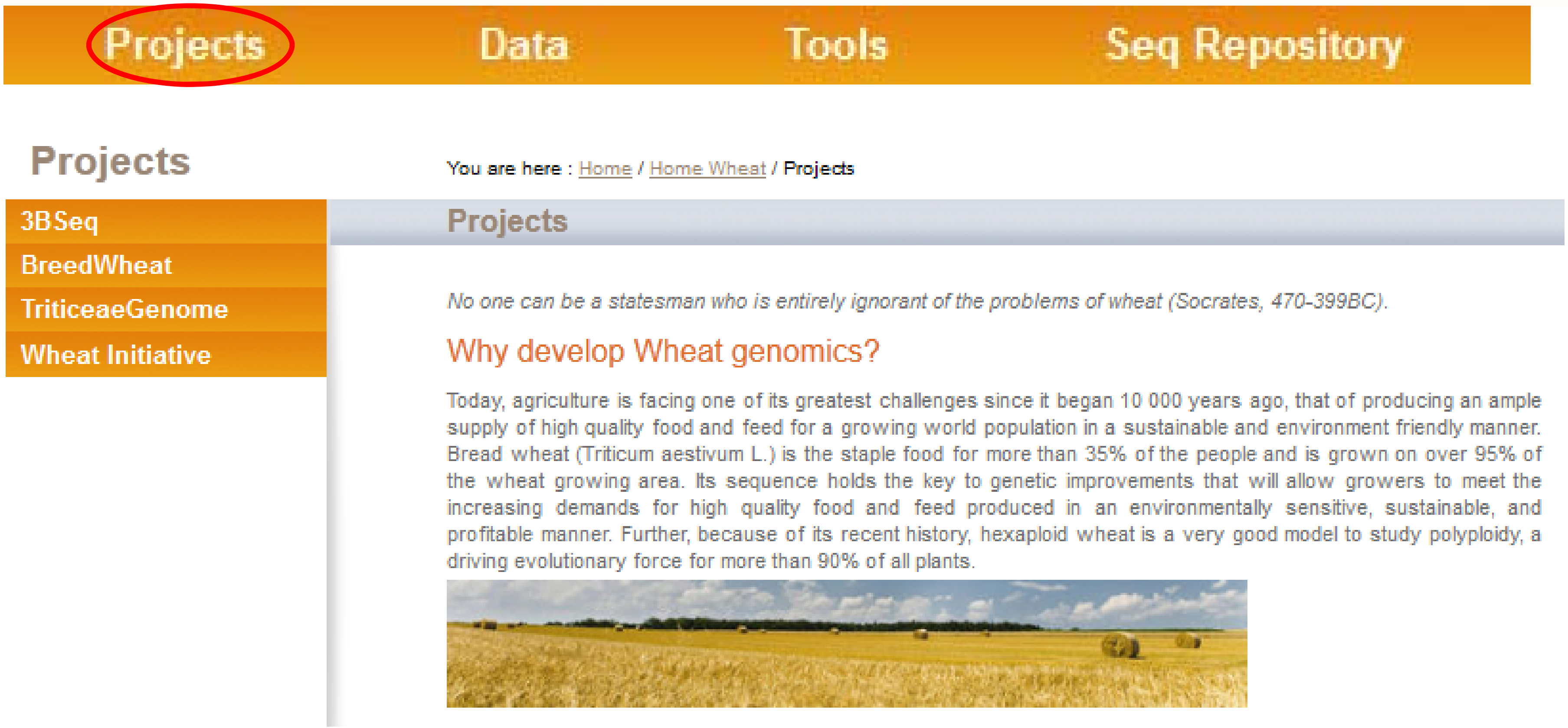
Google-like



Quick Links to data

Search into wheat data in GnpIS the URGI Information system

Wheat@URGI



You are here : Home / Home Wheat / Projects

Projects

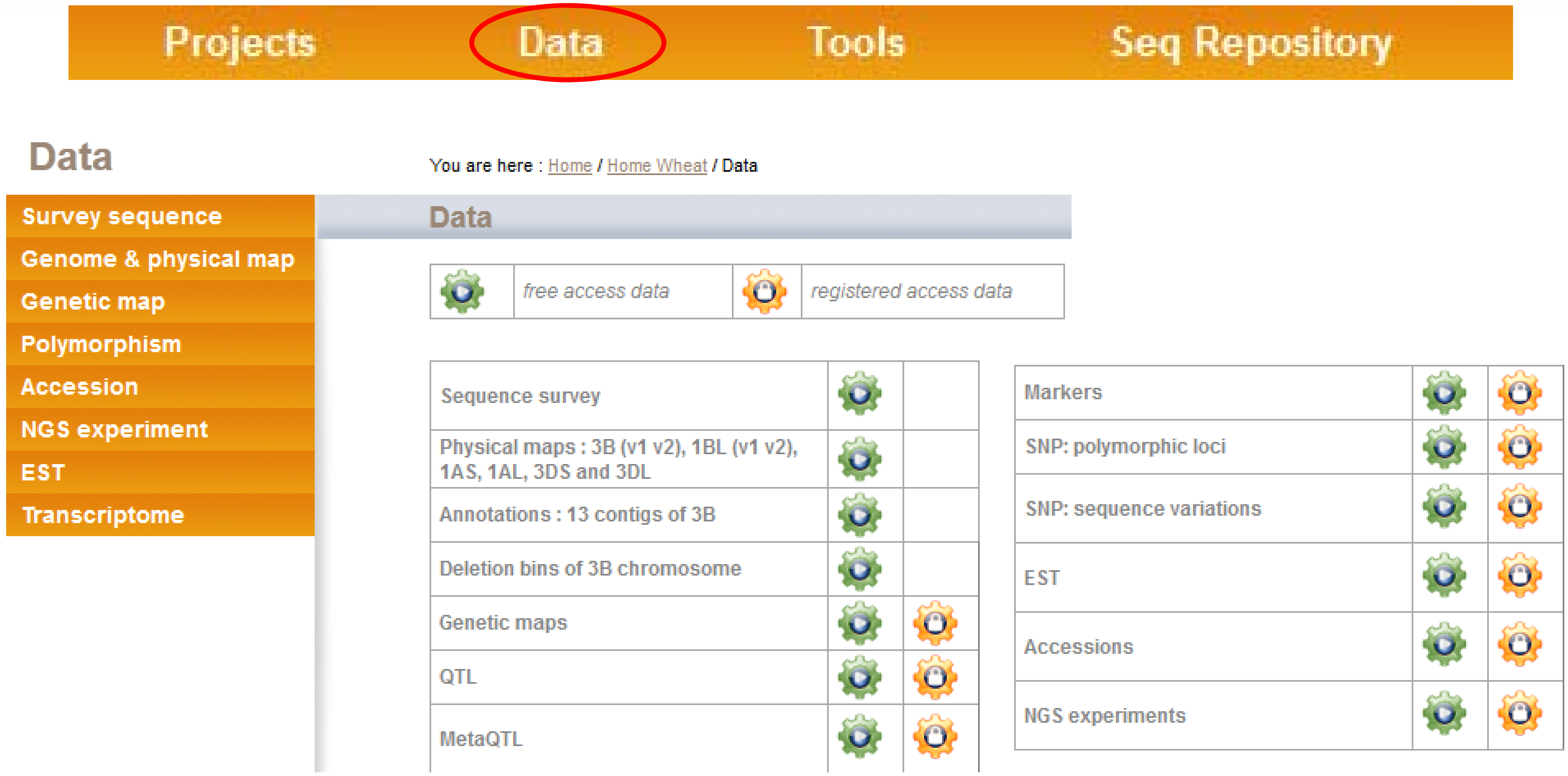
No one can be a statesman who is entirely ignorant of the problems of wheat (Socrates, 470-399BC).

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.

http://wheat-urgi.versailles.inra.fr

Wheat@URGI



You are here : Home / Home Wheat / Data

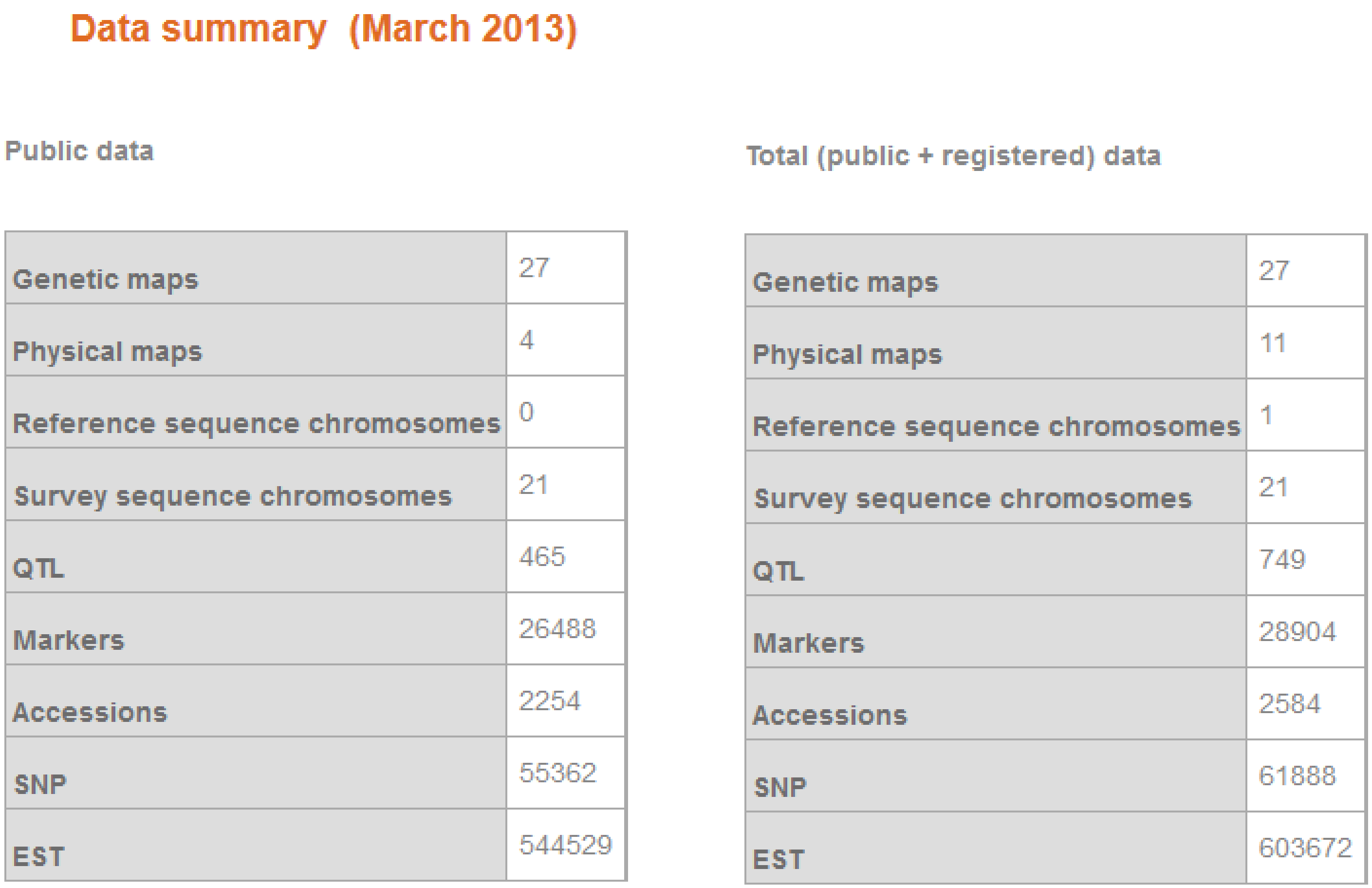
Data

🟩	*free access data*	🟧	*registered access data*

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

Markers	🟩	🟧
SNP: polymorphic loci	🟩	🟧
SNP: sequence variations	🟩	🟧
EST	🟩	🟧
Accessions	🟩	🟧
NGS experiments	🟩	🟧

Wheat@URGI



Data summary (March 2013)

Public data

Genetic maps	27
Physical maps	4
Reference sequence chromosomes	0
Survey sequence chromosomes	21
QTL	465
Markers	26488
Accessions	2254
SNP	55362
EST	544529

Total (public + registered) data

Genetic maps	27
Physical maps	11
Reference sequence chromosomes	1
Survey sequence chromosomes	21
QTL	749
Markers	28904
Accessions	2584
SNP	61888
EST	603672

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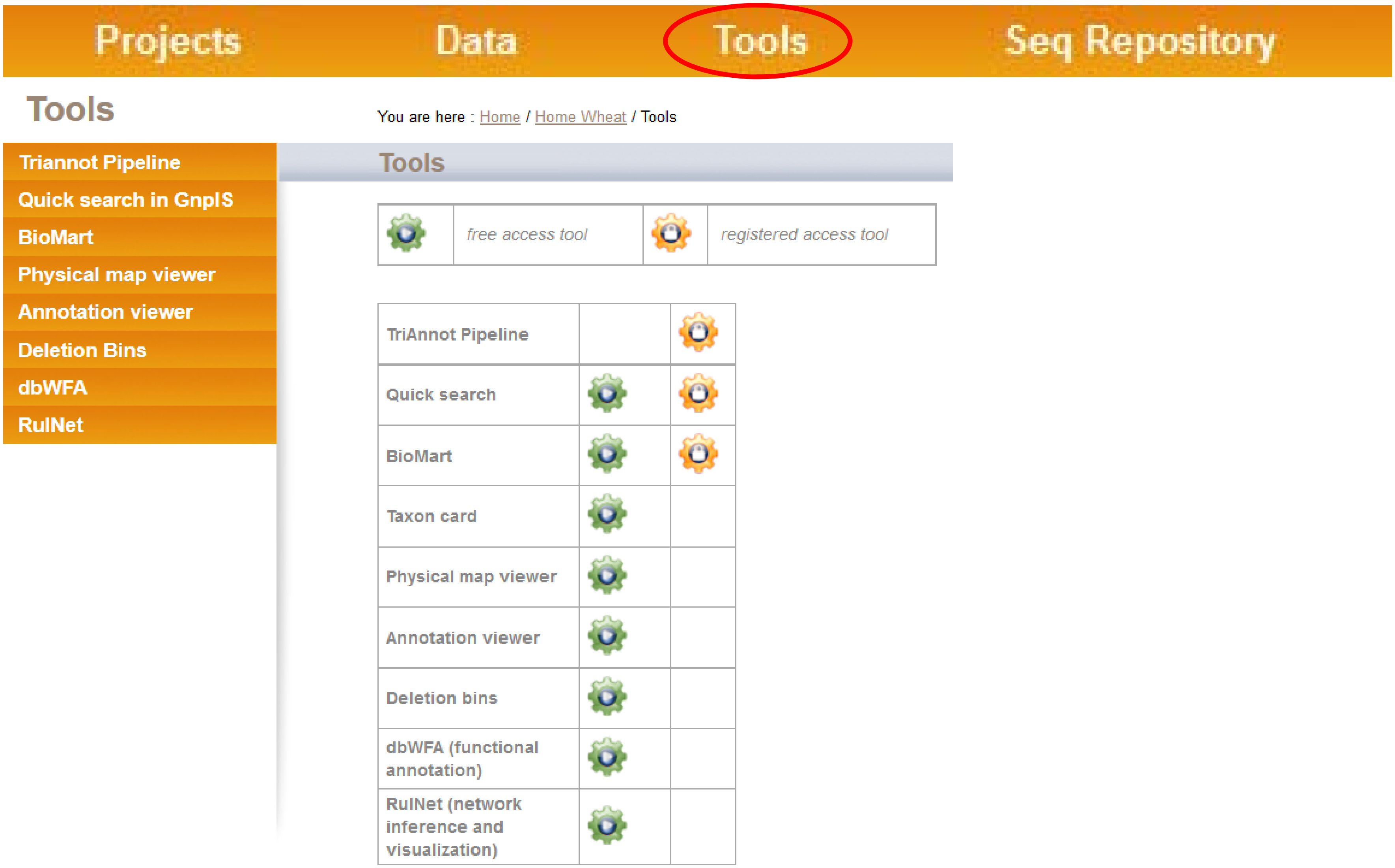


Tools

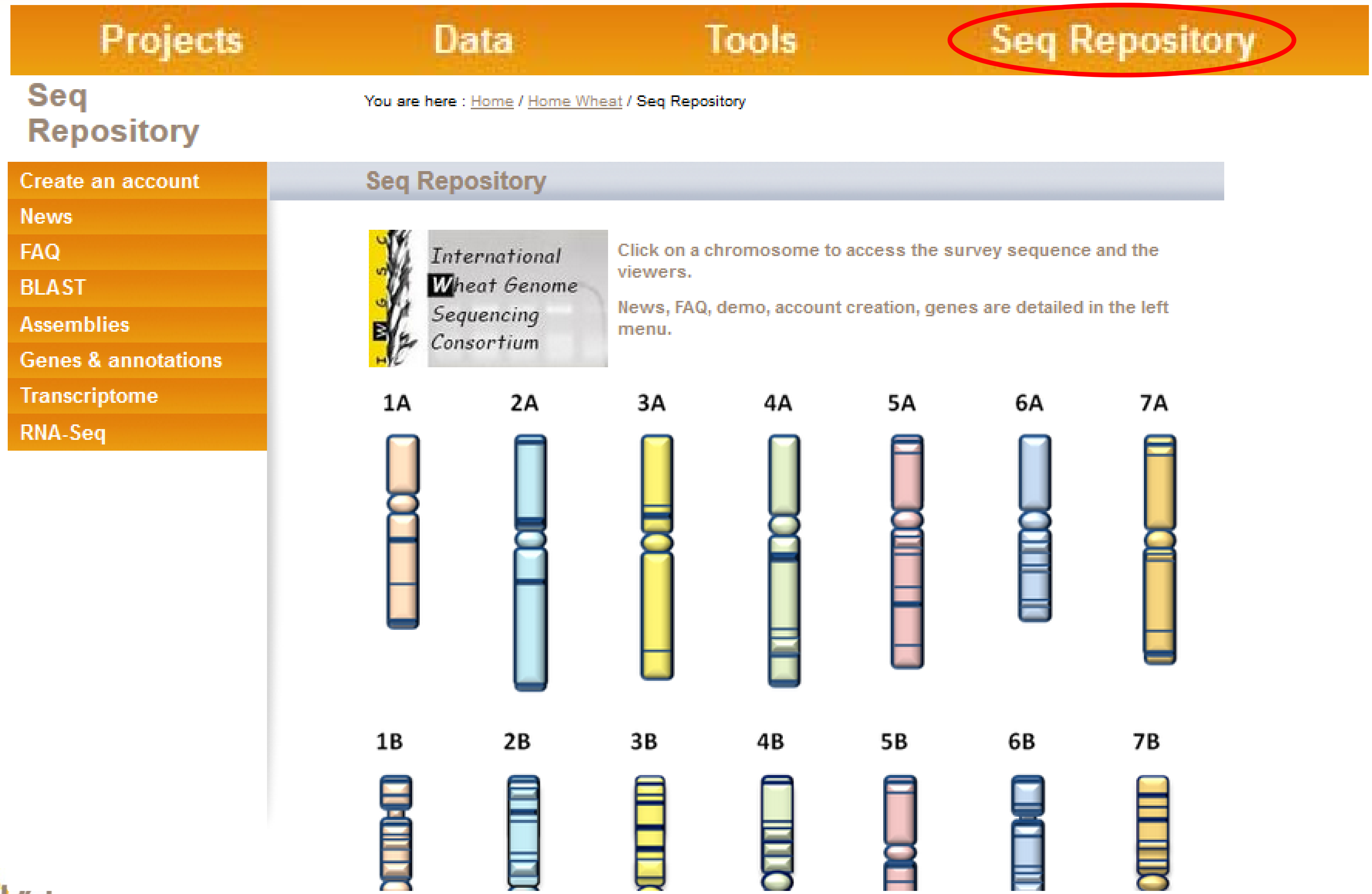
You are here : Home / Home Wheat / Tools

Tools

🟩	*free access tool*	🟧	*registered access tool*

TriAnnot Pipeline		🟧
Quick search	🟩	🟧
BioMart	🟩	🟧
Taxon card	🟩	
Physical map viewer	🟩	
Annotation viewer	🟩	
Deletion bins	🟩	
dbWFA (functional annotation)	🟩	
RulNet (network inference and visualization)	🟩	

Wheat@URGI



You are here : Home / Home Wheat / Seq Repository

Seq Repository

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

News, FAQ, demo, account creation, genes are detailed in the left menu.

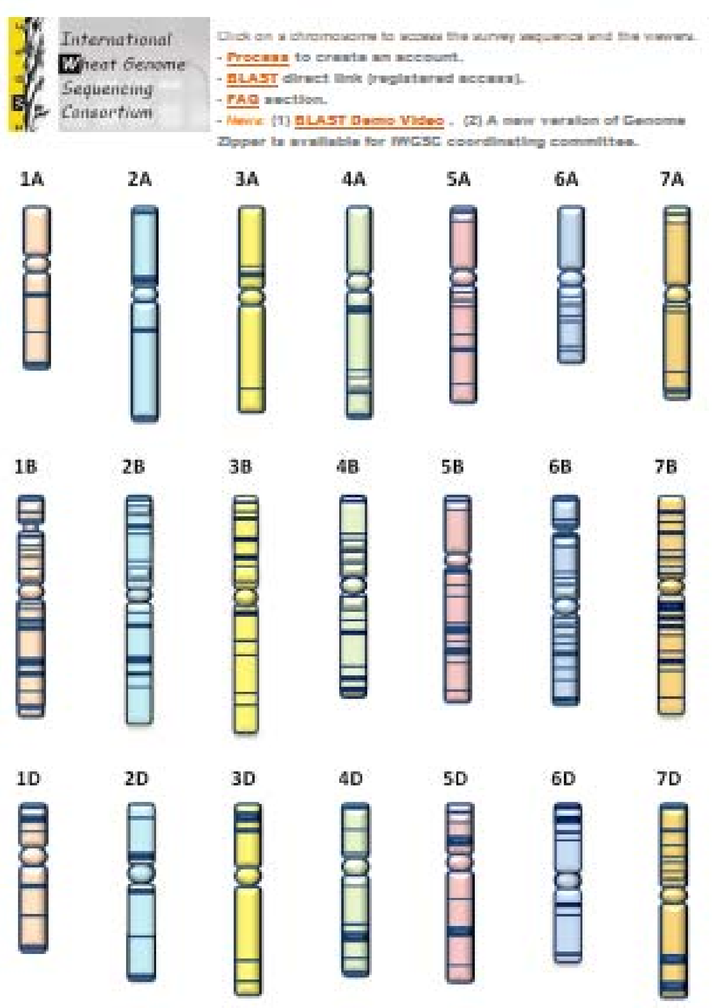
http://wheat-urgi.versailles.inra.fr

Michael Alaux

Survey Sequence

Michael Alaux

Survey Sequence Repository



International Wheat Genome Sequencing Consortium

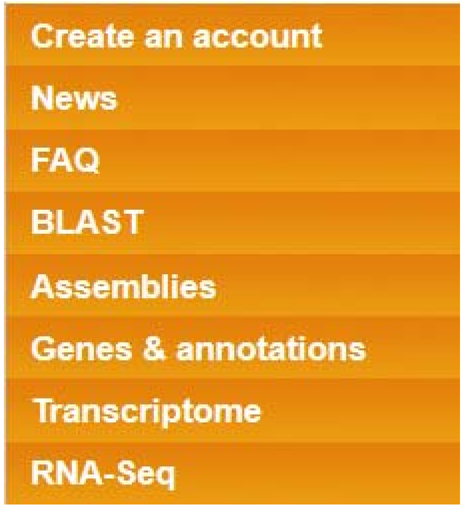
Click on a chromosome to access the survey sequence and the viewers.
- Process to create an account.
- BLAST direct link (registered access).
- FAQ section.
- News: (1) BLAST Demo Video . (2) A new version of Genome Zipper is available for IWGSC coordinating committee.

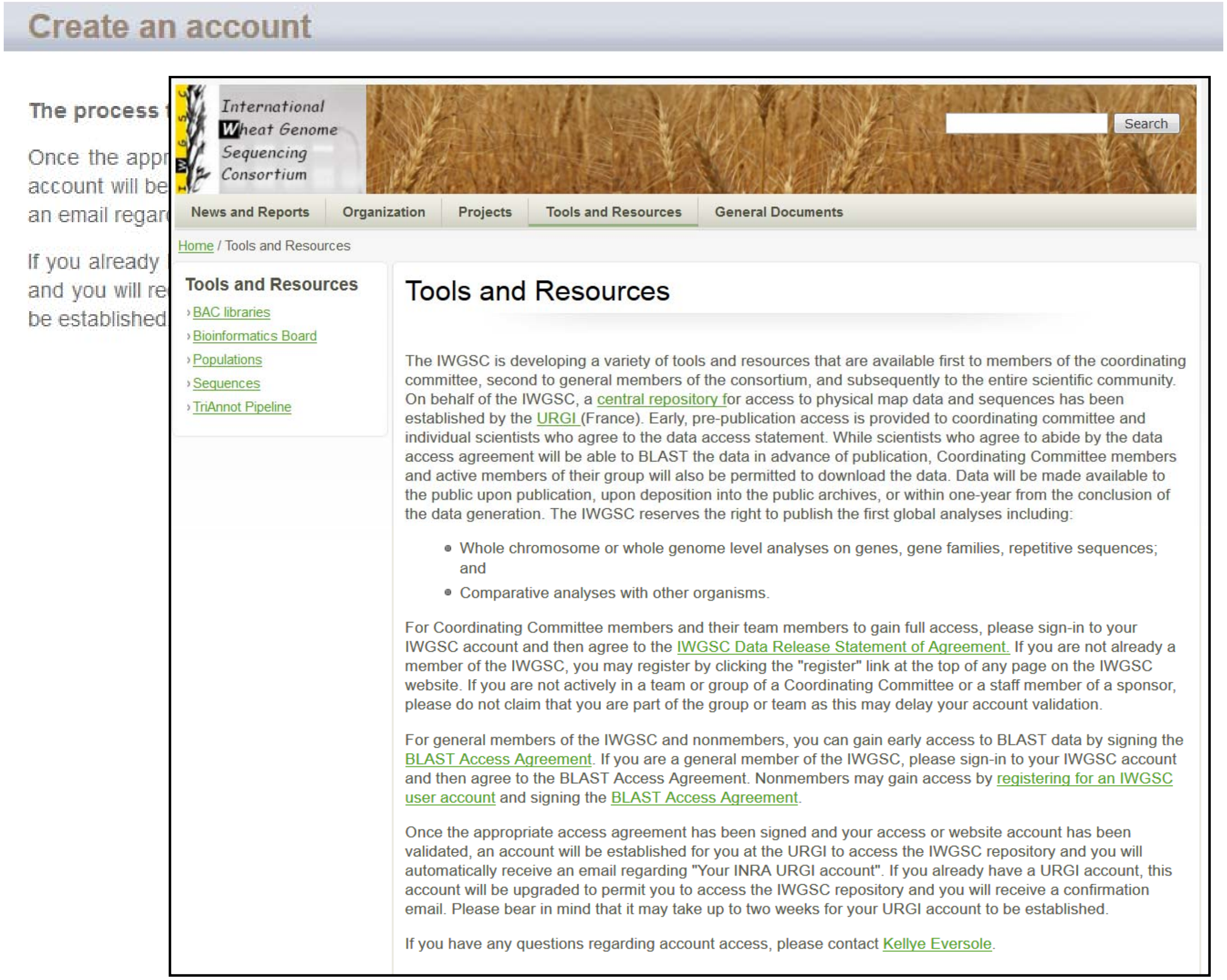
Click on a chromosome to access the survey sequence chromosome arm assembly for:

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

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Survey Sequence Repository





The process

Once the appr account will be an email regar

If you already and you will re be established

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.

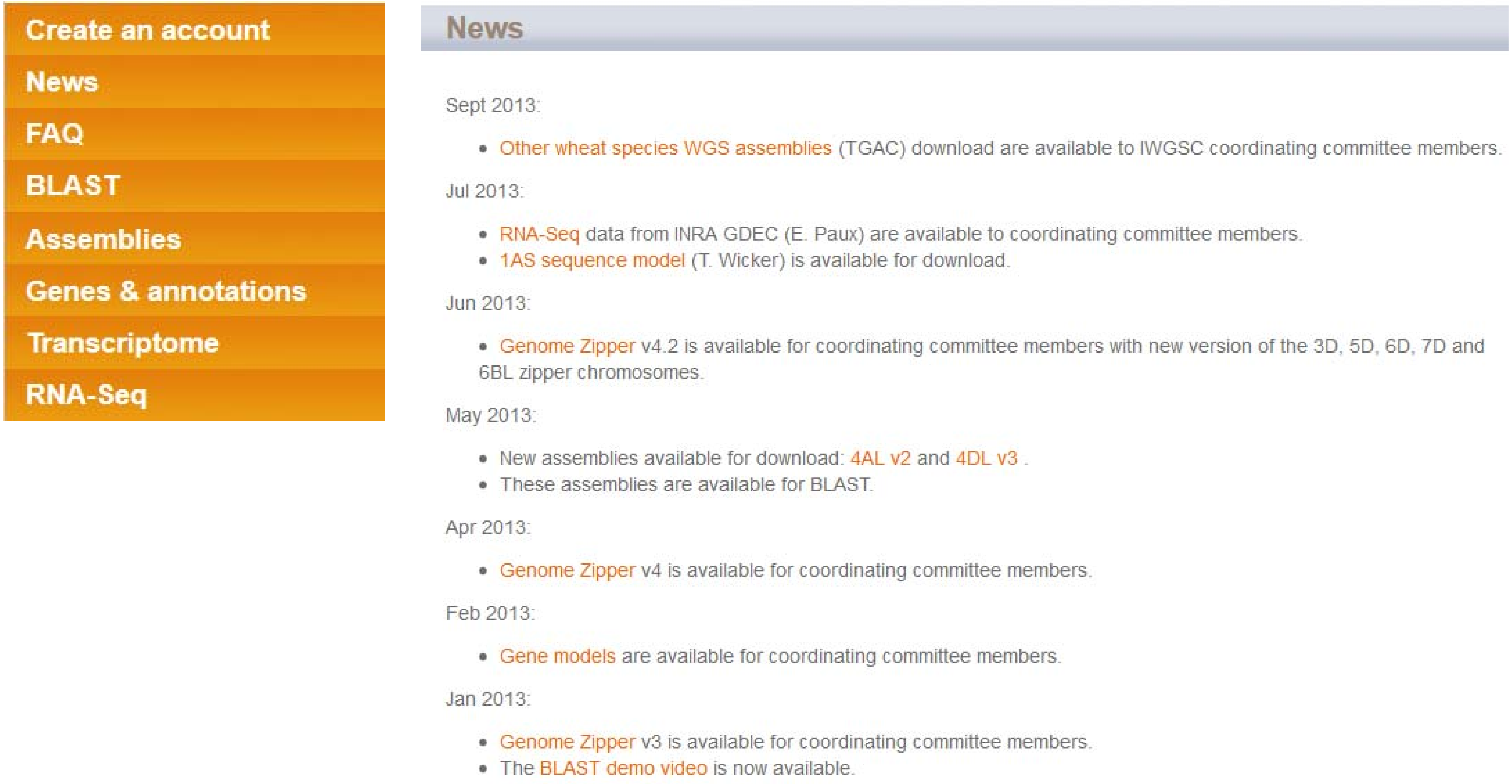
For general members of the IWGSC and nonmembers, you can gain early access to BLAST data by signing the BLAST Access Agreement. If you are a general member of the IWGSC, please sign-in to your IWGSC account and then agree to the BLAST Access Agreement. Nonmembers may gain access by registering for an 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. Please bear in mind that it may take up to two weeks for your URGI account to be established.

If you have any questions regarding account access, please contact Kellye Eversole.

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Survey Sequence Repository



News

Sept 2013:

- Other wheat species WGS assemblies (TGAC) download are available to IWGSC coordinating committee members.

Jul 2013:

- RNA-Seq data from INRA GDEC (E. Paux) are available to coordinating committee members.
- 1AS sequence model (T. Wicker) is available for download.

Jun 2013:

- Genome Zipper v4.2 is available for coordinating committee members with new version of the 3D, 5D, 6D, 7D and 6BL zipper chromosomes.

May 2013:

- New assemblies available for download: 4AL v2 and 4DL v3 .
- These assemblies are available for BLAST.

Apr 2013:

- Genome Zipper v4 is available for coordinating committee members.

Feb 2013:

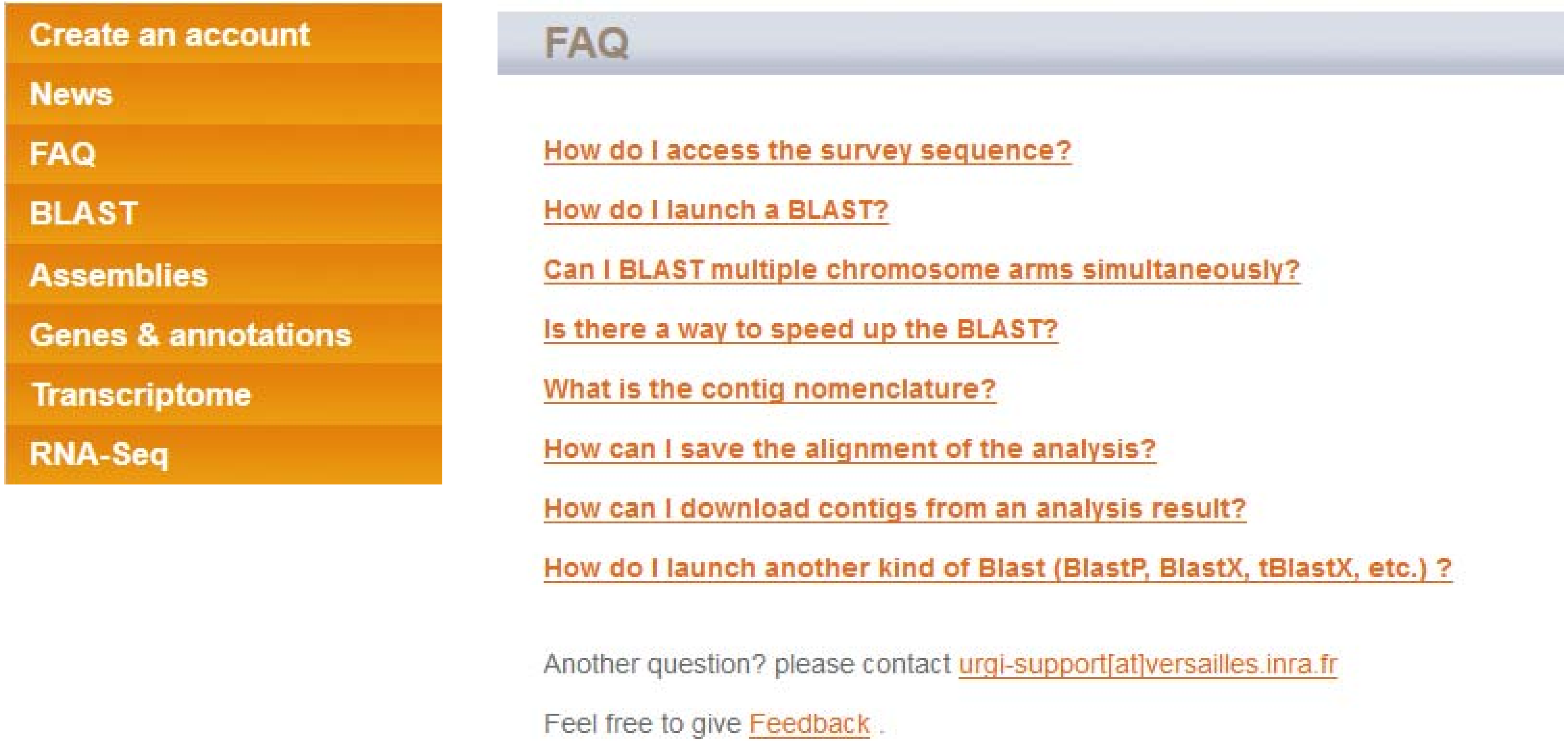
- Gene models are available for coordinating committee members.

Jan 2013:

- Genome Zipper v3 is available for coordinating committee members.
- The BLAST demo video is now available.

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Survey Sequence Repository



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?

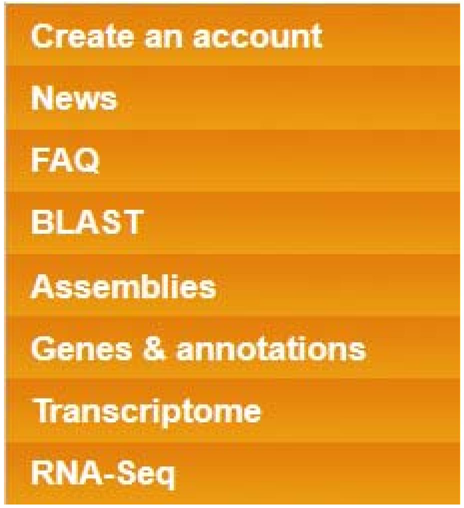
How do I launch another kind of Blast (BlastP, BlastX, tBlastX, etc.) ?

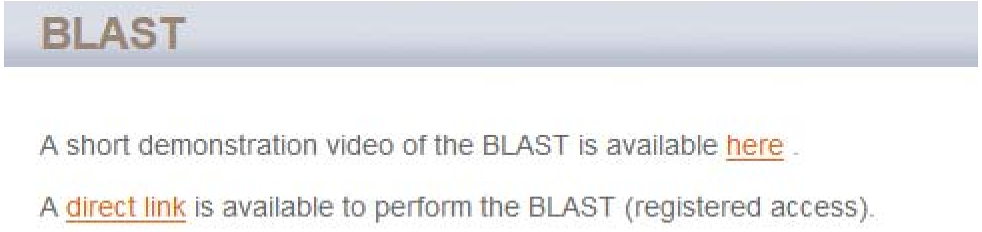
Another question? please contact urgi-support[at]versailles.inra.fr

Feel free to give Feedback .

http://wheat-urgi.versailles.inra.fr/Seq-Repository

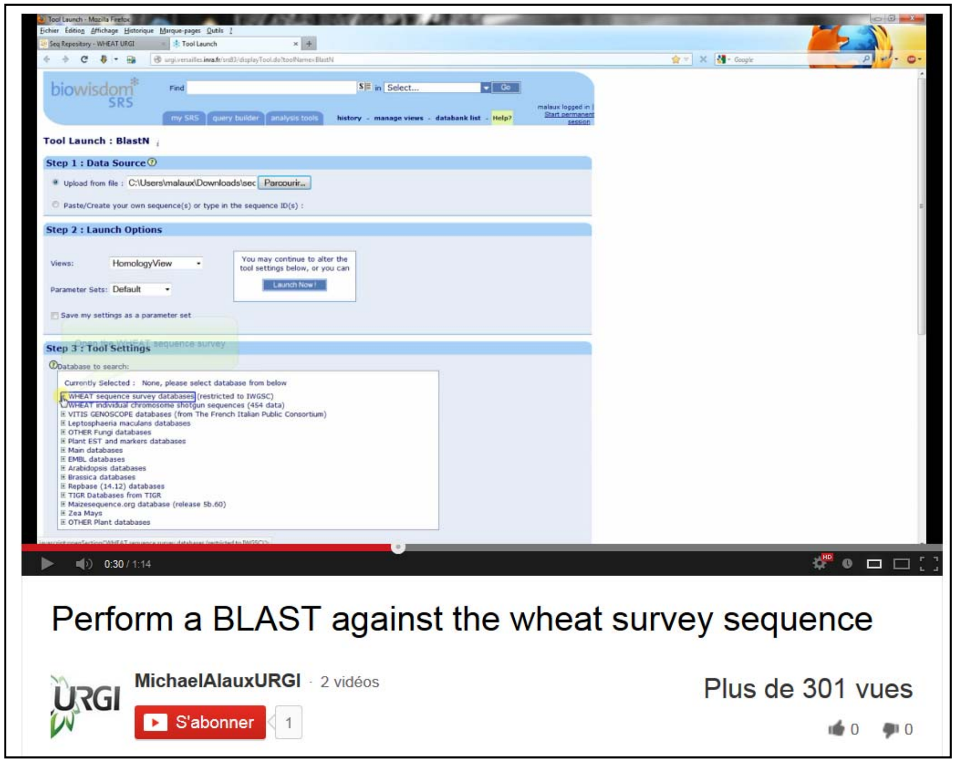
Survey Sequence Repository


- Create an account
- News
- FAQ
- BLAST
- Assemblies
- Genes & annotations
- Transcriptome
- RNA-Seq


BLAST

A short demonstration video of the BLAST is available here .

A direct link is available to perform the BLAST (registered access).



Tool Launch : BlastN

Step 1 : Data Source

● Upload from file : C:\Users\malaux\Downloads\sec 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 Launch Now!

☐ 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)
- WHEAT individual chromosome shotgun sequences (454 data)
- VITIS GENOSCOPE databases (from The French Italian Public Consortium)
- Leptosphaeria maculans databases
- OTHER Fungi databases
- Plant EST and markers databases
- Main databases
- EMBL databases
- Arabidopsis databases
- Brassica databases
- Repbase (14.12) databases
- TIGR Databases from TIGR
- Maizesequence.org database (release 5b.60)
- Zea Mays
- OTHER Plant databases

Perform a BLAST against the wheat survey sequence

MichaelAlauxURGI · 2 vidéos

S'abonner 1

Plus de 301 vues

👍 0 👎 0

http://wheat-urgi.versailles.inra.fr/Seq-Repository

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Survey Sequence Repository

Assemblies

Triticum aestivum (Chinese Spring) survey sequence chromosomes assemblies are available for download (restricted to IWGSC coordinating committee members).

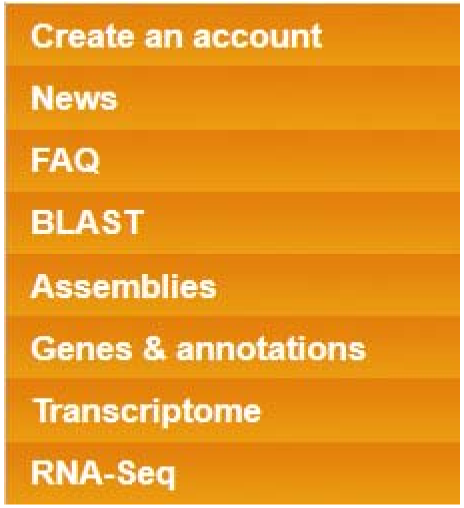
Other wheat species WGS assemblies from TGAC are available for download (restricted to IWGSC coordinating committee members):

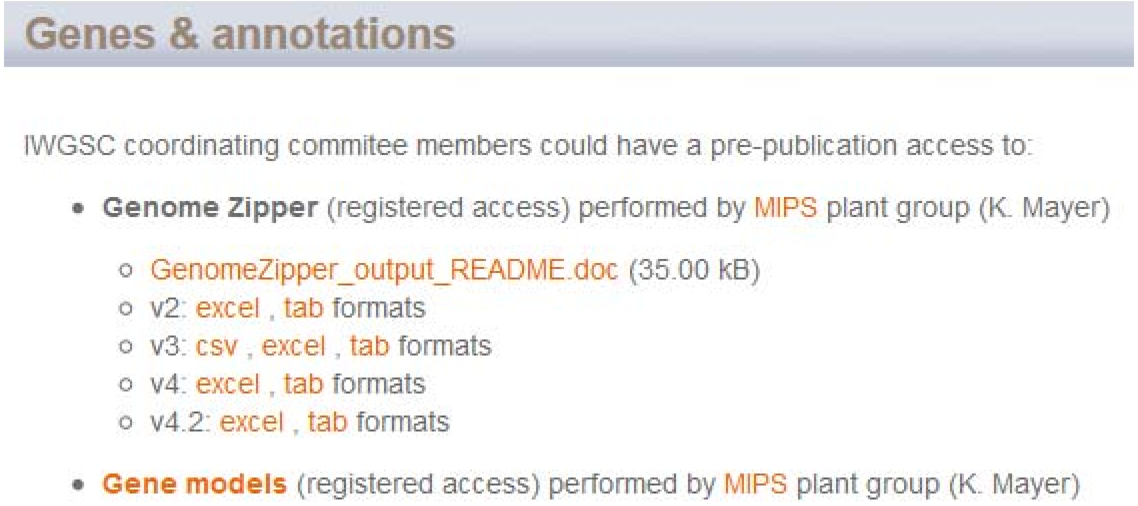
Triticum durum, monococcum, speltoides, strongfield, tauschii, urartu, sharonensis.

TGAC_WGS_durum_v1.fasta.gz
TGAC_WGS_monococcum_v1.fasta.gz
TGAC_WGS_speltoides_v1.fasta.gz
TGAC_WGS_strongfield_v1.fasta.gz
TGAC_WGS_tauschii_v1.fasta.gz
TGAC_WGS_urartu_v1.fasta.gz
TSL_WGS_sharonensis_v1.fasta.gz

http://wheat-urgi.versailles.inra.fr/Seq-Repository

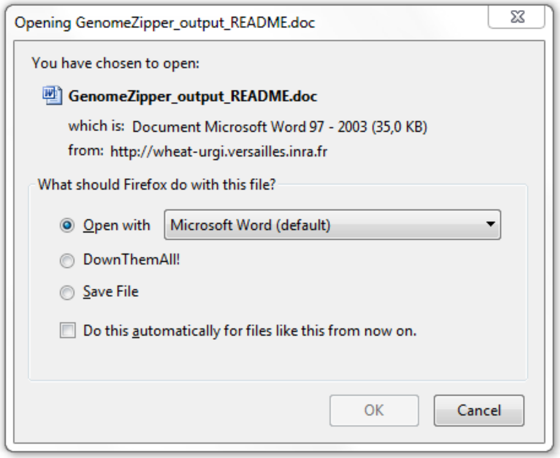
Survey Sequence Repository


Create an account
News
FAQ
BLAST
Assemblies
Genes & annotations
Transcriptome
RNA-Seq


Genes & annotations

IWGSC coordinating commitee members could have a pre-publication access to:

- **Genome Zipper** (registered access) performed by MIPS plant group (K. Mayer)
    - GenomeZipper_output_README.doc (35.00 kB)
    - v2: excel , tab formats
    - v3: csv , excel , tab formats
    - v4: excel , tab formats
    - v4.2: excel , tab formats
- **Gene models** (registered access) performed by MIPS plant group (K. Mayer)


Opening GenomeZipper_output_README.doc

You have chosen to open:

GenomeZipper_output_README.doc

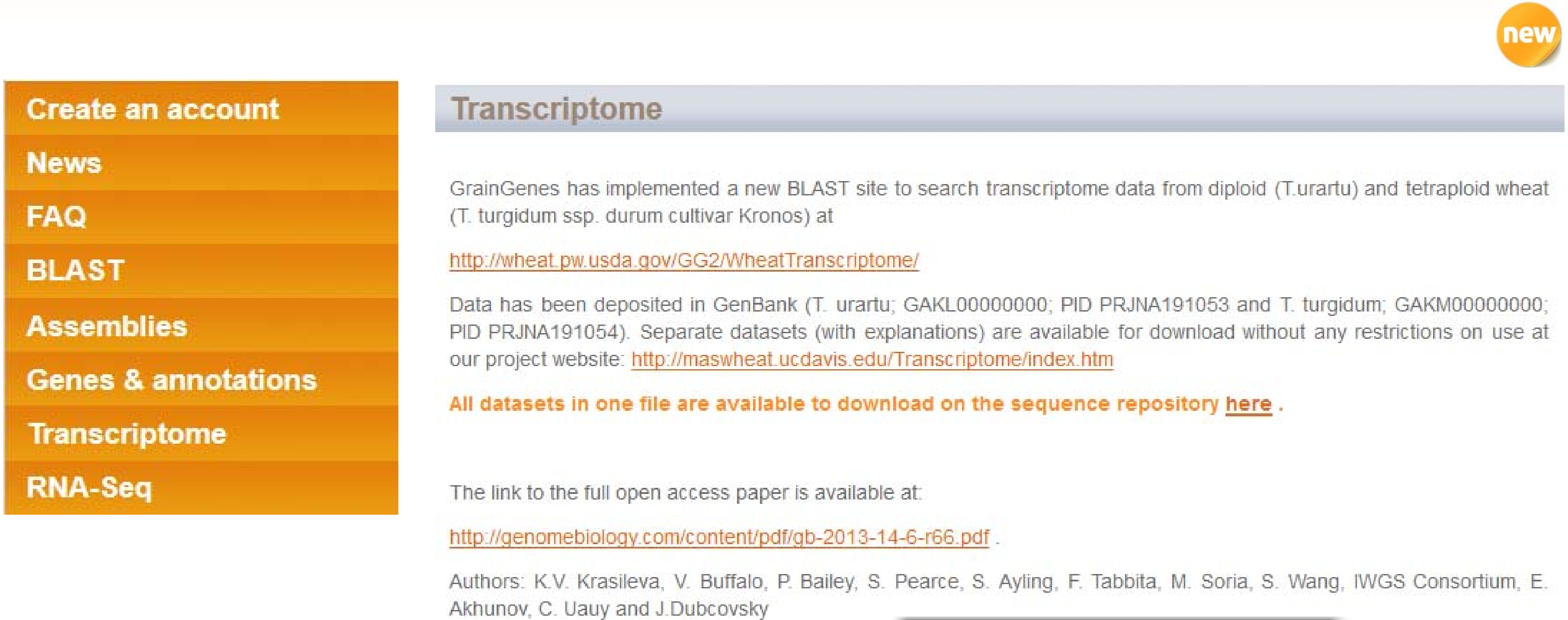
which is: Document Microsoft Word 97 - 2003 (35,0 KB)
from: http://wheat-urgi.versailles.inra.fr

What should Firefox do with this file?

● Open with Microsoft Word (default)
○ DownThemAll!
○ Save File
☐ Do this automatically for files like this from now on.

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Survey Sequence Repository



Transcriptome

GrainGenes has implemented a new BLAST site to search transcriptome data from diploid (T.urartu) and tetraploid wheat (T. turgidum ssp. durum cultivar Kronos) at

http://wheat.pw.usda.gov/GG2/WheatTranscriptome/

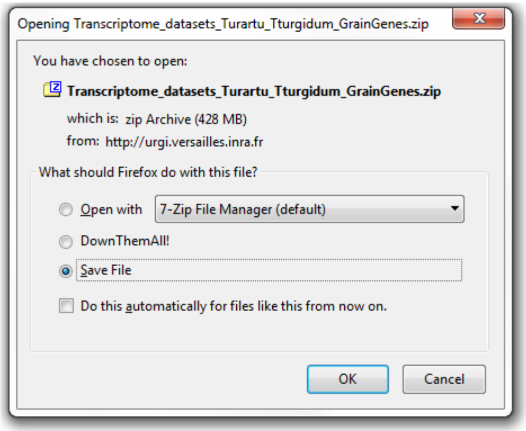
Data has been deposited in GenBank (T. urartu; GAKL00000000; PID PRJNA191053 and T. turgidum; GAKM00000000; PID PRJNA191054). Separate datasets (with explanations) are available for download without any restrictions on use at our project website: http://maswheat.ucdavis.edu/Transcriptome/index.htm

All datasets in one file are available to download on the sequence repository here .

The link to the full open access paper is available at:

http://genomebiology.com/content/pdf/gb-2013-14-6-r66.pdf .

Authors: K.V. Krasileva, V. Buffalo, P. Bailey, S. Pearce, S. Ayling, F. Tabbita, M. Soria, S. Wang, IWGS Consortium, E. Akhunov, C. Uauy and J.Dubcovsky



Opening Transcriptome_datasets_Turartu_Tturgidum_GrainGenes.zip

You have chosen to open:

Transcriptome_datasets_Turartu_Tturgidum_GrainGenes.zip

which is: zip Archive (428 MB)

from: http://urgi.versailles.inra.fr

What should Firefox do with this file?

○ Open with 7-Zip File Manager (default)

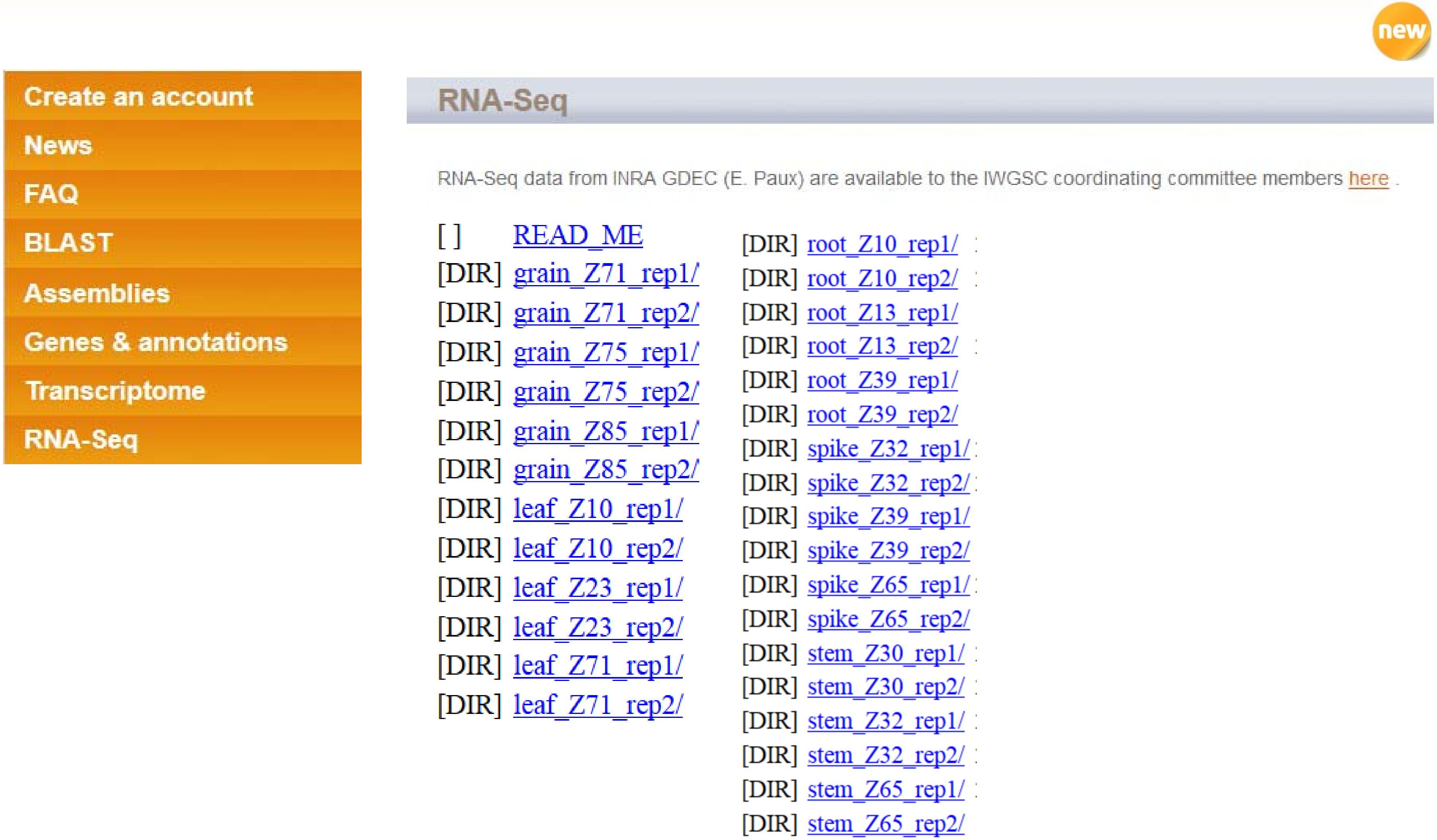
○ DownThemAll!

● Save File

☐ Do this automatically for files like this from now on.

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Survey Sequence Repository



RNA-Seq

RNA-Seq data from INRA GDEC (E. Paux) are available to the IWGSC coordinating committee members here .

[ ] READ_ME
[DIR] grain_Z71_rep1/
[DIR] grain_Z71_rep2/
[DIR] grain_Z75_rep1/
[DIR] grain_Z75_rep2/
[DIR] grain_Z85_rep1/
[DIR] grain_Z85_rep2/
[DIR] leaf_Z10_rep1/
[DIR] leaf_Z10_rep2/
[DIR] leaf_Z23_rep1/
[DIR] leaf_Z23_rep2/
[DIR] leaf_Z71_rep1/
[DIR] leaf_Z71_rep2/
[DIR] root_Z10_rep1/
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[DIR] root_Z13_rep1/
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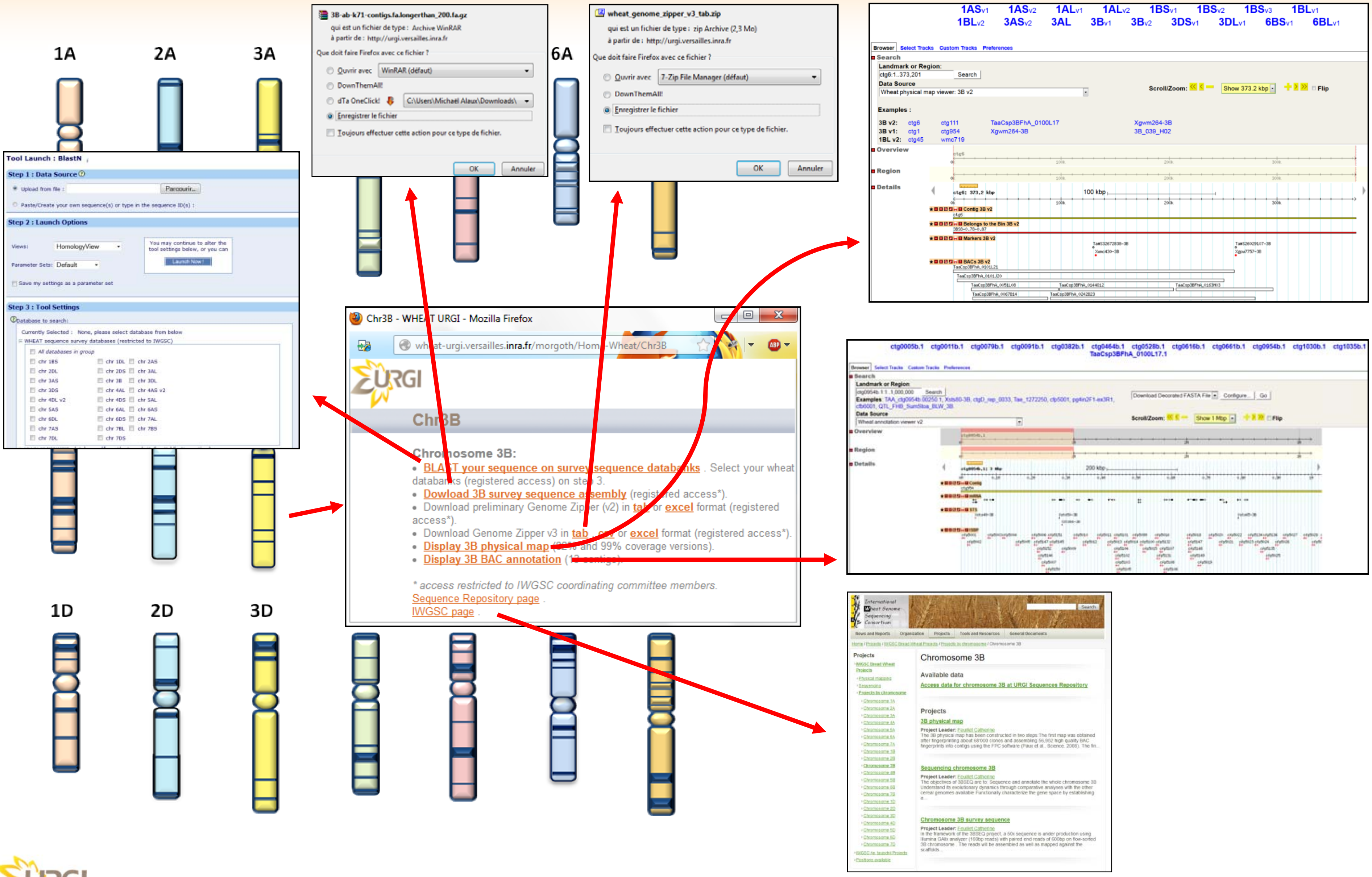
[DIR] spike_Z39_rep2/
[DIR] spike_Z65_rep1/
[DIR] spike_Z65_rep2/
[DIR] stem_Z30_rep1/
[DIR] stem_Z30_rep2/
[DIR] stem_Z32_rep1/
[DIR] stem_Z32_rep2/
[DIR] stem_Z65_rep1/
[DIR] stem_Z65_rep2/

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Survey Sequence Repository



Chr3B - WHEAT URGI - Mozilla Firefox

wheat-urgi.versailles.inra.fr/morgoth/Home-Wheat/Chr3B

Chr3B

Chromosome 3B:

- BLAST your sequence on survey sequence databanks . Select your wheat databanks (registered access) on step 3.
- Dowload 3B survey sequence assembly (registered access*).
- Download preliminary Genome Zipper (v2) in tab or excel format (registered access*).
- Download Genome Zipper v3 in tab , csv or excel format (registered access*).
- Display 3B physical map (92% and 99% coverage versions).
- Display 3B BAC annotation (13 contigs).

** access restricted to IWGSC coordinating committee members.*

Sequence Repository page .

IWGSC page .

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.

OK Annuler

wheat_genome_zipper_v3_tab.zip

qui est un fichier de type : zip Archive (2,3 Mo)

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

Que doit faire Firefox avec ce fichier ?

○ Ouvrir avec 7-Zip File Manager (défaut)

○ DownThemAll!

● Enregistrer le fichier

☐ Toujours effectuer cette action pour ce type de fichier.

OK Annuler

Tool Launch : BlastN

Step 1 : Data Source

● Upload from file : 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 Launch Now !

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

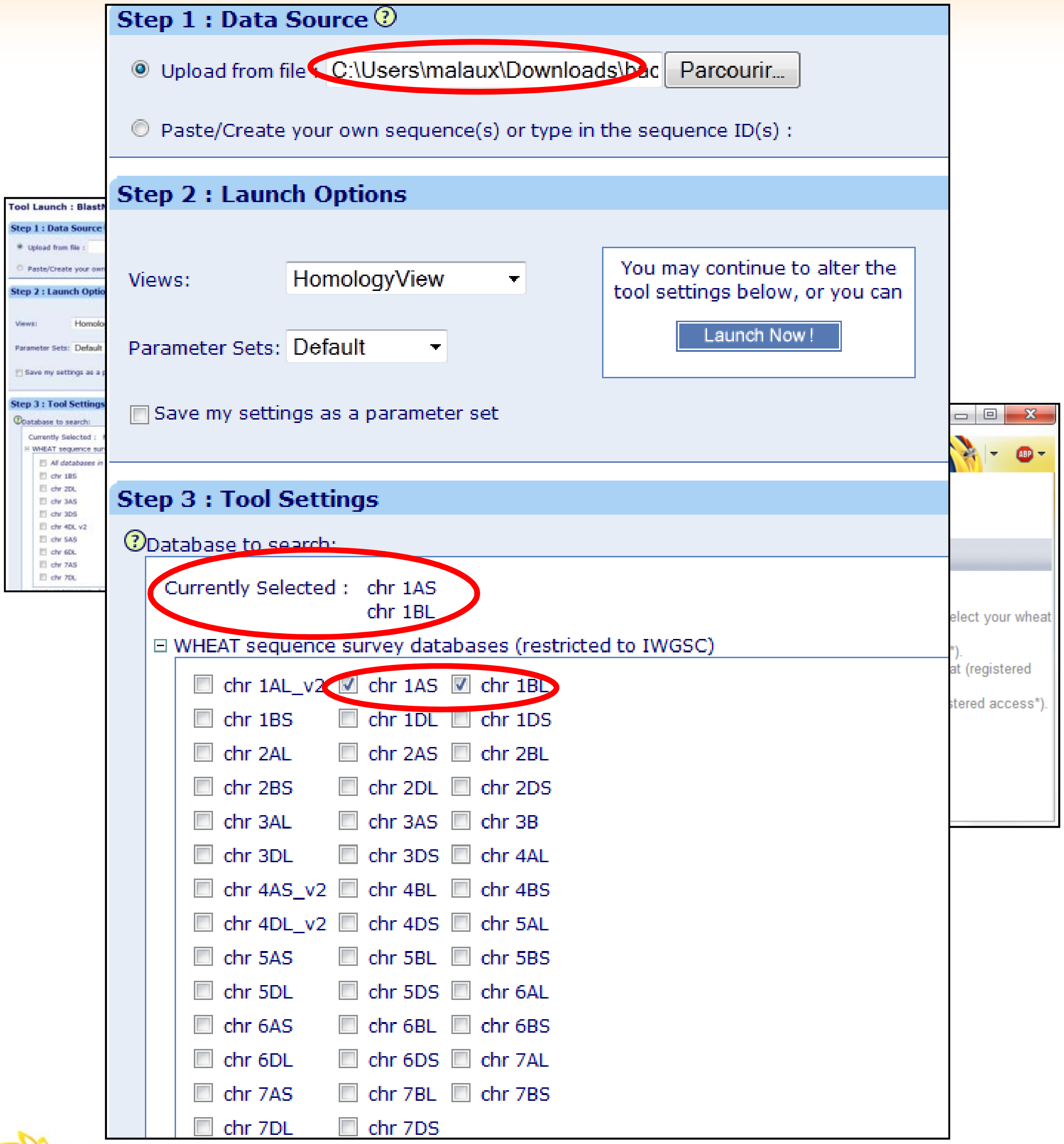
http://wheat-urgi.versailles.inra.fr/Seq-Repository

Michael Alaux

BLAST

Michael Alaux

BLAST



Step 1 : Data Source

● Upload from file : C:\Users\malaux\Downloads\bac

○ 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

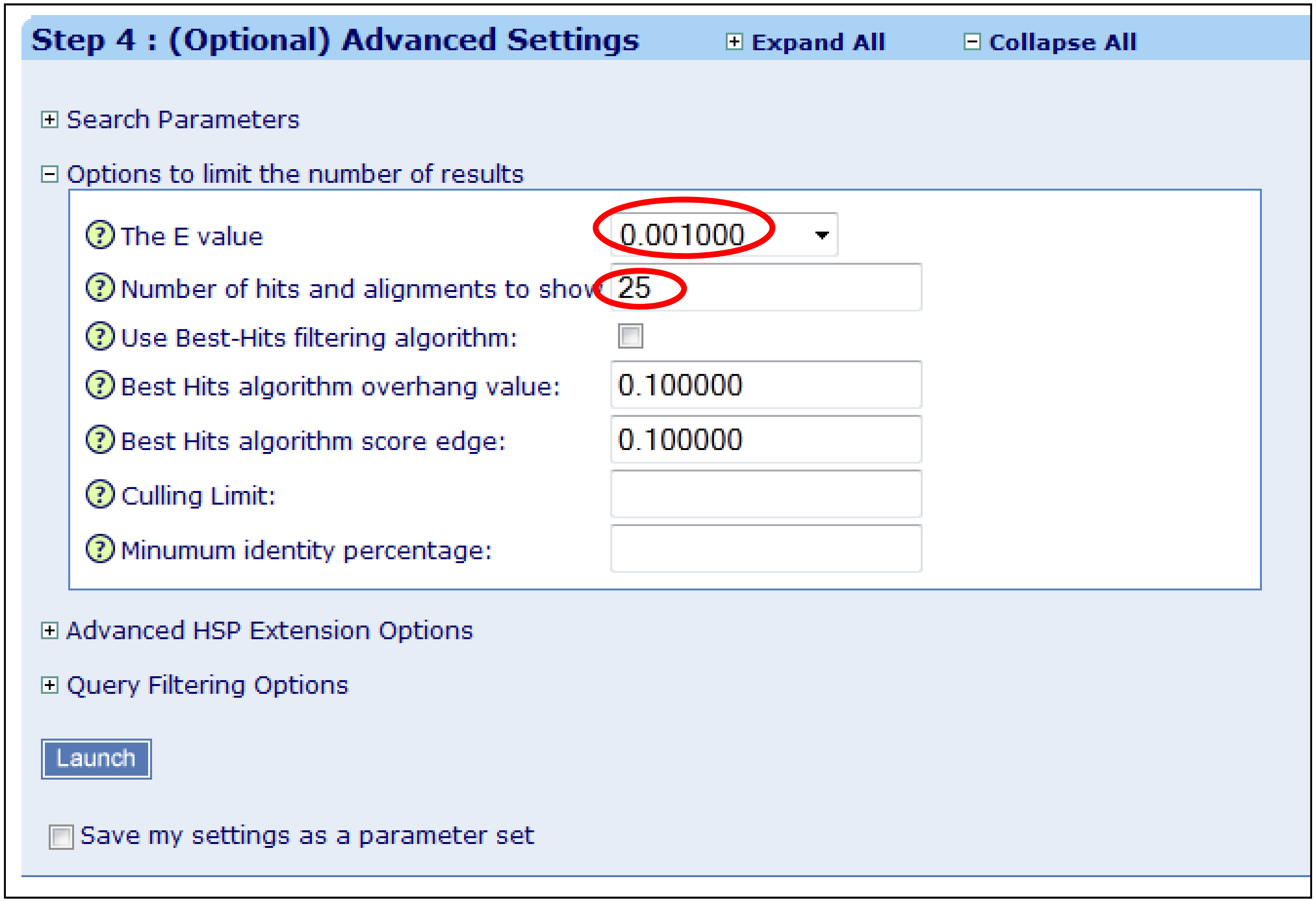
⊟ WHEAT sequence survey databases (restricted to IWGSC)

☐ 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

http://wheat-urgi.versailles.inra.fr/Seq-Repository

BLAST

To speed up your Blast



Step 4 : (Optional) Advanced Settings

⊟ Options to limit the number of results

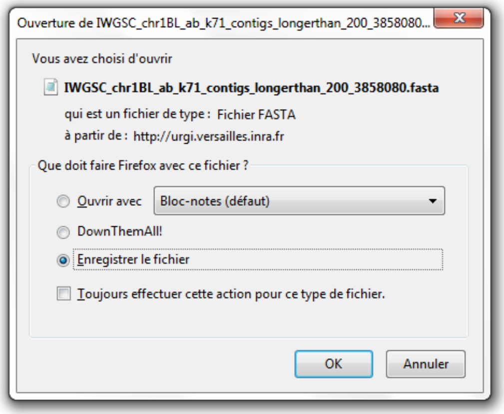
The E value	0.001000
Number of hits and alignments to show	25
Use Best-Hits filtering algorithm:	☐
Best Hits algorithm overhang value:	0.100000
Best Hits algorithm score edge:	0.100000
Culling Limit:	
Minumum identity percentage:	

☐ Save my settings as a parameter set

http://wheat-urgi.versailles.inra.fr/Seq-Repository

BLAST

To download the contigs


Ouverture de IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3858080...

Vous avez choisi d'ouvrir

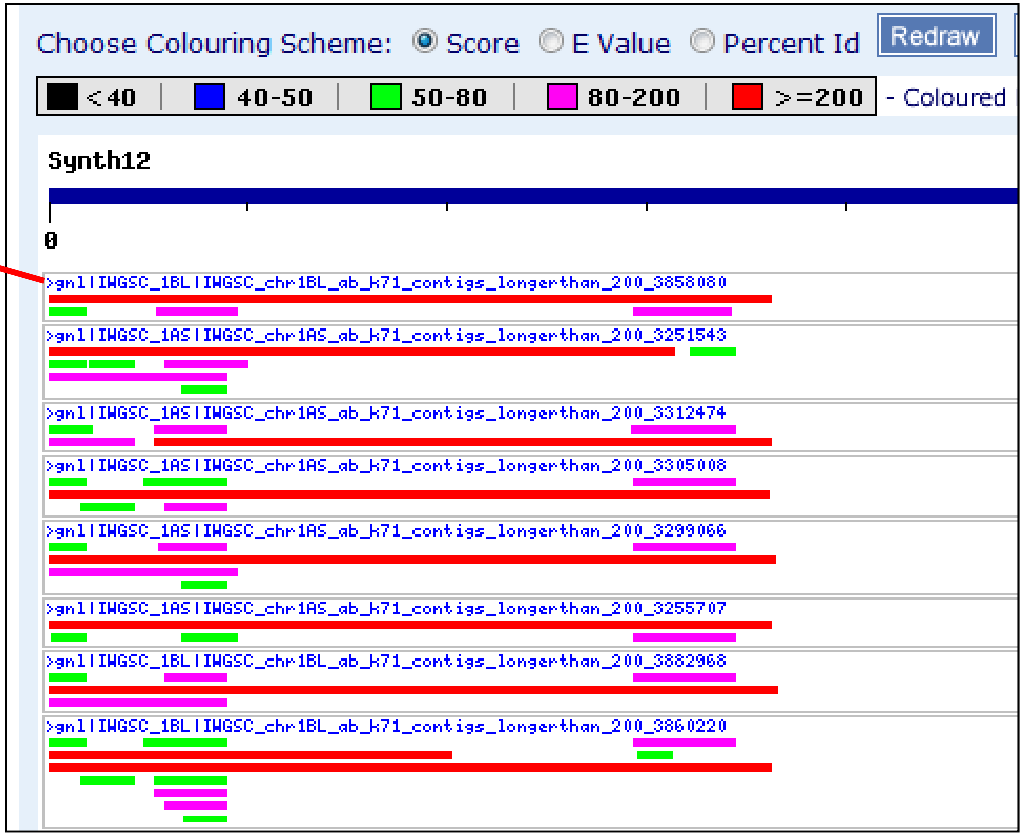
IWGSC_chr1BL_ab_k71_contigs_longerthan_200_3858080.fasta

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

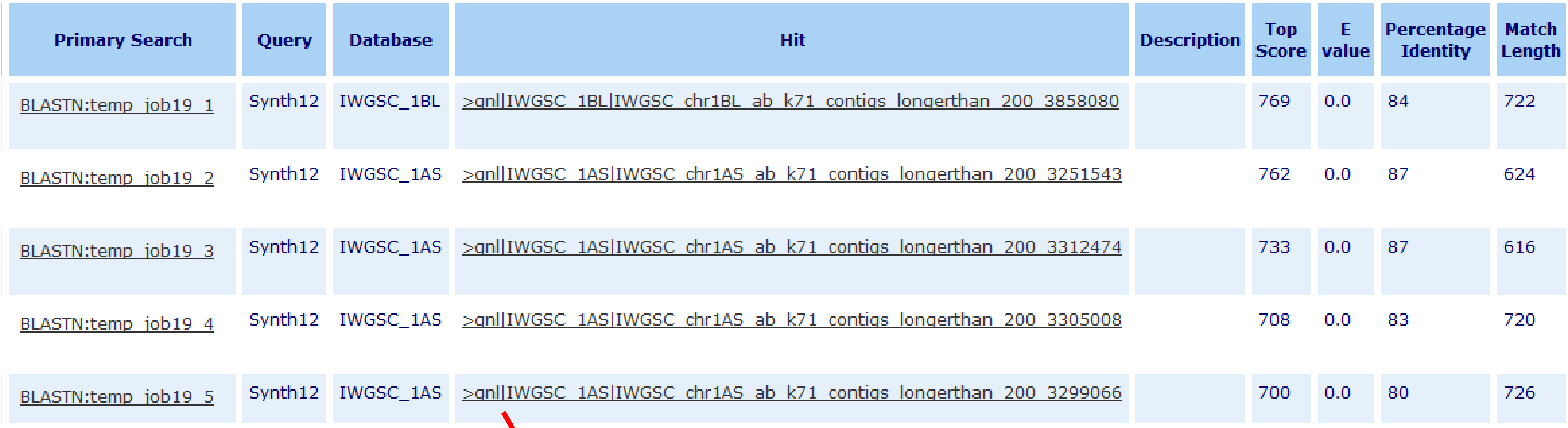
Synth12

>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

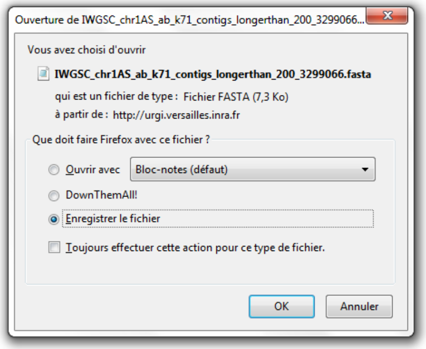
BLAST

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)

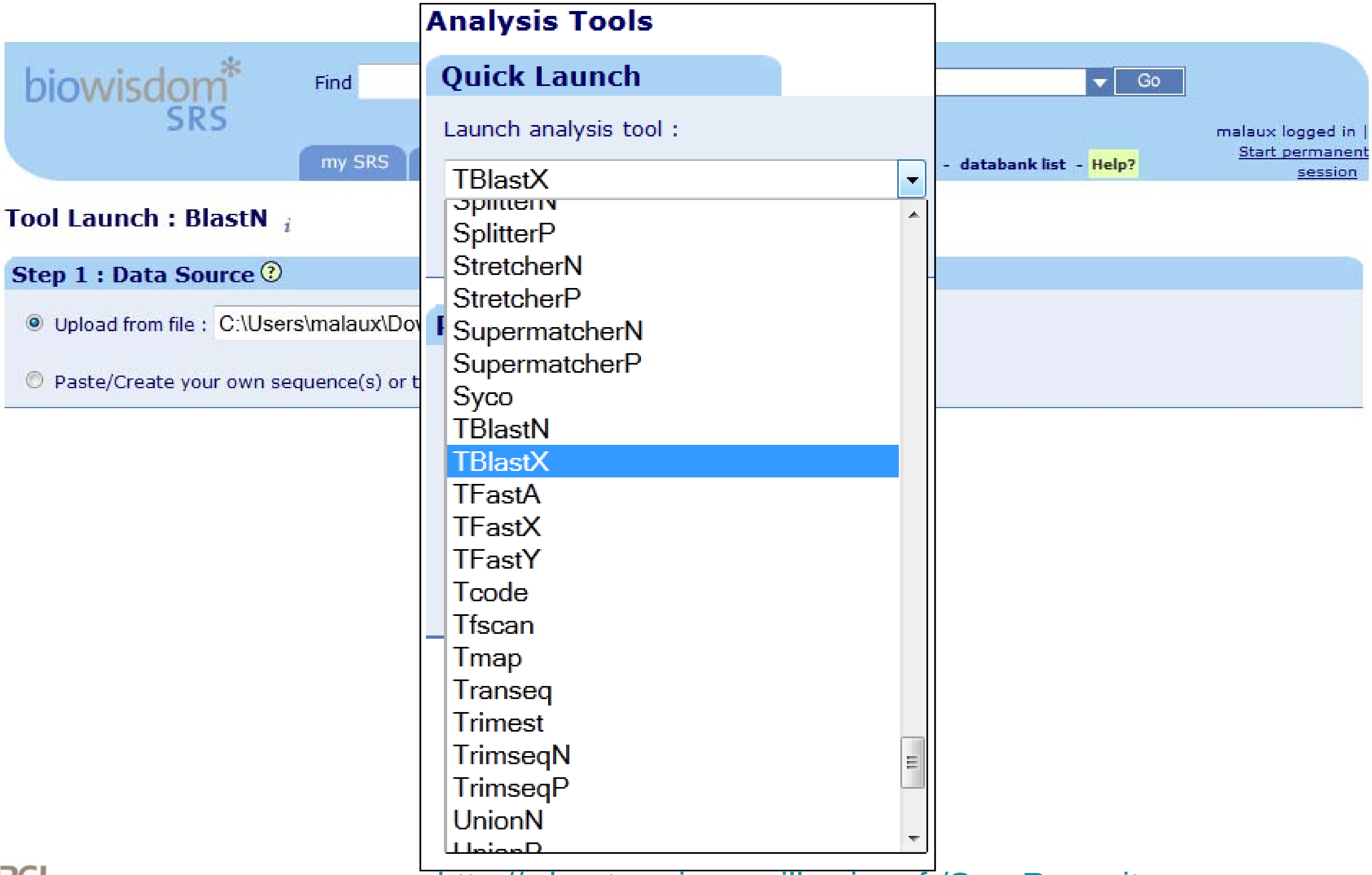
○ DownThemAll!

● Enregistrer le fichier

☐ Toujours effectuer cette action pour ce type de fichier.

BLAST

To launch TBlastX or other tools



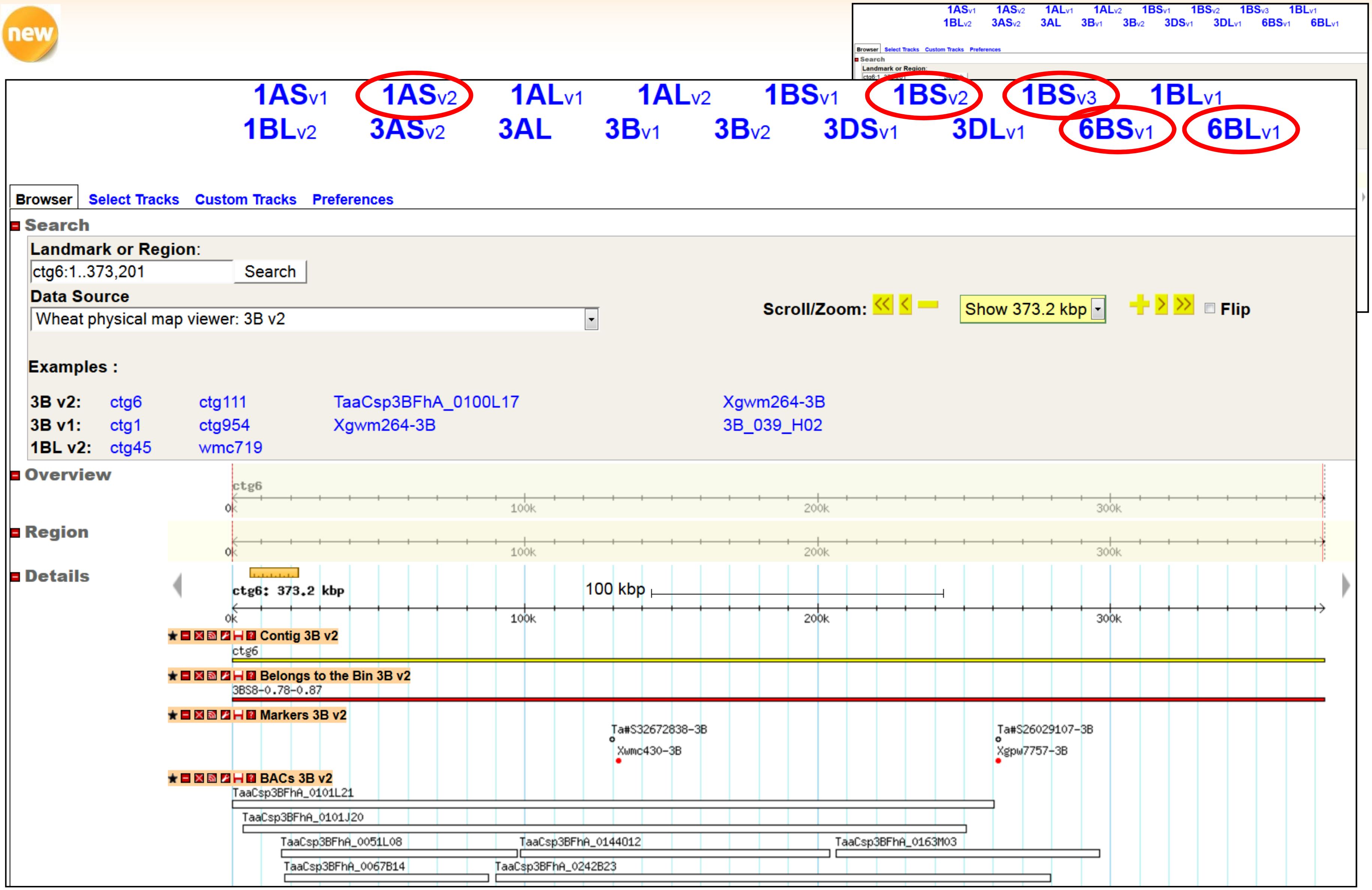
http://wheat-urgi.versailles.inra.fr/Seq-Repository

Physical maps

Michael Alaux

Survey Sequence Repository

new



1AS$_{v1}$ 1AS$_{v2}$ 1AL$_{v1}$ 1AL$_{v2}$ 1BS$_{v1}$ 1BS$_{v2}$ 1BS$_{v3}$ 1BL$_{v1}$
1BL$_{v2}$ 3AS$_{v2}$ 3AL 3B$_{v1}$ 3B$_{v2}$ 3DS$_{v1}$ 3DL$_{v1}$ 6BS$_{v1}$ 6BL$_{v1}$

Browser | Select Tracks | Custom Tracks | Preferences

Search

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

Data Source: Wheat physical map viewer: 3B v2

Scroll/Zoom: Show 373.2 kbp ☐ Flip

Examples :

3B v2:	ctg6	ctg111	TaaCsp3BFhA_0100L17	Xgwm264-3B
3B v1:	ctg1	ctg954	Xgwm264-3B	3B_039_H02
1BL v2:	ctg45	wmc719		

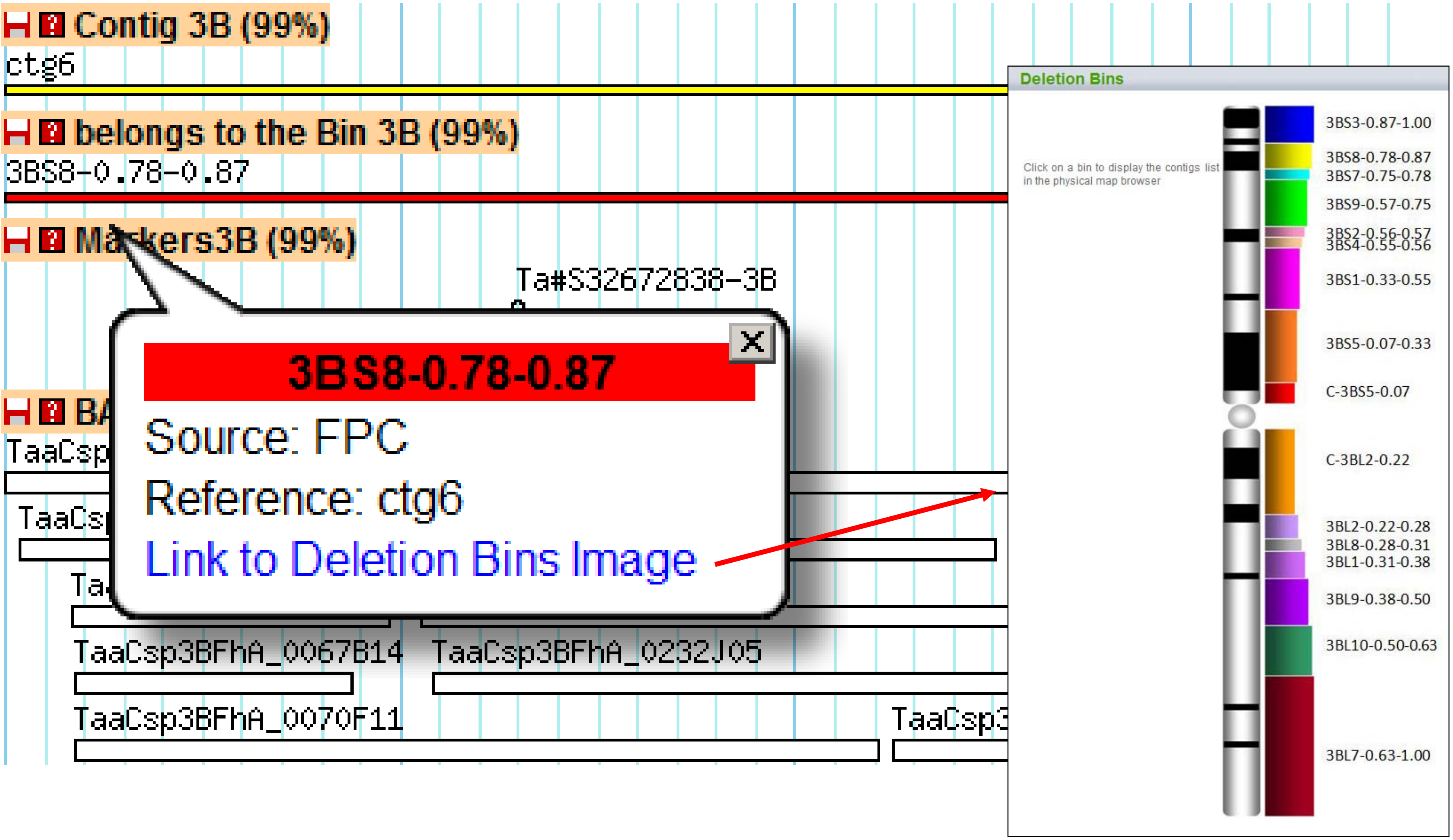
Overview

Region

Details

Michael Alaux

Physical Map Viewer



Contig 3B (99%)
ctg6

belongs to the Bin 3B (99%)
3BS8-0.78-0.87

Markers3B (99%)
Ta#S32672838-3B

3BS8-0.78-0.87
Source: FPC
Reference: ctg6
Link to Deletion Bins Image

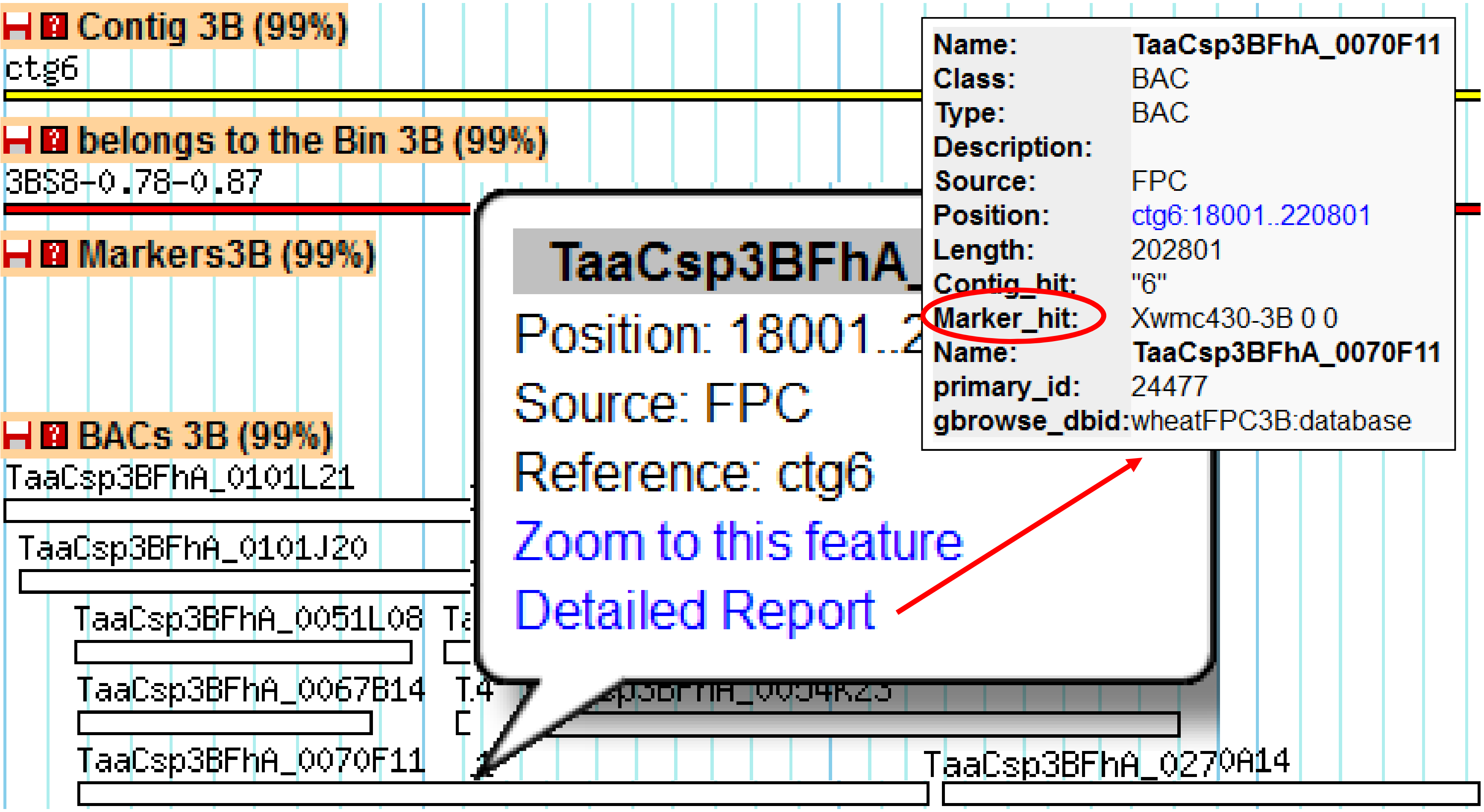
TaaCsp3BFhA_0067B14
TaaCsp3BFhA_0232J05
TaaCsp3BFhA_0070F11

Deletion Bins

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

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

Physical Map Viewer



TaaCsp3BFhA_

Position: 18001..2

Source: FPC

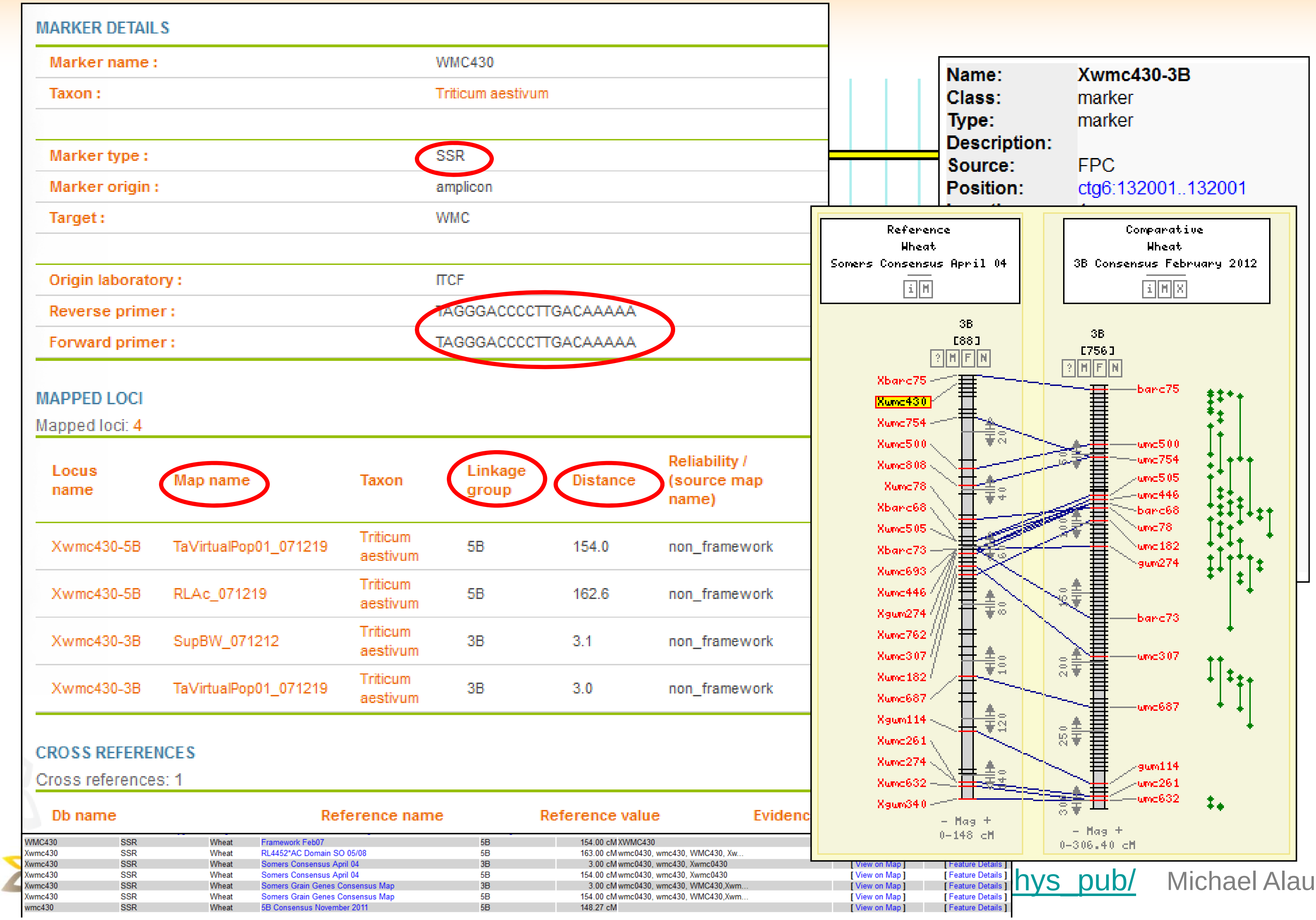
Reference: ctg6

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

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

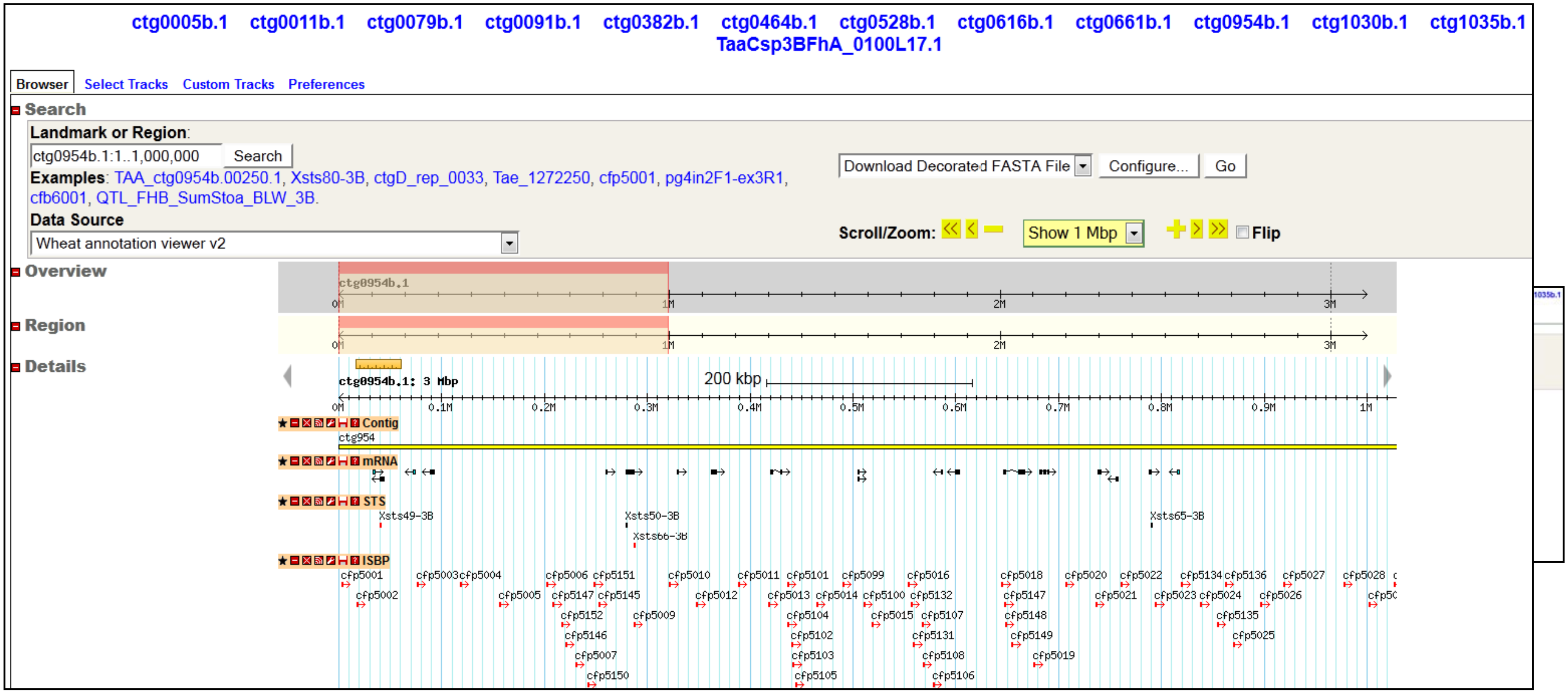
WMC430	SSR	Wheat	Framework Feb07	5B	154.00 cM	XWMC430		
Xwmc430	SSR	Wheat	RL4452*AC Domain SO 05/08	5B	163.00 cM	wmc0430, wmc430, WMC430, Xw...		
Xwmc430	SSR	Wheat	Somers Consensus April 04	3B	3.00 cM	wmc0430, wmc430, Xwmc0430	[View on Map]	[Feature Details]
Xwmc430	SSR	Wheat	Somers Consensus April 04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

Genome annotation

Michael Alaux

Survey Sequence Repository



ctg0005b.1 ctg0011b.1 ctg0079b.1 ctg0091b.1 ctg0382b.1 ctg0464b.1 ctg0528b.1 ctg0616b.1 ctg0661b.1 ctg0954b.1 ctg1030b.1 ctg1035b.1 TaaCsp3BFhA_0100L17.1

Browser | Select Tracks | Custom Tracks | Preferences

Search

Landmark or Region: ctg0954b.1:1..1,000,000 [Search]

Examples: TAA_ctg0954b.00250.1, Xsts80-3B, ctgD_rep_0033, Tae_1272250, cfp5001, pg4in2F1-ex3R1, cfb6001, QTL_FHB_SumStoa_BLW_3B.

Data Source: Wheat annotation viewer v2

Download Decorated FASTA File [Configure...] [Go]

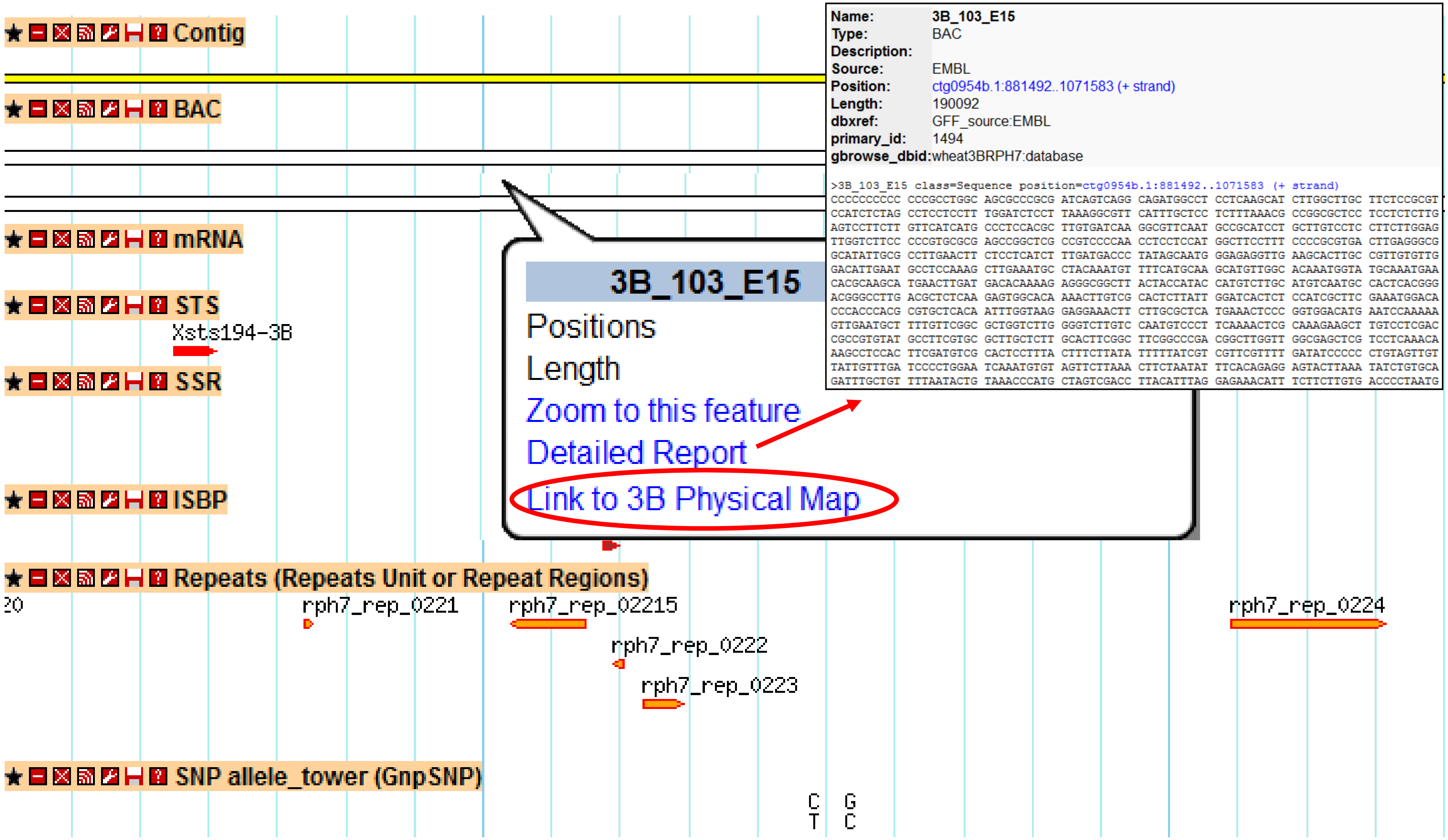
Scroll/Zoom: Show 1 Mbp ☐ **Flip**

Overview

Region

Details

Annotation Viewer Prototype

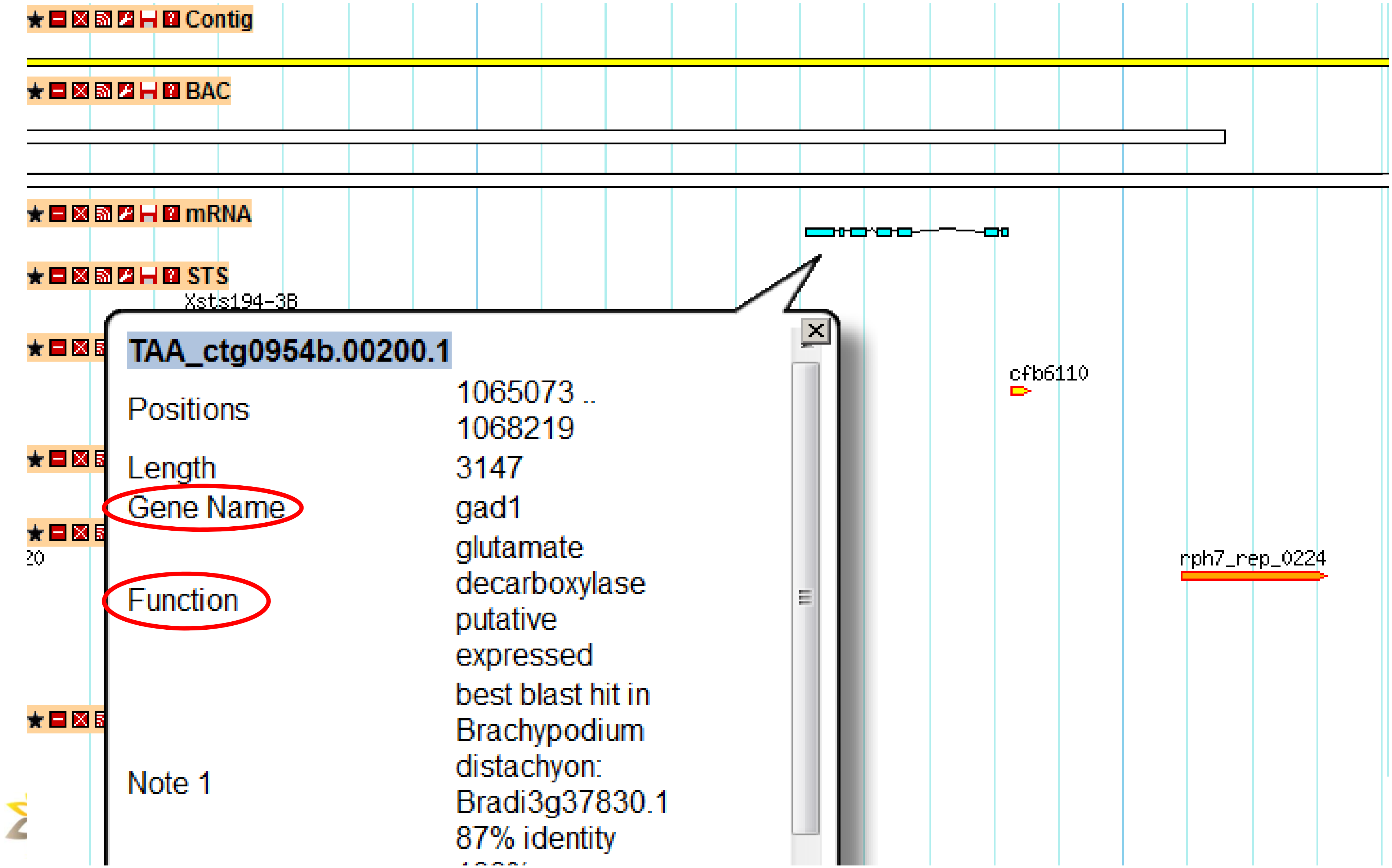


Name:	**3B_103_E15**
Type:	BAC
Description:	
Source:	EMBL
Position:	ctg0954b.1:881492..1071583 (+ strand)
Length:	190092
dbxref:	GFF_source:EMBL
primary_id:	1494
gbrowse_dbid:	wheat3BRPH7:database

```
>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/

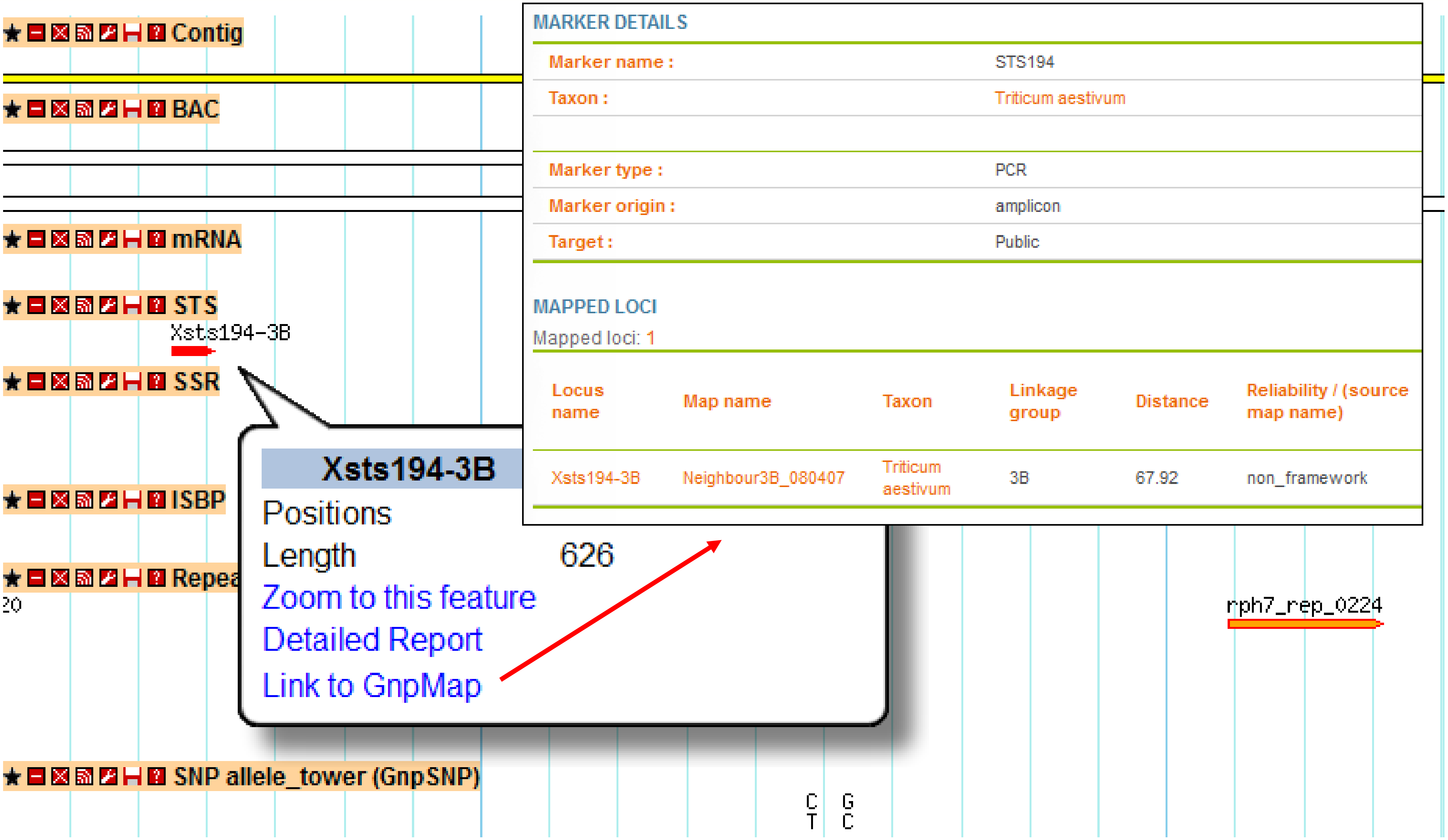
Annotation Viewer Prototype



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

Annotation Viewer Prototype



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

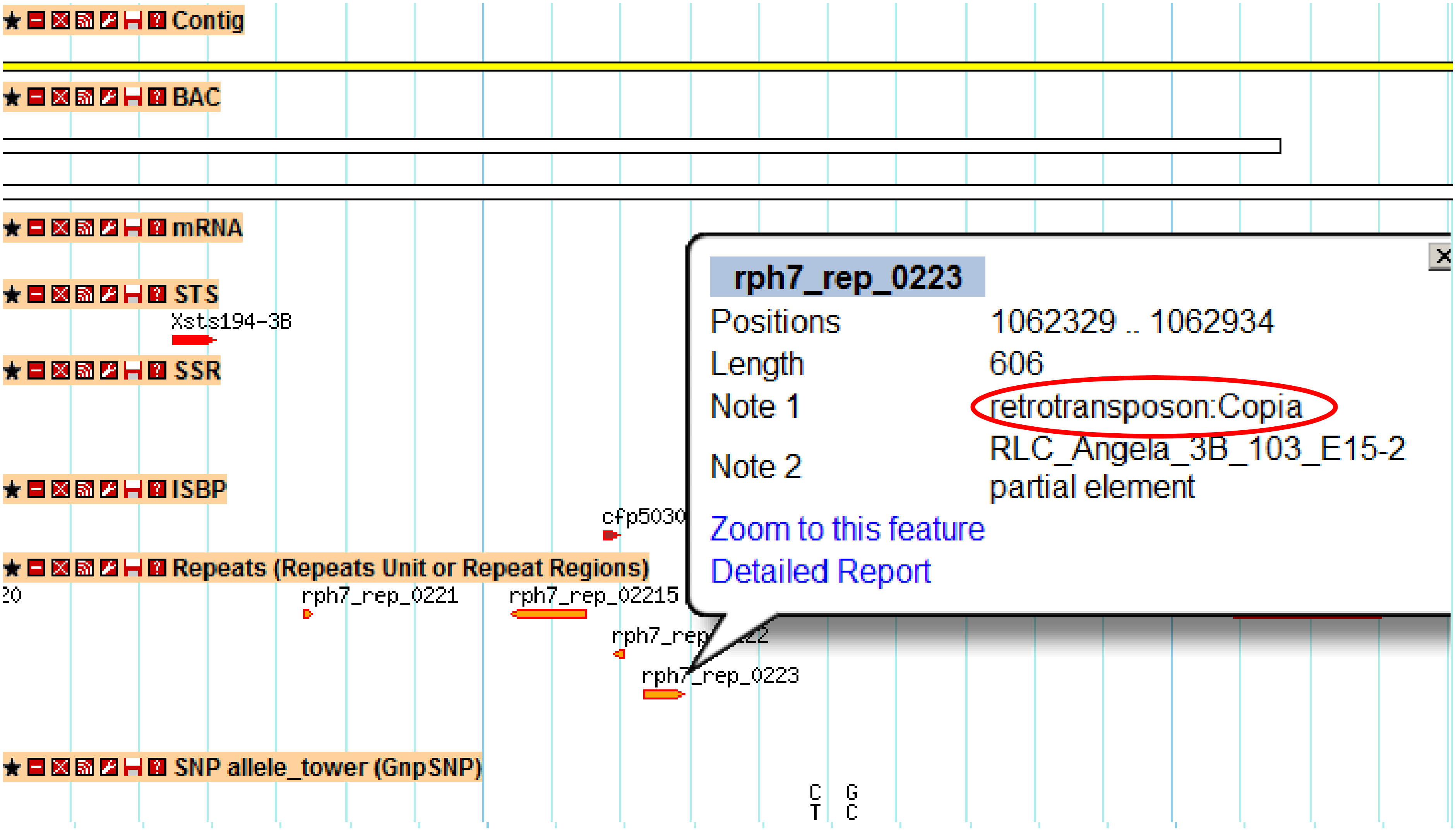
Mapped loci: 1

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/

Michael Alaux

Annotation Viewer Prototype



rph7_rep_0223

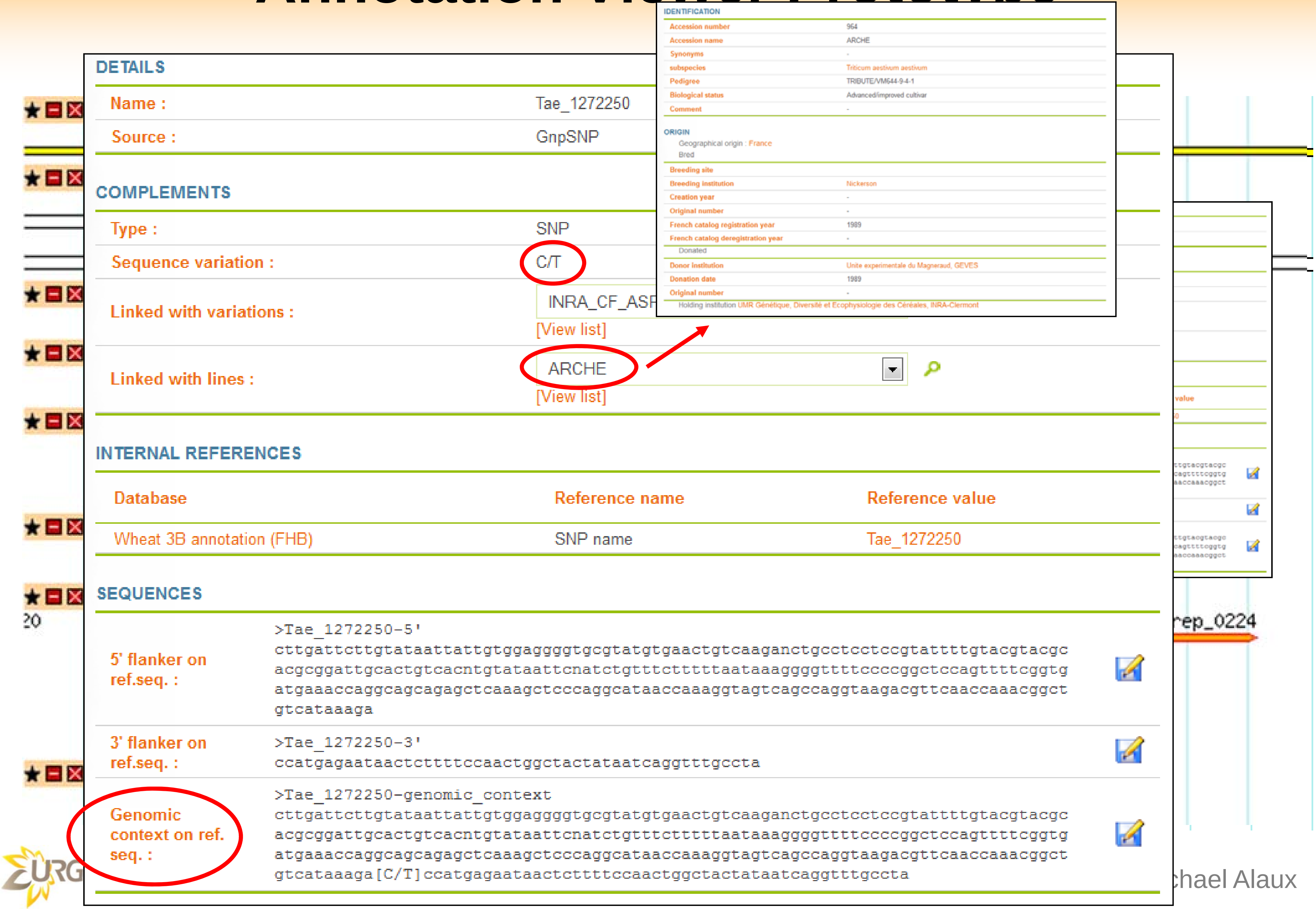
Positions	1062329 .. 1062934
Length	606
Note 1	retrotransposon:Copia
Note 2	RLC_Angela_3B_103_E15-2 partial element

Zoom to this feature

Detailed Report

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

Annotation Viewer Prototype



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

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'
cttgattcttgtataattattgtggaggggtgcgtatgtgaactgtcaaganctgcctcctccgtattttgtacgtacgc
acgcggattgcactgtcacntgtataattcnatctgtttctttttaataaaggggttttccccggctccagttttcggtg
atgaaaccaggcagcagagctcaaagctcccaggcataaccaaaggtagtcagccaggtaagacgttcaaccaaacggct
gtcataaaga
```

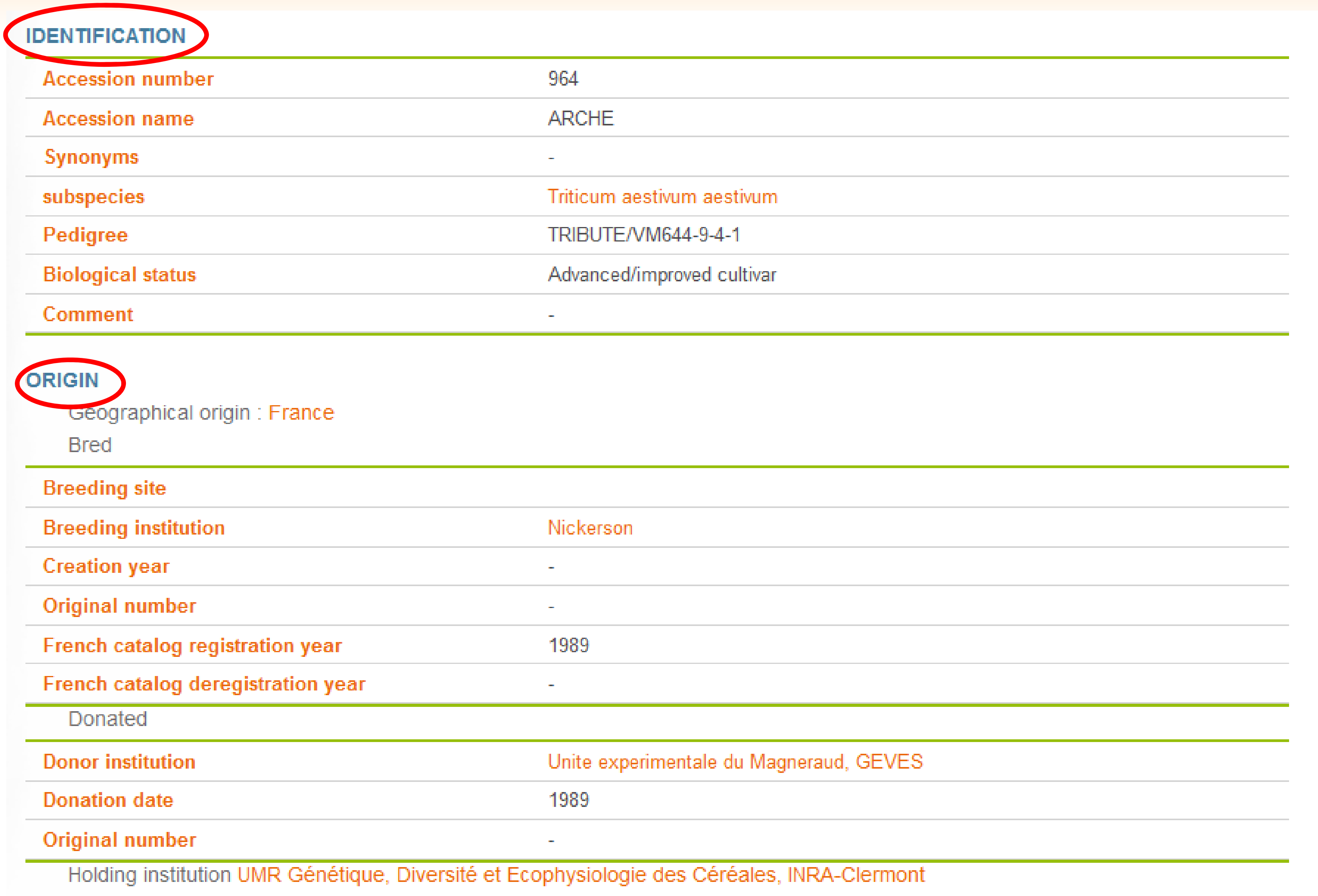
3' flanker on ref.seq. :

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

Genomic context on ref. seq. :

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

Annotation Viewer Prototype



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Synonyms	-
subspecies	Triticum aestivum aestivum
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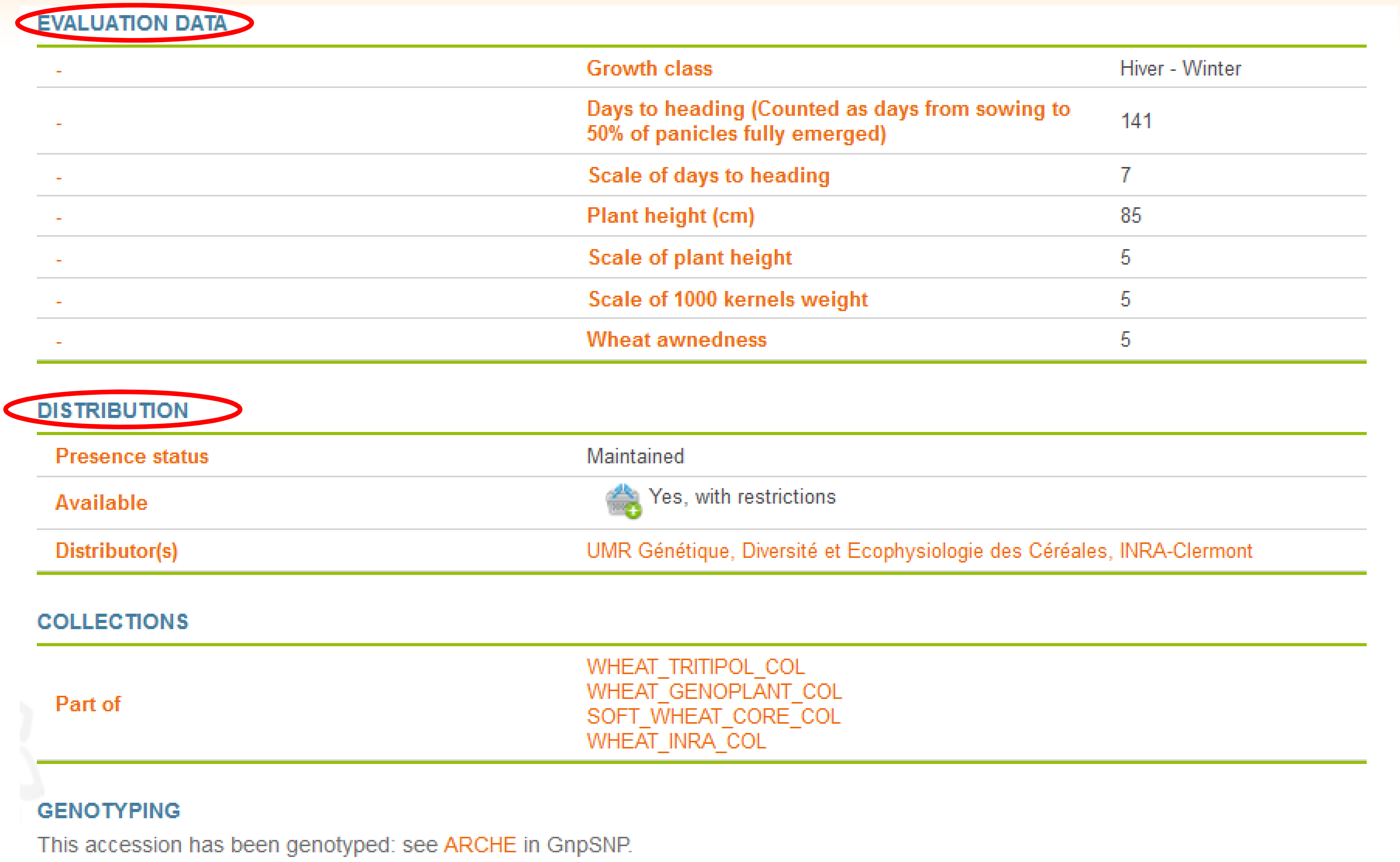
Donation date	1989
Original number	-

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

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

Michael Alaux

Annotation Viewer Prototype



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

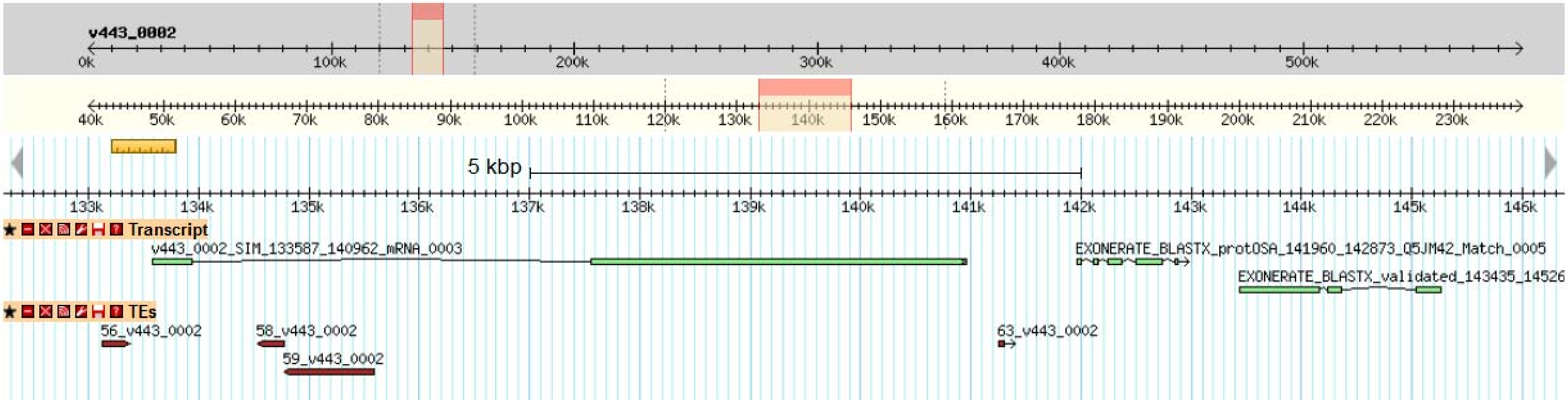
Part of	WHEAT_TRITIPOL_COL WHEAT_GENOPLANT_COL SOFT_WHEAT_CORE_COL WHEAT_INRA_COL

GENOTYPING

This accession has been genotyped: see ARCHE in GnpSNP.

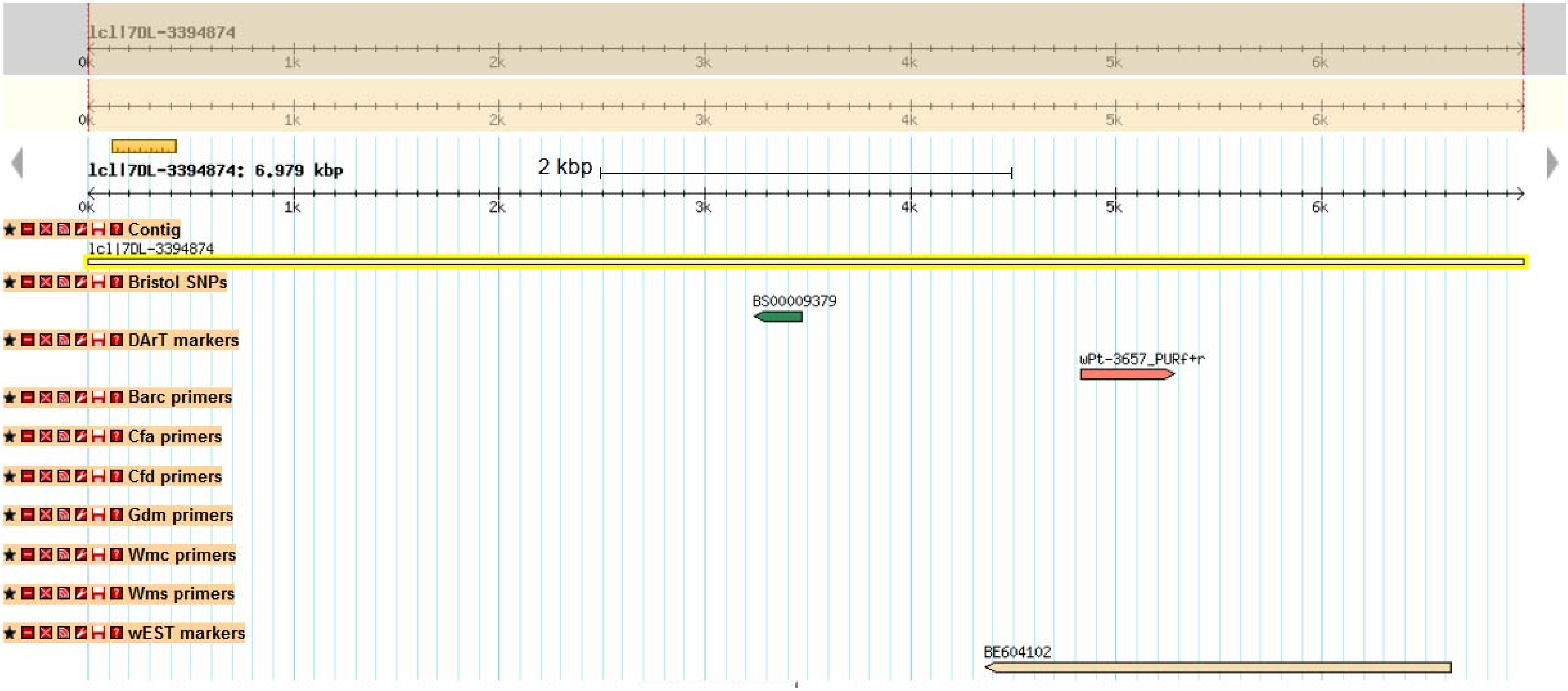
http://urgi.versailles.inra.fr/gb2/gbrowse/wheat_3B_RPH7_pub/

In development: whole 3B annotation viewer



F. Choulet

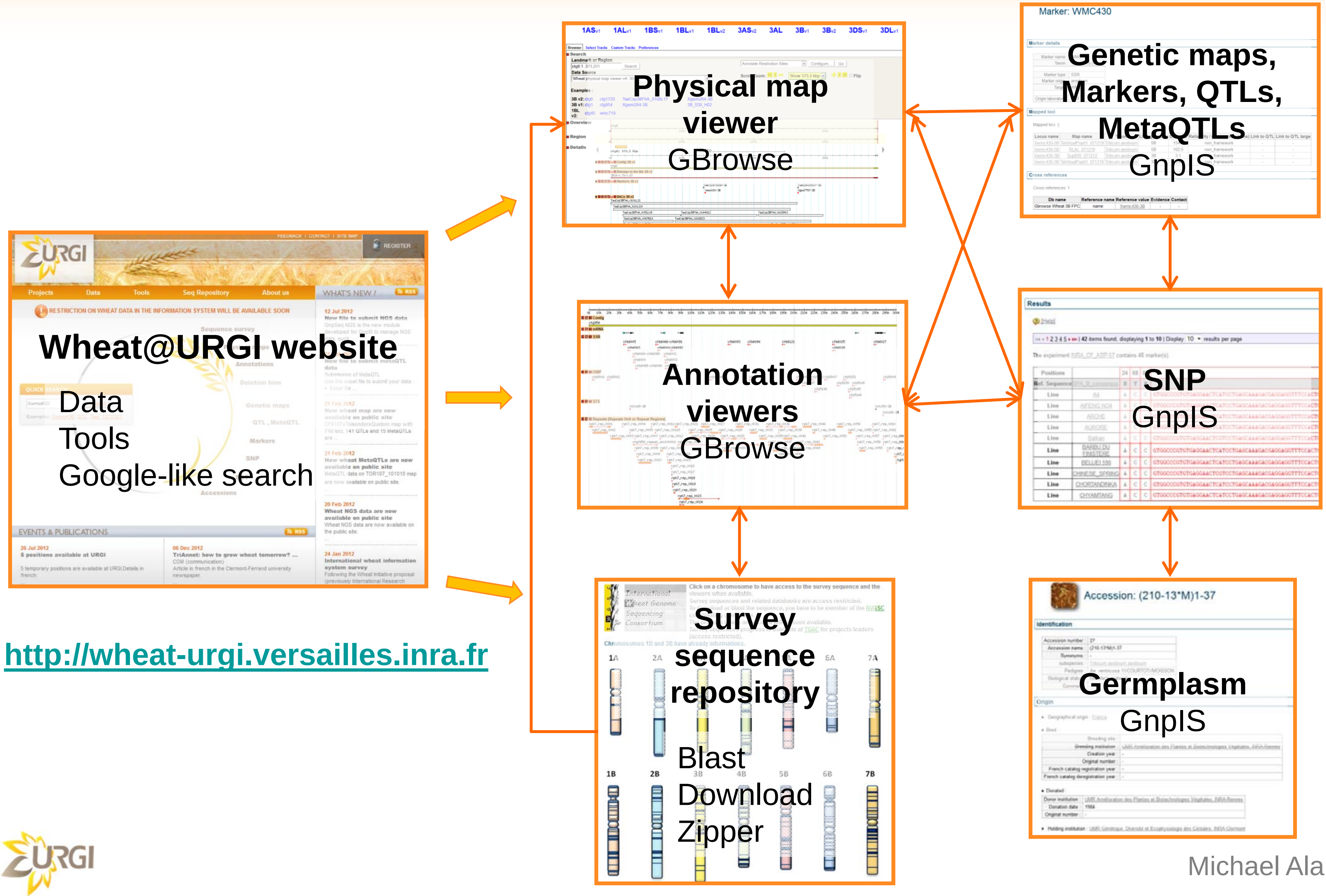
In development: survey seq annotation viewer



C. Pozniak

Michael Alaux

Wheat dataflow overview



Wheat@URGI website

Data
Tools
Google-like search

Physical map viewer
GBrowse

Genetic maps, Markers, QTLs, MetaQTLs
GnpIS

Annotation viewers
GBrowse

SNP
GnpIS

Survey sequence repository

Blast
Download
Zipper

Germplasm
GnpIS

http://wheat-urgi.versailles.inra.fr

Michael Alaux

Acknowlegments

M. Alaux
L. Courderc
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F. Choulet
C. Feuillet

J. Wright
M. Caccamo
S. Ayling

M. Spannagl
M. Martis
K. Mayer

<u>Data producers</u>

Questions

Survey Sequence Repository

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Ask an account

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

Wheat@URGI website

http://wheat-urgi.versailles.inra.fr

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