

GrainGenes Tutorial: The Genome Browser

<https://wheat.pw.usda.gov>

The Genome Browser can be accessed from the GrainGenes Tools dropdown menu or from the Genome Browser icon in Quick Links

The screenshot displays the GrainGenes website interface. At the top, the logo and tagline "A Database for Triticeae and Avena" are visible. The main navigation bar includes "Home", "GrainGenes Tools", "Query Data Types", "Resources", "Collaborations", "About", and "Feedback". The "GrainGenes Tools" dropdown menu is open, listing options such as "Browse GrainGenes", "Quick Queries", "Advanced Queries", "GSP: Genome Specific Primers", "PIECE2", "BLAST", "CMap", and "Genome Browsers". The "Genome Browsers" option is highlighted with a red circle. In the "Quick Links" section, the "Genome Browsers" icon is also circled in red. The "Hot Topics" section features a "Wheat" link, which is also circled in red. The "GrainGenes Updates" section lists recent news items, and the "@GrainGenes Tweets" section shows a tweet about the Wild Emmer Wheat genome assembly.

GrainGenes
A Database for Triticeae and Avena

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Species Portals on GrainGenes

- Annual Wheat Newsletter
- Barley Boulevard
- Barley Genetics Newsletter
- Oat Global
- Oat Newsletter

Upcoming Events

- 8th International Triticeae Symposium, Germany Jun 12 2017 to Jun 16 2017
- Genomic Selection in Plant Breeding Jun 12 2017 to Jun 15 2017
- Triticale Biology, Breeding and Production Jul 2 2017 to Jul 5 2017
- International Cereal Rust and Powdery Mildew Conference, Kruger National Park, South Africa Sep 23 2018 to Sep 28 2018

Quick Links

- Browse GrainGenes
- Genome Browsers**
- CMap

Hot Topics

- Wheat**
- Barley
- Rye

Wild Emmer Wheat genome assembly WEWSeq v.1.0 (genotype Zavitan) is available to BLAST here at GrainGenes

In collaboration with the International Wild Emmer Wheat Genome Sequencing Consortium, GrainGenes is providing pre-publication BLAST service for the Wild Emmer Genome Assembly (Zavitan WEWSeq v.1.0).

For further information, please go to: <https://wheat.pw.usda.gov/GG3/wildemmer>
For our BLAST service, please go to: https://wheat.pw.usda.gov/GG3/wildemmer_blast

Posted on May 16, 2017

GrainGenes Updates

- May 2017: Wild Emmer Wheat (genotype Zavitan) assembly and annotations are available to BLAST at GrainGenes
- May 2017: Tetraploid Wheat Consensus Map
- March 2017: Barley 9K iSelect SNP Data
- March 2017: Hexaploid Oat Consensus Map
- February 2017: Seed Dormancy Data from Chao et al. 2015
- February 2017: A new Tutorials page
- February 2017: 2016 Uniform Regional Hard Red Spring Wheat Nursery
- January 2017: MAS Wheat Data Added
- January 2017: NSGC Durum Wheat Stem Rust genotype and phenotype data are available
- November 2016: A new twitter feed section and a Facebook page
- October 2016: IBGS 2016 abstracts are available on Barley Boulevard
- September 2016: Barley Genetics Newsletter v45 is available under "Species Portal"

more updates....

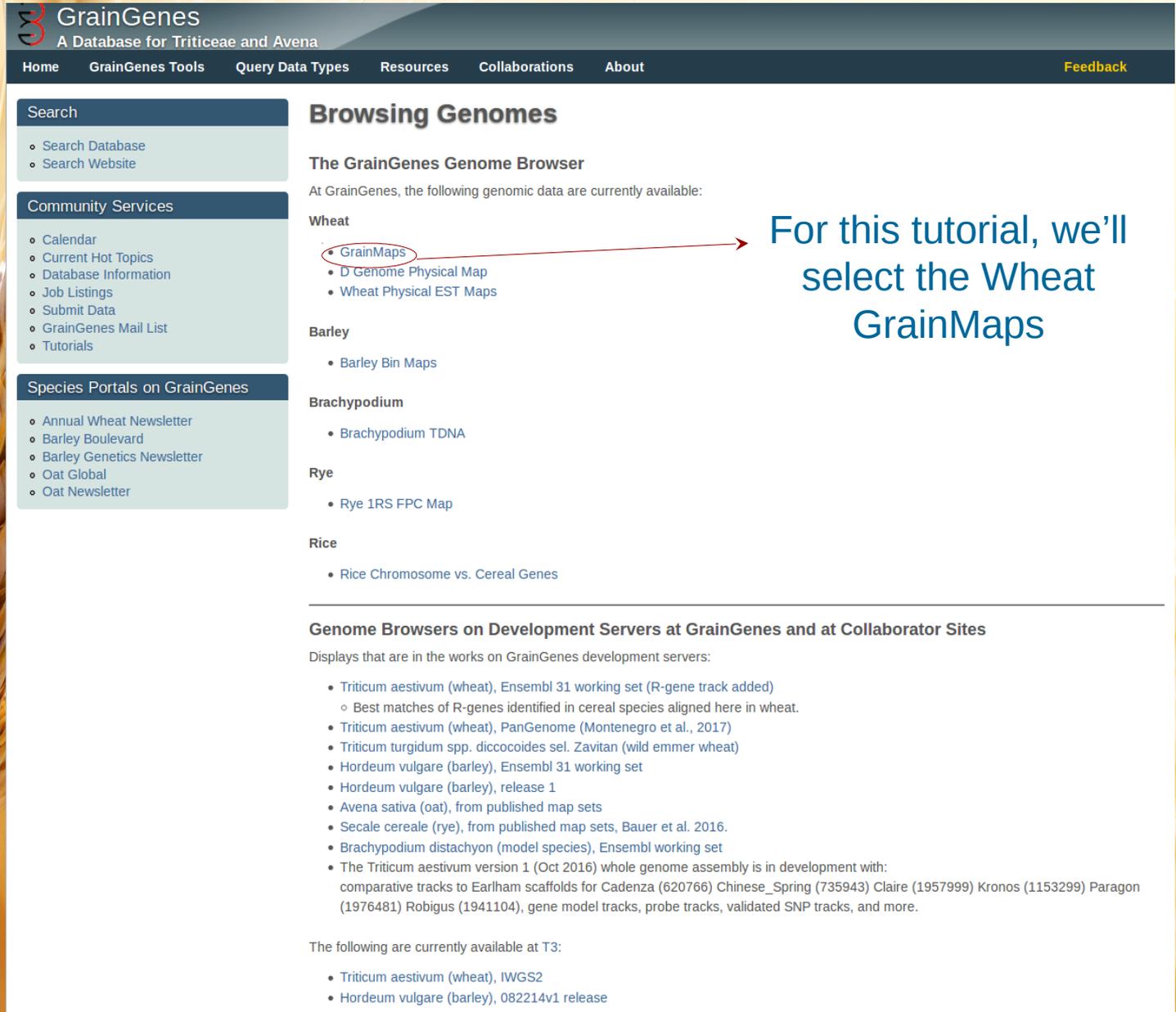
@GrainGenes Tweets

Tweets by @GrainGenes

GrainGenes
@GrainGenes

Tools at GrainGenes:
BLAST sequences against the

Choosing a Genome



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Community Services

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Species Portals on GrainGenes

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- Barley Boulevard
- Barley Genetics Newsletter
- Oat Global
- Oat Newsletter

Browsing Genomes

The GrainGenes Genome Browser

At GrainGenes, the following genomic data are currently available:

Wheat

- GrainMaps**
- D Genome Physical Map
- Wheat Physical EST Maps

Barley

- Barley Bin Maps

Brachypodium

- Brachypodium TDNA

Rye

- Rye 1RS FPC Map

Rice

- Rice Chromosome vs. Cereal Genes

Genome Browsers on Development Servers at GrainGenes and at Collaborator Sites

Displays that are in the works on GrainGenes development servers:

- Triticum aestivum (wheat), Ensembl 31 working set (R-gene track added)
 - Best matches of R-genes identified in cereal species aligned here in wheat.
- Triticum aestivum (wheat), PanGenome (Montenegro et al., 2017)
- Triticum turgidum spp. diccoides sel. Zavitan (wild emmer wheat)
- Hordeum vulgare (barley), Ensembl 31 working set
- Hordeum vulgare (barley), release 1
- Avena sativa (oat), from published map sets
- Secale cereale (rye), from published map sets, Bauer et al. 2016.
- Brachypodium distachyon (model species), Ensembl working set
- The Triticum aestivum version 1 (Oct 2016) whole genome assembly is in development with:
comparative tracks to Earlham scaffolds for Cadenza (620766) Chinese_Spring (735943) Claire (1957999) Kronos (1153299) Paragon (1976481) Robigus (1941104), gene model tracks, probe tracks, validated SNP tracks, and more.

The following are currently available at T3:

- Triticum aestivum (wheat), IWGS2
- Hordeum vulgare (barley), 082214v1 release

- A number of different browsers are available to view which are separated by species
- At the top of the page are completed Gbrowse Genome Browsers offered by GrainGenes
- Below that are Jbrowse instances of genomes that are still under development

The Gbrowse Viewer

- The top of the window lists Genome that we are looking at, as well as our location on the chromosome
- The yellow box offers some instructions for the Landmark or Region Search box and provides examples of valid searches
- Below that are some useful links, for bookmarking a search, uploading your own data, etc.

- There is a Help button if you need assistance, as well as a reset button, which will return the browser to the original configuration of your search if you make changes that you would like to undo

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Genome Browser: GrainMaps

Showing 167 cM from Ta-Synthetic/Opata-1A, positions 0 to 166

Instructions
Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.
Examples: Ta-Synthetic/Opata-1A, *cdo473*, Xcdo473, Xcdo473-1A.

[Bookmark this](#) [\[Upload your own data\]](#) [\[Hide banner\]](#) [\[Share these tracks\]](#) [\[Link to Image\]](#) [\[High-res Image\]](#) [\[Help\]](#) [\[Reset\]](#)

Search
Landmark or Region: Ta-Synthetic/Opata-1A Search

Data Source [Dropdown]

Scroll/Zoom: << < - Show 167 cM + >> >> Flip

Overview

Ta-Synthetic/Opata-1A
 0cM 10cM 20cM 30cM 40cM 50cM 60cM 70cM 80cM 90cM 100cM 110cM 120cM 130cM 140cM 150cM 160cM

Details

← 0cM 10cM 20cM 30cM 40cM 50cM 60cM 70cM 80cM 90cM 100cM 110cM 120cM 130cM 140cM 150cM 160cM →

Locus

Clear highlighting [Update Image](#)

Tracks

General All on All off

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Display Settings

<input checked="" type="checkbox"/> Show grid	Image Width <input type="radio"/> 450 <input type="radio"/> 640 <input checked="" type="radio"/> 800 <input type="radio"/> 1024	Highlight feature(s) (feature1 feature2...) <input type="text"/>
<input checked="" type="checkbox"/> Cache tracks	Track Name Table <input checked="" type="radio"/> Alphabetic <input type="radio"/> Varying	Highlight regions (region1:start..end region2:start..end) <input type="text"/>
<input checked="" type="checkbox"/> Draggable tracks	Key position <input checked="" type="radio"/> Between <input type="radio"/> Beneath <input type="radio"/> Left <input type="radio"/> Right	
<input checked="" type="checkbox"/> Show tooltips		Update Image

The Gbrowse Viewer - Tabs

Genome Browser: GrainMaps

Showing 167 cM from Ta-Synthetic/Opata-1A, positions 0 to 166

Instructions

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.

Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.

Examples: Ta-Synthetic/Opata-1A, *cdo473*, Xcdo473, Xcdo473-1A.

[\[Bookmark this\]](#) [\[Upload your own data\]](#) [\[Hide banner\]](#) [\[Share these tracks\]](#) [\[Link to Image\]](#) [\[High-res Image\]](#) [\[Help\]](#) [\[Reset\]](#)

Search

Landmark or Region:

Ta-Synthetic/Opata-1A

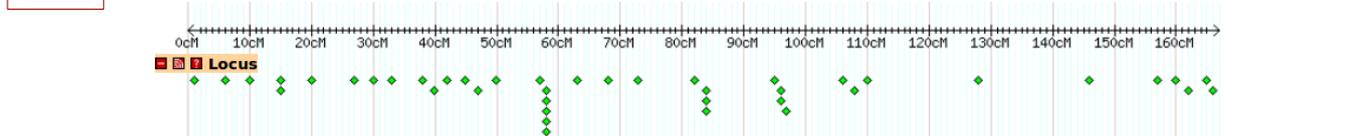
Data Source

Scroll/Zoom: Flip

Overview



Details



Clear highlighting

[Update Image](#)

Tracks

General All on All off

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Display Settings

Show grid 450 640 800 1024

Highlight feature(s) (feature1 feature2...)

Cache tracks Alphabetic Varying

Highlight regions (region1:start..end region2:start..end)

Draggable tracks Between Beneath Left Right

Show tooltips

[Update Image](#)

Add your own tracks

Upload your own data: [\[Help\]](#)

Upload a file No file selected.

Add remote annotations: [\[Help\]](#)

Enter Remote Annotation URL

- The browser itself consists of the number of tabs. The first tab, Overview, shows where the viewer is positioned along the genome
- The Details tab allows you to zoom in on a particular region to view it in higher resolution
- The Tracks and Display settings tabs allow you to customize the viewer by adjusting which tracks are visible and by adding your own tracks, etc.

The Gbrowse Viewer - Navigation

Showing 167 cM from Ta-Synthetic/Opata-1A, positions 0 to 166

Instructions

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.

Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.

Examples: Ta-Synthetic/Opata-1A, *cdo473*, Xcdo473, Xcdo473-1A.

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Search

Landmark or Region:

Ta-Synthetic/Opata-1A Search

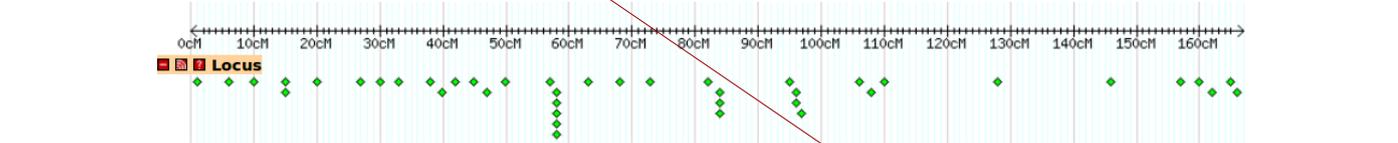
Data Source

Scroll/Zoom: <<< << < Show 167 cM > >> >>> Flip

Overview



Details

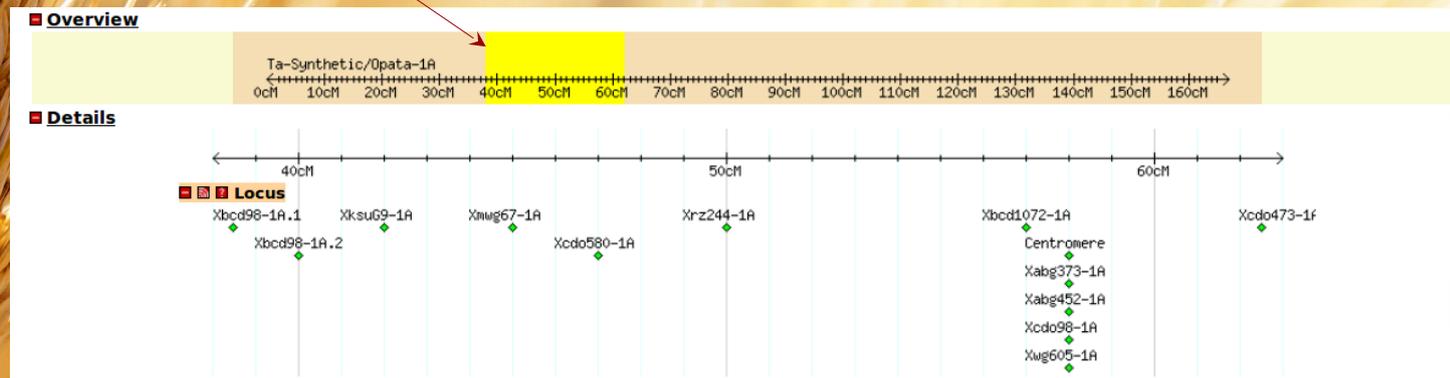


Clear highlighting

Update Image

- The arrows above the Overview bar will allow you to move left and right. The increments that the viewer shifts (either in cM or bp) can be adjusted in the dropdown between the arrows
- The plus or minus signs zoom in and out of the selected region, respectively

- A specific region can be selected from the Overview window by clicking, holding, and dragging your cursor to highlight the desired region.
- To the right is an example of a 24 cM region in finer detail
- To get back to the previous view, you can either zoom out or hit the Reset button



Track Features

GrainGenes
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Genome Browser: GrainMaps

Showing 167 cM from Ta-Synthetic/Opata-1A, positions 0 to 166

- Tracks are shown within the Details Window. In this browser, there are Locus tracks.
- You can collapse tracks by clicking the minus button, share your track, or get more information on the track here

Details

← 0cM 10cM 20cM 30cM 40cM 50cM 60cM 70cM 80cM 90cM 100cM 110cM 120cM 130cM 140cM 150cM 160cM →

Locu: Xbcd265-1A Ta-Synthetic/Opata-1A:96..97

Tracks

General All on All off

Introduction Locus

Display Settings

Show grid Image Width: 450 640 800 1024

Cache tracks Track Name Table: Alphabetic Varying

Draggable tracks Key position: Between Beneath Left Right

Show tooltips

Add your own tracks

Upload your own data: [Help]

Upload a file: No file selected.

Add remote annotations: [Help]

GrainGenes Locus Report: Xbcd265-1A

[Printable Version] [Submit comment/correction]

Locus Xbcd265-1A [Marker Report]

Type RFLP

Chromosome 1A

Chromosome Arm 1AL

Map Ta-Synthetic/Opata-1A 96
[Show all 6]

[Show Nearby Loci]

Map Data Wheat, Synthetic x Opata [GBrowser]
[Show all 6]

Probe BCD265

Homology T16307 e-value: 9e-06 hypothetical protein F40F4.5 - Caenorhabditis elegans
TBA_WHEAT e-value: 5e-21 TUBULIN ALPHA CHAIN

Image BCD265 SO autoradiogram

Possible Orthologs {bcd265} BCD265
[Show all 6]

- All the information in the tracks is clickable. Clicking on a locus feature will take you to a page in GrainGenes with more information on that particular entity, as shown with locus Xbcd265-1A