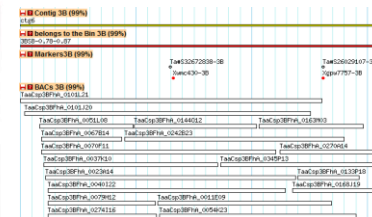
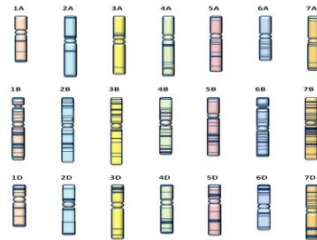


WheatIS: The INRA node presentation

Michael Alaux



Wheat@URGI website



Wheat@URGI

URGI

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, MetaQTL

Markers

SNP

EST

Germplasm

QUICK SEARCH

Xwmc430

Examples: [Xwmc430](#), [QTL](#), [Tae_1272327](#)

ADVANCED TOOLS

[WHEAT3BMINE](#)

WHAT'S NEW ? RSS

21 Nov 2014
2A physical map is now available
2AS and 2AL physical maps are now available for IWGSC partners.
.....

22 Oct 2014
Wheat3BMine is now available
Wheat3BMine, a data warehouse dedicated to wheat chromosome 3B is now available. ...
.....

11 Oct 2014
GnpIS version 14.2 availability
GnpIS version 14.2 is available. Major new functionalities include:
• Sequence Polymorphisms: Genotyping : The ...
.....

03 Sep 2014
New survey sequence gene models (v2.2) available
New version of the survey sequence gene models (v2.2 July 2014) is ...
.....

02 Sep 2014
GBrowse Wheat Survey Sequence Annotation is available
The GBrowse Wheat Survey Sequence Annotation (Markers, SNPs, Gene Models) is now available
.....

02 Sep 2014
7DS physical map is publicly available
7DS physical map is publicly available

EVENTS & PUBLICATIONS RSS

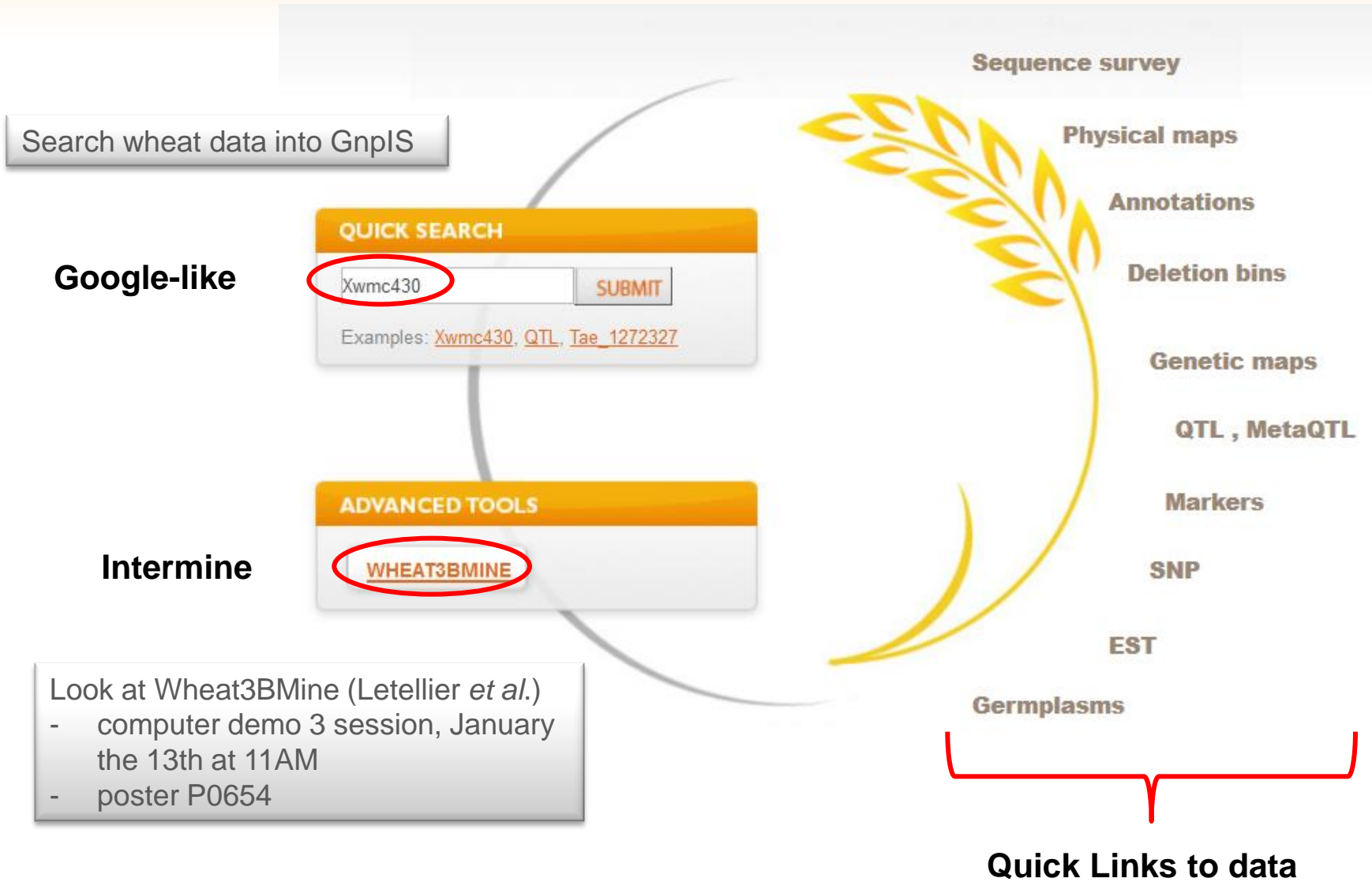
02 Jan 2014
Talks at PAG 2014
Computer demo 1: Saturday 11 at 1.50 PM Wheat 3B Annotation Viewer: Browse ...
.....

02 Jan 2014
IWGSC Sequence Repository: new data and browsers ...
COM (talks)
International Wheat Genetics Symposium (IWGS)
12th 2013, Yokohama, Japan
.....

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



Wheat@URGI



Look at Wheat3BMine (Letellier *et al.*)

- computer demo 3 session, January the 13th at 11AM
- poster P0654

Wheat@URGI

Projects

Data

Tools

Seq Repository

Projects

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

3BSeq

BreedWheat

TriticeaeGenome

Wheatbi

Wheat Initiative

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.



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.
























Wheat@URGI

Projects

Data

Tools

Seq Repository

Sequence survey		
Physical maps		
Annotations (3B pseudomolecule)		
Genetic maps		
QTL		
MetaQTL		
Markers		
SNP: polymorphic loci		
SNP: sequence variations		
Germplasm		
Sequencing experiments (NGS, EST)		
Synten: wheat		
Synten: cereal		
Transcriptome (ProtNBIé project)		
Phenotype (BW project)		

Data summary 22/08/2014

Public data

Genetic maps	27
Physical maps chr. arms	11
Reference sequence chr.	1
Survey sequence chr.	21
QTLs	465
Markers	26881
Germplasms	6797
SNPs: polymorphic loci	1731570
SNPs: sequence variations	204522
ESTs	544529

<http://wheat-urji.versailles.inra.fr>

Michael Alaux



Wheat@URGI

Projects

Data

Tools

Seq Repository

Tools

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

BLAST (Public)

Intermine

TriAnnot Pipeline

Quick search in GnpIS

BioMart

Physical map viewer

Annotation viewer

Deletion Bins








dbWFA

RulNet

Plant Synteny Viewer

Tools

	<i>free access tool</i>		<i>registered access tool</i>
---	-------------------------	---	-------------------------------

BLAST (Public)		
TriAnnot Pipeline		
Intermine		
Quick search		
BioMart		
Physical map viewer		
Annotation viewer		
Deletion bins		
dbWFA (functional annotation)		
RulNet (network inference and visualization)		
Wheat Synteny Viewer		



Wheat@URGI

Projects

Data

Tools

Seq Repository

Seq Repository

You are here : [Home](#) / [Home Wheat](#) / Seq Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

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.

1A



2A



3A



4A



5A



6A



7A



Some GnplS data



Germplasm data

Siregal



Accession: BARBU DU FINISTERE



IDENTIFICATION



Accession number	1232
Accession name	BARBU DU FINISTERE
Synonyms	ECPGR: GVS 1648 [English]
subspecies	<u>Triticum aestivum aestivum</u>
Pedigree	LV
Biological status	Traditional cultivar/landrace
Comment	-

HOLDING

Holding stock center	<u>Small grain cereals BRC</u>
Presence status	Maintained

ORIGIN


Geographical origin :	<u>France</u>
Donated	<u>UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont</u>
Donation date	1987
Original number	-

Germplasm data

EVALUATION DATA

Growth class	winter hiver
Days to heading (in day-degree)	1787
Plant height (cm)	121 cm
Scale of plant height (IPGRI 4.1.2)	high haut
Scale of 1000 kernels weight	low faible - 2000
Scale of spike density (IPGRI 4.2.2)	very low/very sparse très faible/très lâche - 2000
Wheat awnedness (IPGRI 4.2.3)	awned (<= length of spike) barbu (<= à la longueur de l'épi) - 2000
Scale of glume colour (IPGRI 4.2.4)	white yellow blanc jaune - 2000
Scale of glume hairiness (IPGRI 4.2.5)	dense dense - 2000
Scale of grain colour (IPGRI 4.3.1)	dark brown/dark red marron foncé/rouge foncé - 2000
Susceptibility to powdery mildew - Erysiphe graminis f. sp. tritici (CTPS)	very susceptible très sensible - 2011
Susceptibility to head blight - Fusarium spp. (CTPS)	susceptible sensible - 2011
Susceptibility to stripe rust (Puccinia striiformis f. sp. tritici) (CTPS)	little susceptible peu sensible - 2011
Susceptibility to leaf rust (Puccinia triticina) (CTPS)	susceptible sensible - 2011

DISTRIBUTION

Distributor(s)	UMR Génétique, Diversité et Ecophysiologie des Céréales, INRA-Clermont Available from Multilateral System (MLS) 
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COLLECTIONS

Part of	BREEDWHEAT COL SOFT WHEAT CORE COL SOFT WHEAT FAO COL WHEAT INRA COL
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GENOTYPING

This accession has been genotyped: see [BARBU DU FINISTERE](#) in the polymorphisms module.

Phenotyping data

lotNumber	fertiliser	trialName	trialSite	bloc	subBloc	plot	Grain yield (harvesting machine)(GY)
37339-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	4086	67.2105
36499-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3091	74.994
37342-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	4096	63.382000000000005
36314-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3081	63.0604
36340-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3084	65.2098
36589-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3097	58.443599999999996
37337-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	4079	60.603300000000004
3572-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3077	70.7252
37338-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3077	70.7252
37340-2011	HN: High Nitrogen	CHA-2012	Arvalis-Chalons	1	4	3077	70.7252

Ephesis data export 

A	B	C	D
lotNumber	fertiliser	trialName	trialSite
Query param Lot Numbers : Grain yield (harvesting mac			
"37339-2011	HN: High Nit	CHA-2012	Arvalis-Chal
36499-2011	HN: High Nit	CHA-2012	Arvalis-Chal
37342-2011	HN: High Nit	CHA-2012	Arvalis-Chal
36314-2011	HN: High Nit	CHA-2012	Arvalis-Chal
36340-2011	HN: High Nit	CHA-2012	Arvalis-Chal
36589-2011	HN: High Nit	CHA-2012	Arvalis-Chal
37337-2011	HN: High Nit	CHA-2012	Arvalis-Chal
3572-2011	HN: High Nit	CHA-2012	Arvalis-Chal
37338-2011	HN: High Nit	CHA-2012	Arvalis-Chal
37340-2011	HN: High Nit	CHA-2012	Arvalis-Chal

_data24.580140357102177_isatab_data.zip - WinRAR (Version d'évaluation)

Fichier Commandes Outils Favoris Options Aide

Ajouter Extraire vers Tester Afficher Supprimer Rechercher Assistant Informations Antivirus Commentaire

_data24.580140357102177_isatab_data.zip - ZIP archive, la taille non compressée est de 87 764

Nom	Taille	Compressé	Type	Modifié
Dossier de fichiers				
s_Study_CHA-2012_tdf.csv	205	115	Fichier CSV Microsoft Excel	05/11/2014 16:12
Investigation.txt	444	271	Document texte	05/11/2014 16:12
a_CHA-2012_processed_data.csv	7 127	1 786	Fichier CSV Microsoft Excel	05/11/2014 16:12
s_Study_CHA-2012(CHA-2012).txt	13 956	1 940	Document texte	05/11/2014 16:12
Assay_s_Study_CHA-2012(CHA-2012).txt	21 621	1 765	Document texte	05/11/2014 16:12
ephehis_data.csv	44 411	1 738	Fichier CSV Microsoft Excel	05/11/2014 16:13

Total 87 764 octets dans les fichiers 6



SNP discovery data

DETAILS

Name :	contig05927_111_BS00079614
Ref. Sequences :	<input type="text" value="7AS_4182395"/>  
Position on ref. seq. :	-1
Source :	Breadwheat SNP discovery for "BBSRC" experiment




COMPLEMENTS

Type :	SNP
Sequence variation :	A/G 

MAPPING INFORMATIONS (NGS)

Reference Genome :	IWGSC Survey Sequences
Taxon (mapping) :	Triticum aestivum
Chromosome :	7AS

SEQUENCES

5' flanker on ref.seq. :	>contig05927_111_BS00079614-5' CTAATGGAACCAATGGCAAACCTAGCAGAGG	
3' flanker on ref.seq. :	>contig05927_111_BS00079614-3' AGACGACGAAGCCAAAATGGCGCAAGTTGT	
Genomic context on ref. seq. :	>contig05927_111_BS00079614-genomic_context CTAATGGAACCAATGGCAAACCTAGCAGAGG [A/G] AGACGACGAAGCCAAAATGGCGCAAGTTGT	

Genotyping data

GENOTYPE RESULTS

1-10 of 6,720,835 | Display 10 results per page

Marker	Accession	Genotype type	Genotype	Quality type	Quality	Experiment	Genotyping array
BGABW022597	ITMI-15	genotype	A/A			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-21	genotype	G/G			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-23	genotype	G/G			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-33	genotype	G/G			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-43	genotype	A/A			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-50	genotype	A/A			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-2	genotype	G/G			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-56	genotype	G/G			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-64	genotype	A/A			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set
BGABW022597	ITMI-71	genotype	G/G			Axiom_WP1_ITMI_callsGenotyped	Axiom_WP1_ITMI_callsGenotyped Set

1 - 100 of 75515

Marker \ Accession	ITMI-109	ITMI-108	ITMI-Sn	ITMI-106	ITMI-105	ITMI-1	ITMI-104	ITMI-101	ITMI-110	ITMI-111
BGABW020868	G/G	G/G	T/T	G/T	T/T	T/T	G/G	G/G	T/T	T/T
BGABW020867	T/T	T/T	C/C	C/T	C/C	C/C	T/T	T/T	C/C	C/C
BGABW020764	G/G	G/G	A/A	A/A	A/A	A/A	G/G	G/G	A/A	A/A
BGABW021805	C/C	C/C	C/C	C/C	C/C	C/C	C/C	A/A	A/A	A/A
BGABW021803	G/G	G/G	G/G	G/G	G/G	G/G	G/G	A/A	A/A	A/A
BGABW021705	A/A	G/G	A/A	A/A	G/G	A/G	G/G	A/A	G/G	A/A
BGABW020860	G/G	A/A	G/G	G/G	A/A	G/G	A/A	G/G	G/G	A/A
BGABW021909	T/T	T/T	T/T	G/G	T/T	G/G	G/G	T/T	G/G	G/G
BGABW021992	G/G	G/G	G/G	G/G	G/G	A/A	G/G	A/A	A/A	A/A
BGABW020762	C/C	T/T	T/T	C/C	C/C	C/C	C/C	T/T	C/C	T/T
BGABW020763	A/A	G/G	G/G	A/A	A/A	A/A	A/A	G/G	A/A	G/G
BGABW020761	T/T	C/C	C/C	T/T	T/T	T/T	T/T	C/C	T/T	C/C
BGABW021912	C/C	C/C	T/T	C/C	T/T	C/C	T/T	T/T	C/C	C/C
BGABW022027	G/G	G/G	G/G	A/A	A/A	A/A	A/A	G/G	A/A	A/A
BGABW021786	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
BGABW022226	C/C	C/C	T/T	T/T	C/C	C/C	T/T	C/C	C/C	C/C
BGABW021880	G/G	C/C	C/C	C/C	G/G	C/C	C/C	C/C	G/G	G/G
BGABW021881	C/C	T/T	T/T	T/T	C/C	T/T	T/T	T/T	C/C	C/C
BGABW022223	G/G	G/G	A/A	G/G	A/A	A/A	G/G	G/G	A/A	A/A



Association data

Filters:

Traits Treatments Locations Years Chromosomes Models Values

pval < Add filter

Filtered fields	Filter type	Treshold value(s)	Delete filter
pval	<	0.5	✕

Refresh results

GRAPHICAL DISPLAY

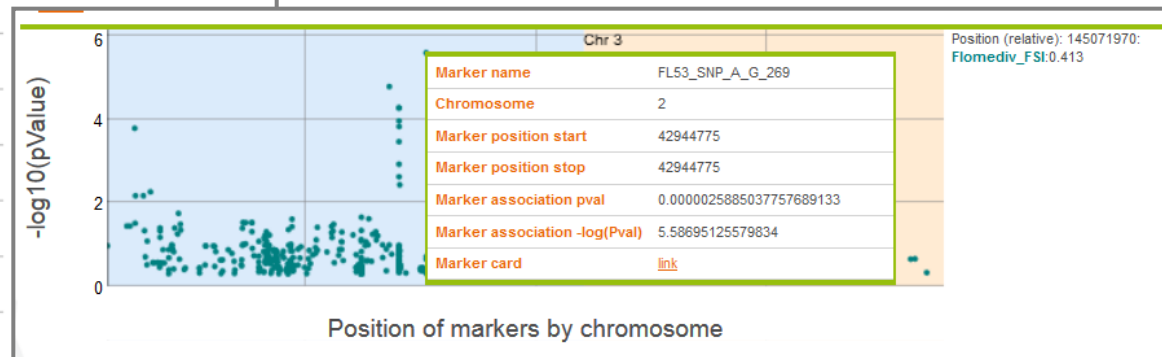
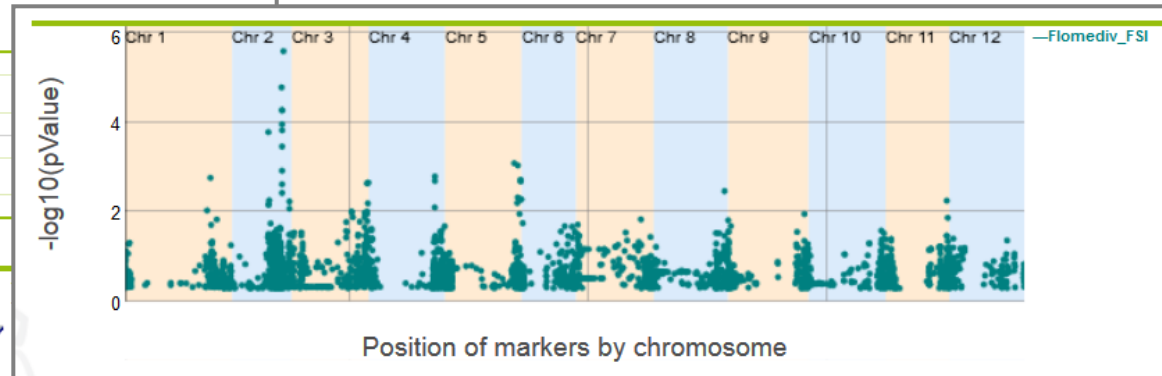
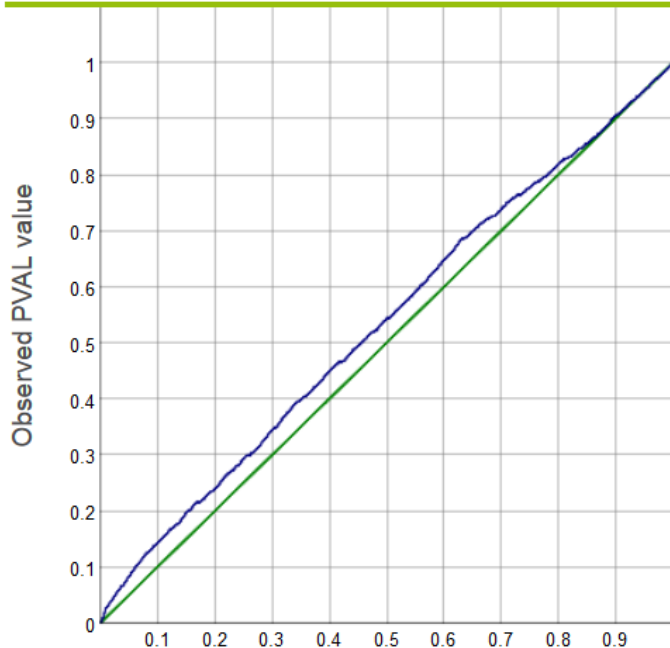
Draw QQPlot :

pval

Draw Manhattan Plot:

$-\log(pval)$

Plots:



Sequence Repository

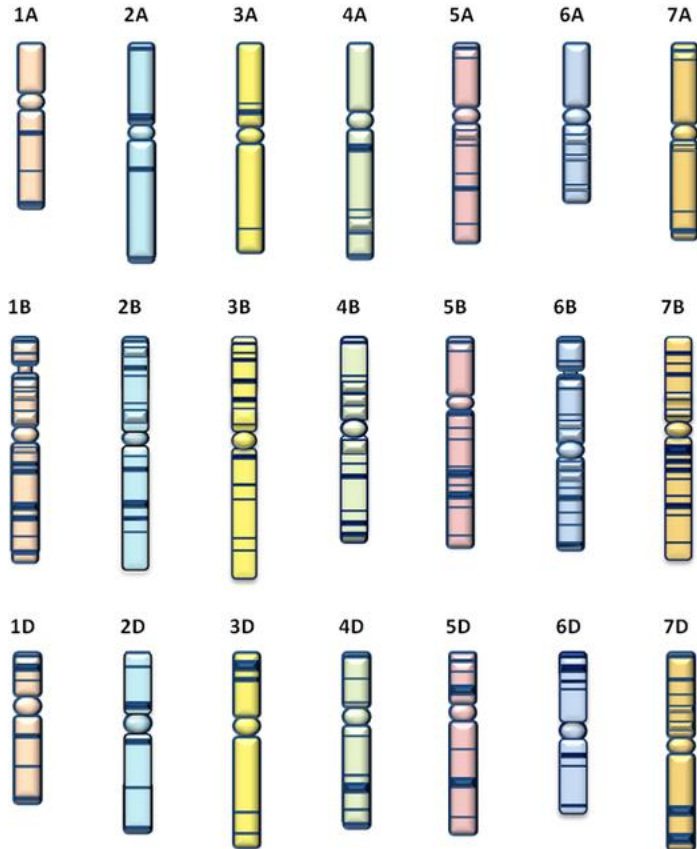


Sequence Repository



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

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



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

BLAST (**Public**)

Download (**Public**)

Browsers:

- Physical maps
- Annotated reference sequence **3B (Public)**
- Annotated survey sequence (**Public**)



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

Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

Jan 2015:

- New physical maps available to **display** : 2A, 4A, 7B and 7DS.
- **Wheat3BMine** , a data warehouse dedicated to wheat chr. 3B is available.
- New bank available to **BLAST** : 4A individual chr shotgun.

Sept 2014:

- Aegilops tauschii scaffolds available for **BLAST** at **ATGSP** .
- Summary of the different CSS assemblies and versions: **IWGSC-CSS_assembly-version-overview_Sep2014.xls**

August 2014:

- IWGSC **survey sequence browser** is now **publicly** available.
- New version of the survey sequence **gene models** (v2.2 July 2014) is **publicly** available.

June 2014:

Other wheat species WGS assemblies are publicly available for **BLAST** : *Triticum durum*, cv. Cappelli, *Triticum durum*, cv. Strongfield, *Triticum monococcum*, *Aegilops speltoides*, *Aegilops sharonensis*, *Triticum urartu*, *Aegilops tauschii*.

April 2014:

- **Access Status** webpage is available to display all the resources and their access (public, community, etc.).
- **3B reference sequence databanks** (whole chromosome and CDS only) are available to **BLAST** .

March 2014:

- **Public BLAST** to query survey sequence and 454 assemblies is **available** .
- **3B data** (Genomic DNA, CDSs, annotation of features and a README) are **publicly** available for **download** .
- **POPSEQ** data are **publicly** available for **download** .
- **GenomeZipper** data are now **publicly** available.
- New **oriented RNA-Seq library** is **publicly** available.

Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

		Data access agreement					
		Public	General access	Project team data access	Other	Contacts	Publication
Survey sequence	BLAST	x				IWGSC	IWGSC, PMID:25035500
	Download	x				IWGSC	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome Science
	Genome Zipper (v5)	x				Mihaela Martis, Klaus Mayer	
	Gene models (nov13)	x				Manuel Spannagl, Klaus Mayer	
	POPSEQ	x				Nils Stein	
	Browser	x				IWGSC, Curtis Pozniak, Eduard Akhunov	
Other wheat species WGS assemblies	Download	x				Jon Wright, Mario Caccamo	
RNA-Seq (oriented and non-oriented)	Download	x				Lise Pingault, Etienne Paux	

Sequence Repository

Create an account

News

Access Status

FAQ

✓ BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

- **Public BLAST**

A **BLAST** is now **publicly available** to query the *Triticum aestivum* **survey sequence** assemblies, the **3B reference sequence** (whole chromosome and CDS only), **454 assemblies** and **other wheat species** assemblies.

- SRS BLAST

A short demonstration video of the SRS BLAST is available [here](#) .

A [direct link](#) is available to perform a SRS BLAST (registered access).

- External BLAST

Aegilops tauschii scaffolds available for [BLAST](#) at [ATGSP](#) .

Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

Triticum aestivum (Chinese Spring) survey sequence chromosomes assemblies are **publicly available** for [download](#) , [BLAST](#) and in a [browser](#) .

Summary of the different CSS assemblies and versions (TGAC): [IWGSC-CSS assembly-version-overview_Sep2014.xls](#) (30.50 kB)

Some individual chromosome shotgun (454 data) are also **publicly available** for [BLAST](#) .

Other wheat species WGS assemblies (TGAC, TSL) are **publicly available** for [download](#) and [BLAST](#) :

- *Triticum durum*, cv. Cappelli (listed as durum_v1)
- *Triticum durum*, cv. Strongfield
- *Triticum monococcum*
- *Aegilops speltoides*
- *Aegilops. sharonensis*
- *Triticum urartu*
- *Aegilops tauschii*

Triticum durum cv. Cappelli

The cultivar Senatore Cappelli (know as Cappelli) is an historical durum wheat genotype selected from a North African landrace by N. Strampelli and registered in 1915. Cappelli is one of the founders of the Italian durum wheat breeding program and it is present in the pedigree of many durum wheat cultivars released in southern Europe in the XXth century. Cappelli has been largely grown in Mediterranean regions since the late 1950s.

Cappelli is characterized by an elevated water use efficiency (Rizza et al., 2012 Field Crops Research 125, 49–60).

Triticum durum cv. Strongfield

Strongfield durum wheat was developed by Dr. John Clarke during his tenure at Agriculture and Agri-Food Canada. "Strongfield" expresses high grain yield, high grain protein concentration coupled with low grain cadmium concentration. Canadian durum wheat production represents 60% of durum wheat traded globally and Strongfield currently occupies 65% of the total planted area of durum wheat in Canada. A detailed description of the variety has been published (Clarke et al. 2005; Can J. Plant Sci., 83: 651-654 see <http://pubs.aic.ca/doi/abs/10.4141/P04-119>).

Aegilops tauschii scaffolds available for [BLAST](#) at [ATGSP](#)

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

Michael Alaux



Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

✓ Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

3B reference sequence (F. Choulet):

- Display the 3B pseudomolecule using the 3B wheat annotation viewer (**publicly available**).
- Download the 3B data : Genomic DNA, CDSs, annotation of features and a README (**publicly available**).
- BLAST the 3B reference sequence: whole chromosome or CDS only (nucleotide and peptide) (**publicly available**).

Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

- **Gene models** performed by MIPS plant group (K. Mayer) are **publicly available**

- Feb. 2013 version
- Nov. 2013 version (README file included)
- Jul. 2014 (version v2.2)

Major changes are:

a.) we re-named the genome assembly scaffolds from the old e.g ">10" identifiers to ">ta_iwgsc_1al_v2_10" identifiers for the fasta files of CLEANED and repeat-masked genome sequences and adapted the ids in the annotation GTF files accordingly.

b.) we fixed an issue with missing stop codons in the gene prediction fasta and GTF files

NO structural changes were made between v2.1 and v2.2 annotation, all gene identifiers remain stable, so this update can be considered cosmetic and mainly attributed to better user convenience.

Re-named genome assembly: genome_assembly/genome_arm_assemblies_CLEANED/ and genome_assembly/genome_arm_assemblies_CLEANED_REPMASKED/
gene predictions incl. changelog, README, ...: genePrediction_v2.2/

- **Genome Zipper** performed by MIPS plant group (K. Mayer) is **publicly available**

- 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
- v5: excel , tab formats

- **POPSEQ** performed by IPK (N. Stein) is **publicly available**

- Mar. 2014 version (README file included)

- **1AS sequence model** (T. Wicker) is publicly available for download.

Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and
data submission

RNA-Seq data from INRA GDEC (L. Pingault, E. Paux) are **publicly** available to [download](#).

Deep transcriptome sequencing was conducted on two RNA-Seq library types:

(i) **non-oriented library** (TruSeq, Illumina) sequenced on Illumina HiSeq2000 2x100bp (PE) for 15 different conditions corresponding to five wheat organs (root, leaf, stem, spike, grain) at three developmental stages each in duplicates

(ii) **oriented library** (ScriptSeq, Epicentre) sequenced on Illumina HiSeq2000 1x100bp (SE) for five conditions corresponding to five wheat organs (root, leaf, stem, spike, grain) without duplicates.

Mapping RNA-Seq reads to the chromosome 3B reference sequence allowed to validate gene prediction, as well as to identify a significant number of novel transcribed regions in which no gene structure was predicted and that might correspond to long non-coding RNAs. Transcription profiles, alternative splicing and expression breadth were also studied, providing new insights into the structural and functional compartmentalization of the wheat chromosome 3B. In combination with the IWGSC survey sequences, these data also proved to be extremely useful to decipher the specific evolutionary history of wheat chromosomes as well as to study the relative expression of homoeologous and paralogous copies of wheat genes.

[] [README](#)

[DIR] grain_Z71_rep1/	[DIR] root_Z10_rep1/
[DIR] grain_Z71_rep2/	[DIR] root_Z10_rep2/
[DIR] grain_Z75_rep1/	[DIR] root_Z13_rep1/
[DIR] grain_Z75_rep2/	[DIR] root_Z13_rep2/
[DIR] grain_Z85_rep1/	[DIR] root_Z39_rep1/
[DIR] grain_Z85_rep2/	[DIR] root_Z39_rep2/
[DIR] leaf_Z10_rep1/	[DIR] spike_Z32_rep1/
[DIR] leaf_Z10_rep2/	[DIR] spike_Z32_rep2/
[DIR] leaf_Z23_rep1/	[DIR] spike_Z39_rep1/
[DIR] leaf_Z23_rep2/	[DIR] spike_Z39_rep2/
[DIR] leaf_Z71_rep1/	[DIR] spike_Z65_rep1/
[DIR] leaf_Z71_rep2/	[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/

Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

IWGSC, A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome, *Science* 2014

doi: 10.1126/science.1251788

You can access all the related data (survey sequence assemblies, gene models, genome zipper, POPSEQ) as it existed at the time of manuscript submission [here](#) .



Sequence Repository

Create an account

News

Access Status

FAQ

BLAST

Assemblies

Reference sequence

Genes & annotations

Physical maps

Transcriptome

RNA-Seq

Publication

Support to assembly and

data submission

- [BAC sequence assembly](#)

Frederic Choulet talk about 3B pseudomolecule assembly at PAG 2014 IWGSC Standard and Protocol session:

[iwgscStdProtocolesPAG2014_Choulet.pptx](#) (756.23 kB)

- [Data submission](#)

Physical map

Send your FPC file to [michael.alaux \[at\] versailles.inra.fr](mailto:michael.alaux@versailles.inra.fr).

Notice that [LTC software](#) could generate a FPC file. Questions about LTC software could be send to Zeev Freenkel ([zvfrenkel \[at\] gmail.com](mailto:zvfrenkel@gmail.com)).

FPC file sample for 3B with BACs, contigs, markers and deletion bins:

[FPC_3B_example.fpc](#) (1.64 kB)

Reference sequence annotation

Send your sequence and gff3 files to [michael.alaux \[at\] versailles.inra.fr](mailto:michael.alaux@versailles.inra.fr).

GFF3 files sample for 3B with genes, RNAs, markers, BACs, transposable elements:

[Ref_Seq_Annot_3B_GeneModel_example.gff](#) (5.46 kB)

[Ref_Seq_Annot_3B_Markers_example.gff](#) (704 B)

[Ref_Seq_Annot_3B_Repeats_example.gff](#) (1.52 kB)



Sequence Repository: 3B example

BLAST parameter settings

Enter query sequences here in fasta format.

Or upload sequence fasta file (max 2M):

Program: Group: Database(s):

currently selected database(s):

Basic Search - using default BLAST parameter settings

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!

Enregistrer le fichier

Toujours effectuer cette action pour ce type de fichier.

Ouverture de wheat_genome_zipper_v5_excel.tar.gz

Vous avez choisi d'ouvrir:

wheat_genome_zipper_v5_excel.tar.gz
 qui est un fichier de type: Archive WinRAR (7.0 Mo)
 à partir de: https://urgi.versailles.inra.fr

Que doit faire Firefox avec ce fichier ?

Ouvrir avec WinRAR archiver (défaut)

DownThemAll!

dTa OneClick!

Enregistrer le fichier

Toujours effectuer cette action pour ce type de fichier.

Wheat annotation viewer: 3B: 9.999 kbp from traes3bPseudomoleculeV1:9,577,253..9,587,252

Browser:

Search:

Landmark of Region:

Examples: [traes3bPseudomoleculeV1.9.577.253..9.587.252](#), [traes3bPseudomoleculeV1.264.818.124..269.148.123](#), [Traes3bPseudomoleculeV1.443.0010](#)

Data Source:

Wheat annotation viewer: 3B:

Chromosome 3B:

- [BLAST on survey sequence databanks \(Public BLAST\)](#).
- [Download 3B survey sequence assembly](#).
- [Download Gene models, GenomeZipper and POPSEQ data](#).
- [Display 3B physical map \(82% and 99% coverage versions\)](#).
- [Display 3B annotated pseudomolecule browser](#)
- [Display survey sequence annotation browser](#).

[Sequence Repository page](#) .
[IWGSC page](#) .

Chromosome 3B

Available data
 Access data for chromosome 3B at URGI Sequences Repository

Projects
 3B physical map

Sequencing chromosome 3B

Project Leader: [Toussaint Catherine](#)

Chromosome 3B survey sequence

Project Leader: [Toussaint Catherine](#)

Gene model mRNA

50K size exons SNPs

Enriched SNPs markers

CFC markers

DAT gbs markers

DAT v3 markers

Wheat EST markers

Wheat

Barc

BLAST



BLAST

BLAST parameter settings

Enter query sequences here in [Fasta format](#)

Or upload sequence fasta file (max 2M): bacSynth12_debut.tfa

Program

Group

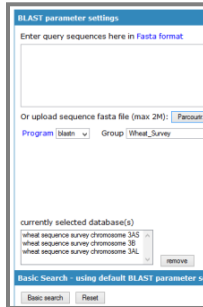
Database(s)

- Wheat_Reference
- Wheat_454
- Wheat_Markers
- Wheat_other_species_WGS
- Wheat_Survey

currently selected database(s)

- Wheat reference sequence chromosome 3B
- wheat sequence survey chromosome 3DL
- wheat sequence survey chromosome 3DS

Basic Search - using default BLAST parameter settings



BLAST

Advanced Search - setting your favorite parameters below

Expect threshold	<input type="text" value="0.0001"/>
Word size	<input type="text" value="11"/>
Max target sequences	<input type="text" value="50"/>
Match/Mismatch scores	<input type="text" value="2,-3"/>
Gap costs	<input type="text" value="Existence: 5, Extension: 2"/>
Filter	<input checked="" type="checkbox"/> Low complexity regions
Mask	<input checked="" type="checkbox"/> Mask for lookup table only <input type="checkbox"/> Mask for lower case letters
Alignment	<input type="checkbox"/> Perform ungapped alignment
Alignment output format	<input type="text" value="pairwise"/>
Other parameters	<input type="text"/>

BLAST

Filter current page by score:

Show for each query sequence

where cutoff criterion \geq for Similarity percentage

Blast score

Filter

Query	Subject	Score	Identities (Query length)	Percentage	Expect
Synth12	traes3bPseudomoleculeV1	2796	1554/1555 (1560)	99	0.0
Synth12	IWGSC_chr3DL_ab_k71_contigs_longerthan_200_6919237	787	631/768 (1560)	82	0.0
Synth12	IWGSC_chr3DL_ab_k71_contigs_longerthan_200_6956789	740	607/726 (1560)	84	0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3D				0.0
Synth12	IWGSC_chr3DL_ab_k95_contigs_longerthan_200_552567				0.0
Synth12	IWGSC_chr3DL_ab_k71_contigs_longerthan_200_6939577	652	457/525 (1560)	87	0.0
Synth12	IWGSC_chr3DL_ab_k71_contigs_longerthan_200_6955649	648	565/714 (1560)	79	0.0
Synth12	v443_0679	641	592/740 (1560)	80	0.0

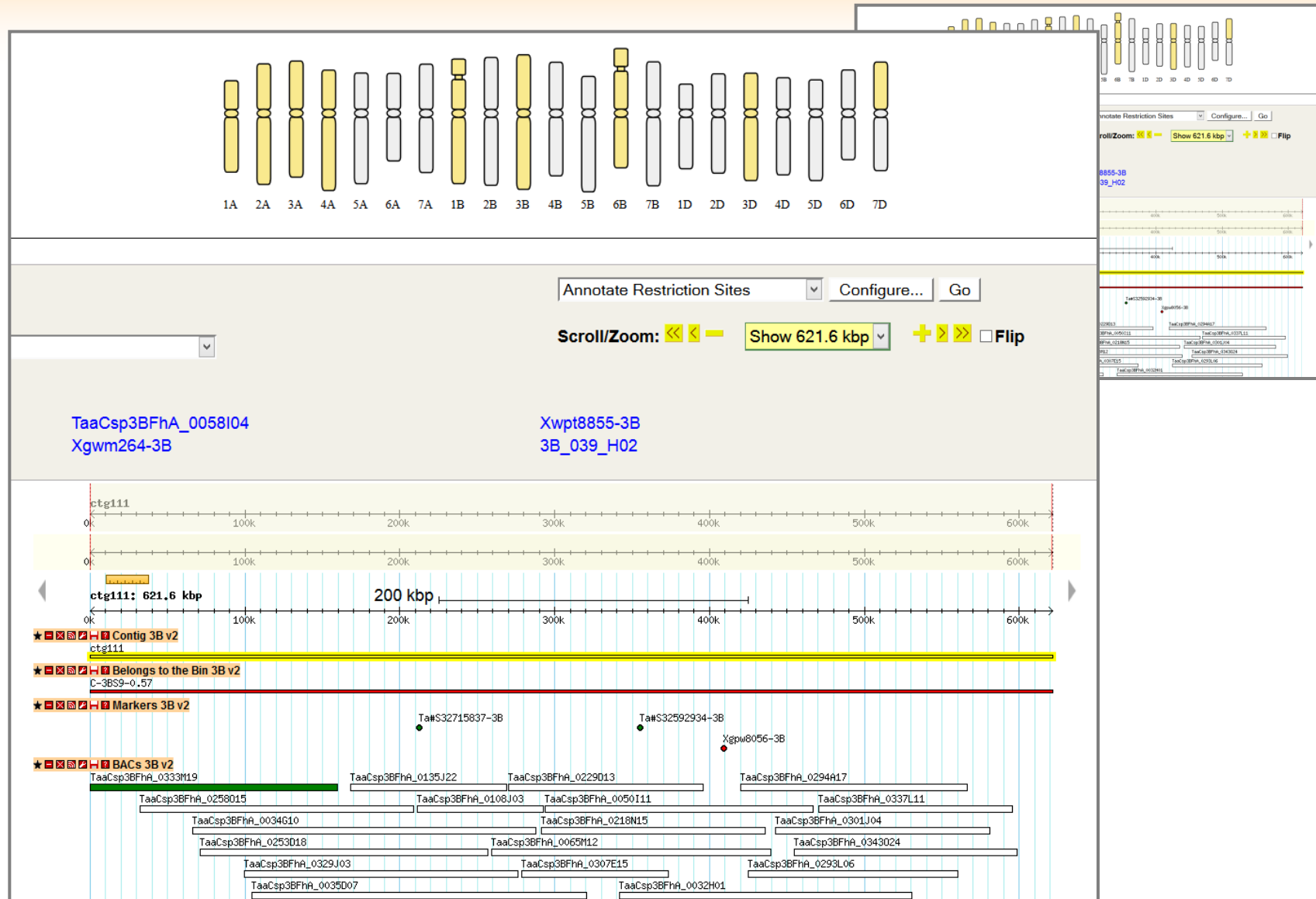
Category	Start	End	Direction
Scaffold	v443_0679	...	→
Pseudomolecule	→
BAC	→
Gap	-
Markers	→
CDS	→
ncRNA	→
rRNA	→
tRNA	→
TES	→



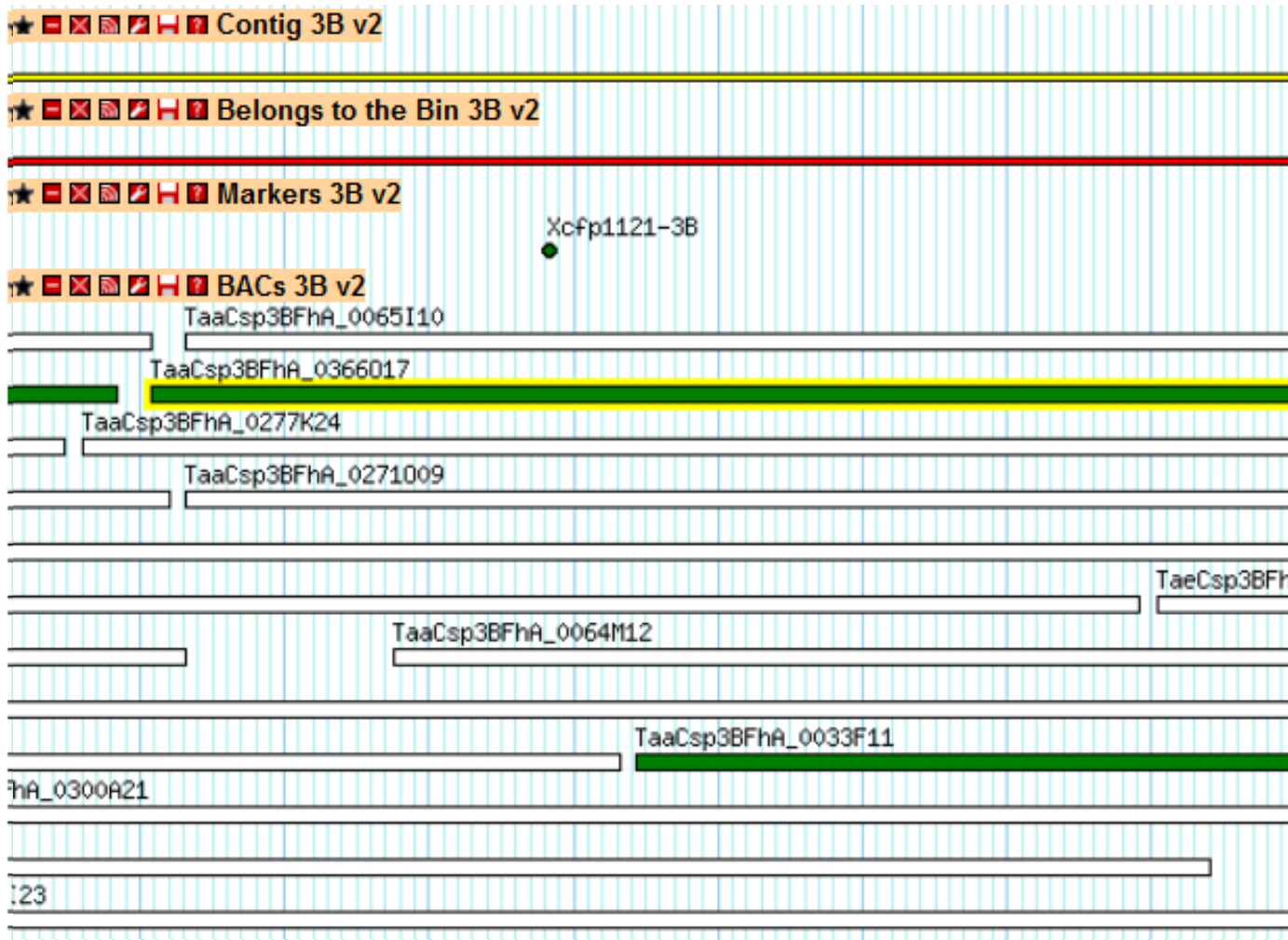
Physical maps



Physical maps



Physical maps



Physical contig

Deletion bin

Markers

BACs

Physical maps

★ Contig 3B v2

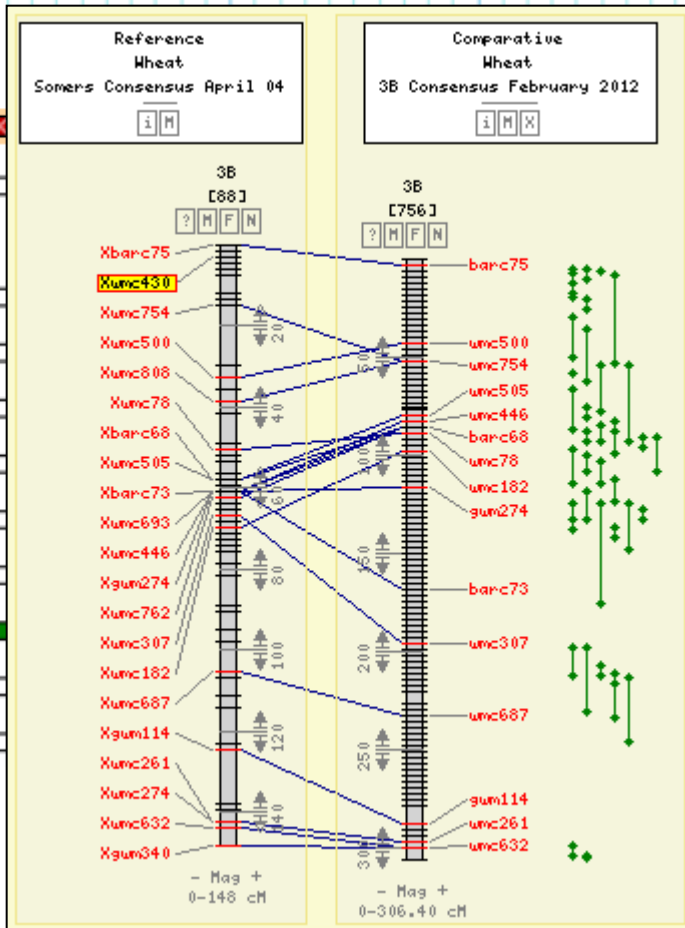
★ Belongs to the Bin 3B v2

★ Markers 3B v2

XwPt2748-3B

XwPt7341-3B

XwPt8855-3B



XwPt8855-3B

Position: 1268401..1268401
Source: FPC
Reference: ctg344
[Zoom to this feature](#)
[Detailed Report](#)
[Link to Marker card in GnpIS](#)
[External link to CMap \(CCG Murdoch\)](#)
[Link to Annotation](#)

Physical maps

MARKER DETAILS

Marker name :	WPT8855
Taxon :	Triticum aestivum
Marker type :	DArT type
Marker origin :	amplicon
Target :	Triticarte
Origin laboratory :	Triticarte

MAPPED LOCI

Mapped loci: 2

genetic maps			chr	cM.		QTL	MetaQTL	
Locus name	Map name	Taxon	Linkage group	Distance	Reliability / (source map name)	Link to QTL	Link to QTL large	Link to MetaQTL
XwPt-8855-3A	CF9107xToisonDorxQuebon	Triticum aestivum	3A	224.6	-	-	-	-
Xwpt8855-3B	Neighbour3B_080407	Triticum aestivum	3B	52.35	non_framework	-	-	-

CROSS REFERENCES

Cross references : 1

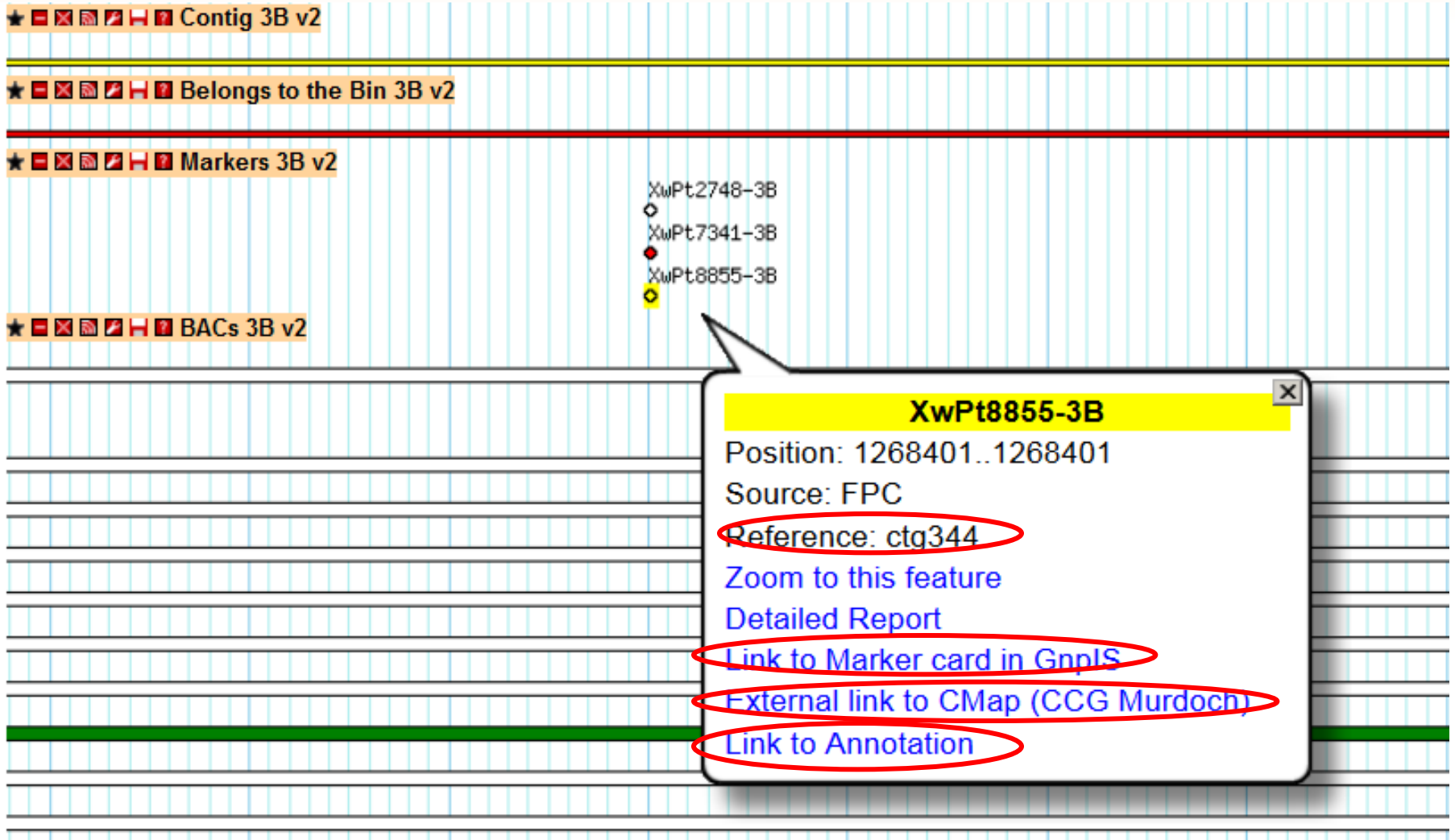
Db name
Gbrowse Wheat physical map : 3B

MARKER SEQUENCES

Sequence name	Sequence type	Sequence
WMC430_Forward	Primer forward	TAGGGACCCCTTGACAAAAA
WMC430_Reverse	Primer reverse	TAGGGACCCCTTGACAAAAA

Primers

Physical maps



3B reference sequence annotation



3B annotation

Wheat annotation viewer: 3B: 4.33 Mbp from traes3bPseudomoleculeV1:264,818,124..269,148,123

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

Search

Landmark or Region:
traes3bPseudomoleculeV1: Search

Examples: traes3bPseudomoleculeV1:9,577,253..9,587,252, traes3bPseudomoleculeV1:264,818,124..269,148,123, TRAES3BF037300090CFD_t1, XwPt8855-3B, v443_0010.

Data Source
Wheat annotation viewer: 3B

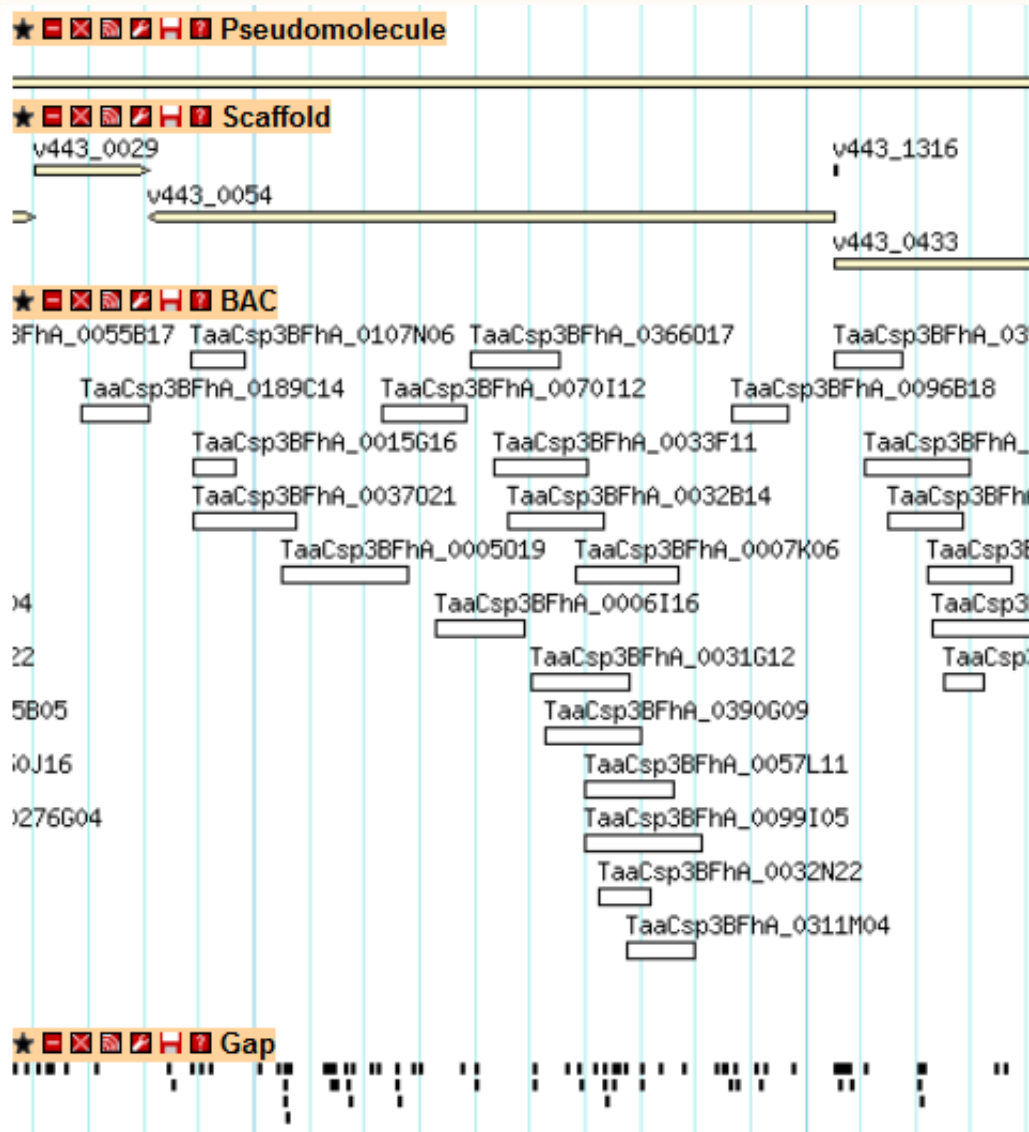
Download Decorated FASTA File

Scroll/Zoom: Show 4.33 Mbp Flip

Overview

The figure displays a genomic map of wheat chromosome 3B. At the top, a scale bar for 'traes3bPseudomoleculeV1' ranges from 0M to 700M. Below it, a zoomed-in view shows a 1 Mbp region from 265M to 269M. The map is divided into three main tracks: Pseudomolecule, Scaffold, and BAC. The Pseudomolecule track shows a single continuous line. The Scaffold track shows several scaffolds labeled v443_0029, v443_0054, v443_1316, v443_0144, v443_0431, v443_0432, v443_0351, and v443_0058. The BAC track shows numerous BAC clones, each represented by a horizontal bar with its ID. The BAC clones are arranged in a grid-like pattern, with some overlapping. The IDs include: 3FhA_0055B17, TaaCsp3BFhA_0107N06, TaaCsp3BFhA_0366D17, TaaCsp3BFhA_0350N06, TaaCsp3BFhA_0108A03, TaaCsp3BFhA_0179G05, TaaCsp3BFhA_0040K10, TaaCsp3BFhA_0330K17, TaaCsp3BFhA_0008K09, TaaCsp3BFhA_0189C14, TaaCsp3BFhA_0070I12, TaaCsp3BFhA_0096B18, TaaCsp3BFhA_0364E08, TaaCsp3BFhA_0021I24, TaaCsp3BFhA_0190J01, TaaCsp3BFhA_0122K10, TaaCsp3BFhA_0005G05, TaaCsp3BFhA_0015G16, TaaCsp3BFhA_0033F11, TaaCsp3BFhA_0012M19, TaaCsp3BFhA_0262L21, TaaCsp3BFhA_0281C13, TaaCsp3BFhA_0358L24, TaaCsp3BFhA_0053N21, TaaCsp3BFhA_0077G, TaaCsp3BFhA_0037O21, TaaCsp3BFhA_0032B14, TaaCsp3BFhA_0304O06, TaaCsp3BFhA_0228P04, TaaCsp3BFhA_0182E12, TaaCsp3BFhA_0035N08, TaaCsp3BFhA_0068F18, TaaCsp3BFhA_0, TaaCsp3BFhA_0005O19, TaaCsp3BFhA_0007K06, TaaCsp3BFhA_0282K15, TaaCsp3BFhA_0015D03, TaaCsp3BFhA_0152A16, TaaCsp3BFhA_0222N21, TaaCsp3BFhA_0006I16, TaaCsp3BFhA_0068K01, TaaCsp3BFhA_0066O04, TaaCsp3BFhA_0122K10, TaaCsp3BFhA_0227D05, TaaCsp3BFhA_0031G12, TaaCsp3BFhA_0100L22, TaaCsp3BFhA_0007P15, TaaCsp3BFhA_0374P15, TaaCsp3BFhA_022, TaaCsp3BFhA_0390G09, TaaCsp3BFhA_0353C24, TaaCsp3BFhA_0382J08, TaaCsp3BFhA_0342C14, TaaCsp3BF, TaaCsp3BFhA_0057L11, TaaCsp3BFhA_0002I12, TaaCsp3BFhA_0099I05, TaaCsp3BFhA_0015O20, TaaCsp3BFhA_0032N22, TaaCsp3BFhA_0057K23, TaaCsp3BF, TaaCsp3, TaaCsp3.

3B annotation



Pseudomolecule

Scaffolds

BACs

Gaps

3B annotation: Scaffold

Scaffold

v443_0029 v443_0054 v443_1316 v443_0433 v443_0054

3FhA_0055B17 TaaCsp3BFh

v443_0054

Positions	264810342 .. 266051024
Length	1240683
Reference	traes3bPseudomoleculeV1

[Zoom to this feature](#)
[Detailed Report](#)
[Download Fasta](#)

```
>traes3bPseudomoleculeV1:264810342..266051024
tgatgatagttcgggctatccggacacccccctagtccaggactccctcaccactacttcca
tgacatccactaccggttgctggaacgactacttctctacgacccggtgaccattccttc
cttcaacgtactcgttccacctgaaaatgcacacttcaaaggataaaacaatgagacgat
caccocgtggaccgaatgcatgtgtattgtatgaggtgctcgtgtttgcaccggtatcgaa
ttgtcgttgcatgccccctcttttccatgccaccgacacgtgtaaaccoggtatctgg
gatcaccaccacatcttttgcattgtccgcactccacatcttcgtttgcaccgacatcc
cgatgagttatcggaaccaagatgttactgtggcatcattttcggattctttgcccggc
accctttctttccacggtgacaaatgtttcatatcatgctcatgtcaacatttccataaa
attgcataaaccttgatatgtctaccacatcatggttaacaacatttatatggttaaatt
tgttgttggcattaaaattgcttaatgacatggggatttctatggaattattggttgta
tttccggcctcattttaaactttcctaaatagtttagtttaattatacttcacctcttgcca
tgtttaacaacattttaatattggttgggtacataaaacaagagagaactaaataattgaatg
tgggtgtttcgtcaatatgcaactcgtttgcatattgagctccacttaacttataatattgt
ttgttgcactttgccatgccatgcctcattaaaccgaacatgcatcatacttggttgtgc
atcatgccatgtttatgcttgtgtgtttaccatgttgtttgtctctttccggttgagctt
tctccagtaattgttgcggattgtgaggatttgttgcacttcttcgtttgtctcttccat
ggactcgttcttcttcttcttgggatctcaggcaagatgaccattaccttcgatatcact
```

3B annotation: BAC

The image shows a genomic browser interface with a list of BAC features on the left and a detailed view of a specific feature on the right. The features listed include TaaCsp3BFhA_0055B17, TaaCsp3BFhA_0107N06, TaaCsp3BFhA_0366017, TaaCsp3BFhA_0350N06, TaaCsp3BFhA_0108A03, TaaCsp3BFhA_0189C14, TaaCsp3BFhA_0070I12, TaaCsp3BFhA_0096B18, TaaCsp3BFhA_0364E08, TaaCsp3BFhA_0015G16, TaaCsp3BFhA_0033F11, TaaCsp3BFhA_0012M19, TaaCsp3BFhA_0262L21, TaaCsp3BFhA_0037021, TaaCsp3BFhA_000501, and TaaCsp3BFhA_0311M04. A tooltip for TaaCsp3BFhA_0366017 is open, showing its position (265393621 .. 265554831), length (161211), and reference (traes3bPseudomoleculeV1). The tooltip also contains links for 'Zoom to this feature', 'Detailed Report', 'Link to 3B Physical Map', and 'Download Fasta'. A second window shows a contig map with various features highlighted in green, including TaaCsp3BFhA_0366017 and TaaCsp3BFhA_0033F11.

★ [Icons] BAC

3FhA_0055B17 TaaCsp3BFhA_0107N06 TaaCsp3BFhA_0366017 TaaCsp3BFhA_0350N06 TaaCsp3BFhA_0108A03 TaaCsp3BFhA_0189C14 TaaCsp3BFhA_0070I12 TaaCsp3BFhA_0096B18 TaaCsp3BFhA_0364E08 TaaCsp3BFhA_0015G16 TaaCsp3BFhA_0033F11 TaaCsp3BFhA_0012M19 TaaCsp3BFhA_0262L21 TaaCsp3BFhA_0037021 TaaCsp3BFhA_000501 TaaCsp3BFhA_0311M04

14
22
5B05
10J16
1276G04

TaaCsp3BFhA_0366017

Positions 265393621 .. 265554831
Length 161211
Reference traes3bPseudomoleculeV1
[Zoom to this feature](#)
[Detailed Report](#)
[Link to 3B Physical Map](#)
[Download Fasta](#)

★ [Icons] Contig 3B v2
★ [Icons] Belongs to the Bin 3B v2
★ [Icons] Markers 3B v2 Xcfp1121-3B
★ [Icons] BACs 3B v2
TaaCsp3BFhA_0065I10
TaaCsp3BFhA_0366017
TaaCsp3BFhA_0277K24
TaaCsp3BFhA_0271009
TaaCsp3BFhA_0064M12
TaaCsp3BFhA_0033F11
hA_0300A21
23

3B annotation

★ Pseudomolecule

★ Scaffold

★ BAC

★ Gap

★ Markers

★ mRNA

★ ncRNA

★ rRNA

★ tRNA

★ TEs

XwPt8855-3B



TRAES3BF053100220CFD_t1



Markers

Genes

TE



3B annotation: Marker

MARKER DETAILS

Marker name : WPT8855
 Taxon : [Triticum aestivum](#)
 Marker type : DArT
 Marker origin : amplicon
 Target : Triticate
 Origin laboratory : Triticate

MAPPED LOCI
 Mapped loci: 2

Locus name	Map name	Taxon	Linkage group	Distance	Reliability / (source map name)	Link to QTL	Link to QTL large	Link to MetaQTL
XwPt-8855-3A	CF9107xToisonDorxQuebon	Triticum aestivum	3A	224.6	-	-	-	-
Xwpt8855-3B	Neighbour3B_080407	Triticum aestivum	3B	52.35	non_framework	-	-	-

CROSS REFERENCES
 Cross references : 1

Db name	Reference name	Reference value	Evidence	Contact
Gbrowse Wheat physical map : 3B	name	XwPt8855-3B	-	-

Tooltip 1: XwPt8855-3B
 Positions: 9584806 .. 9585578
 Length: 773
 Reference: traes3bPseudomoleculeV1

Tooltip 2: XwPt8855-3B
 Position: 1268401..1268401
 Source: FPC
 Reference: ctg344
[Link to this feature](#)
[Failed Report](#)
[Link to Marker card in GnpIS](#)
[External link to CMap \(CCG Murdoch\)](#)
[Link to Annotation](#)

3B annotation: Gene

traes3bPseudomoleculeV1

0M 100M 200M

563530k 563540k 563550k 563560k 563570k 563580k

563627k 563627k 563627k

★ Pseudomolecule

★ Scaffold

★ BAC

★ Gap

★ mRNA

TRAES3BF037300090CFD_t1

TRAES3BF037300090CFD_t1

Positions	563626983 .. 563627455
Length	473
Note	Known_function - YMF19_WHEAT SwissProt databank Putative ATP synthase protein YMF19 OS Triticum aestivum GN YMF19 PE 2 SV 1
Reference	traes3bPseudomoleculeV1
Status	High Confidence

[Zoom to this feature](#)

[Detailed Report](#)

[Download Fasta](#)

3B annotation: TE

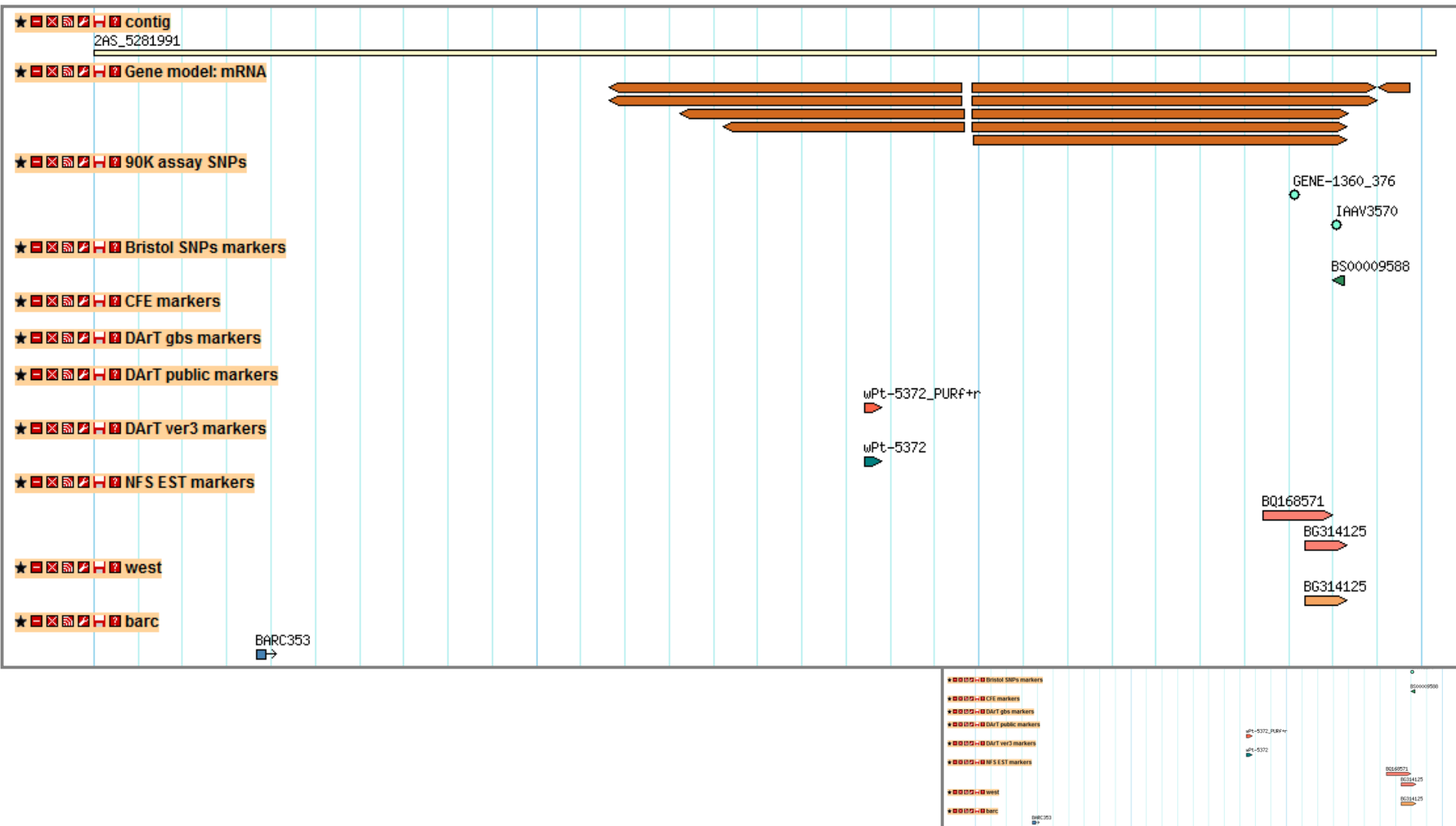
The screenshot shows a genome browser interface with several tracks on the left side, each with a star icon and a set of colored icons representing different annotation types. The tracks are: Pseudomolecule, Scaffold, BAC, Gap, Markers, mRNA, ncRNA, rRNA, tRNA, and TEs. A red arrow points to a specific TE element in the TEs track. A pop-up window titled '270_v443_0531' provides details for this element:

Positions	9576729 .. 9576991
Length	263
Reference	traes3bPseudomoleculeV1
Status	complete
Post	DTX_famn1 263bp 1..263
TE Family	DTX_famn1
Zoon DNA Transposon Superfamily (DTX)	
Detailed Report	
Download Fasta	

Survey sequence browser



Survey sequence



Survey sequence

Markers

All on All off

- | | | |
|--------------------------|-------------------------|---------------------|
| ✓ ☆ 90K assay SNPs | ✓ ☆ CFE markers | ✓ ☆ NFS EST markers |
| ✓ ☆ barc | ✓ ☆ DArT gbs markers | ✓ ☆ west |
| ✓ ☆ Bristol SNPs markers | ✓ ☆ DArT public markers | ✓ ☆ wmc primers |
| ✓ ☆ Cfa primers | ✓ ☆ DArT ver3 markers | ✓ ☆ Wms primers |
| ✓ ☆ Cfd primers | ✓ ☆ gdm primers | |

Wheat dataflow overview

Wheat@URGI website

Projects Data Tools Seq Repository About us

Sequence survey

Annotations

Deletion sites

Genetic maps

GTL / MetaGTL

Markers

SNP

22 Oct 2014
WheatBMine is now available
WheatBMine is a data warehouse dedicated to wheat chromosome 5B

02 Sep 2014
GnpIS version 4.2 availability
GnpIS version 4.2 is available. Major new functionalities include:
- Sequence
- Polymorphisms/Genotyping: The ...

02 Sep 2014
New survey sequence gene models (v2.2) available
New version of the survey sequence gene models (v2.2 July 2014) is ...

02 Sep 2014
GBrowse Wheat Survey sequence Annotation is available
The GBrowse Wheat Survey sequence Annotation (Markers, SNP, Gene Models) is now available

02 Sep 2014
73S physical map is publicly available
73S physical map is publicly available

02 Jan 2014
Talks at PAG
Computer demo
Annotation View

Sequence repository

Chromosomes 1B and 3B have already informations.

1A 2A 6A 7A

1B 2B 6B 7B

Blast
Download
Browsers

Physical maps browser GBrowse

Annotation browser

- 3B ref
- Survey seq

GBrowse / JBrowse

BLAST

- 3B ref
- Survey seq

Marker: WMC430

Genetic maps, Markers, QTLs, MetaQTLs GnpIS

SNPs GnpIS

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

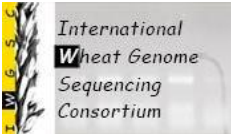
Germplasm GnpIS

Phenotyping GnpIS

Genotyping GnpIS

Association GnpIS

Acknowledgments



Questions

Wheat@URGI website

<http://wheat-urgj.versailles.inra.fr>

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