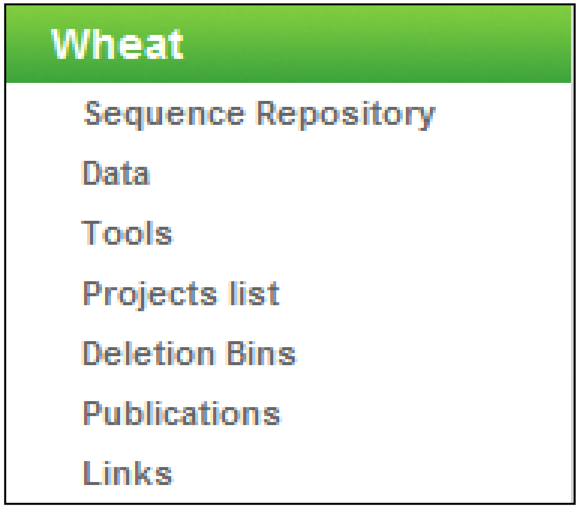
International Wheat Genome Sequencing Consortium

IWGSC Sequence Repository

Michaël Alaux

IWGSC Prague 2011

Wheat bioinformatics at URGI



Wheat

- Sequence Repository
- Data
- Tools
- Projects list
- Deletion Bins
- Publications
- Links

Species

- Vitis
- Wheat
  - Sequence Repository
  - Data
  - Tools
  - Projects list
  - Deletion Bins
  - Publications
  - Links
- Botrytis
- Leptosphaeria
- Microbotryum
- Venturia
- Arabidopsis
- Oryza
- Populus
- Maize
- Medicago
- Pisum
- Flax

You are here : Home / Species / Wheat

Wheat

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

New Sequence Repository first version available

Why develop Wheat genomics?

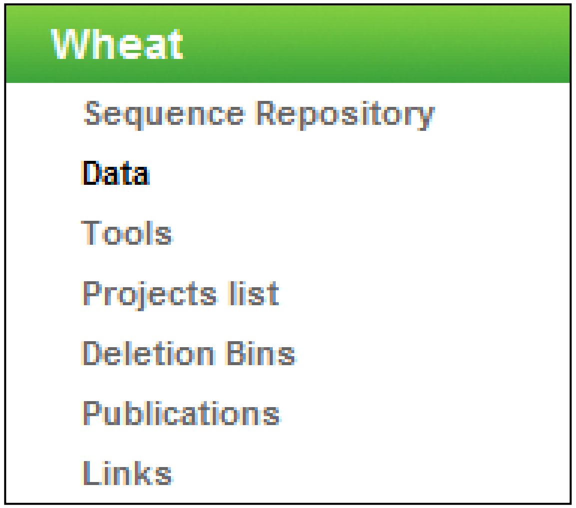
Today, agriculture is facing one of its greatest challenges since it began 10 000 years ago, that of producing an ample supply of high quality food and feed for a growing world population in a sustainable and environment friendly manner. Bread wheat (Triticum aestivum L.) is the staple food for more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

Wheat bioinformatics at URGI



Wheat

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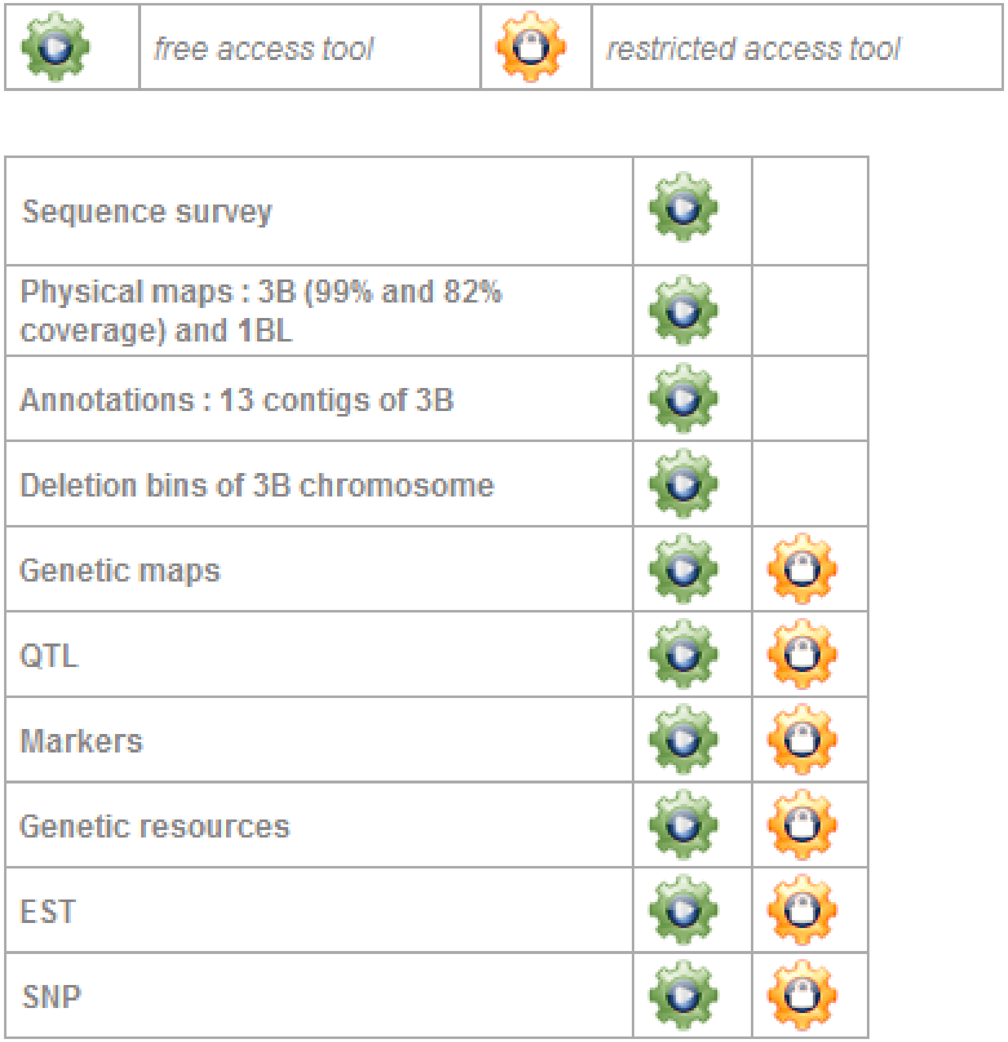
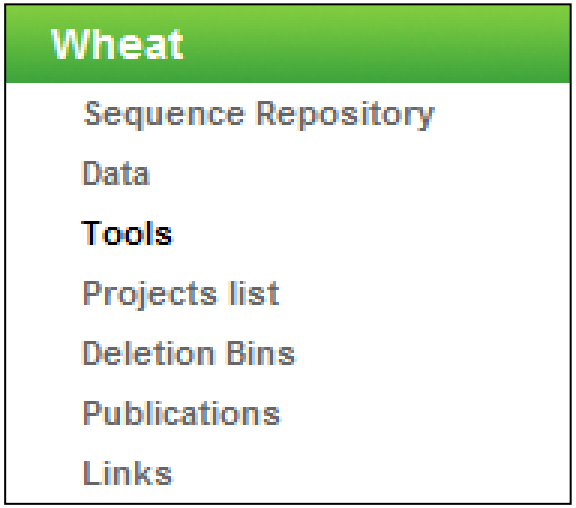


▶	*free access tool*	🔒	*restricted access tool*

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

Wheat bioinformatics at URGI



Wheat

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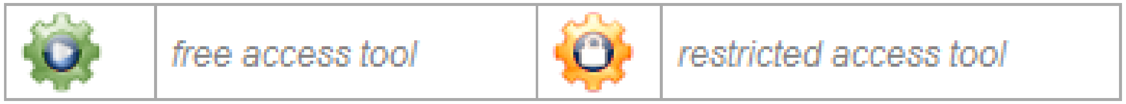
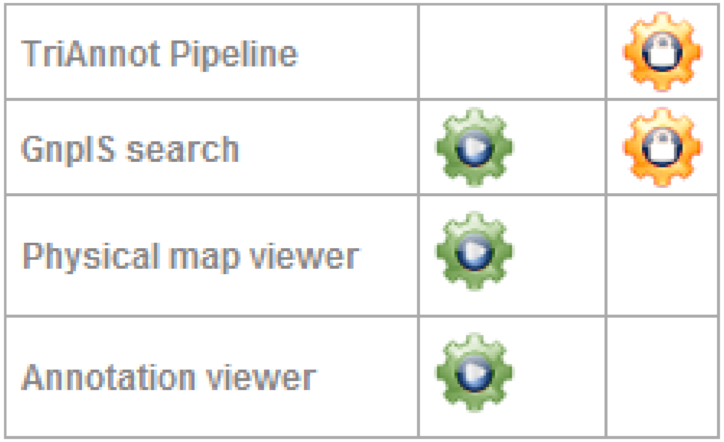
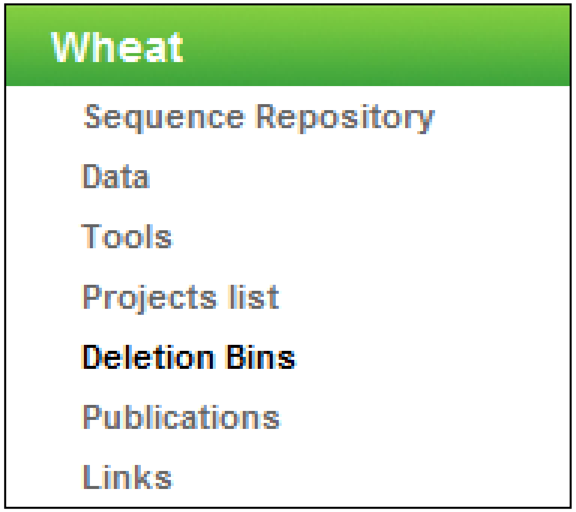


🟢	*free access tool*	🟠	*restricted access tool*



TriAnnot Pipeline		🟠
GnpIS search	🟢	🟠
Physical map viewer	🟢	
Annotation viewer	🟢	

Wheat bioinformatics at URGI



Wheat

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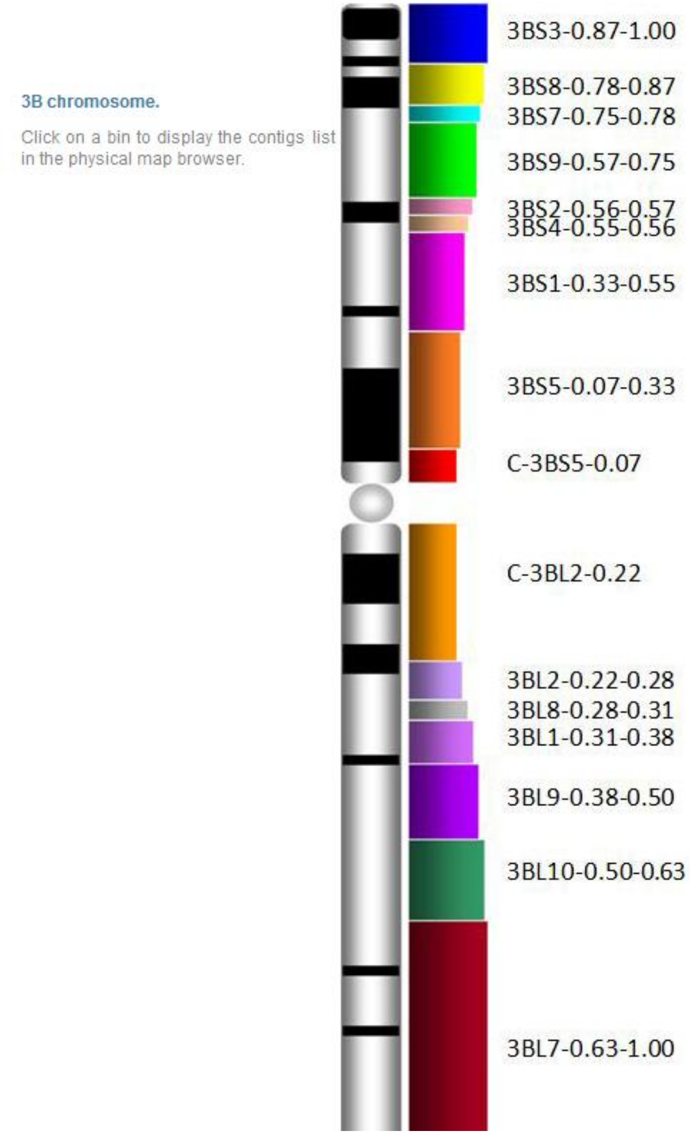
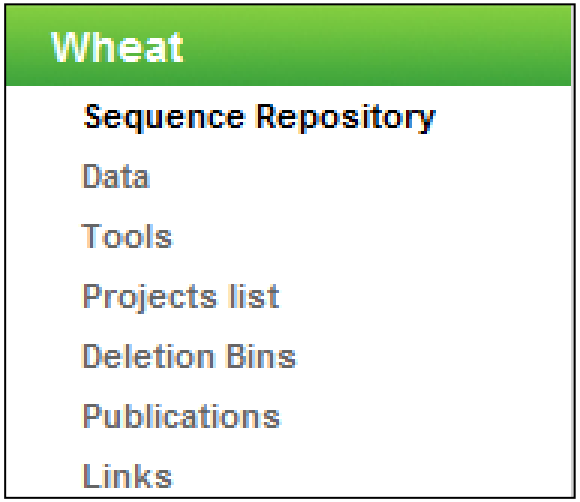


3B chromosome.

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

Wheat bioinformatics at URGI



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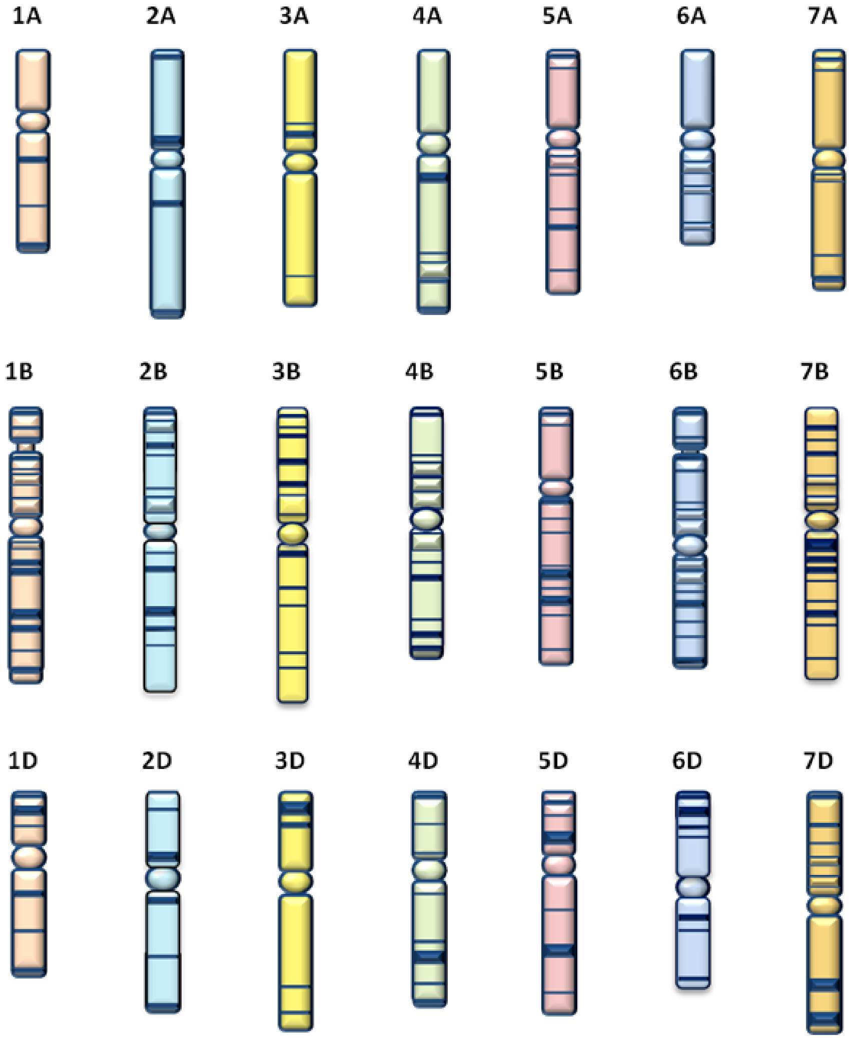


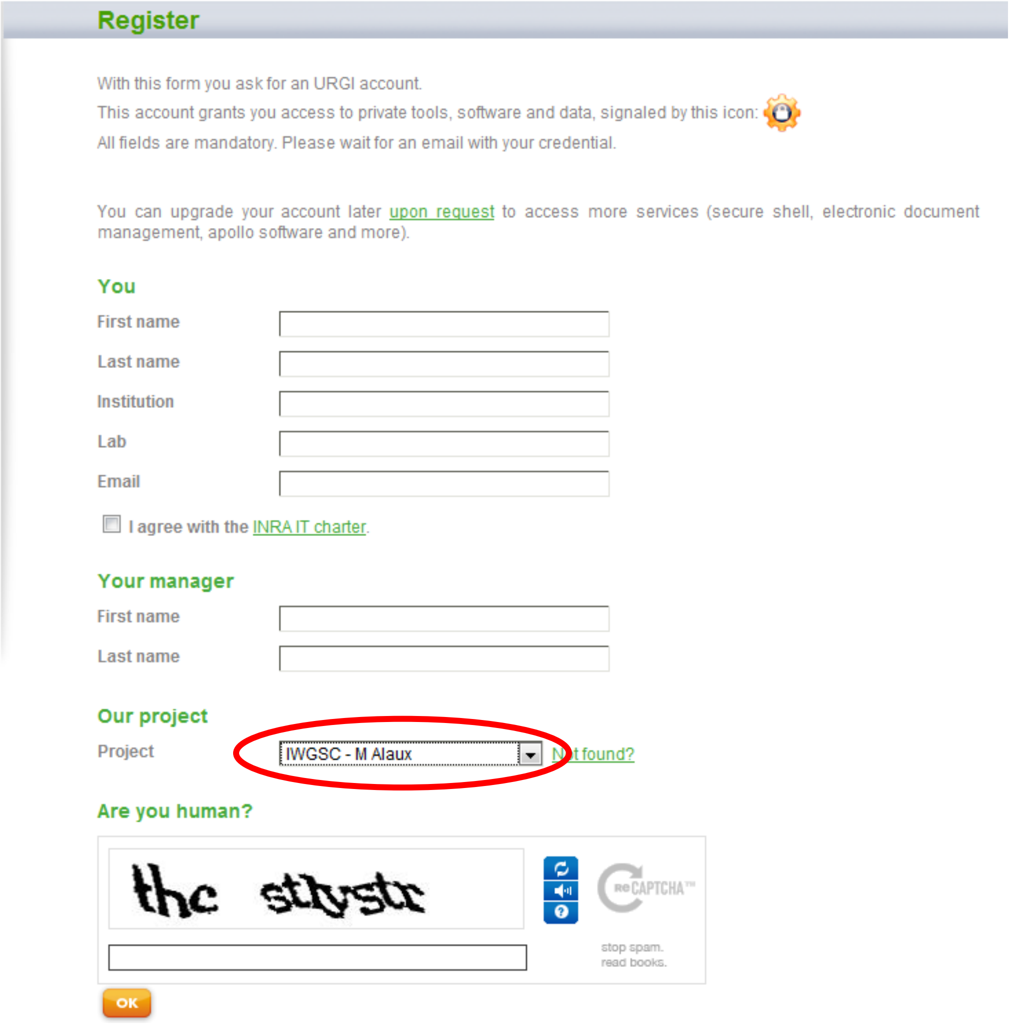
http://urgi.versailles.inra.fr/index.php/urgi/Species/Wheat

Sequence Repository

- IWGSC initiative
- Click on a chromosome to have access to the survey sequence, blast search and viewers when available.
- Survey sequences and blast search are access restricted:
  - to members of the IWGSC coordinating committee in the first time.
  - ask an URGI account (please select project name: IWGSC): http://urgi.versailles.inra.fr/index.php/urgi/Register

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

Sequence Repository



Register

With this form you ask for an URGI account.
This account grants you access to private tools, software and data, signaled by this icon:
All fields are mandatory. Please wait for an email with your credential.

You can upgrade your account later upon request to access more services (secure shell, electronic document management, apollo software and more).

You

First name
Last name
Institution
Lab
Email

☐ I agree with the INRA IT charter.

Your manager

First name
Last name

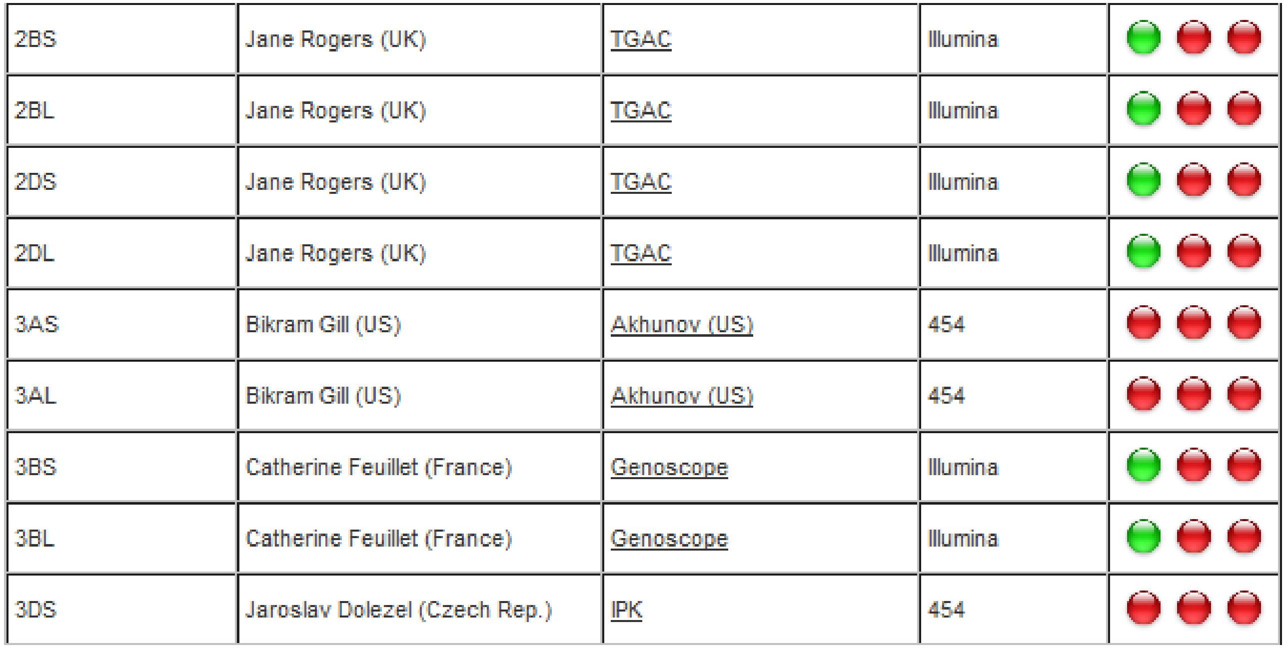
Our project

Project: IWGSC - M Alaux

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

Sequence Repository

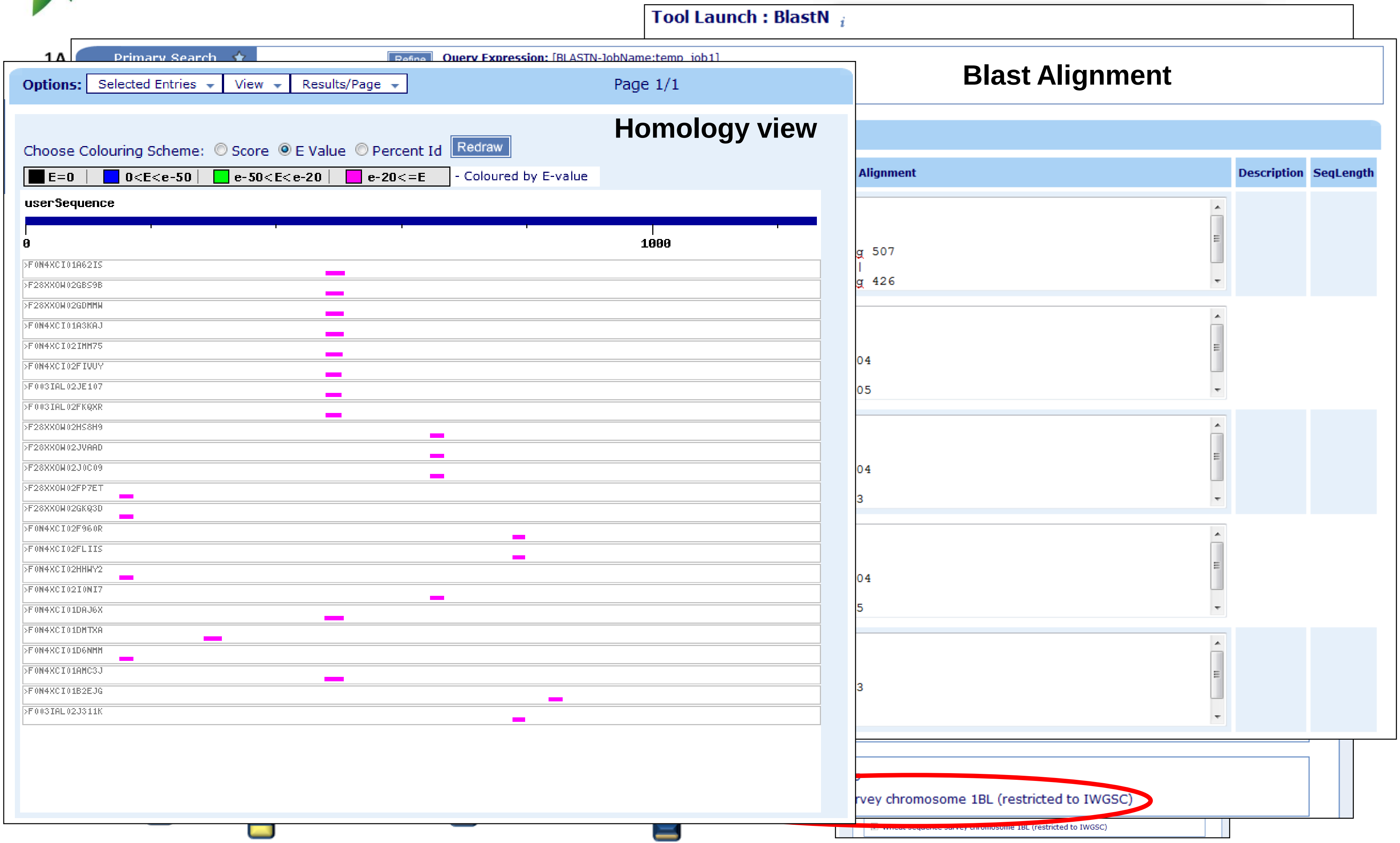
- Chromosomes 1B and 3B have already informations.
- Link to survey sequences progress available at TGAC for projects leaders (access restricted) :



2BS	Jane Rogers (UK)	TGAC	Illumina	🟢 🔴 🔴
2BL	Jane Rogers (UK)	TGAC	Illumina	🟢 🔴 🔴
2DS	Jane Rogers (UK)	TGAC	Illumina	🟢 🔴 🔴
2DL	Jane Rogers (UK)	TGAC	Illumina	🟢 🔴 🔴
3AS	Bikram Gill (US)	Akhunov (US)	454	🔴 🔴 🔴
3AL	Bikram Gill (US)	Akhunov (US)	454	🔴 🔴 🔴
3BS	Catherine Feuillet (France)	Genoscope	Illumina	🟢 🔴 🔴
3BL	Catherine Feuillet (France)	Genoscope	Illumina	🟢 🔴 🔴
3DS	Jaroslav Dolezel (Czech Rep.)	IPK	454	🔴 🔴 🔴

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

Sequence Repository



Tool Launch : BlastN

Primary Search

Query Expression: [BLASTN-JobName:temp_job1]

Blast Alignment

Homology view

Options: Selected Entries ▾ | View ▾ | Results/Page ▾

Page 1/1

Choose Colouring Scheme: ○ Score ● E Value ○ Percent Id [Redraw]

■ E=0 | 🟦 0<E<e-50 | 🟩 e-50<E<e-20 | 🟪 e-20<=E - Coloured by E-value

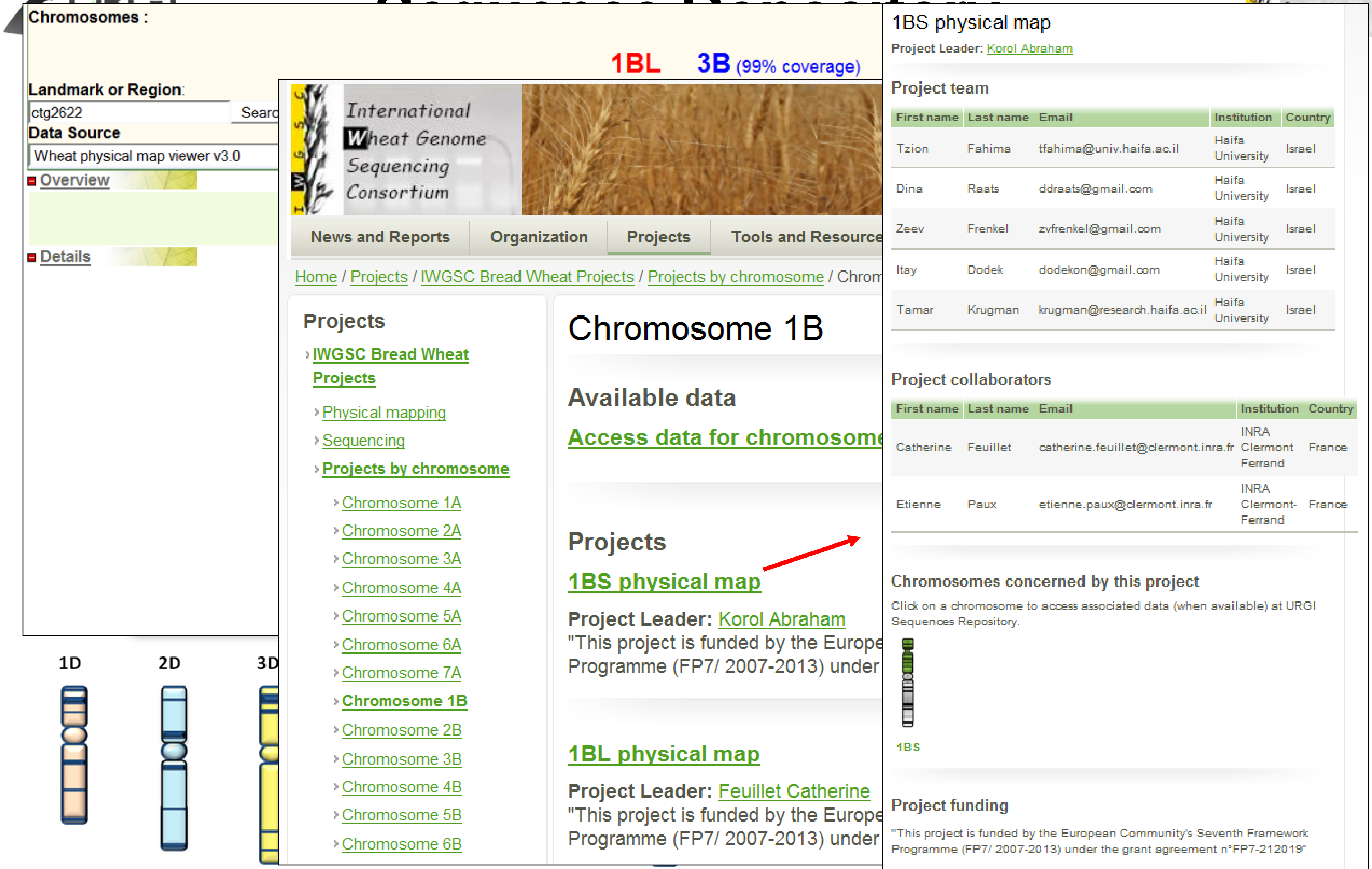
userSequence

0 … 1000

>F0N4XCI01A62IS
>F28XXOW02GBS9B
>F28XXOW02GDMMW
>F0N4XCI01A3KAJ
>F0N4XCI02IMM75
>F0N4XCI02FIVUY
>F003IAL02JE107
>F003IAL02FKQXR
>F28XXOW02HS8H9
>F28XXOW02JVAAD
>F28XXOW02J0C09
>F28XXOW02FP7ET
>F28XXOW02GKQ3D
>F0N4XCI02F960R
>F0N4XCI02FLIIS
>F0N4XCI02HHWY2
>F0N4XCI02I0NI7
>F0N4XCI01DAJ6X
>F0N4XCI01DMTXA
>F0N4XCI01D6NMM
>F0N4XCI01AMC3J
>F0N4XCI01B2EJG
>F003IAL02J311K

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

Sequence Repository



Chromosomes :

1BL 3B (99% coverage)

Landmark or Region:

ctg2622

Data Source

Wheat physical map viewer v3.0

International Wheat Genome Sequencing Consortium

Home / Projects / IWGSC Bread Wheat Projects / Projects by chromosome / Chrom

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 1B

Available data

Access data for chromosome

Projects

1BS physical map

Project Leader: Korol Abraham

"This project is funded by the Europe
Programme (FP7/ 2007-2013) under

1BL physical map

Project Leader: Feuillet Catherine

"This project is funded by the Europe
Programme (FP7/ 2007-2013) under

1BS physical map

Project Leader: Korol Abraham

Project team

First name	Last name	Email	Institution	Country
Tzion	Fahima	tfahima@univ.haifa.ac.il	Haifa University	Israel
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Zeev	Frenkel	zvfrenkel@gmail.com	Haifa University	Israel
Itay	Dodek	dodekon@gmail.com	Haifa University	Israel
Tamar	Krugman	krugman@research.haifa.ac.il	Haifa University	Israel

Project collaborators

First name	Last name	Email	Institution	Country
Catherine	Feuillet	catherine.feuillet@clermont.inra.fr	INRA Clermont Ferrand	France
Etienne	Paux	etienne.paux@clermont.inra.fr	INRA Clermont-Ferrand	France

Chromosomes concerned by this project

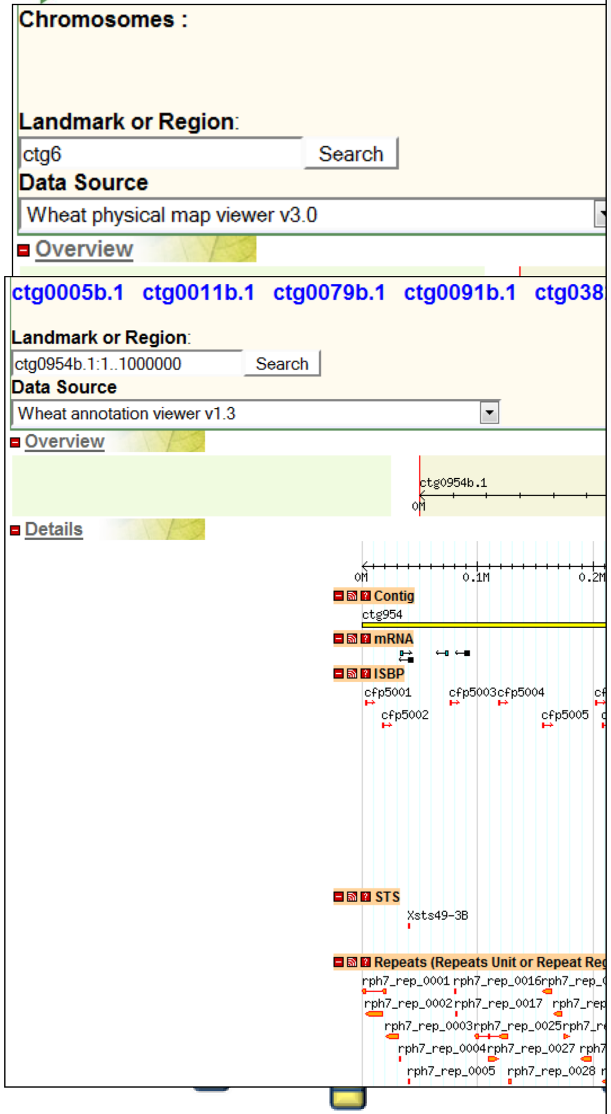
Click on a chromosome to access associated data (when available) at URGI Sequences Repository.

Project funding

"This project is funded by the European Community's Seventh Framework Programme (FP7/ 2007-2013) under the grant agreement n°FP7-212019"

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

Sequence Repository



Chromosomes :

Landmark or Region:

ctg6 Search

Data Source

Wheat physical map viewer v3.0

Overview

ctg0005b.1 ctg0011b.1 ctg0079b.1 ctg0091b.1 ctg038

Landmark or Region:

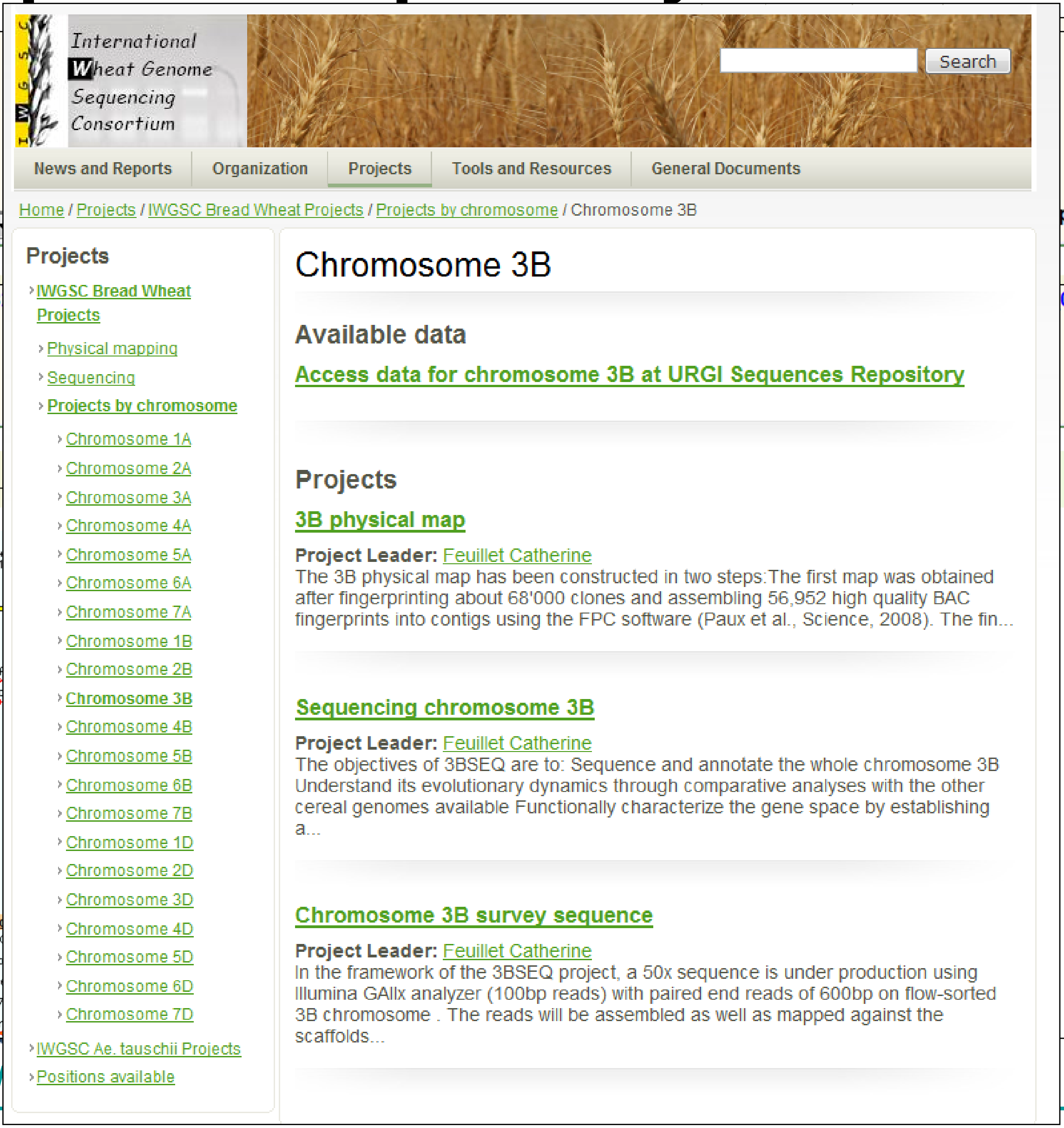
ctg0954b.1:1..1000000 Search

Data Source

Wheat annotation viewer v1.3

Overview

Details



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/ itory

Wheat physical map viewer

- Versions
  - v2.0 to 2.4
    - contig centric view
    - published version of the 3B FPC
    - add of deletion bin track
    - deletion bins chromosome image
    - index of all features in "Landmark or Region" (wildcard)
    - speed improvement with GBrowse 1.70 and MySQL 5
    - link to BAC annotation viewer
    - external link to CMap composite maps (R. Appels)

Paux *et al.*
Science (2008)
322:101-104

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

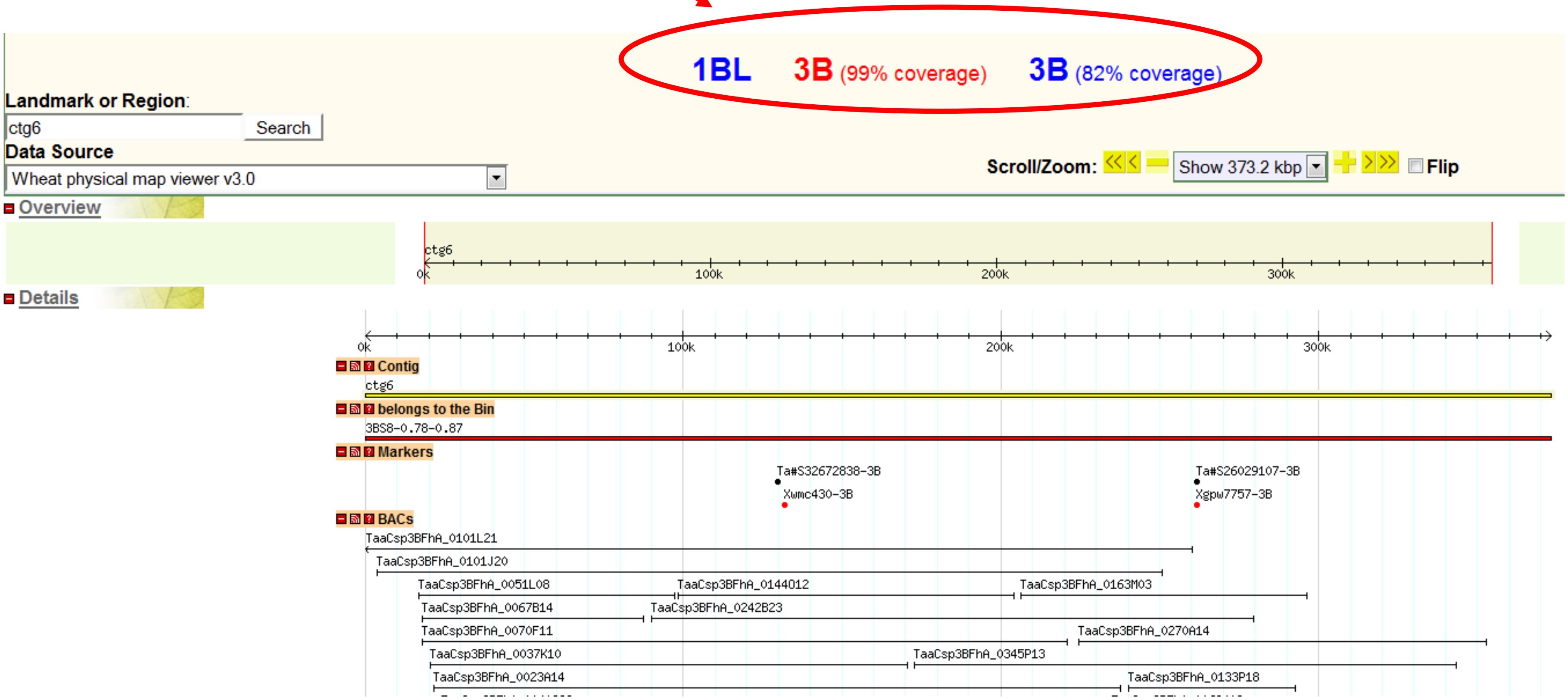
Wheat physical map viewer

- v3.0
  - add new version of 3B FPC assembly (99% coverage) & 1BL physical map *(E. Paux, R. Philippe)*

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat physical map viewer

Select your physical map



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

Landmark or Region: ctg6

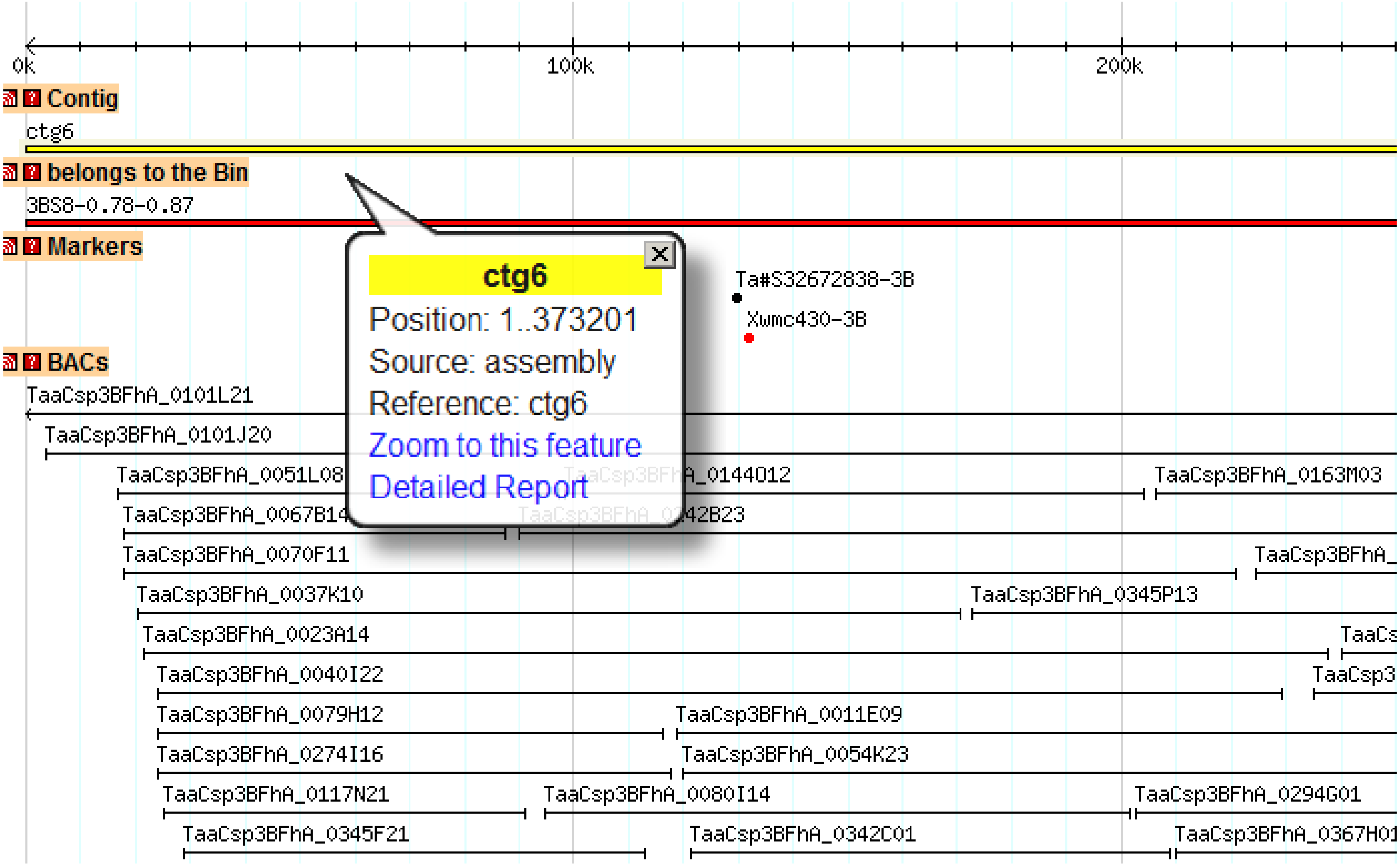
Data Source: Wheat physical map viewer v3.0

Scroll/Zoom: Show 373.2 kbp ☐ Flip

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat physical map viewer

Contig



ctg6

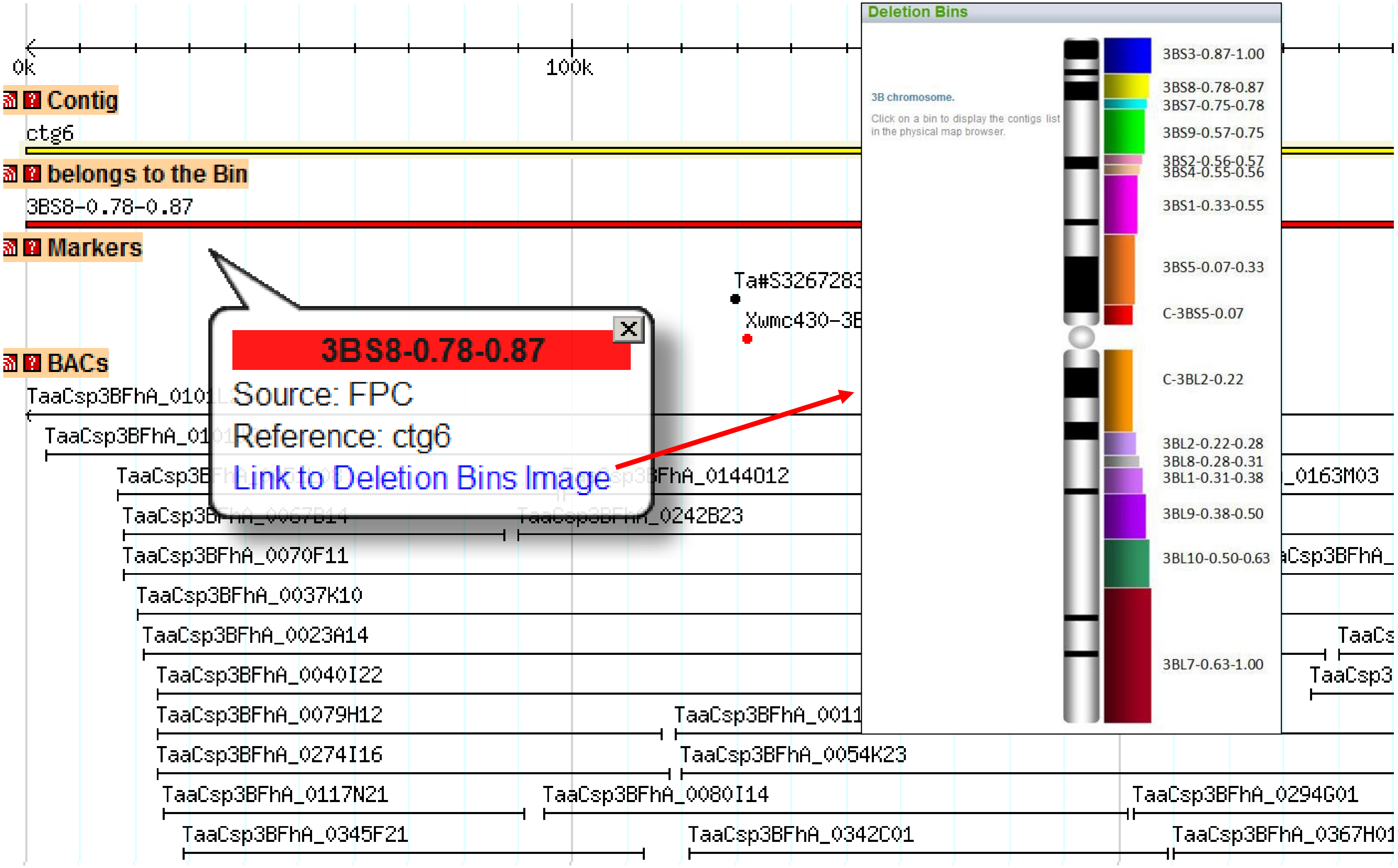
Position: 1..373201

Source: assembly

Reference: ctg6

Wheat physical map viewer

Deletion bin



3BS8-0.78-0.87

Source: FPC

Reference: ctg6

Link to Deletion Bins Image

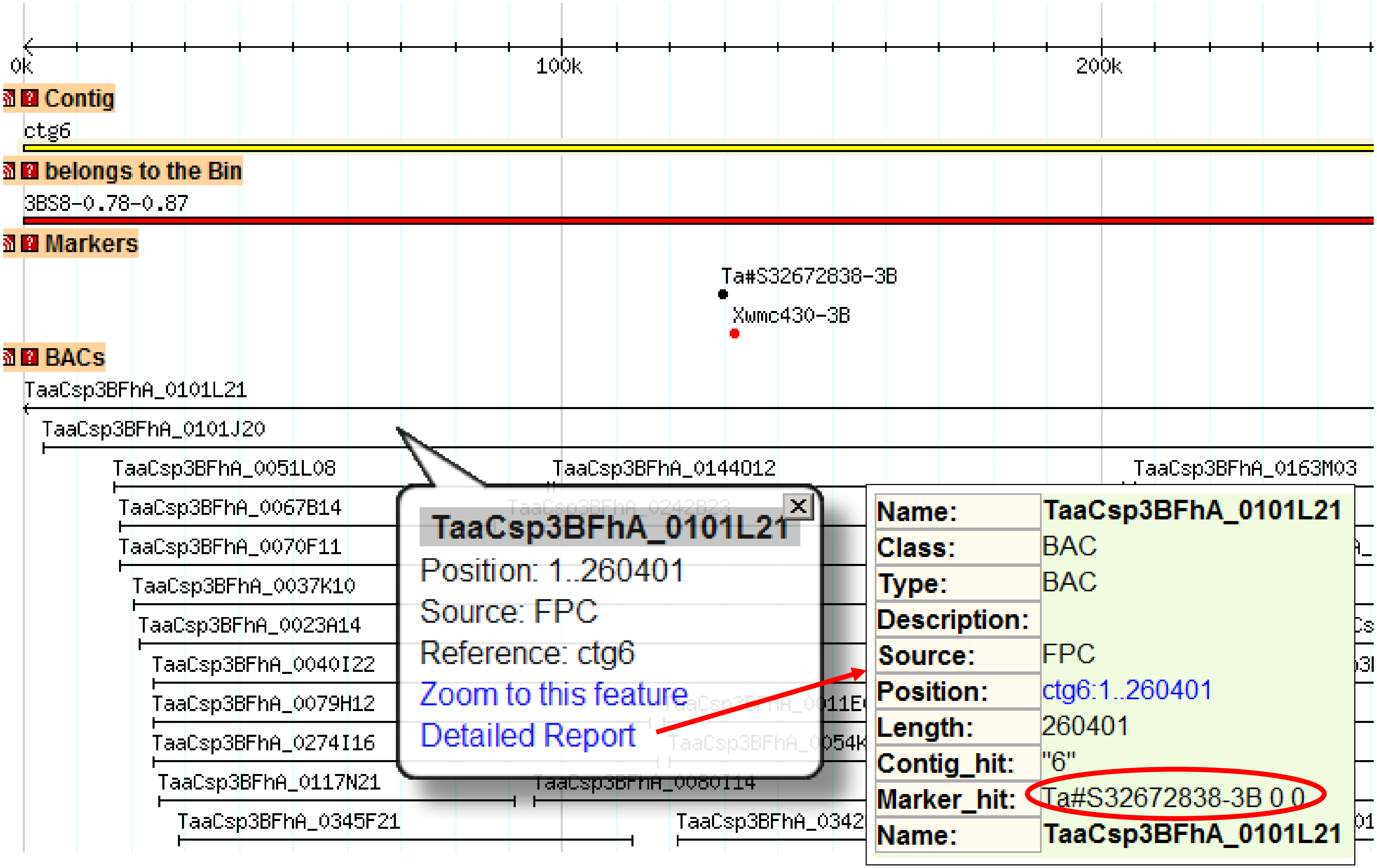
3B chromosome.

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

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat physical map viewer

BACs



TaaCsp3BFhA_0101L21

Position: 1..260401

Source: FPC

Reference: ctg6

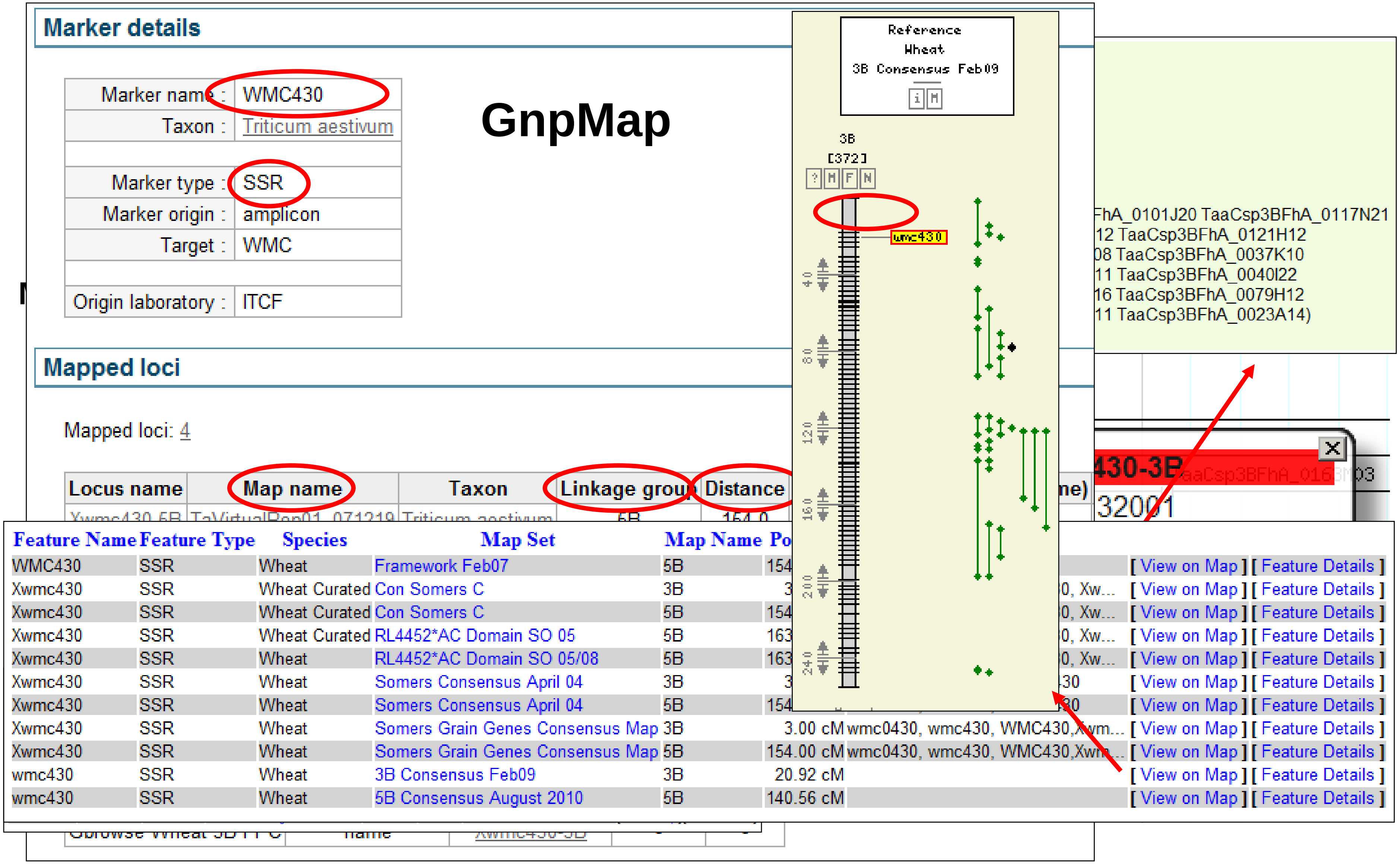
Zoom to this feature

Detailed Report

Name:	**TaaCsp3BFhA_0101L21**
Class:	BAC
Type:	BAC
Description:	
Source:	FPC
Position:	ctg6:1..260401
Length:	260401
Contig_hit:	"6"
Marker_hit:	Ta#S32672838-3B 0 0
Name:	**TaaCsp3BFhA_0101L21**

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat physical map viewer



Marker details

Marker name :	WMC430
Taxon :	Triticum aestivum
Marker type :	SSR
Marker origin :	amplicon
Target :	WMC
Origin laboratory :	ITCF

GnpMap

Mapped loci

Mapped loci: 4

Locus name	Map name	Taxon	Linkage group	Distance
Xwmc430-5B	TaVirtualPop01_071219	Triticum aestivum	5B	154.0

FhA_0101J20 TaaCsp3BFhA_0117N21
12 TaaCsp3BFhA_0121H12
08 TaaCsp3BFhA_0037K10
11 TaaCsp3BFhA_0040I22
16 TaaCsp3BFhA_0079H12
11 TaaCsp3BFhA_0023A14)

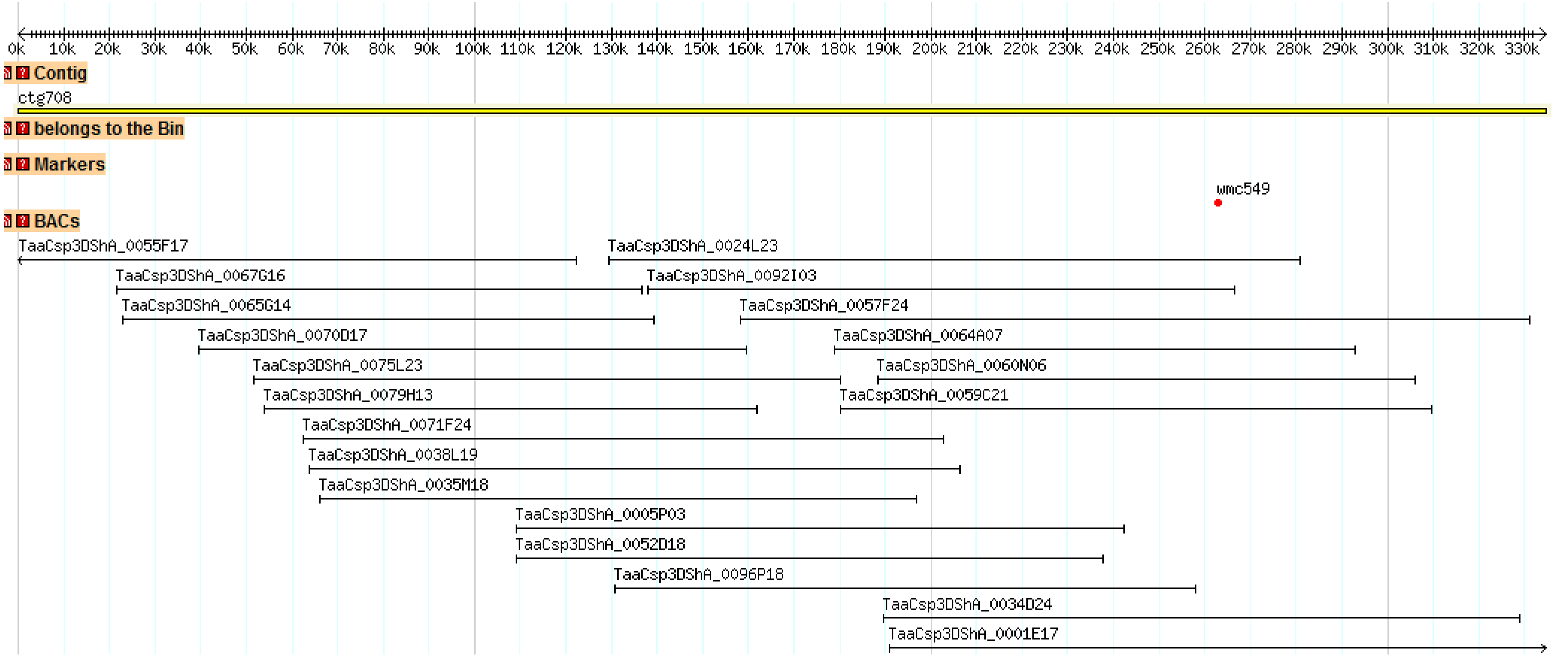
430-3B TaaCsp3BFhA_0163M03
32001

Feature Name	Feature Type	Species	Map Set	Map Name	Po		
WMC430	SSR	Wheat	Framework Feb07	5B	154		[View on Map] [Feature Details]
Xwmc430	SSR	Wheat Curated	Con Somers C	3B	3	0, Xw...	[View on Map] [Feature Details]
Xwmc430	SSR	Wheat Curated	Con Somers C	5B	154	0, Xw...	[View on Map] [Feature Details]
Xwmc430	SSR	Wheat Curated	RL4452*AC Domain SO 05	5B	163	0, Xw...	[View on Map] [Feature Details]
Xwmc430	SSR	Wheat	RL4452*AC Domain SO 05/08	5B	163	0, Xw...	[View on Map] [Feature Details]
Xwmc430	SSR	Wheat	Somers Consensus April 04	3B	3	30	[View on Map] [Feature Details]
Xwmc430	SSR	Wheat	Somers Consensus April 04	5B	154	30	[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	3B Consensus Feb09	3B	20.92 cM		[View on Map] [Feature Details]
wmc430	SSR	Wheat	5B Consensus August 2010	5B	140.56 cM		[View on Map] [Feature Details]

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat physical map viewer

- in development
  - add 3DS physical map in restricted access *(J. Bartos, J. Dolezel)*

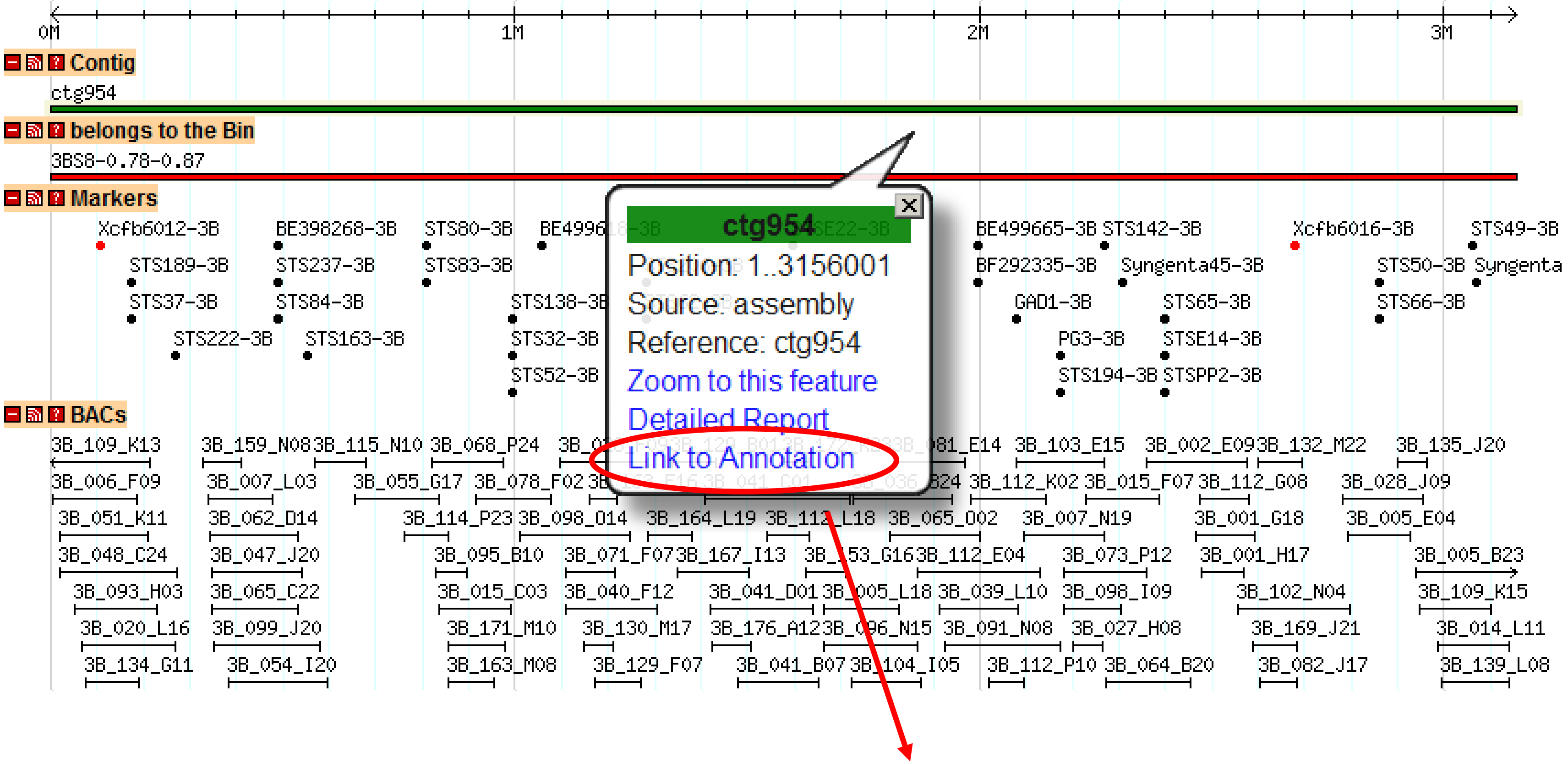


  - using GBrowse 2

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat physical map viewer

Contig or BAC in green are annotated



ctg954

Position: 1..3156001

Source: assembly

Reference: ctg954

Zoom to this feature

Detailed Report

Link to Annotation

Link to annotation viewer

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

Wheat annotation viewer

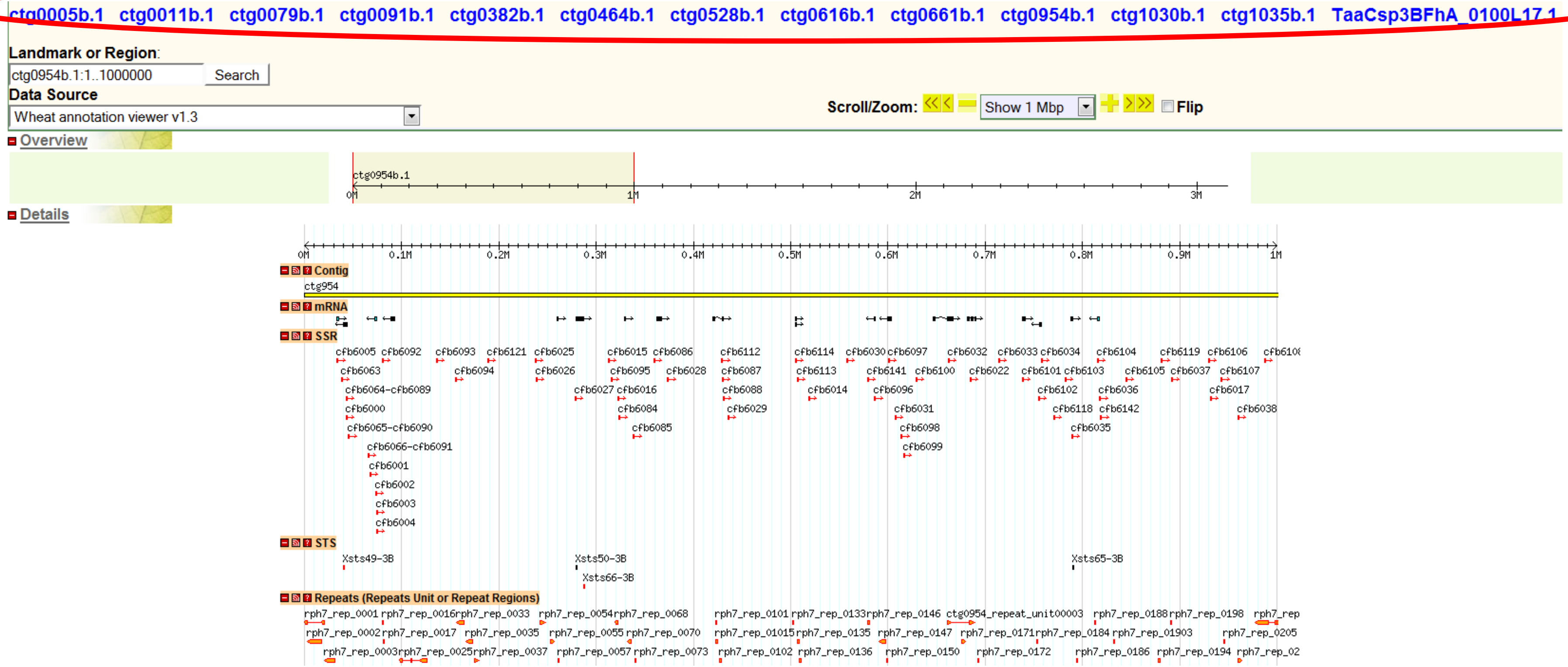
- Versions
  - v1.1
    - GBrowse 1.70
    - Contig 954 (FHB locus) of 3B chromosome
  - v1.2
    - Publicly available
  - v1.3
    - 12 new annotated 3B contigs *(F. Choulet)*
  - in development
    - All 3B BACs will be automatically annotated using TriAnnot *(P. Leroy)* in the frame of the 3BSeq project

Choulet *et al.*
Plant Cell. 2010 Jun 25.

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat3B_RPH7_pub/

Wheat annotation viewer

Select your annotated contig or BAC



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

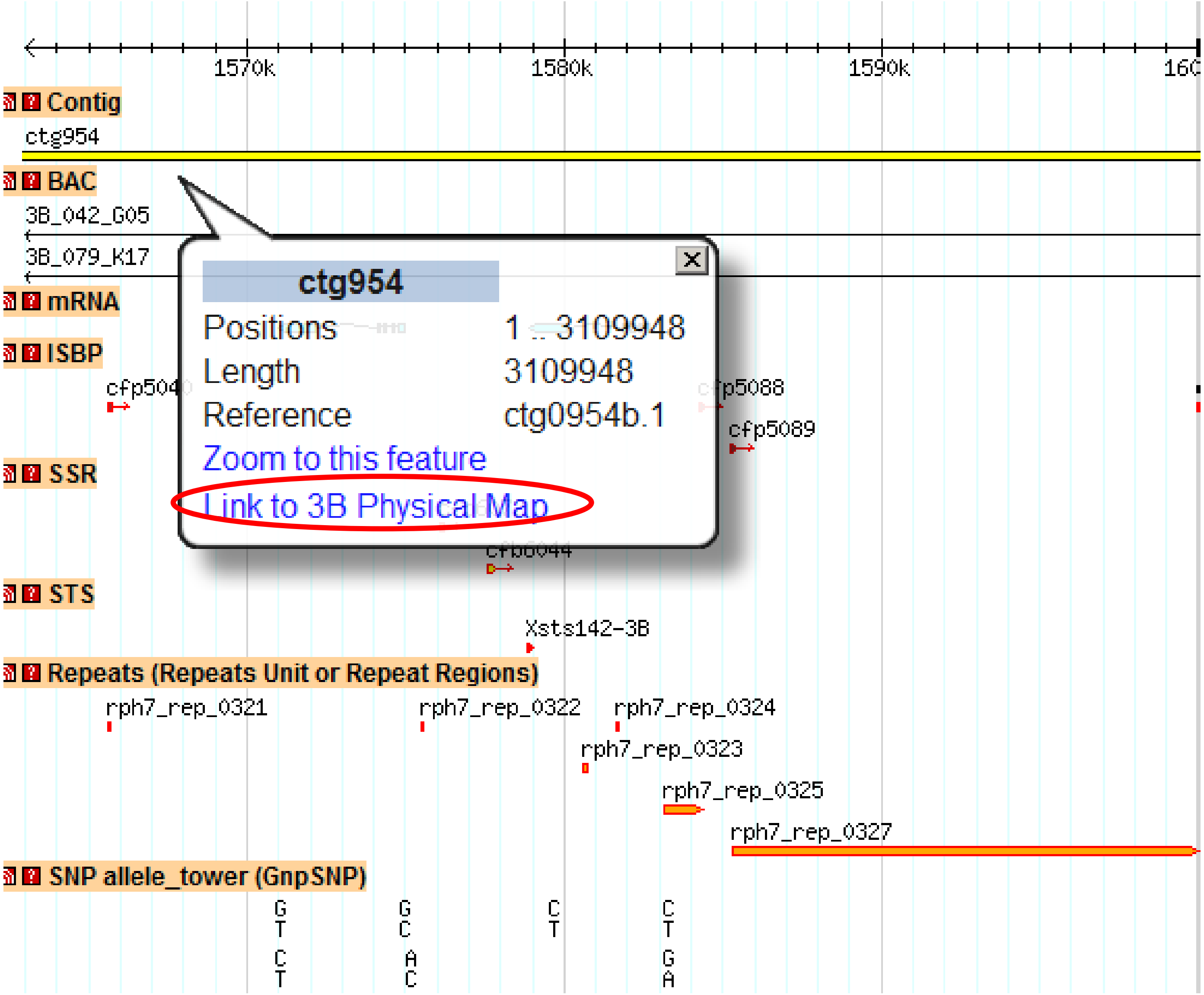
Landmark or Region: ctg0954b.1:1..1000000 Search

Data Source: Wheat annotation viewer v1.3

Scroll/Zoom: Show 1 Mbp ☐ **Flip**

Wheat annotation viewer

Contig



ctg954

Positions	1 .. 3109948
Length	3109948
Reference	ctg0954b.1

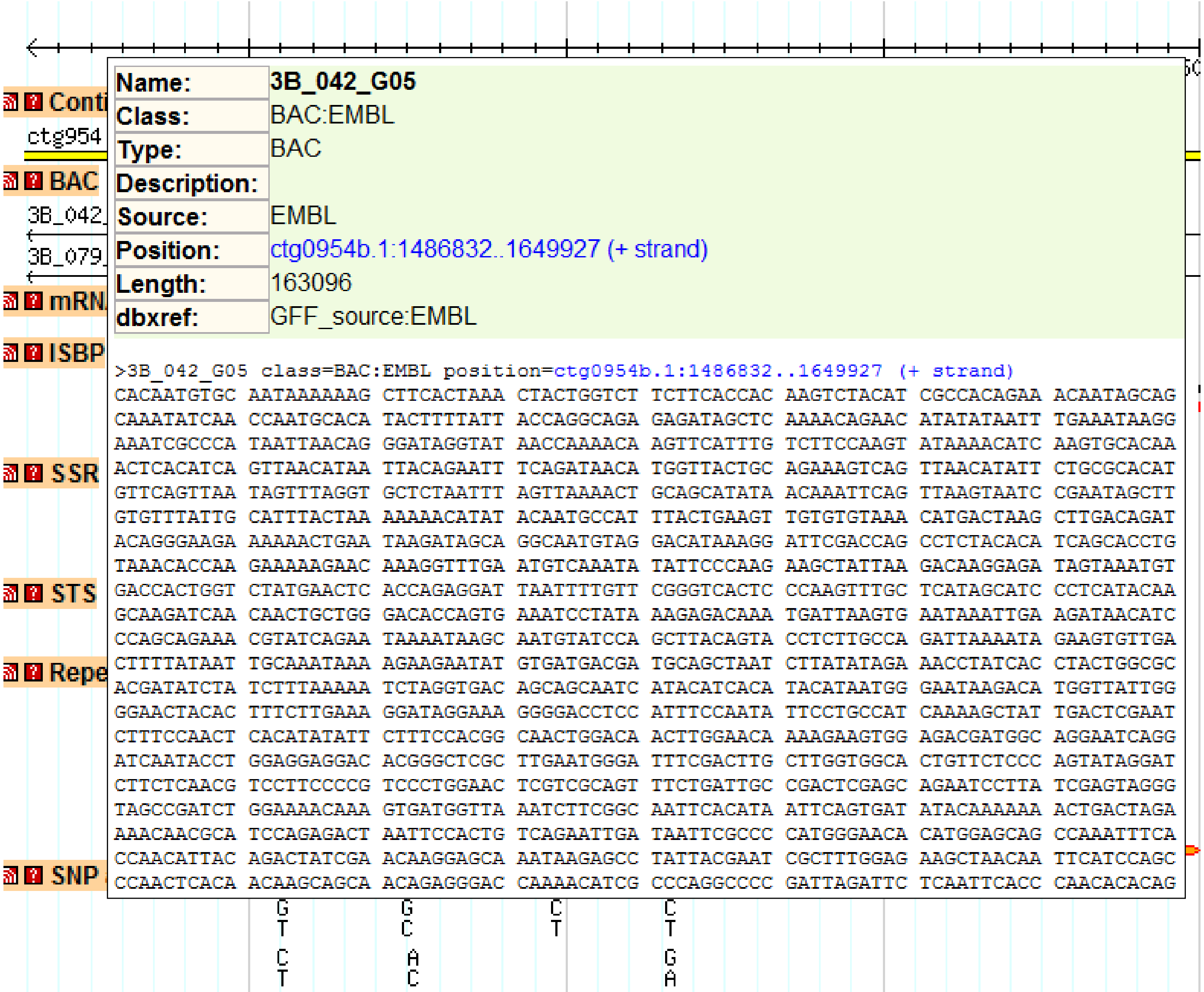
Zoom to this feature

Link to 3B Physical Map

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat3B_RPH7_pub/

Wheat annotation viewer

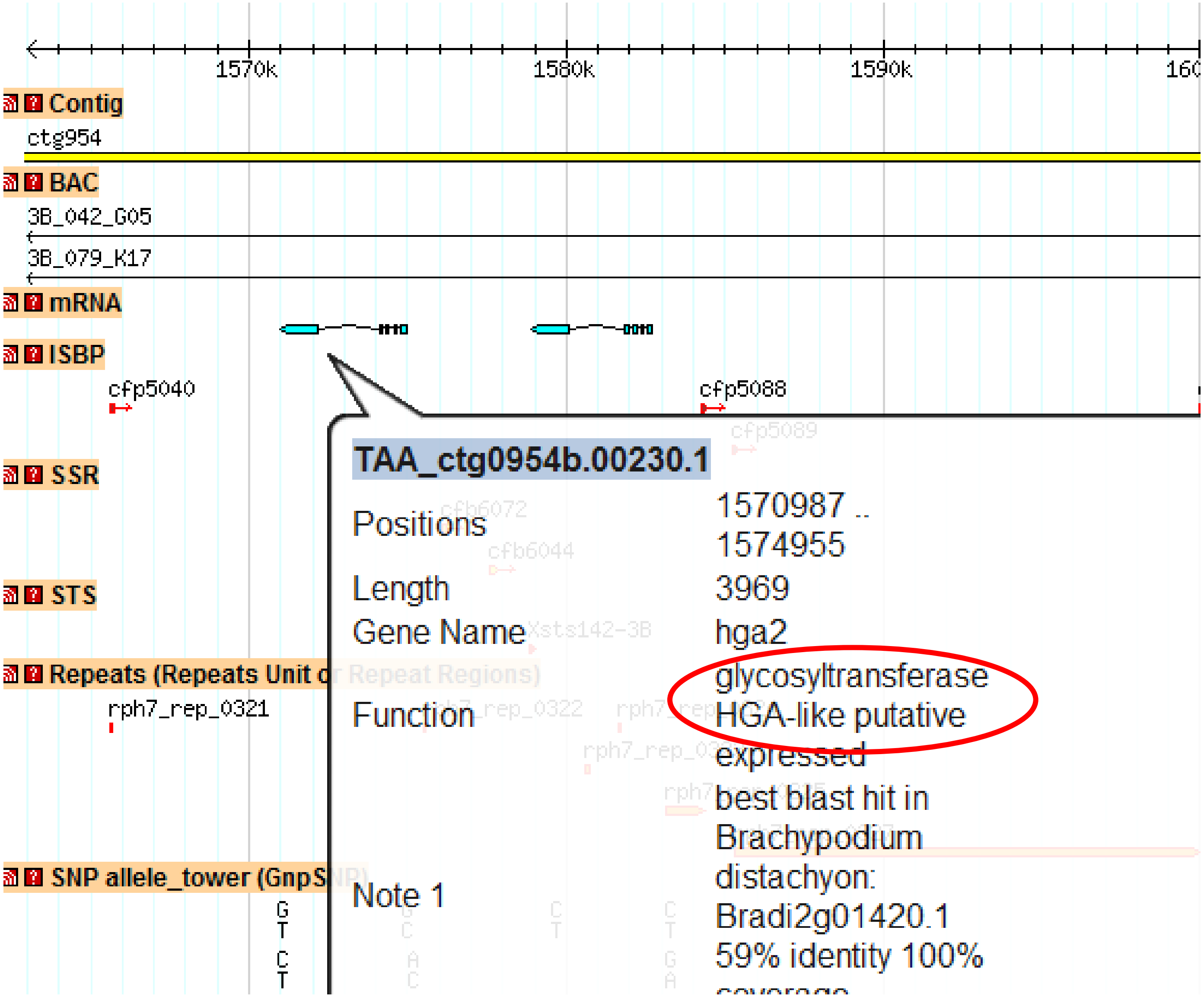
BAC



Name:	**3B_042_G05**
Class:	BAC:EMBL
Type:	BAC
Description:	
Source:	EMBL
Position:	ctg0954b.1:1486832..1649927 (+ strand)
Length:	163096
dbxref:	GFF_source:EMBL

```
>3B_042_G05 class=BAC:EMBL position=ctg0954b.1:1486832..1649927 (+ strand)
CACAATGTGC AATAAAAAAG CTTCACTAAA CTACTGGTCT TCTTCACCAC AAGTCTACAT CGCCACAGAA ACAATAGCAG
CAAATATCAA CCAATGCACA TACTTTTATT ACCAGGCAGA GAGATAGCTC AAAACAGAAC ATATATAATT TGAAATAAGG
AAATCGCCCA TAATTAACAG GGATAGGTAT AACCAAAACA AGTTCATTTG TCTTCCAAGT ATAAAACATC AAGTGCACAA
ACTCACATCA GTTAACATAA TTACAGAATT TCAGATAACA TGGTTACTGC AGAAAGTCAG TTAACATATT CTGCGCACAT
GTTCAGTTAA TAGTTTAGGT GCTCTAATTT AGTTAAAACT GCAGCATATA ACAAATTCAG TTAAGTAATC CGAATAGCTT
GTGTTTATTG CATTTACTAA AAAAACATAT ACAATGCCAT TTACTGAAGT TGTGTGTAAA CATGACTAAG CTTGACAGAT
ACAGGGAAGA AAAAACTGAA TAAGATAGCA GGCAATGTAG GACATAAAGG ATTCGACCAG CCTCTACACA TCAGCACCTG
TAAACACCAA GAAAAAGAAC AAAGGTTTGA ATGTCAAATA TATTCCCAAG AAGCTATTAA GACAAGGAGA TAGTAAATGT
GACCACTGGT CTATGAACTC ACCAGAGGAT TAATTTTGTT CGGGTCACTC CCAAGTTTGC TCATAGCATC CCTCATACAA
GCAAGATCAA CAACTGCTGG GACACCAGTG AAATCCTATA AAGAGACAAA TGATTAAGTG AATAAATTGA AGATAACATC
CCAGCAGAAA CGTATCAGAA TAAAATAAGC AATGTATCCA GCTTACAGTA CCTCTTGCCA GATTAAAATA GAAGTGTTGA
CTTTTATAAT TGCAAATAAA AGAAGAATAT GTGATGACGA TGCAGCTAAT CTTATATAGA AACCTATCAC CTACTGGCGC
ACGATATCTA TCTTTAAAAA TCTAGGTGAC AGCAGCAATC ATACATCACA TACATAATGG GAATAAGACA TGGTTATTGG
GGAACTACAC TTTCTTGAAA GGATAGGAAA GGGGACCTCC ATTTCCAATA TTCCTGCCAT CAAAAGCTAT TGACTCGAAT
CTTTCCAACT CACATATATT CTTTCCACGG CAACTGGACA ACTTGGAACA AAAGAAGTGG AGACGATGGC AGGAATCAGG
ATCAATACCT GGAGGAGGAC ACGGGCTCGC TTGAATGGGA TTTCGACTTG CTTGGTGGCA CTGTTCTCCC AGTATAGGAT
CTTCTCAACG TCCTTCCCCG TCCCTGGAAC TCGTCGCAGT TTCTGATTGC CGACTCGAGC AGAATCCTTA TCGAGTAGGG
TAGCCGATCT GGAAAACAAA GTGATGGTTA AATCTTCGGC AATTCACATA ATTCAGTGAT ATACAAAAAA ACTGACTAGA
AAACAACGCA TCCAGAGACT AATTCCACTG TCAGAATTGA TAATTCGCCC CATGGGAACA CATGGAGCAG CCAAATTTCA
CCAACATTAC AGACTATCGA ACAAGGAGCA AATAAGAGCC TATTACGAAT CGCTTTGGAG AAGCTAACAA TTCATCCAGC
CCAACTCACA ACAAGCAGCA ACAGAGGGAC CAAAACATCG CCCAGGCCCC GATTAGATTC TCAATTCACC CAACACACAG
```

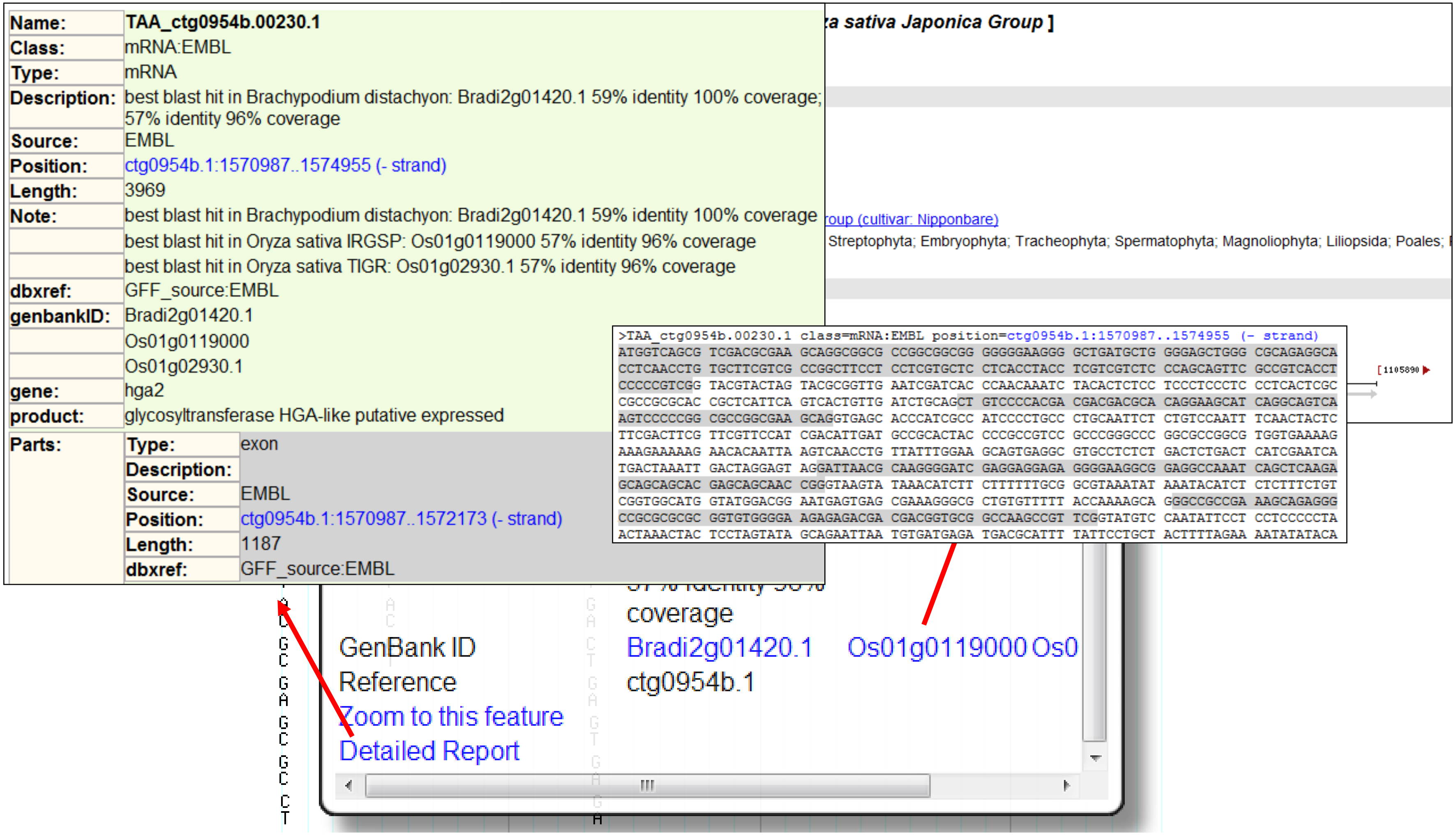
Wheat annotation viewer



TAA_ctg0954b.00230.1

Positions	1570987 .. 1574955
Length	3969
Gene Name	hga2
Function	glycosyltransferase HGA-like putative expressed
Note 1	best blast hit in Brachypodium distachyon: Bradi2g01420.1 59% identity 100%

Wheat annotation viewer



Name:	**TAA_ctg0954b.00230.1**
Class:	mRNA:EMBL
Type:	mRNA
Description:	best blast hit in Brachypodium distachyon: Bradi2g01420.1 59% identity 100% coverage; 57% identity 96% coverage
Source:	EMBL
Position:	ctg0954b.1:1570987..1574955 (- strand)
Length:	3969
Note:	best blast hit in Brachypodium distachyon: Bradi2g01420.1 59% identity 100% coverage
	best blast hit in Oryza sativa IRGSP: Os01g0119000 57% identity 96% coverage
	best blast hit in Oryza sativa TIGR: Os01g02930.1 57% identity 96% coverage
dbxref:	GFF_source:EMBL
genbankID:	Bradi2g01420.1
	Os01g0119000
	Os01g02930.1
gene:	hga2
product:	glycosyltransferase HGA-like putative expressed

Parts:		
	Type:	exon
	Description:	
	Source:	EMBL
	Position:	ctg0954b.1:1570987..1572173 (- strand)
	Length:	1187
	dbxref:	GFF_source:EMBL

ta sativa Japonica Group]

roup (cultivar: Nipponbare)

Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales;

```
>TAA_ctg0954b.00230.1 class=mRNA:EMBL position=ctg0954b.1:1570987..1574955 (- strand)
ATGGTCAGCG TCGACGCGAA GCAGGCGGCG CCGGCGGCGG GGGGGAAGGG GCTGATGCTG GGGAGCTGGG CGCAGAGGCA
CCTCAACCTG TGCTTCGTCG CCGGCTTCCT CCTCGTGCTC CTCACCTACC TCGTCGTCTC CCAGCAGTTC GCCGTCACCT
CCCCCGTCGG TACGTACTAG TACGCGGTTG AATCGATCAC CCAACAAATC TACACTCTCC TCCCTCCCTC CCTCACTCGC
CGCCGCGCAC CGCTCATTCA GTCACTGTTG ATCTGCAGCT GTCCCCACGA CGACGACGCA CAGGAAGCAT CAGGCAGTCA
AGTCCCCCGG CGCCGGCGAA GCAGGTGAGC ACCCATCGCC ATCCCCTGCC CTGCAATTCT CTGTCCAATT TCAACTACTC
TTCGACTTCG TTCGTTCCAT CGACATTGAT GCCGCACTAC CCCGCCGTCC GCCCGGGCCC GGCGCCGGCG TGGTGAAAAG
AAAGAAAAAG AACACAATTA AGTCAACCTG TTATTTGGAA GCAGTGAGGC GTGCCTCTCT GACTCTGACT CATCGAATCA
TGACTAAATT GACTAGGAGT AGGATTAACG CAAGGGGATC GAGGAGGAGA GGGGAAGGCG GAGGCCAAAT CAGCTCAAGA
GCAGCAGCAC GAGCAGCAAC CGGGTAAGTA TAAACATCTT CTTTTTTGCG GCGTAAATAT AAATACATCT CTCTTTCTGT
CGGTGGCATG GTATGGACGG AATGAGTGAG CGAAAGGGCG CTGTGTTTTT ACCAAAAGCA GGGCCGCCGA AAGCAGAGGG
CCGCGCGCGC GGTGTGGGGA AGAGAGACGA CGACGGTGCG GCCAAGCCGT TCGGTATGTC CAATATTCCT CCTCCCCCTA
ACTAAACTAC TCCTAGTATA GCAGAATTAA TGTGATGAGA TGACGCATTT TATTCCTGCT ACTTTTAGAA AATATATACA
```

coverage

GenBank ID	Bradi2g01420.1	Os01g0119000 Os0
Reference	ctg0954b.1	

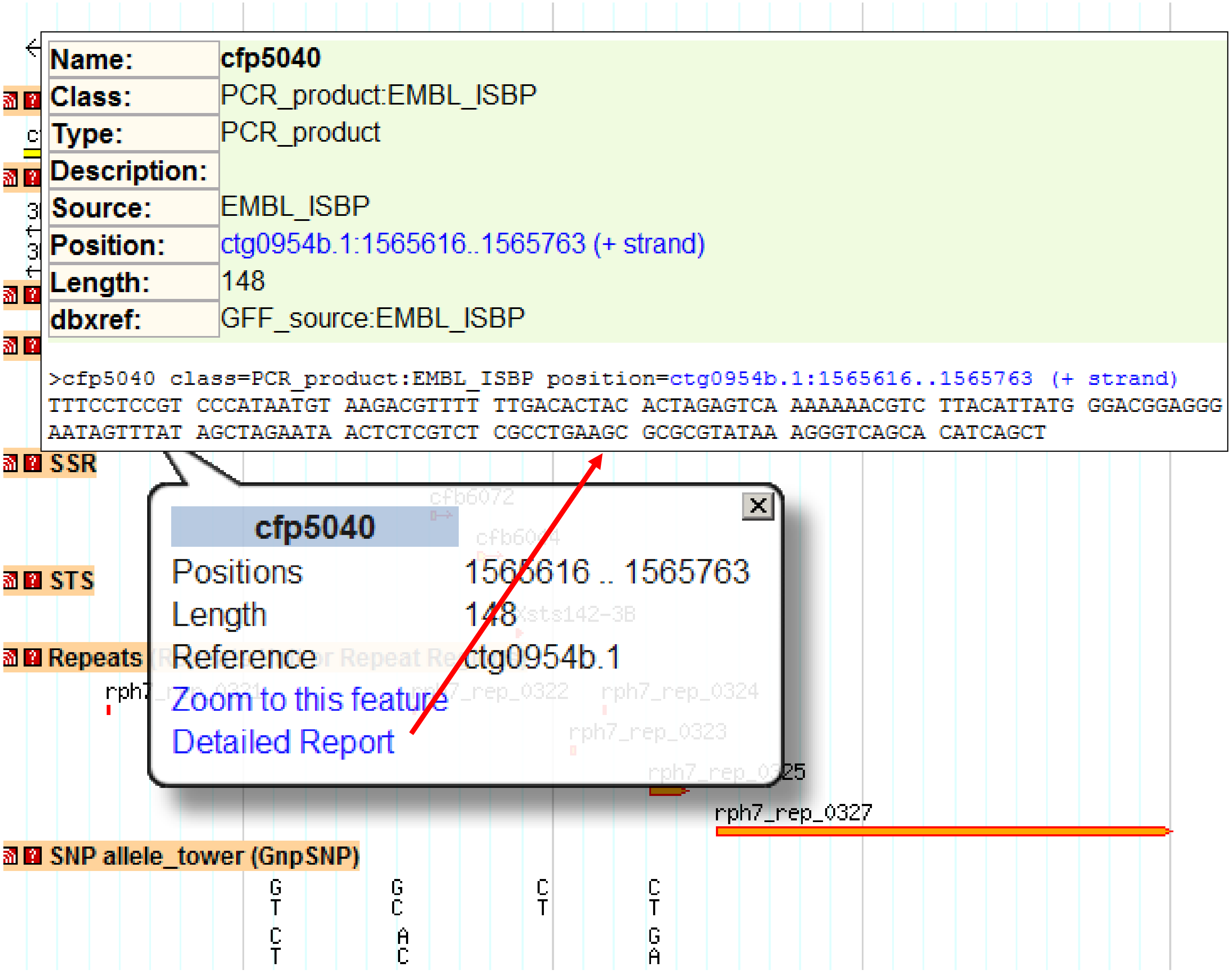
Zoom to this feature

Detailed Report

Wheat annotation viewer

ISBP

SSR



Name:	**cfp5040**
Class:	PCR_product:EMBL_ISBP
Type:	PCR_product
Description:	
Source:	EMBL_ISBP
Position:	ctg0954b.1:1565616..1565763 (+ strand)
Length:	148
dbxref:	GFF_source:EMBL_ISBP

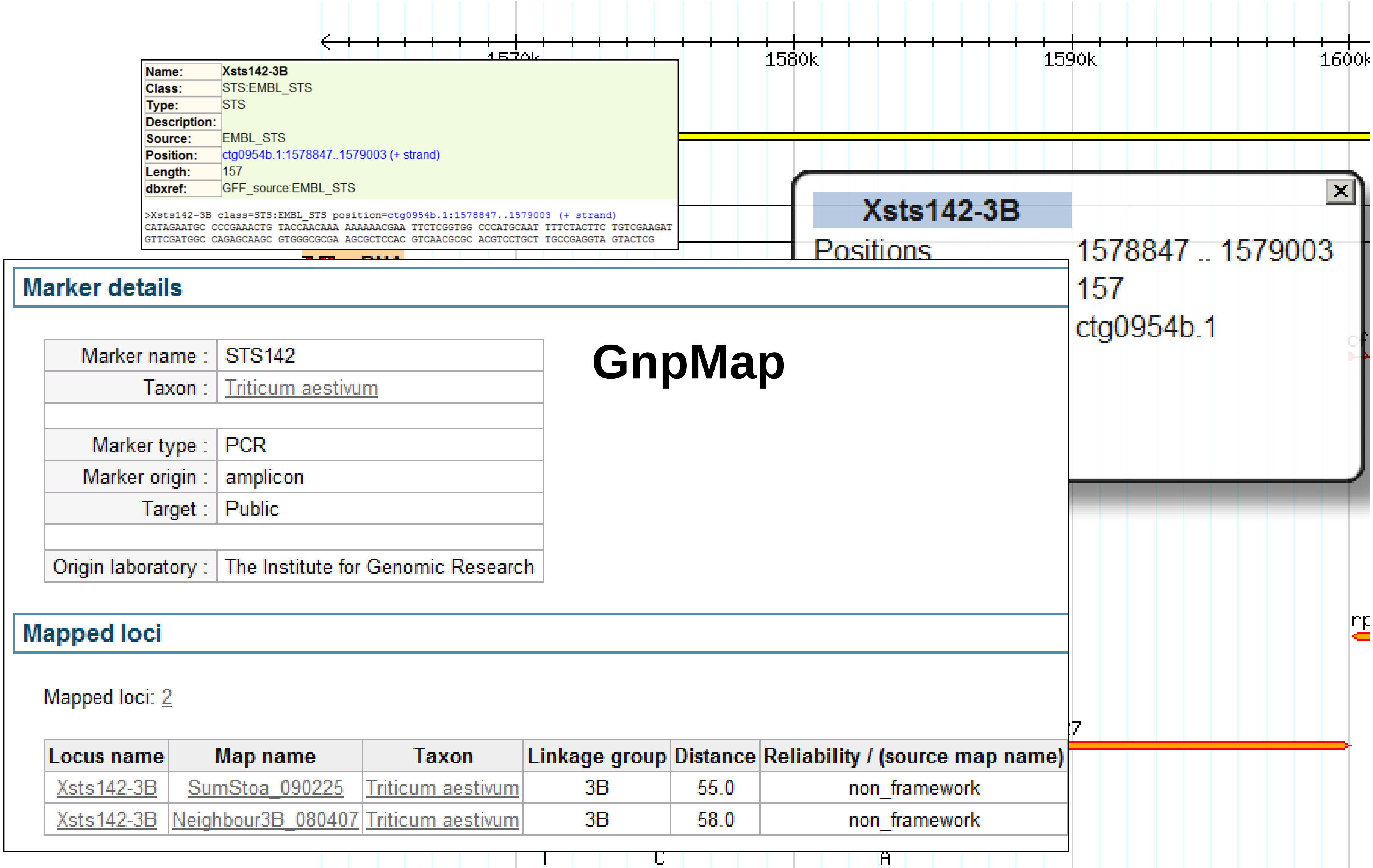
```
>cfp5040 class=PCR_product:EMBL_ISBP position=ctg0954b.1:1565616..1565763 (+ strand)
TTTCCTCCGT CCCATAATGT AAGACGTTTT TTGACACTAC ACTAGAGTCA AAAAAACGTC TTACATTATG GGACGGAGGG
AATAGTTTAT AGCTAGAATA ACTCTCGTCT CGCCTGAAGC GCGCGTATAA AGGGTCAGCA CATCAGCT
```

cfp5040	
Positions	1565616 .. 1565763
Length	148
Reference	ctg0954b.1

Zoom to this feature

Detailed Report

Wheat annotation viewer



Name:	Xsts142-3B
Class:	STS:EMBL_STS
Type:	STS
Description:	
Source:	EMBL_STS
Position:	ctg0954b.1:1578847..1579003 (+ strand)
Length:	157
dbxref:	GFF_source:EMBL_STS

```
>Xsts142-3B class=STS:EMBL_STS position=ctg0954b.1:1578847..1579003 (+ strand)
CATAGAATGC CCCGAAACTG TACCAACAAA AAAAAACGAA TTCTCGGTGG CCCATGCAAT TTTCTACTTC TGTCGAAGAT
GTTCGATGGC CAGAGCAAGC GTGGGCGCGA AGCGCTCCAC GTCAACGCGC ACGTCCTGCT TGCCGAGGTA GTACTCG
```

Xsts142-3B

Positions	1578847 .. 1579003
	157
	ctg0954b.1

GnpMap

Marker details

Marker name :	STS142
Taxon :	Triticum aestivum
Marker type :	PCR
Marker origin :	amplicon
Target :	Public
Origin laboratory :	The Institute for Genomic Research

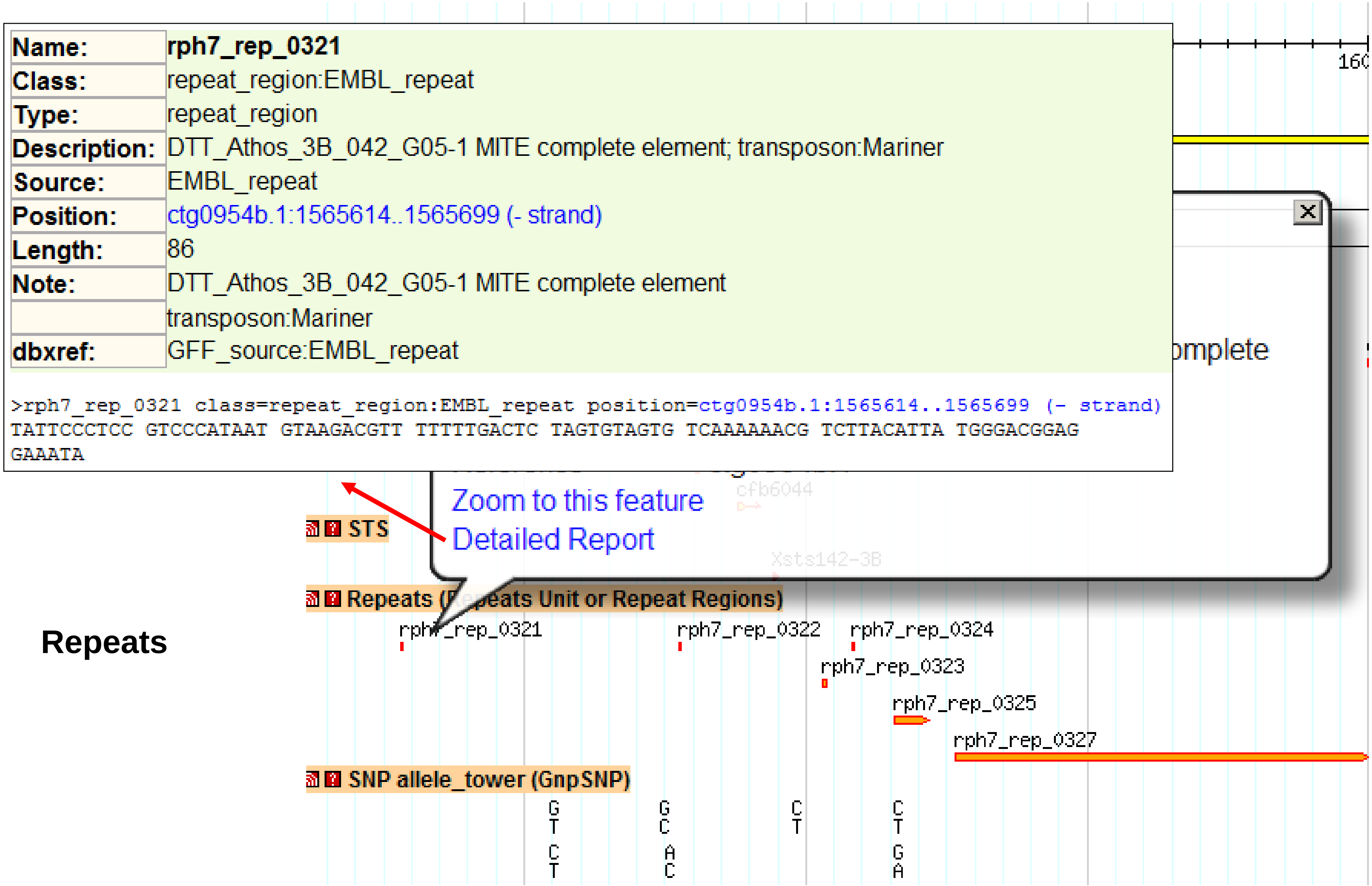
Mapped loci

Mapped loci: 2

Locus name	Map name	Taxon	Linkage group	Distance	Reliability / (source map name)
Xsts142-3B	SumStoa_090225	Triticum aestivum	3B	55.0	non_framework
Xsts142-3B	Neighbour3B_080407	Triticum aestivum	3B	58.0	non_framework

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat3B_RPH7_pub/

Wheat annotation viewer

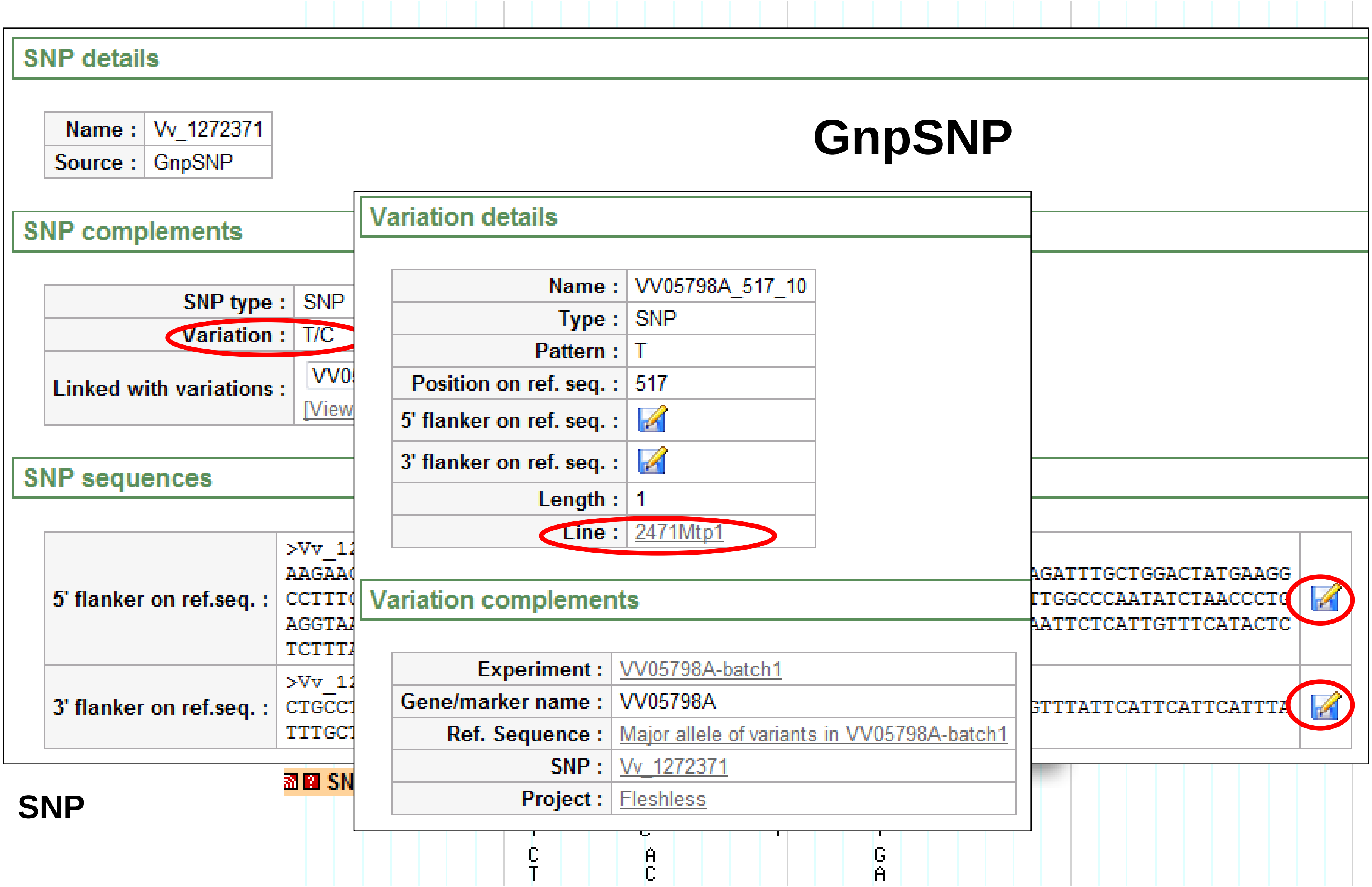


Name:	**rph7_rep_0321**
Class:	repeat_region:EMBL_repeat
Type:	repeat_region
Description:	DTT_Athos_3B_042_G05-1 MITE complete element; transposon:Mariner
Source:	EMBL_repeat
Position:	ctg0954b.1:1565614..1565699 (- strand)
Length:	86
Note:	DTT_Athos_3B_042_G05-1 MITE complete element
	transposon:Mariner
dbxref:	GFF_source:EMBL_repeat

```
>rph7_rep_0321 class=repeat_region:EMBL_repeat position=ctg0954b.1:1565614..1565699 (- strand)
TATTCCCTCC GTCCCATAAT GTAAGACGTT TTTTTGACTC TAGTGTAGTG TCAAAAAACG TCTTACATTA TGGGACGGAG
GAAATA
```

Repeats

Wheat annotation viewer



GnpSNP

SNP details

Name :	Vv_1272371
Source :	GnpSNP

SNP complements

SNP type :	SNP
Variation :	T/C
Linked with variations :	VV0 [View

SNP sequences

5' flanker on ref.seq. :

```
>Vv_12
AAGAA                   AGATTTGCTGGACTATGAAGG
CCTTT                   TTGGCCCAATATCTAACCCTG
AGGTA                   AATTCTCATTGTTTCATACTC
TCTTT
```

3' flanker on ref.seq. :

```
>Vv_12
CTGCC                   GTTTATTCATTCATTCATTTA
TTTGC
```

SN

Variation details

Name :	VV05798A_517_10
Type :	SNP
Pattern :	T
Position on ref. seq. :	517
5' flanker on ref. seq. :	✎
3' flanker on ref. seq. :	✎
Length :	1
Line :	2471Mtp1

Variation complements

Experiment :	VV05798A-batch1
Gene/marker name :	VV05798A
Ref. Sequence :	Major allele of variants in VV05798A-batch1
SNP :	Vv_1272371
Project :	Fleshless

SNP

Take-Home Message

IWGSC Sequence Repository with links to Survey sequence, Blast search, Physical map and Annotation viewers.

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

Sequence Repository

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

Physical map viewer

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

BAC annotation viewer

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat3B_RPH7_pub/

URGI website for wheat

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

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URGI

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K. Eversole

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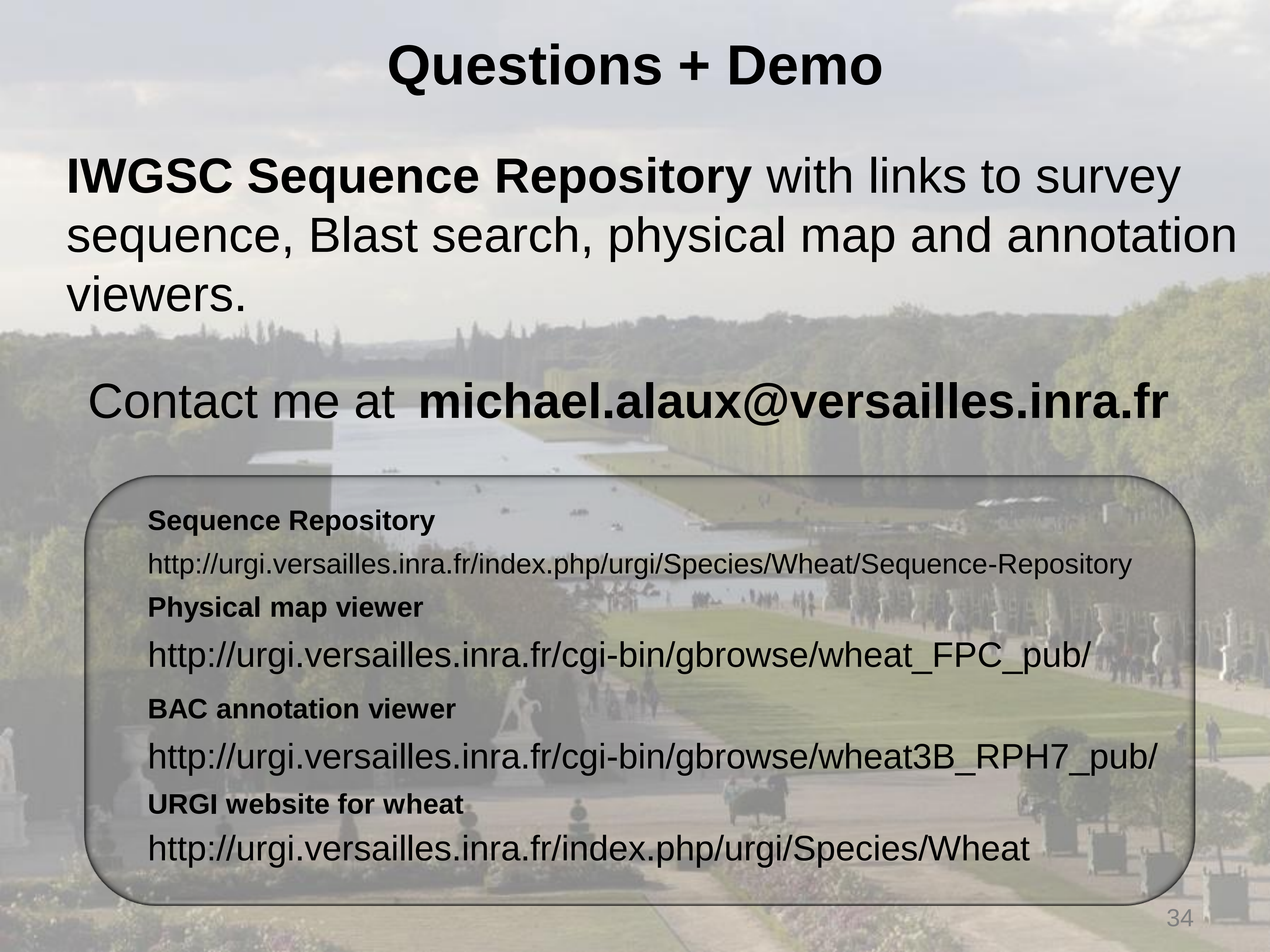

Questions + Demo

IWGSC Sequence Repository with links to survey sequence, Blast search, physical map and annotation viewers.

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

Sequence Repository

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

Physical map viewer

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat_FPC_pub/

BAC annotation viewer

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/wheat3B_RPH7_pub/

URGI website for wheat

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