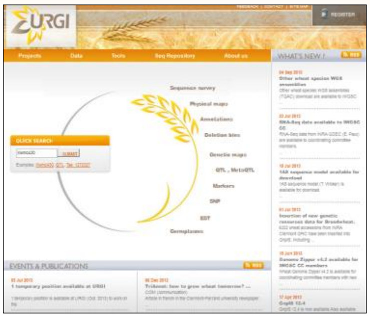
IWGSC Sequence Repository at URGI :
New features and Blast tool

Michael Alaux

PAG 2014 – IWGSC Standards and Protocol

Wheat@URGI website

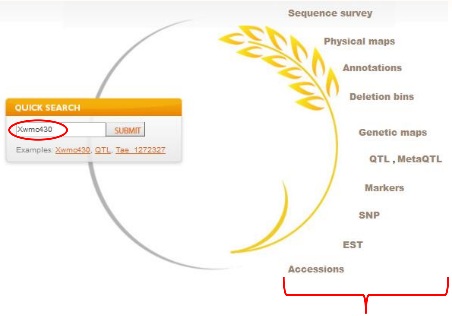
Wheat@URGI



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

Wheat@URGI

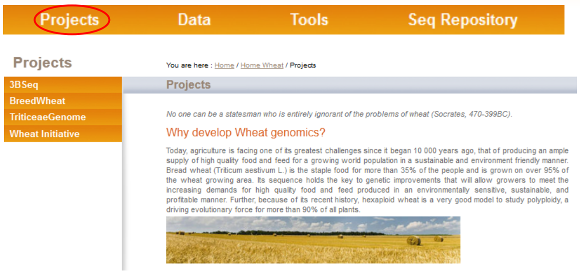
Google-like



Search into wheat data in GnpIS the URGI Information system

Quick Links to data

Wheat@URGI



You are here : Home / Home Wheat / Projects

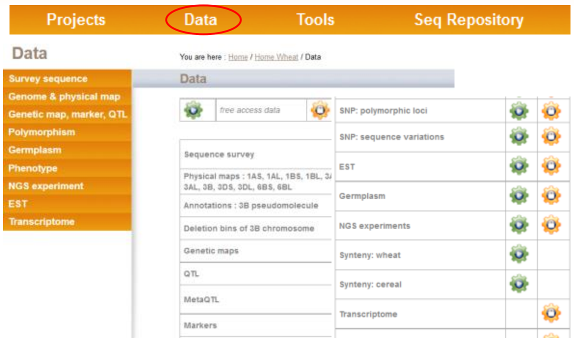
Projects

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.

Wheat@URGI



You are here : Home / Home Wheat / Data

Data

⚙ free access data ⚙

Sequence survey

Physical maps : 1AS, 1AL, 1BS, 1BL, 3AL, 3B, 3DS, 3DL, 6BS, 6BL

Annotations : 3B pseudomolecule

Deletion bins of 3B chromosome

Genetic maps

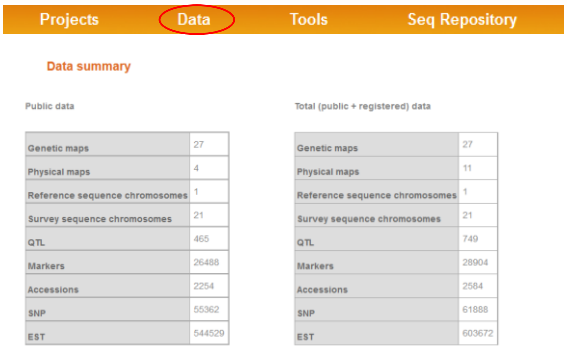
QTL

MetaQTL

Markers

SNP: polymorphic loci	⚙	⚙
SNP: sequence variations	⚙	⚙
EST	⚙	⚙
Germplasm	⚙	⚙
NGS experiments	⚙	⚙
Synteny: wheat	⚙	
Synteny: cereal	⚙	
Transcriptome		⚙
Phenotype: BW project		⚙

Wheat@URGI



Data summary

Public data

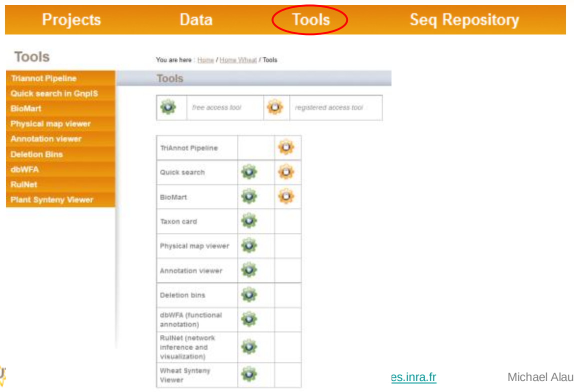
Genetic maps	27
Physical maps	4
Reference sequence chromosomes	1
Survey sequence chromosomes	21
QTL	465
Markers	26488
Accessions	2254
SNP	55362
EST	544529

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

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

Wheat@URGI



You are here : Home / Home Wheat / Tools

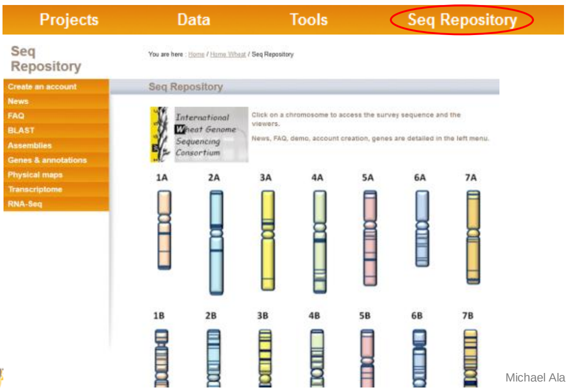
Tools

⚙	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 Synteny Viewer	⚙	

es.inra.fr

Wheat@URGI



You are here : Home / Home Wheat / Seq Repository

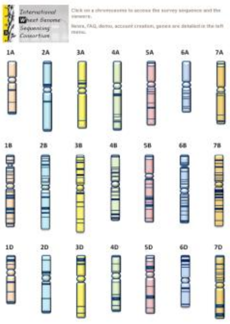
Seq Repository

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

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

Sequence Repository

Sequence Repository



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

BLAST search (Blast agreement, public Blast will be available soon)

Download (Public)

Viewers:

- ❑ Physical maps 
- ❑ Annotated reference sequence 3B (Public)

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

Survey Sequence Repository

News

Jan 2014:

- Survey sequence assemblies and Gene models download are **publicly** available.
- 3B annotated pseudomolecule is **publicly** available.
- 2D physical map (WGP data) is **publicly** available to download.
- 3B RNA-Seq data (15 conditions) are **publicly** available to download.

Dec 2013:

- New Gene models version is available for coordinating committee members.

Oct 2013:

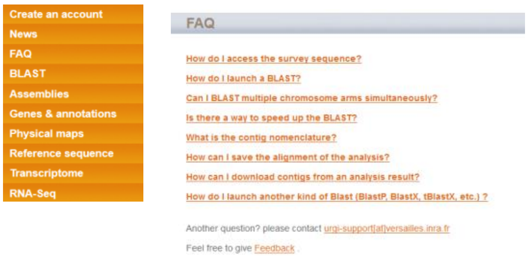
- 7B physical map data (Odd-Arne Olsen) are available upon request though an MTA.

Sept 2013:

- Chromosomes assemblies are now available for download to "Blast agreement" members.
- Other wheat species WGS assemblies (TGAC) download are available to IWGSC coordinating com

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

Survey Sequence Repository



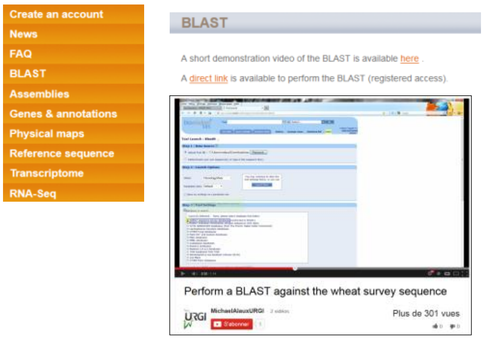
FAQ

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 .

Survey Sequence Repository



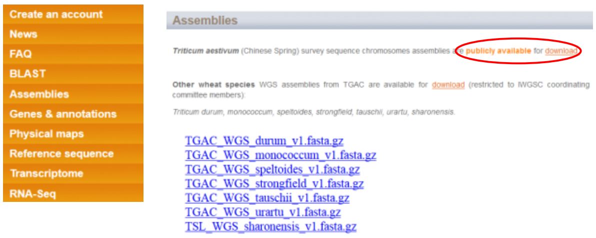
BLAST

A short demonstration video of the BLAST is available here .

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

Perform a BLAST against the wheat survey sequence

Survey Sequence Repository



Assemblies

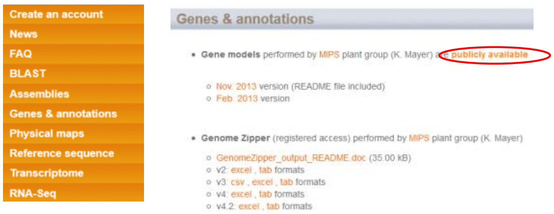
Triticum aestivum (Chinese Spring) survey sequence chromosomes assemblies are **publicly available** for download

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

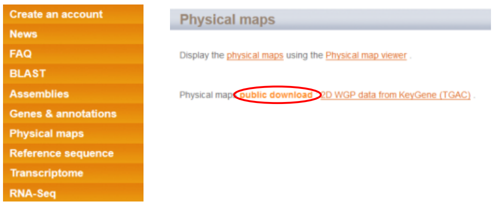
Survey Sequence Repository



Genes & annotations

- **Gene models** performed by MIPS plant group (K. Mayer) are **publicly available**
    - Nov. 2013 version (README file included)
    - Feb. 2013 version
- **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

Survey Sequence Repository

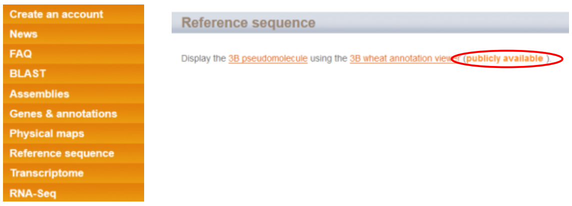


Physical maps

Display the physical maps using the Physical map viewer .

Physical map **public download** 2D WGP data from KeyGene (TGAC) .

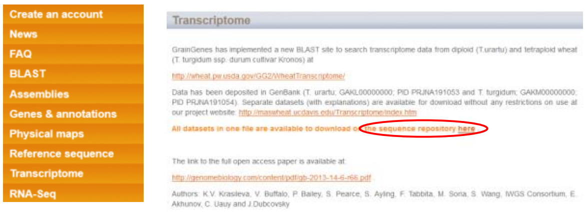
Survey Sequence Repository



Reference sequence

Display the 3B pseudomolecule using the 3B wheat annotation viewer (**publicly available**).

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

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

Survey Sequence Repository

RNA-Seq

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

Deep transcriptome sequencing was conducted on 15 different conditions corresponding to five wheat organs at three developmental stages each. Mapping RNAseq reads to the chromosome 3B reference sequence allowed to validate gene prediction, as well 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 to study the relative expression of homoeologous and paralogous copies of wheat genes.

```
[ ]   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/
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[DIR] stem_Z32_rep2/
[DIR] stem_Z65_rep1/
[DIR] stem_Z65_rep2/
```
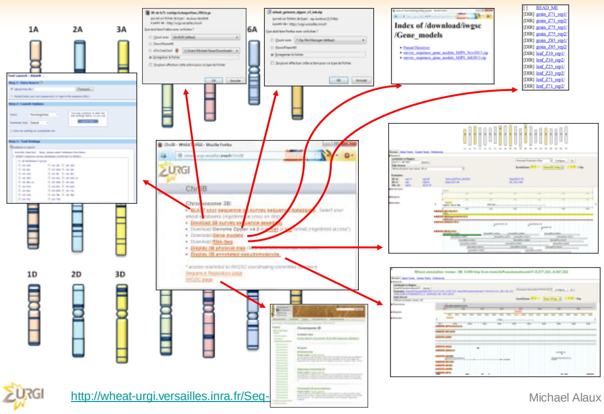

http://wheat-urgi.versailles.inra.fr/Seq-Repository

Sequence Repository: 3B



Chr3B

Chromosome 3B:

- BLAST your sequence on survey sequence databases
- Download 3B survey sequence assembly
- Download Genome Zipper v4.2 in excel or txt format (registered access*)
- Download Gene models
- Download RNA-Seq
- Display 3B physical map
- Display 3B annotated pseudomolecule

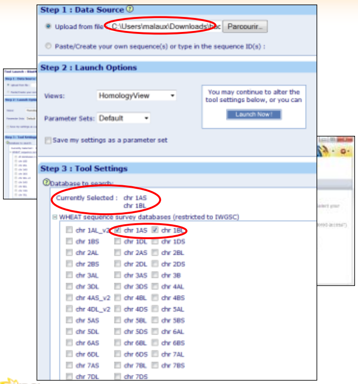
Sequence Repository page

IWGSC page

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

BLAST

BLAST



Step 1 : Data Source

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

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

Step 2 : Launch Options

Views: HomologyView

Parameter Sets: Default

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 : chr 1AS
chr 1BL

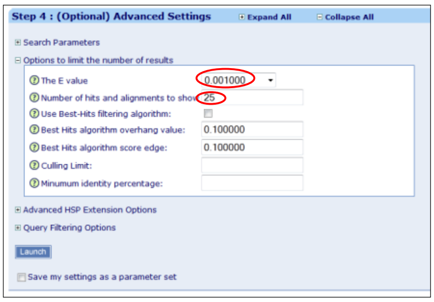
⊟ WHEAT sequence survey databases (restricted to IWGSC)

☐ 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

https://urgi.versailles.inra.fr/srs83/displayTool.do?toolName=BlastN

BLAST

To speed up your Blast



Step 4 : (Optional) Advanced Settings

⊟ Options to limit the number of results

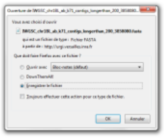
The E value	0.001000
Number of hits and alignments to show	25
Use Best-Hits filtering algorithm:	☐
Best Hits algorithm overhang value:	0.100000
Best Hits algorithm score edge:	0.100000
Culling Limit:	
Minumum identity percentage:	

☐ Save my settings as a parameter set

https://urgi.versailles.inra.fr/srs83/displayTool.do?toolName=BlastN

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

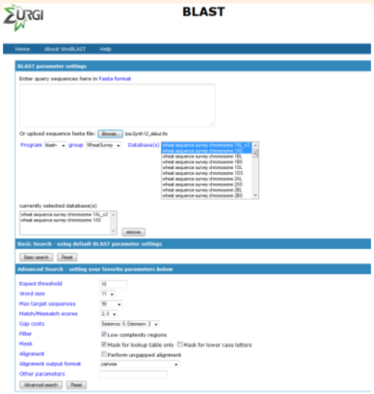
☐ Toujours effectuer cette action pour ce type de fichier.

Homology View

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

https://urgi.versailles.inra.fr/srs83/displayTool.do?toolName=BlastN

Public BLAST (soon available)



BLAST

BLAST parameter settings

Enter query sequences here in Fasta format

Or upload sequence fasta file: Browse... bacSynth12_debut.tfa

Program blastn group WheatSurvey Database(s)

wheat sequence survey chromosome 1AL_v2
wheat sequence survey chromosome 1AS
wheat sequence survey chromosome 1BL
wheat sequence survey chromosome 1BS
wheat sequence survey chromosome 1DL
wheat sequence survey chromosome 1DS
wheat sequence survey chromosome 2AL
wheat sequence survey chromosome 2AS
wheat sequence survey chromosome 2BL
wheat sequence survey chromosome 2BS

currently selected database(s)

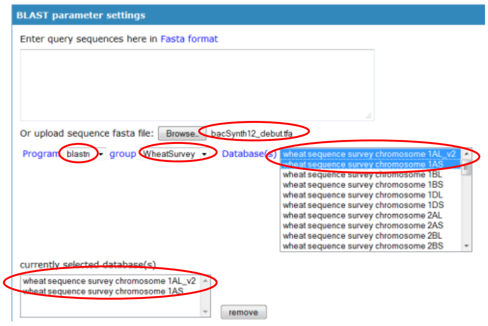
wheat sequence survey chromosome 1AL_v2
wheat sequence survey chromosome 1AS

Basic Search - using default BLAST parameter settings

Advanced Search - setting your favorite parameters below

Expect threshold 10
Word size 11
Max target sequences 50
Match/Mismatch scores 2-3
Gap costs Existence: 5, Extension: 2
Filter ☑ Low complexity regions
Mask ☑ Mask for lookup table only ☐ Mask for lower case letters
Alignment ☐ Perform ungapped alignment
Alignment output format pairwise
Other parameters

Public BLAST (soon available)



BLAST parameter settings

Enter query sequences here in Fasta format

Or upload sequence fasta file: Browse... bacSynth12_debut.tfa

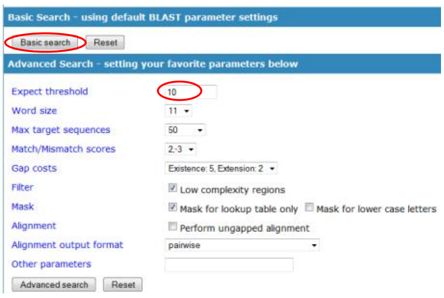
Program blastn group WheatSurvey Database(s)

wheat sequence survey chromosome 1AL_v2
wheat sequence survey chromosome 1AS
wheat sequence survey chromosome 1BL
wheat sequence survey chromosome 1BS
wheat sequence survey chromosome 1DL
wheat sequence survey chromosome 1DS
wheat sequence survey chromosome 2AL
wheat sequence survey chromosome 2AS
wheat sequence survey chromosome 2BL
wheat sequence survey chromosome 2BS

currently selected database(s)

wheat sequence survey chromosome 1AL_v2
wheat sequence survey chromosome 1AS

Public BLAST (soon available)

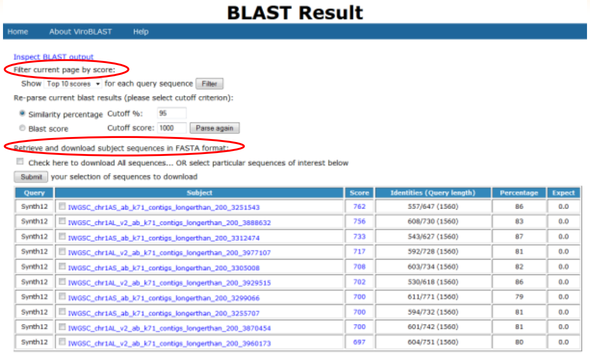


Basic Search - using default BLAST parameter settings

Advanced Search - setting your favorite parameters below

Expect threshold 10
Word size 11
Max target sequences 50
Match/Mismatch scores 2-3
Gap costs Existence: 5, Extension: 2
Filter ☑ Low complexity regions
Mask ☑ Mask for lookup table only ☐ Mask for lower case letters
Alignment ☐ Perform ungapped alignment
Alignment output format pairwise
Other parameters

Public BLAST (soon available)



BLAST Result

Inspect BLAST output

Filter current page by score:

Show Top 10 scores for each query sequence Filter

Re-parse current blast results (please select cutoff criterion):

● Similarity percentage Cutoff %: 95
○ Blast score Cutoff score: 1000 Parse again

Retrieve and download subject sequences in FASTA format:

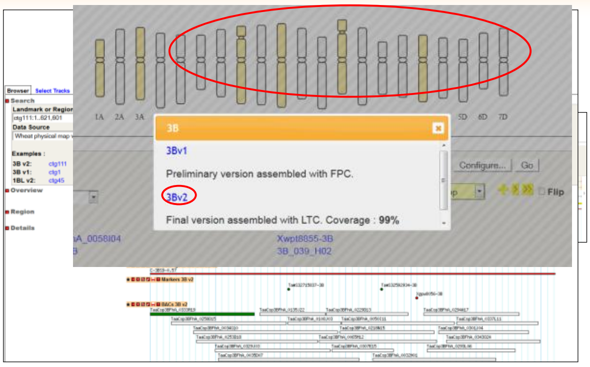
☐ Check here to download All sequences... OR select particular sequences of interest below

Submit your selection of sequences to download

Query	Subject	Score	Identities (Query length)	Percentage	Expect
Synth12	☐ IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3251543	762	557/647 (1560)	86	0.0
Synth12	☐ IWGSC_chr1AL_v2_ab_k71_contigs_longerthan_200_3888632	756	608/730 (1560)	83	0.0
Synth12	☐ IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3312474	733	543/627 (1560)	87	0.0
Synth12	☐ IWGSC_chr1AL_v2_ab_k71_contigs_longerthan_200_3977107	717	592/728 (1560)	81	0.0
Synth12	☐ IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3305008	708	603/734 (1560)	82	0.0
Synth12	☐ IWGSC_chr1AL_v2_ab_k71_contigs_longerthan_200_3929515	702	530/618 (1560)	86	0.0
Synth12	☐ IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3299066	700	611/771 (1560)	79	0.0
Synth12	☐ IWGSC_chr1AS_ab_k71_contigs_longerthan_200_3255707	700	594/732 (1560)	81	0.0
Synth12	☐ IWGSC_chr1AL_v2_ab_k71_contigs_longerthan_200_3870454	700	601/742 (1560)	81	0.0
Synth12	☐ IWGSC_chr1AL_v2_ab_k71_contigs_longerthan_200_3960173	697	604/751 (1560)	80	0.0

Physical maps

Physical map viewer



3B

3Bv1

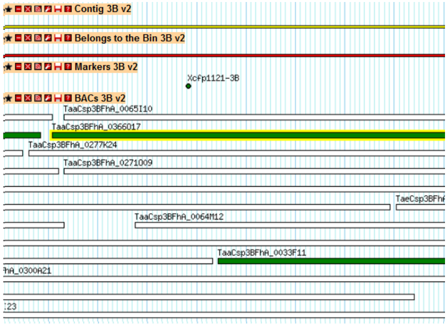
Preliminary version assembled with FPC.

3Bv2

Final version assembled with LTC. Coverage : **99%**

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

Physical map viewer 3B v2



Physical contig

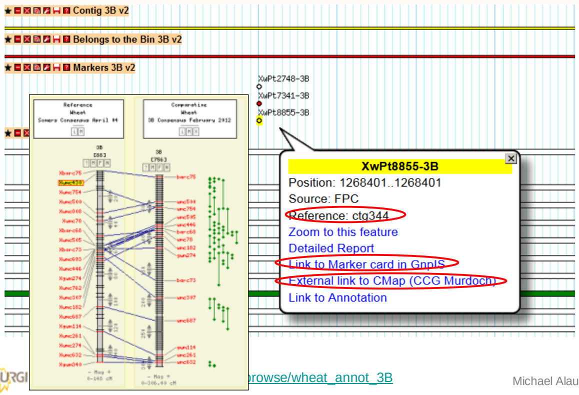
Deletion bin

Markers

BACs

https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

Physical map viewer 3B v2



XwPt8855-3B

Position: 1268401..1268401

Source: FPC

Reference: ctg344

Zoom to this feature

Detailed Report

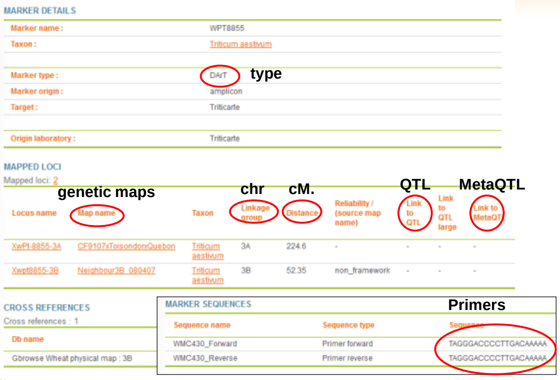
Link to Marker card in GnpIS

External link to CMap (CCG Murdoch)

Link to Annotation

rowse/wheat_annot_3B

Physical map viewer



MARKER DETAILS

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

type

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

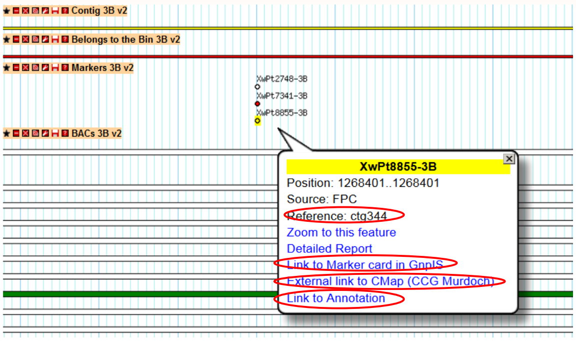
MARKER SEQUENCES

Primers

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

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

Physical map viewer



XwPt8855-3B

Position: 1268401..1268401

Source: FPC

Reference: ctg344

Zoom to this feature

Detailed Report

Link to Marker card in GnpIS

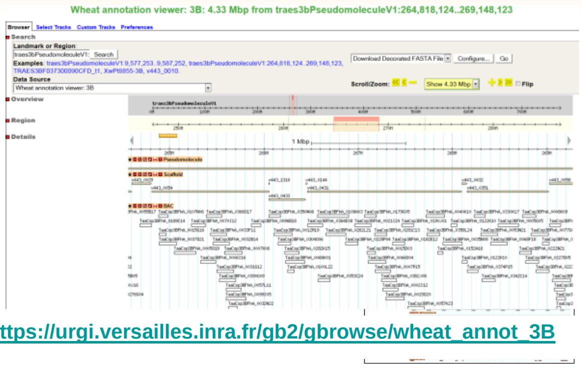
External link to CMap (CCG Murdoch)

Link to Annotation

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

3B reference sequence annotation

3B annotation viewer



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

Landmark or Region: traes3bPseudomoleculeV1:

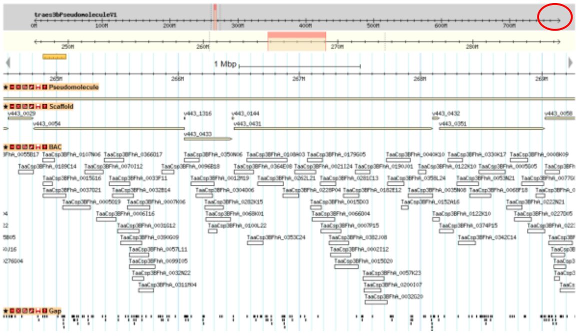
Examples: traes3bPseudomoleculeV1:9,577,253..9,587,252, traes3bPseudomoleculeV1:264,818,124..269,148,123, TRAES3BF037300090CFD_t1, XwPt8855-3B, v443_0010.

Data Source: Wheat annotation viewer: 3B

https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

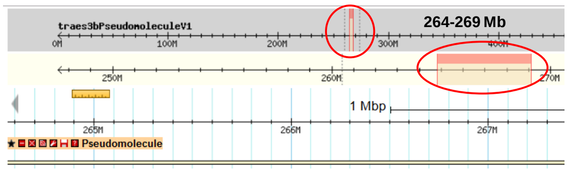
3B annotation viewer

774 Mb pseudomolecule + non anchored scaffolds (1450)

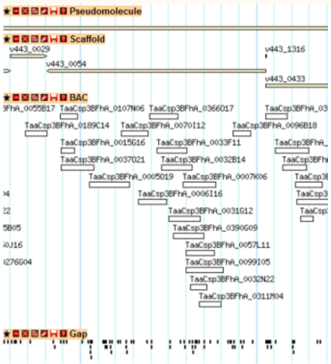


3B annotation viewer: Pseudomolecule

Position on the pseudomolecule



3B annotation viewer



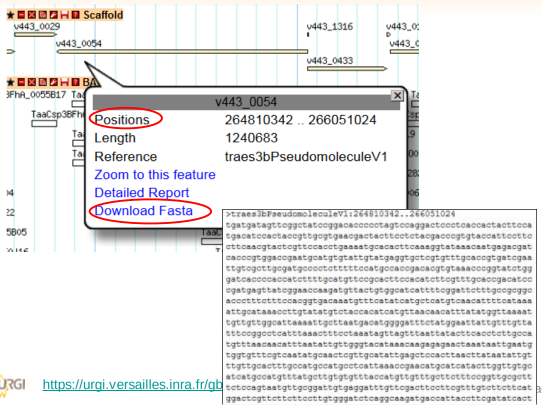
Pseudomolecule

Scaffolds

BACs

Gaps

3B annotation viewer: Scaffold



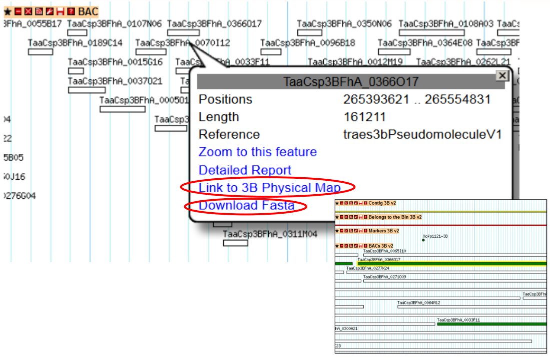
v443_0054

Positions	264810342 .. 266051024
Length	1240683
Reference	traes3bPseudomoleculeV1

Zoom to this feature
Detailed Report
Download Fasta

```
>traes3bPseudomoleculeV1:264810342..266051024
tgatgatagttcggctatccggacacccccctagtccaggactccctcaccactacttcca
tgacatccactaccgttgcgtgaacgactacttcctctacgacccgtgtaccattccttc
cttcaacgtactcgttccacctgaaaatgcacacttcaaaggtataaacaatgagacgat
cacccgtggaccgaatgcatgtgtattgtatgaggtgctcgtgtttgcaccgtgatcgaa
ttgtcgcttgcgatgccccctctttttccatgccaccgacacgtgtaaacccggtatctgg
gatcaccccaccatcttttgcatgttccgcacttccacatcttcgtttgcaccgacatcc
cgatgagttatcggaaccaagatgttactgtggcatcattttcggattctttgccgcggc
accctttctttccacggtgacaaatgtttcatatcatgctcatgtcaacattttcataaa
attgcataaaccttgtatatgtctaccacatcatgttaacaacatttatatggttaaaat
tgttgttggcattaaaattgcttaatgacatggggatttctatggaattattgtttgtta
tttccggcctcatttaaactttcctaaatagttagtttaattatacttcacctcttgcca
tgtttaacaacatttaatattgttgggtacataaacaagagagaactaaataattgaatg
tggtgtttcgtcaatatgcaactcgttgcatattgagctccacttaacttataatattgt
ttgttgcactttgccatgccatgcctcattaaaccgaacatgcatcatacttggttgtgc
atcatgccatgtttatgcttgtgtgtttaccatgttgtttgcttctttccggttgcgctt
tctccagtaatgttgcggattgtgaggatttgttcgacttccttcgtttgtcttcttcat
ggactcgttcttcttccttgtgggatctcaggcaagatgaccattaccttcgatatcact
```

3B annotation viewer: BAC

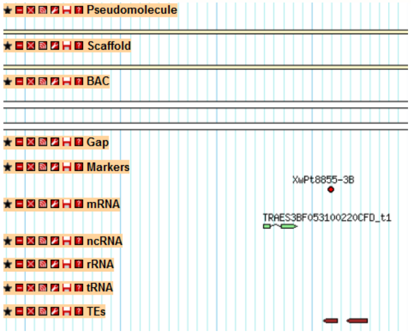


TaaCsp3BFhA_0366O17

Positions	265393621 .. 265554831
Length	161211
Reference	traes3bPseudomoleculeV1

Zoom to this feature
Detailed Report
Link to 3B Physical Map
Download Fasta

3B annotation viewer



Markers

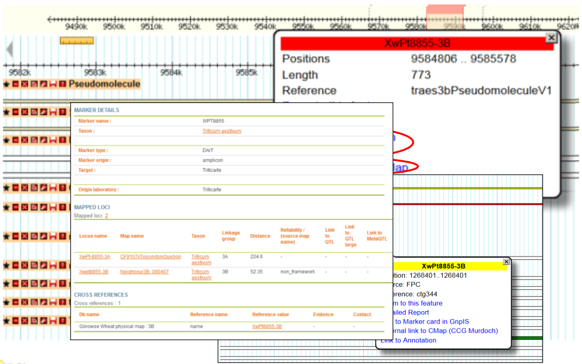
mRNA (genes)

Other RNA

TE

https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

3B annotation viewer: Marker



XwPt8855-3B

Positions 9584806 .. 9585578

Length 773

Reference traes3bPseudomoleculeV1

MARKER DETAILS

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

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	CF9107xToisondonQuebon	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	-	-

XwPt8855-3B

tion: 1268401..1268401

rce: FPC

erence: ctg344

m to this feature

ailed Report

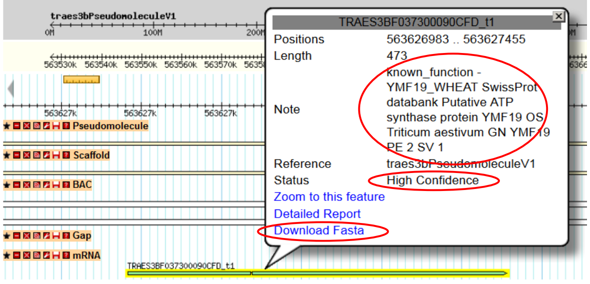
to Marker card in GnpIS

ernal link to CMap (CCG Murdoch)

Link to Annotation

https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

3B annotation viewer: Gene



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

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https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

3B annotation viewer: other RNA

mRNA

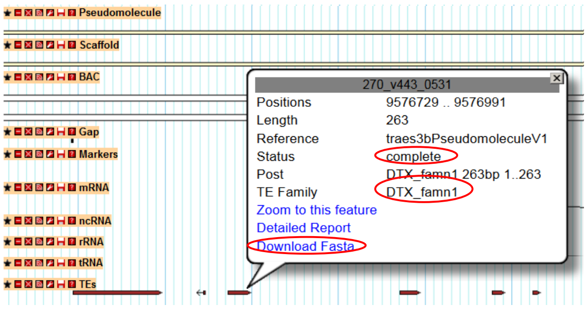
ncRNA

rRNA

tRNA

https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

3B annotation viewer: TE



270_v443_0531

Positions	9576729 .. 9576991
Length	263
Reference	traes3bPseudomoleculeV1
Status	complete
Post	DTX_famn1 263bp 1..263
TE Family	DTX_famn1

Zoom to this feature

Detailed Report

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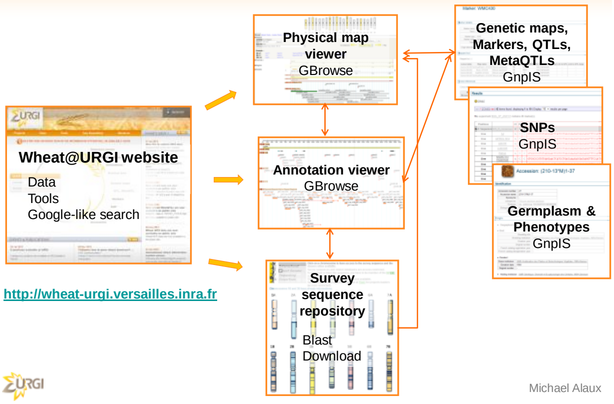
DNA Transposon Superfamily (DTX)

https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

Wheat dataflow overview



Wheat@URGI website

Data

Tools

Google-like search

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

Physical map viewer

GBrowse

Annotation viewer

GBrowse

Survey sequence repository

Blast

Download

Genetic maps, Markers, QTLs, MetaQTLs

GnpIS

SNPs

GnpIS

Germplasm & Phenotypes

GnpIS

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M. Caccamo

M. Spannagl
M. Martis
K. Mayer

Data producers

Questions

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

Wheat@URGI website
http://wheat-urgi.versailles.inra.fr

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