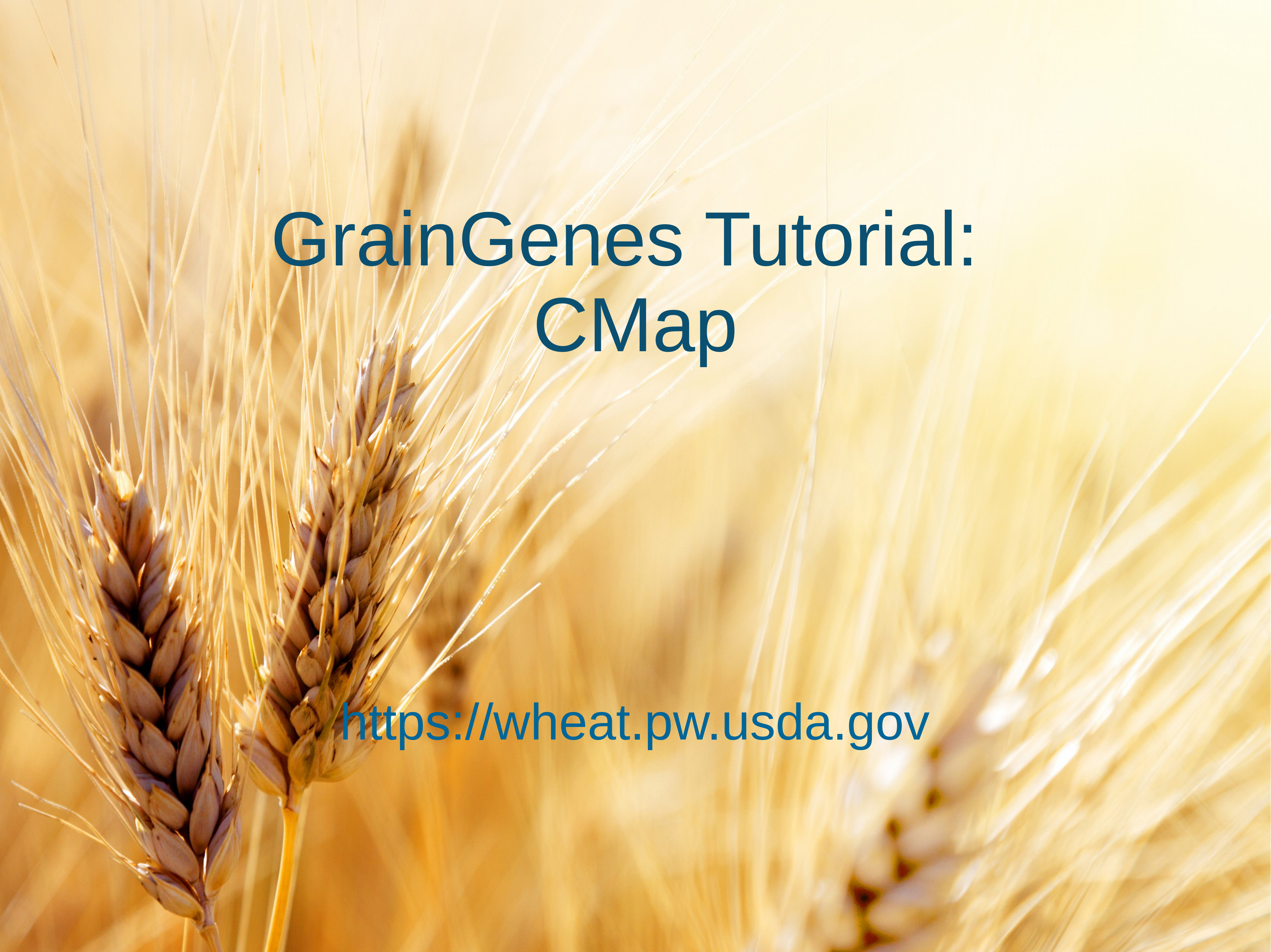
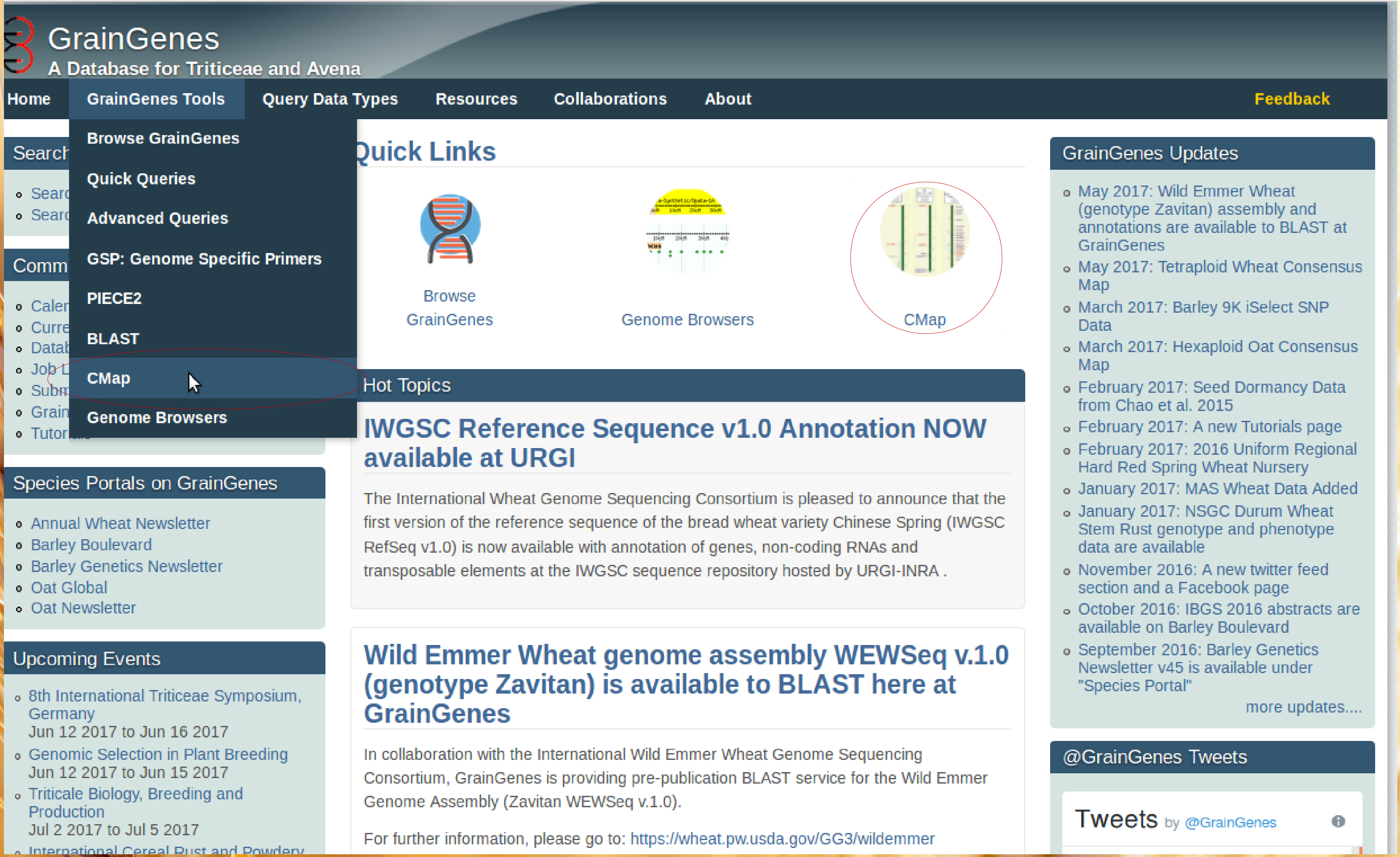


GrainGenes Tutorial: CMap

https://wheat.pw.usda.gov

CMap can be accessed from the GrainGenes Tools dropdown menu or from the Quick Links panel on the GrainGenes homepage



Hot Topics

IWGSC Reference Sequence v1.0 Annotation NOW available at URGI

The International Wheat Genome Sequencing Consortium is pleased to announce that the first version of the reference sequence of the bread wheat variety Chinese Spring (IWGSC RefSeq v1.0) is now available with annotation of genes, non-coding RNAs and transposable elements at the IWGSC sequence repository hosted by URGI-INRA .

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

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

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

CMap – Map Selection

GrainGenes CMap

CMap is the official map display for the new GrainGenes database, **GrainGenes SQL**. It also allows the maps to be compared side by side much more satisfactorily.

Currently **GrainGenes CMap** includes two Data Sources:

- GrainGenes
- Wheat Composite

Data Source GrainGenes contains the same set of maps that can be viewed with the ACEDB map display in GrainGenes Classic. The two databases are synchronized weekly.

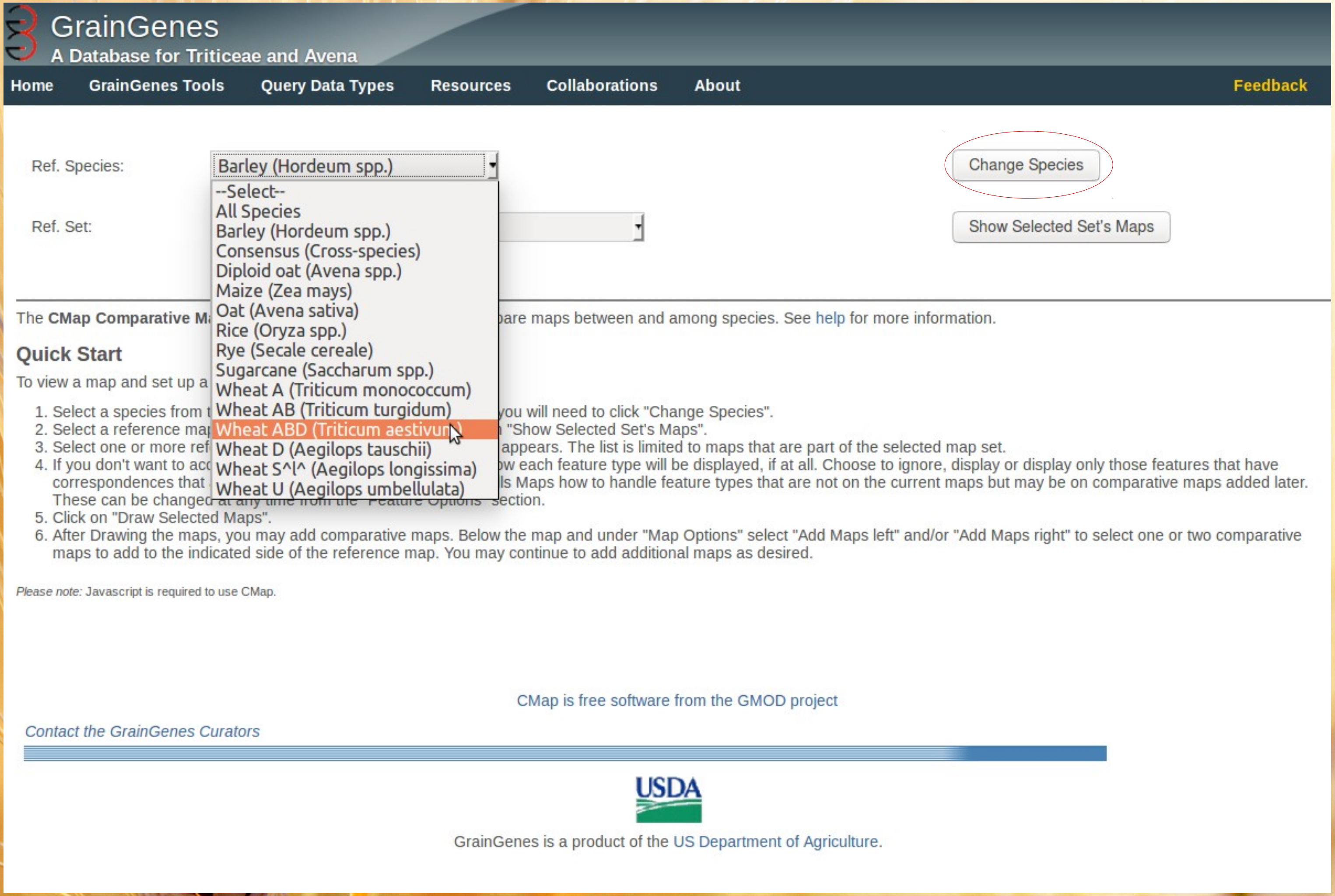
Data Source Wheat Composite contains the composite wheat map compiled by Rudi Appels, integrating twelve maps and 3700 loci. Nine of the component maps are also included so you can line them up next to the composite map and see the differences in marker order that exist. This is the same process Rudi is using to build and refine the composite map. Many more current maps are available at Rudi's Genica site.

We thank Ken Youens-Clark, Ben Faga, Gramene and GMOD for the fine comparative map display software CMap and for its ongoing improvements.

CMap is free software from the GMOD project.

From the CMap start page, you can choose between two Data Sources: GrainGenes maps and the Wheat Composite Map. For this tutorial, we will choose the GrainGenes maps.

CMap –
Reference Map Selection



The **CMap Comparative Ma** pare maps between and among species. See help for more information.

Quick Start

To view a map and set up a

1. Select a species from t you will need to click "Change Species".
2. Select a reference ma "Show Selected Set's Maps".
3. Select one or more ref appears. The list is limited to maps that are part of the selected map set.
4. If you don't want to acc ow each feature type will be displayed, if at all. Choose to ignore, display or display only those features that have correspondences that ls Maps how to handle feature types that are not on the current maps but may be on comparative maps added later. These can be changed at any time from the "Feature Options" section.
5. Click on "Draw Selected Maps".
6. After Drawing the maps, you may add comparative maps. Below the map and under "Map Options" select "Add Maps left" and/or "Add Maps right" to select one or two comparative maps to add to the indicated side of the reference map. You may continue to add additional maps as desired.

Please note: Javascript is required to use CMap.

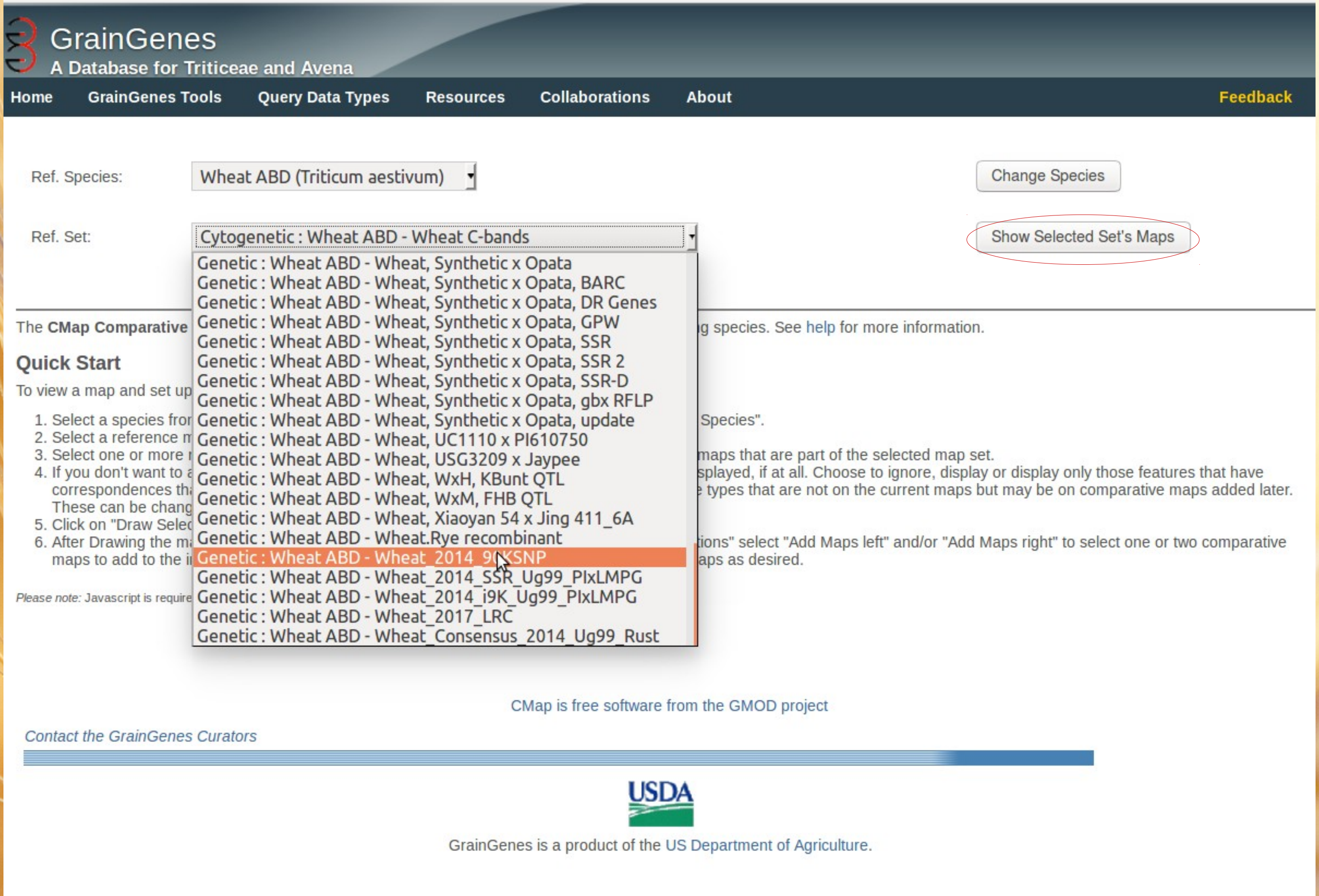
CMap is free software from the GMOD project

Contact the GrainGenes Curators

GrainGenes is a product of the US Department of Agriculture.

To select a reference map, choose a species from the dropdown.
In this tutorial, we will select hexaploid wheat (Triticum aestivum)
Once selected, click the Change Species button.

CMap –
Reference Map Selection



Ref. Species: Wheat ABD (Triticum aestivum)

Ref. Set: Cytogenetic : Wheat ABD - Wheat C-bands

Genetic : Wheat ABD - Wheat, Synthetic x Opata
Genetic : Wheat ABD - Wheat, Synthetic x Opata, BARC
Genetic : Wheat ABD - Wheat, Synthetic x Opata, DR Genes
Genetic : Wheat ABD - Wheat, Synthetic x Opata, GPW
Genetic : Wheat ABD - Wheat, Synthetic x Opata, SSR
Genetic : Wheat ABD - Wheat, Synthetic x Opata, SSR 2
Genetic : Wheat ABD - Wheat, Synthetic x Opata, SSR-D
Genetic : Wheat ABD - Wheat, Synthetic x Opata, gbx RFLP
Genetic : Wheat ABD - Wheat, Synthetic x Opata, update
Genetic : Wheat ABD - Wheat, UC1110 x PI610750
Genetic : Wheat ABD - Wheat, USG3209 x Jaypee
Genetic : Wheat ABD - Wheat, WxH, KBunt QTL
Genetic : Wheat ABD - Wheat, WxM, FHB QTL
Genetic : Wheat ABD - Wheat, Xiaoyan 54 x Jing 411_6A
Genetic : Wheat ABD - Wheat.Rye recombinant
Genetic : Wheat ABD - Wheat_2014_90KSNP
Genetic : Wheat ABD - Wheat_2014_SSR_Ug99_PlxLMPG
Genetic : Wheat ABD - Wheat_2014_i9K_Ug99_PlxLMPG
Genetic : Wheat ABD - Wheat_2017_LRC
Genetic : Wheat ABD - Wheat_Consensus_2014_Ug99_Rust

The **CMap Comparative**

g species. See help for more information.

Quick Start

To view a map and set up

1. Select a species fror
2. Select a reference m
3. Select one or more r
4. If you don't want to a
   correspondences tha
   These can be chang
5. Click on "Draw Selec
6. After Drawing the ma
   maps to add to the ir

Species".

maps that are part of the selected map set.
splayed, if at all. Choose to ignore, display or display only those features that have
e types that are not on the current maps but may be on comparative maps added later.

tions" select "Add Maps left" and/or "Add Maps right" to select one or two comparative
aps as desired.

Please note: Javascript is require

CMap is free software from the GMOD project

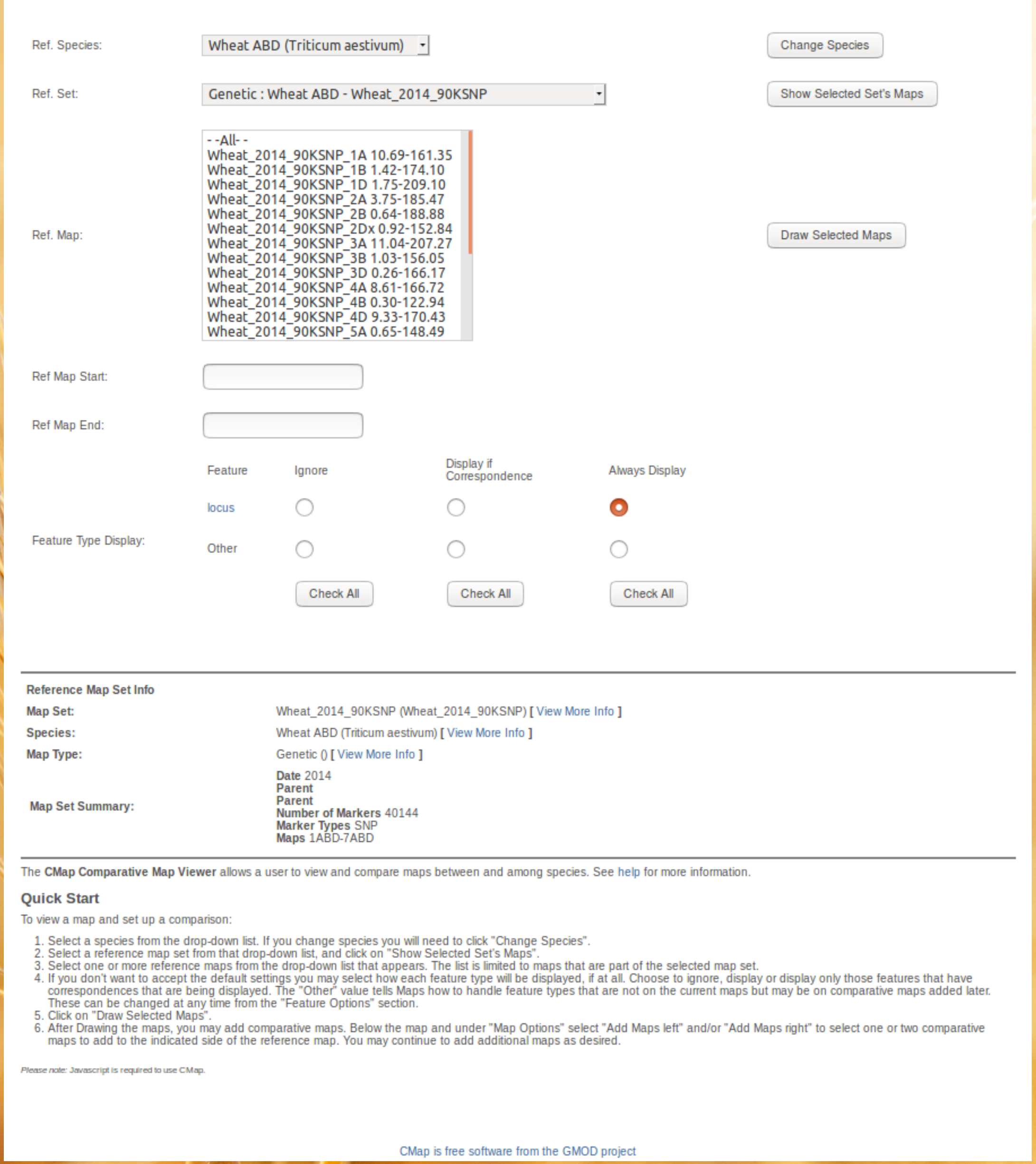
Contact the GrainGenes Curators

USDA

GrainGenes is a product of the US Department of Agriculture.

Then we can select a reference map from the Reference set dropdown.
In this tutorial, we will select the Wheat 90K SNP Array map () set as our reference.
Once selected, click the Show Selected Set's Maps button.

CMap –
Reference Map Selection



Ref. Species: Wheat ABD (Triticum aestivum)

Ref. Set: Genetic : Wheat ABD - Wheat_2014_90KSNP

Ref. Map:
--All--
Wheat_2014_90KSNP_1A 10.69-161.35
Wheat_2014_90KSNP_1B 1.42-174.10
Wheat_2014_90KSNP_1D 1.75-209.10
Wheat_2014_90KSNP_2A 3.75-185.47
Wheat_2014_90KSNP_2B 0.64-188.88
Wheat_2014_90KSNP_2Dx 0.92-152.84
Wheat_2014_90KSNP_3A 11.04-207.27
Wheat_2014_90KSNP_3B 1.03-156.05
Wheat_2014_90KSNP_3D 0.26-166.17
Wheat_2014_90KSNP_4A 8.61-166.72
Wheat_2014_90KSNP_4B 0.30-122.94
Wheat_2014_90KSNP_4D 9.33-170.43
Wheat_2014_90KSNP_5A 0.65-148.49

Ref Map Start:

Ref Map End:

Feature Type Display:

Feature	Ignore	Display if Correspondence	Always Display
locus	○	○	●
Other	○	○	○

Reference Map Set Info

Map Set: Wheat_2014_90KSNP (Wheat_2014_90KSNP) [View More Info]

Species: Wheat ABD (Triticum aestivum) [View More Info]

Map Type: Genetic () [View More Info]

Map Set Summary:
Date 2014
Parent
Parent
Number of Markers 40144
Marker Types SNP
Maps 1ABD-7ABD

The **CMap Comparative Map Viewer** allows a user to view and compare maps between and among species. See help for more information.

Quick Start

To view a map and set up a comparison:

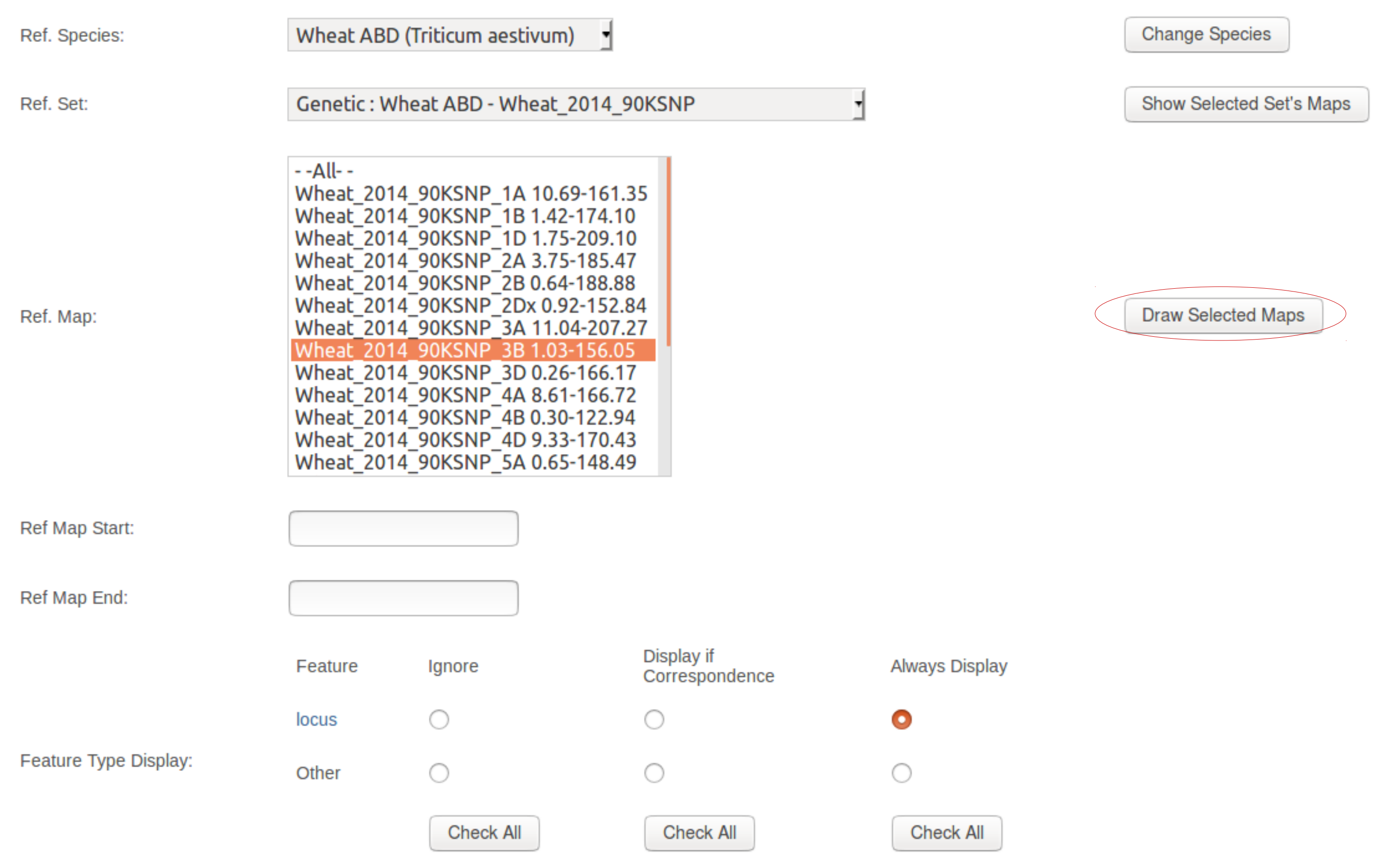
1. Select a species from the drop-down list. If you change species you will need to click "Change Species".
2. Select a reference map set from that drop-down list, and click on "Show Selected Set's Maps".
3. Select one or more reference maps from the drop-down list that appears. The list is limited to maps that are part of the selected map set.
4. If you don't want to accept the default settings you may select how each feature type will be displayed, if at all. Choose to ignore, display or display only those features that have correspondences that are being displayed. The "Other" value tells Maps how to handle feature types that are not on the current maps but may be on comparative maps added later. These can be changed at any time from the "Feature Options" section.
5. Click on "Draw Selected Maps".
6. After Drawing the maps, you may add comparative maps. Below the map and under "Map Options" select "Add Maps left" and/or "Add Maps right" to select one or two comparative maps to add to the indicated side of the reference map. You may continue to add additional maps as desired.

Please note: Javascript is required to use CMap.

CMap is free software from the GMOD project

- Next, we can select which maps from the reference map set we wish to see.
- From the Reference Map panels, we can select –All-- to view all the maps in the map set.
- We can select multiple consecutive maps by clicking the first map, holding shift and then releasing on the last map.
- Non-consecutive maps can be selected with Ctrl-click.
- Selected maps will be highlighted in orange.

CMap –
Reference Map Selection



Ref. Species: Wheat ABD (Triticum aestivum)

Ref. Set: Genetic : Wheat ABD - Wheat_2014_90KSNP

Ref. Map:
- -All- -
Wheat_2014_90KSNP_1A 10.69-161.35
Wheat_2014_90KSNP_1B 1.42-174.10
Wheat_2014_90KSNP_1D 1.75-209.10
Wheat_2014_90KSNP_2A 3.75-185.47
Wheat_2014_90KSNP_2B 0.64-188.88
Wheat_2014_90KSNP_2Dx 0.92-152.84
Wheat_2014_90KSNP_3A 11.04-207.27
Wheat_2014_90KSNP_3B 1.03-156.05
Wheat_2014_90KSNP_3D 0.26-166.17
Wheat_2014_90KSNP_4A 8.61-166.72
Wheat_2014_90KSNP_4B 0.30-122.94
Wheat_2014_90KSNP_4D 9.33-170.43
Wheat_2014_90KSNP_5A 0.65-148.49

Ref Map Start:

Ref Map End:

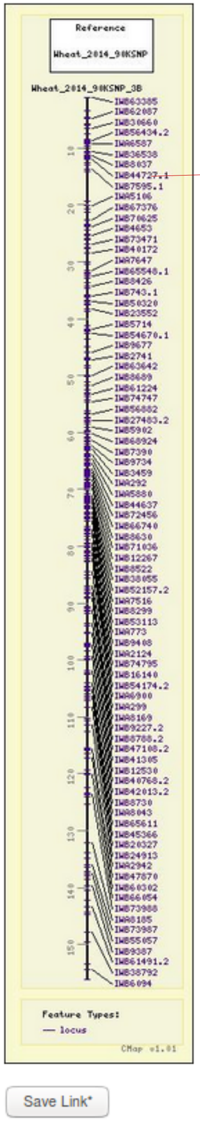
Feature Type Display:

Feature	Ignore	Display if Correspondence	Always Display
locus	○	○	●
Other	○	○	○

- If you wish to compare maps between map sets, it is usually best to choose one map at a time
- Below the Reference Map window, we can adjust which regions of the selected map we wish to view, and which features (loci, qtl, etc.) we want shown
- For this tutorial, we will look at the map for chromosome 3B
- To view the selected maps, click Draw Selected Maps

CMap –
The Map Viewer

- A chromosomal view will be shown of the selected map
- By clicking on a locus feature, we can learn more about the feature location and correspondences
- Note that for dense maps, not all markers will be shown automatically



*Bookmarks for this page will fail after this session expires. Use the "Save Link" button to create a permanent link

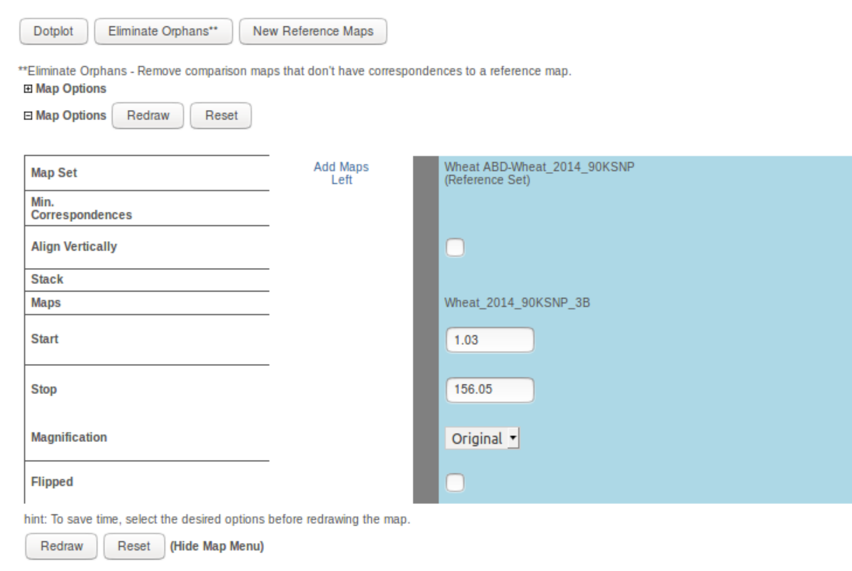
Feature "IWB7204"

Feature Name:	IWB7204	
Aliases:	BS00022669_51	[View Alias Details]
Accession ID:	140768	
Feature Type:	locus	[View Feature Type Info]
Map:	Species: Wheat ABD Map Set: Wheat_2014_90KSNP Map Name: Wheat_2014_90KSNP_3B	[View Map Details]
Start:	13.78	
Stop:	13.78	

Correspondences

Feature	Accession	Map	Map Type	Aliases	Evidence Type	Actions
IWB7204	321529	Wheat AB-Wheat_AB, Simeto x Levante-Wheat_AB, Simeto x Levante 3B_1	Genetic	None	Automated name-based	[Correspondence Details] [View On Map

CMap –
Comparing Maps



**Eliminate Orphans - Remove comparison maps that don't have correspondences to a reference map.

Start: 1.03

Stop: 156.05

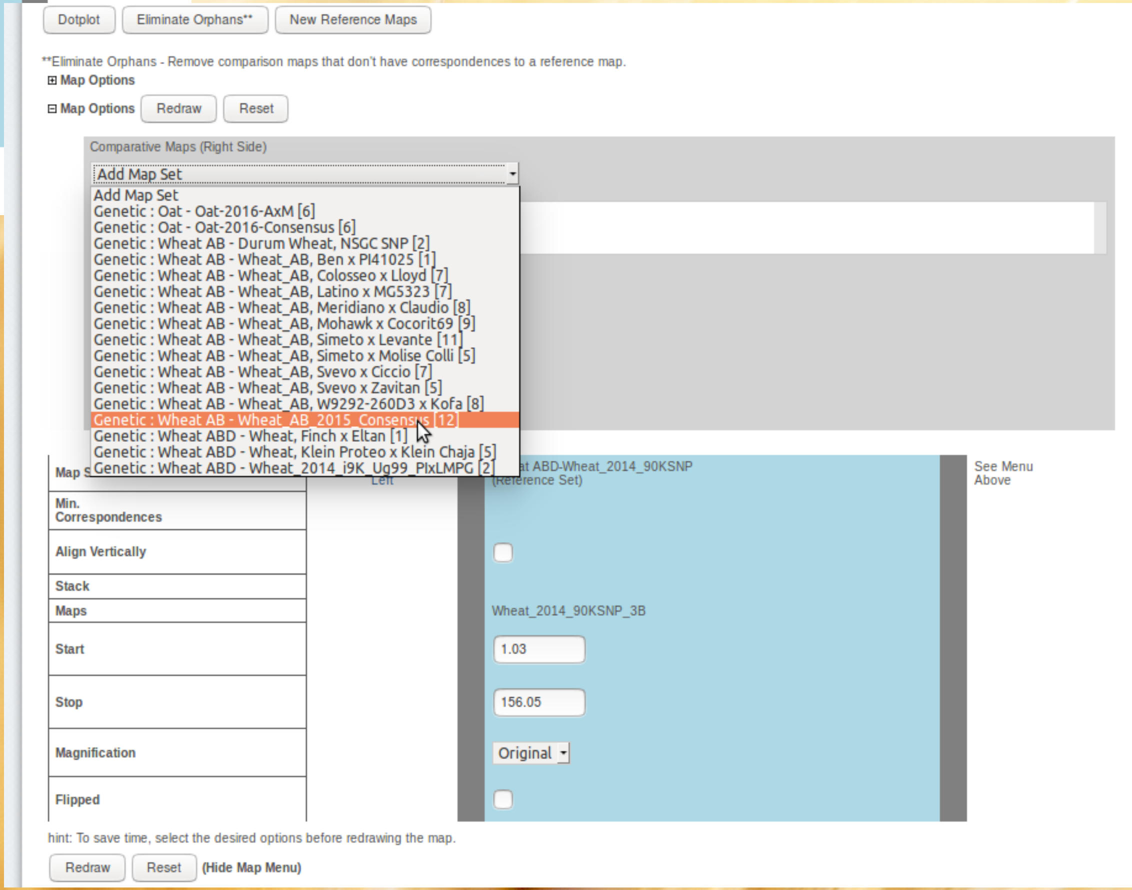
Magnification: Original

Flipped: ☐

hint: To save time, select the desired options before redrawing the map.

Below the map view is a Map Options Panel which shows the current map and buttons on either side: Draw Maps Left and Draw Maps Right

- By clicking Draw Maps Right, a Panel Appears where you are prompted to select from a list of maps which have correspondences to the reference map.
- The number in brackets next to the map name shows how many maps have correspondences within the map set



**Eliminate Orphans - Remove comparison maps that don't have correspondences to a reference map.

Start: 1.03

Stop: 156.05

Magnification: Original

Flipped: ☐

hint: To save time, select the desired options before redrawing the map.

CMap –
Comparing Maps

Comparative Maps (Right Side)

Genetic : Wheat AB - Wheat_AB_2015_Consensus [12]

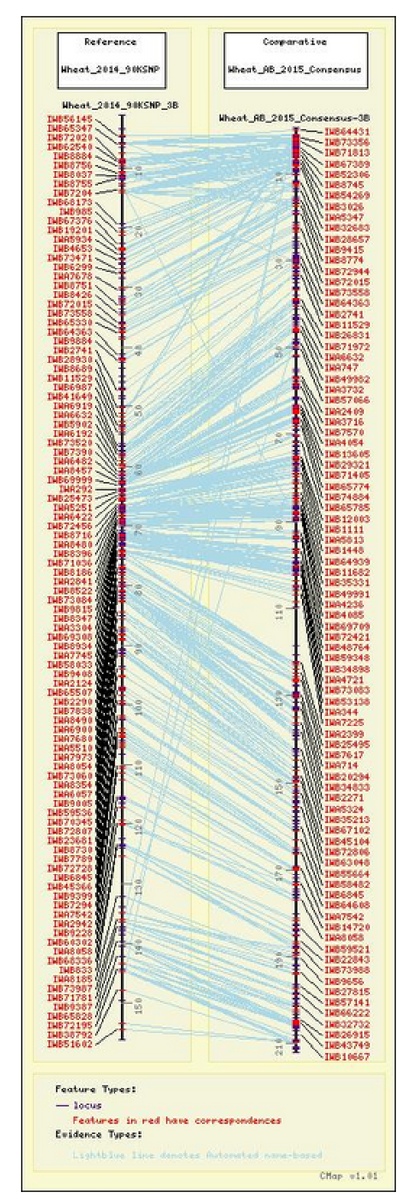
Wheat_AB_2015_Consensus-2B [4,4]
Wheat_AB_2015_Consensus-3A [48,48]
Wheat_AB_2015_Consensus-3B [2900,2900]

Min. Correspondences: 0

Stack 1 ☐

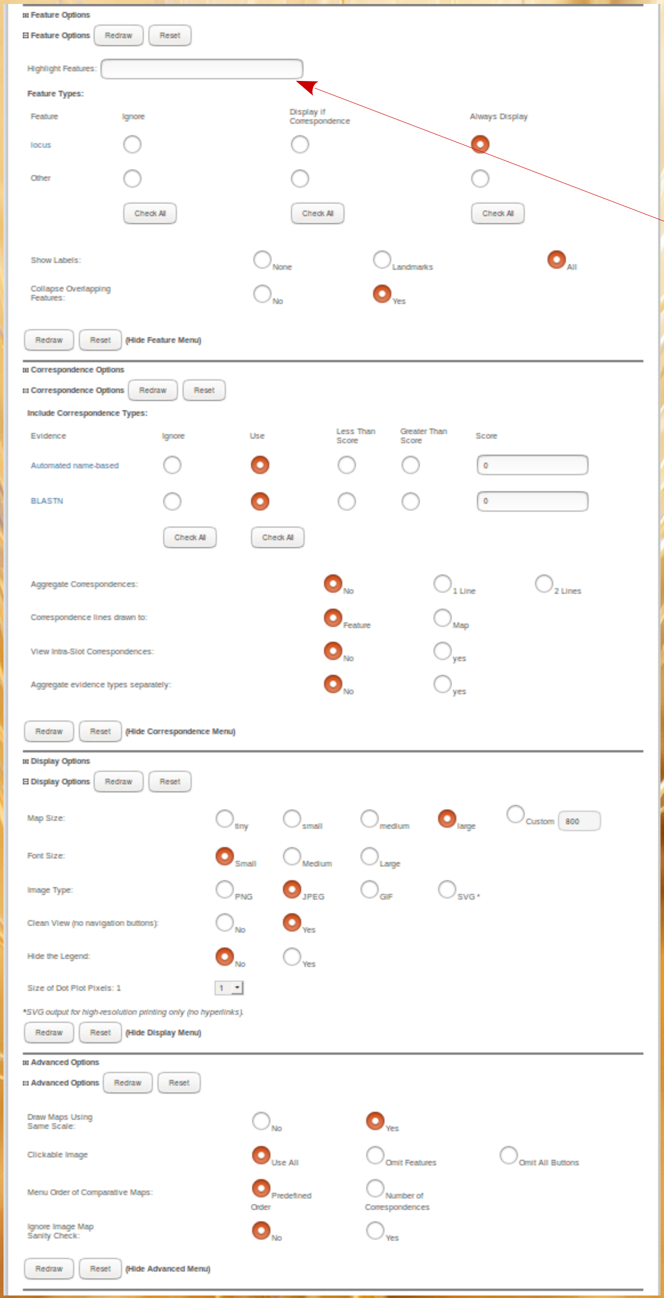
Format:
Name [Total correspondences to slot,
Max correspondences to single map]

- After selecting a map set from the dropdown, we are prompted to choose a map within the mapset to draw. The number in brackets next to the map name shows how many features are shared between the reference map and this map.
- After selecting a map, click Add Maps to draw
- The map will appear next to the Reference map, with blue lines drawn between shared features. Features that have correspondences will be red in red



Feature Types:
— locus
Features in red have correspondences
Evidence Types:
Lightblue line denotes Automated name-based

CMap –
Highlight Features



⊞ Feature Options

⊟ Feature Options Redraw Reset

Highlight Features:

Feature Types:

Feature	Ignore	Display if Correspondence	Always Display
locus	○	○	●
Other	○	○	○
	Check All	Check All	Check All

Show Labels: ○ None ○ Landmarks ● All

Collapse Overlapping Features: ○ No ● Yes

Redraw Reset **(Hide Feature Menu)**

⊞ Correspondence Options

⊞ Correspondence Options Redraw Reset

Include Correspondence Types:

Evidence	Ignore	Use	Less Than Score	Greater Than Score	Score
Automated name-based	○	●	○	○	0
BLASTN	○	●	○	○	0
	Check All	Check All			

Aggregate Correspondences: ● No ○ 1 Line ○ 2 Lines

Correspondence lines drawn to: ● Feature ○ Map

View Intra-Slot Correspondences: ● No ○ yes

Aggregate evidence types separately: ● No ○ yes

Redraw Reset **(Hide Correspondence Menu)**

⊞ Display Options

⊟ Display Options Redraw Reset

Map Size: ○ tiny ○ small ○ medium ● large ○ Custom 800

Font Size: ● Small ○ Medium ○ Large

Image Type: ○ PNG ● JPEG ○ GIF ○ SVG *

Clean View (no navigation buttons): ○ No ● Yes

Hide the Legend: ● No ○ Yes

Size of Dot Plot Pixels: 1 1

**SVG output for high-resolution printing only (no hyperlinks).*

Redraw Reset **(Hide Display Menu)**

⊞ Advanced Options

⊞ Advanced Options Redraw Reset

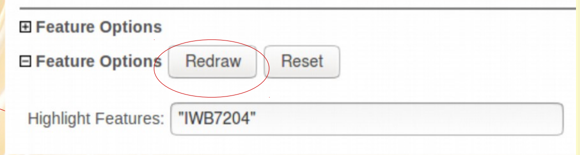
Draw Maps Using Same Scale: ○ No ● Yes

Clickable Image ● Use All ○ Omit Features ○ Omit All Buttons

Menu Order of Comparative Maps: ● Predefined Order ○ Number of Correspondences

Ignore Image Map Sanity Check: ● No ○ Yes

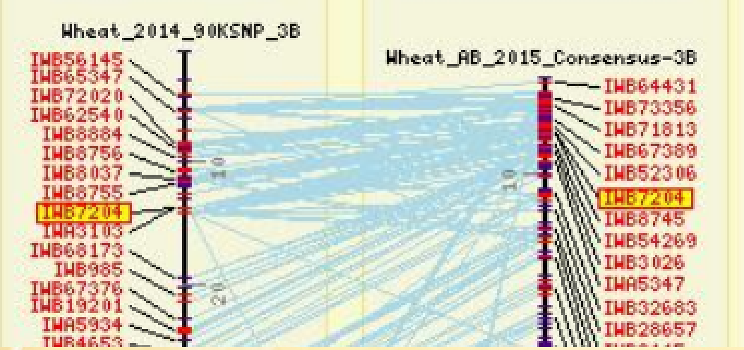
Redraw Reset **(Hide Advanced Menu)**



⊞ Feature Options

⊟ Feature Options Redraw Reset

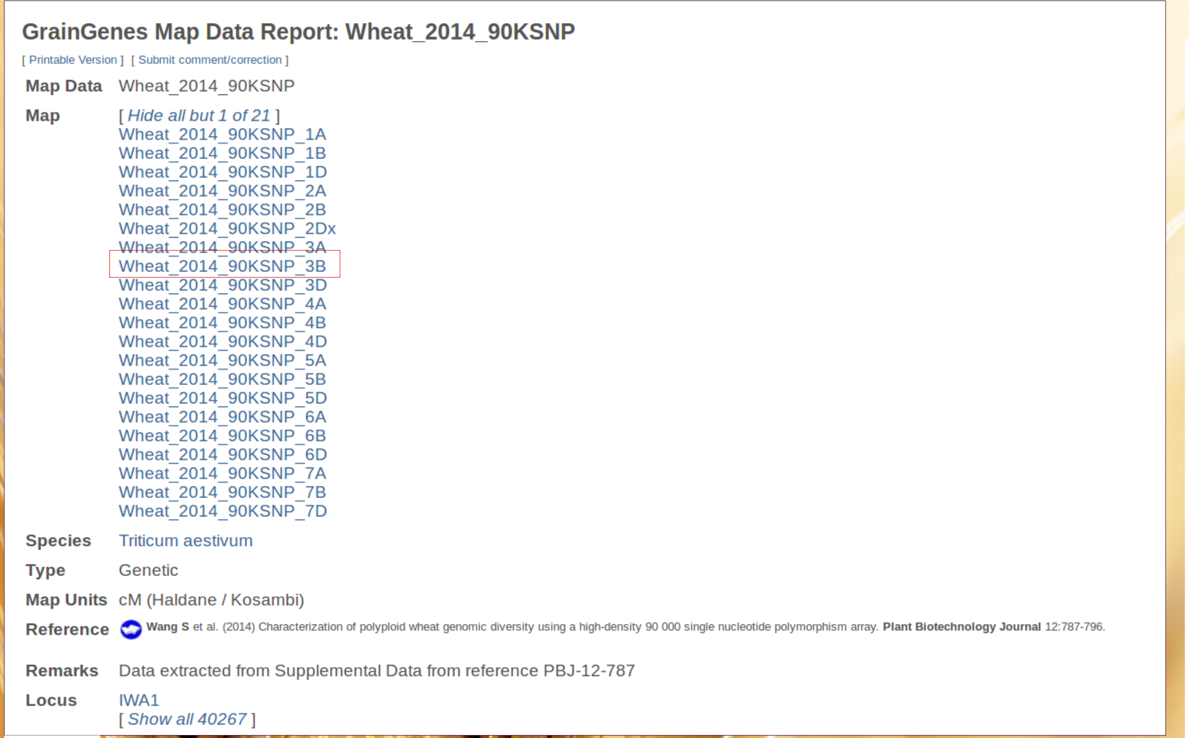
Highlight Features: "IWB7204"



- Scrolling down on the map view page, there are many options to edit the size of the map display, which features and correspondences are shown, and other advanced options
- One notable option is the Highlight Features option, which allows you to identify individual loci or other features in drawn maps
- By typing in a feature name, or list of names separated by commas, and clicking the Redraw button, the map will be redrawn with that feature or list of features highlighted in yellow

CMap –
Navigation from Report Pages

1)

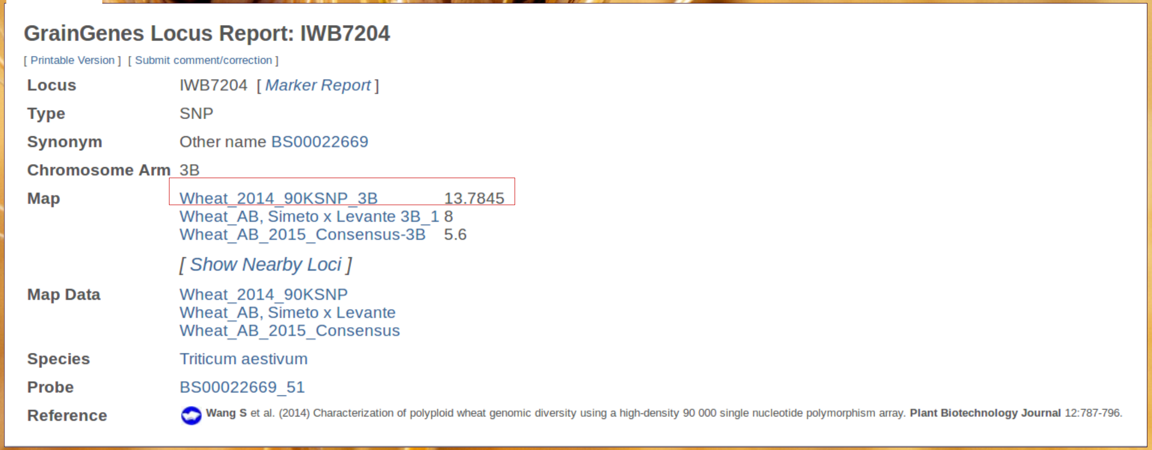


GrainGenes Map Data Report: Wheat_2014_90KSNP

[Printable Version] [Submit comment/correction]

Map Data	Wheat_2014_90KSNP
Map	[*Hide all but 1 of 21*] Wheat_2014_90KSNP_1A Wheat_2014_90KSNP_1B Wheat_2014_90KSNP_1D Wheat_2014_90KSNP_2A Wheat_2014_90KSNP_2B Wheat_2014_90KSNP_2Dx Wheat_2014_90KSNP_3A Wheat_2014_90KSNP_3B Wheat_2014_90KSNP_3D Wheat_2014_90KSNP_4A Wheat_2014_90KSNP_4B Wheat_2014_90KSNP_4D Wheat_2014_90KSNP_5A Wheat_2014_90KSNP_5B Wheat_2014_90KSNP_5D Wheat_2014_90KSNP_6A Wheat_2014_90KSNP_6B Wheat_2014_90KSNP_6D Wheat_2014_90KSNP_7A Wheat_2014_90KSNP_7B Wheat_2014_90KSNP_7D
Species	Triticum aestivum
Type	Genetic
Map Units	cM (Haldane / Kosambi)
Reference	**Wang S** et al. (2014) Characterization of polyploid wheat genomic diversity using a high-density 90 000 single nucleotide polymorphism array. **Plant Biotechnology Journal** 12:787-796.
Remarks	Data extracted from Supplemental Data from reference PBJ-12-787
Locus	IWA1 [*Show all 40267*]

2)



GrainGenes Locus Report: IWB7204

[Printable Version] [Submit comment/correction]

Locus	IWB7204 [*Marker Report*]	
Type	SNP	
Synonym	Other name BS00022669	
Chromosome Arm	3B	
Map	Wheat_2014_90KSNP_3B	13.7845
	Wheat_AB, Simeto x Levante 3B_1	8
	Wheat_AB_2015_Consensus-3B	5.6
	[*Show Nearby Loci*]	
Map Data	Wheat_2014_90KSNP Wheat_AB, Simeto x Levante Wheat_AB_2015_Consensus	
Species	Triticum aestivum	
Probe	BS00022669_51	
Reference	**Wang S** et al. (2014) Characterization of polyploid wheat genomic diversity using a high-density 90 000 single nucleotide polymorphism array. **Plant Biotechnology Journal** 12:787-796.	

The CMap viewer is interconnected with the GrainGenes database, and there are two ways to navigate to the CMap page from the database browser:

1) Map Data Report pages allow you to select individual maps. Clicking on them will open a new tab with the CMap view of this map

2) Locus Report pages list all of the maps that contain that specific locus as well as the position of that locus. By clicking, you can view the map in CMap with the locus highlighted in yellow