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IWGSC sequence repository: how to facilitate pseudomolecule assembly?

Michael M. Alaux, Frédéric Choulet, Loïc Couderc, Françoise F. Alfama-Depauw, Véronique Jamilloux, Thomas Letellier, Raphaël-Gauthier R.-G. Flores, Claire Guerche, Mikaël Loaec, Etienne Paux, et al.

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IWGSC Sequence Repository: How to facilitate pseudomolecule assembly ?

Michael Alaux



Wheat@URGI website



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Wheat@URGI

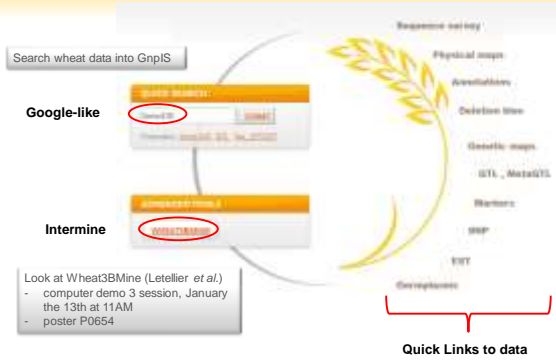


<http://wheat-urgi.versailles.inra.fr>



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Projects
Data
Tools
Seq Repository

Tools

- BLAST (Public)
- Access Status
- FASTQ
- BLAST
- Annotations
- Reference sequence
- Genes & annotations
- Physical maps
- Transcriptome
- RNA-Seq
- Publication
- Support to assembly and data submissions

ailles.inra.fr
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Sequence Repository

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Sequence Repository

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>

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Sequence Repository

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Seq-2012:

- Wheat genome maps available in **FASTA** (3x, 4x, 5x and 7x)
- **FASTQ** (3x, 4x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (5x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (7x) available on **URGI** or **NCBI** or **ENA**

Seq-2014:

- **FASTQ** (3x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (4x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (5x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (7x) available on **URGI** or **NCBI** or **ENA**

Seq-2015:

- **FASTQ** (3x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (4x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (5x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (7x) available on **URGI** or **NCBI** or **ENA**

Seq-2016:

- **FASTQ** (3x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (4x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (5x) available on **URGI** or **NCBI** or **ENA**
- **FASTQ** (7x) available on **URGI** or **NCBI** or **ENA**

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Seq-2012	Seq-2014			Seq-2015			Seq-2016		
	FASTQ	FASTQ	FASTQ	FASTQ	FASTQ	FASTQ	FASTQ	FASTQ	FASTQ
3x	3x	4x	5x	3x	4x	5x	3x	4x	5x
4x	4x	5x	7x	4x	5x	7x	4x	5x	7x
5x	5x	7x		5x	7x		5x	7x	
7x	7x			7x			7x		

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Sequence Repository

Navigation sidebar (checked items):

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- News
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- Physical maps
- Transcriptions
- IRW-Seq
- Publication
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Main content area:

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

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Sequence Repository

The screenshot shows the 'Sequence Repository' website. On the left is a vertical navigation menu with items: 'Create an account', 'Home', 'Access Status', 'FAQ', 'BLAST', 'Accessories', 'Reference sequences', 'Genes & annotations', 'Physical maps', 'Transcriptome', 'BIM-Seq', 'Publication', and 'Support to assembly and data submission'. The main content area features a 'New' section with a 'Create account' button and a 'Public BLAST' section with a 'Public BLAST' button. Below these are sections for 'Reference sequences' and 'Genes & annotations'.



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

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Sequence Repository: 3B example

The diagram illustrates a 3B example of sequence repository usage. It features a central screenshot of the 'Sequence Repository' interface with several red arrows pointing to other screenshots. These arrows indicate a workflow: from the main site to a specific sequence entry, then to a BLAST search interface, and finally to the results of a BLAST search. The screenshots show various details of the repository, including sequence lists and search parameters.



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BLAST

BLAST



- **Public BLAST**
<https://urgi.versailles.inra.fr/blast/>
- More than 250 000 BLAST searches the past 2 years !



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<https://urgi.versailles.inra.fr/blast/>

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BLAST

The screenshot shows the BLAST search interface. The 'Database' dropdown menu is highlighted with a red circle, showing a list of available databases including 'Arabidopsis thaliana', 'Glycine max', and 'Oryza sativa'. The interface also includes fields for 'Query sequence', 'Program', and 'Database', along with a 'Search' button.



<https://urgi.versailles.inra.fr/blast/>

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BLAST

The screenshot shows the 'Advanced search' options for the BLAST search interface. It includes fields for 'Expect threshold', 'Matrix', 'Masking', 'Filter', 'Mask', 'Alignment', and 'Output format'. There are also checkboxes for 'Low complexity regions', 'Mask for low-complexity regions', and 'Perform ungapped alignment'. A 'Search' button is visible at the bottom.



<https://urgi.versailles.inra.fr/blast/>

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Physical maps



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Physical maps



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

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Physical maps



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

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Physical maps



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

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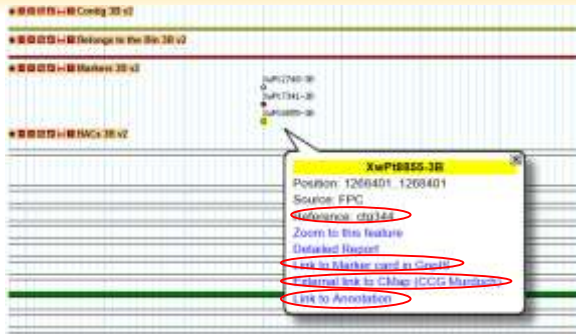
Physical maps



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

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Physical maps



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

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3B reference sequence annotation



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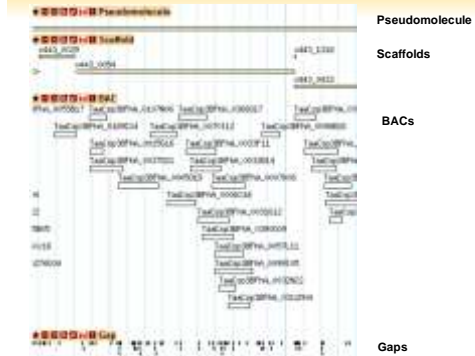
3B annotation



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

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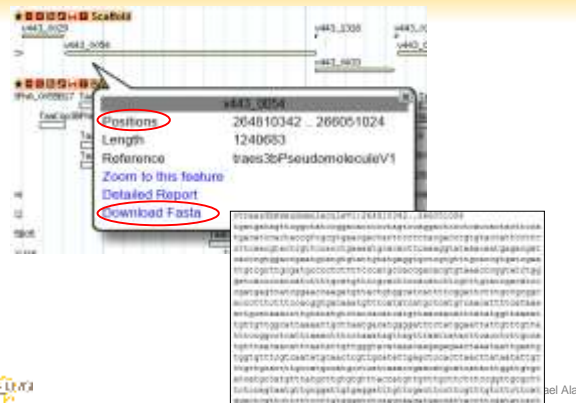
3B annotation



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

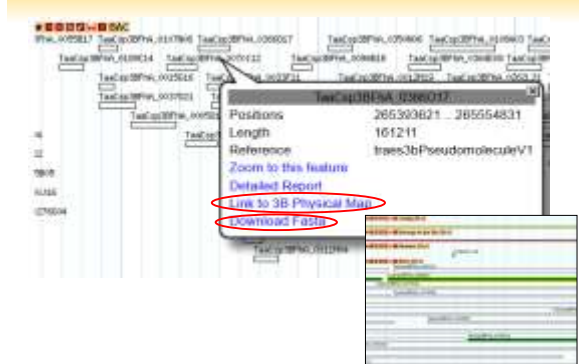
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3B annotation: Scaffold



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3B annotation: BAC



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

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3B annotation



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

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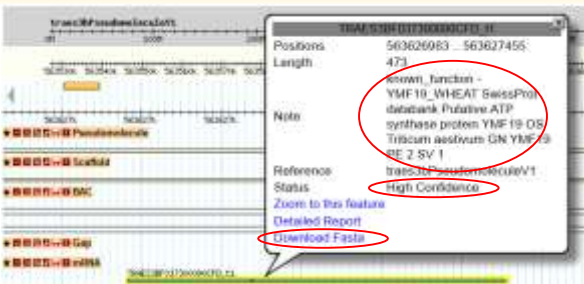
3B annotation: Marker



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

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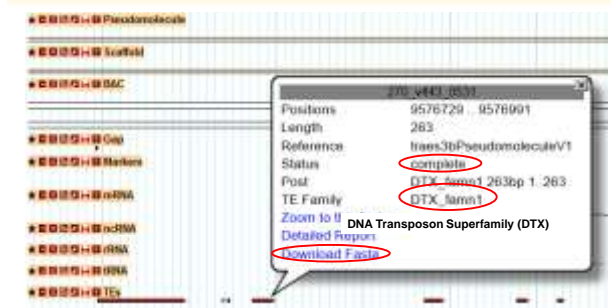
3B annotation: Gene



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

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3B annotation: TE



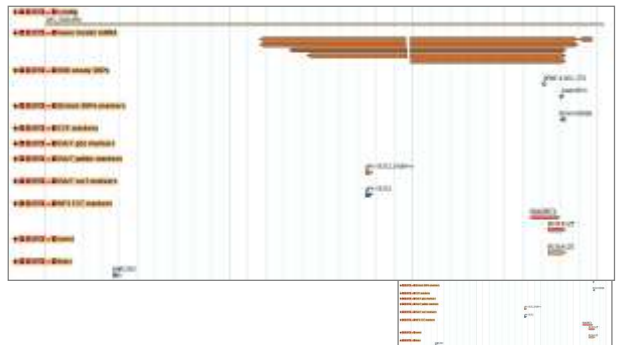
https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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Survey sequence browser



Survey sequence



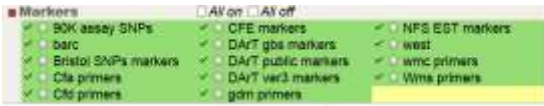
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https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_survey_sequence_annotation

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Survey sequence



Support to assembly and data submission



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

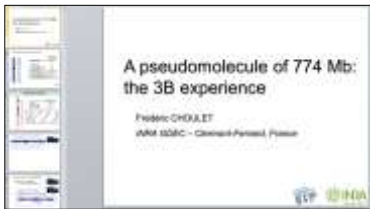
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BAC sequence assembly

4 BAC (sequence assembly)
 Frédéric Choulet, Stéphane Baudouin, Frédéric Choulet, Stéphane Baudouin, Frédéric Choulet, Stéphane Baudouin
<http://urgi.versailles.inra.fr/Seq-Repository>



- 3B MTP BAC sequencing
- 3B physical map
- Assembly and scaffolding
- Ordering scaffolds
- Perform the Annotation
- Bioinformatic tools

BAC sequence assembly

What are the needs?
 i.e. distribute the bioinformatics softwares



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

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Data submission



Wheat dataflow overview



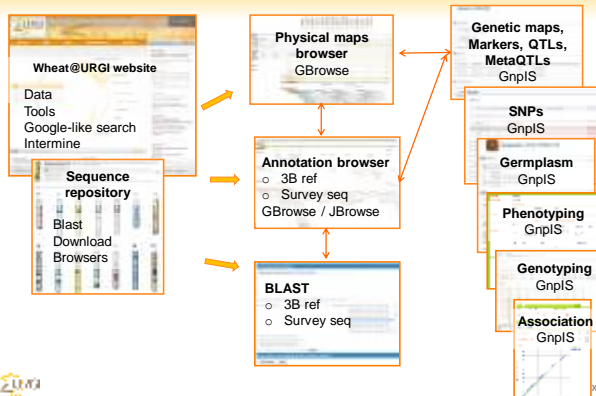
<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Wheat dataflow overview



Acknowledgments



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Letellier T.
Couderc L.
Alfama F.
Jamilloux V.
Flores R.
Guerche C.
Loaec M.
Steinbach D.
Quesneville H.



Choulet F.
Paux E.



Rogers J.
Eversole K.

All data providers



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Questions

Sequence Repository

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

BLAST (public)

<https://urgi.versailles.inra.fr/blast/>

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



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