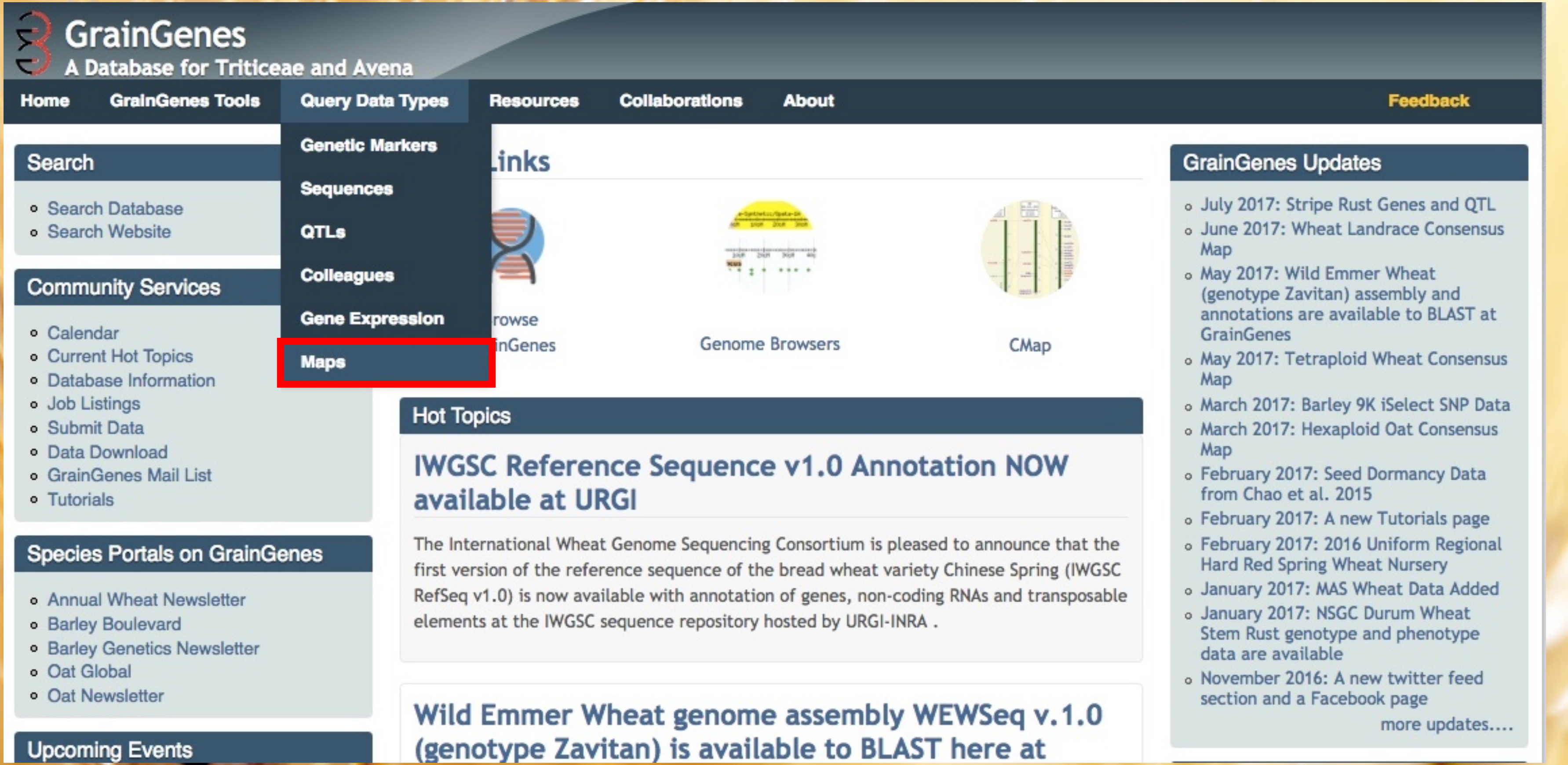
GrainGenes Tutorial:

Viewing GWAS QTLs in CMap

GrainGenes contains an increasing amount of data from peer-reviewed publications of genome-wide association studies (GWAS). Many of the QTLs found in these studies for various important traits can be viewing in the CMap Viewer with relative map positions on consensus maps. To view a summary of some of the maps held in GrainGenes, go to the Maps section under Query Data Types.



IWGSC Reference Sequence v1.0 Annotation NOW available at URGI

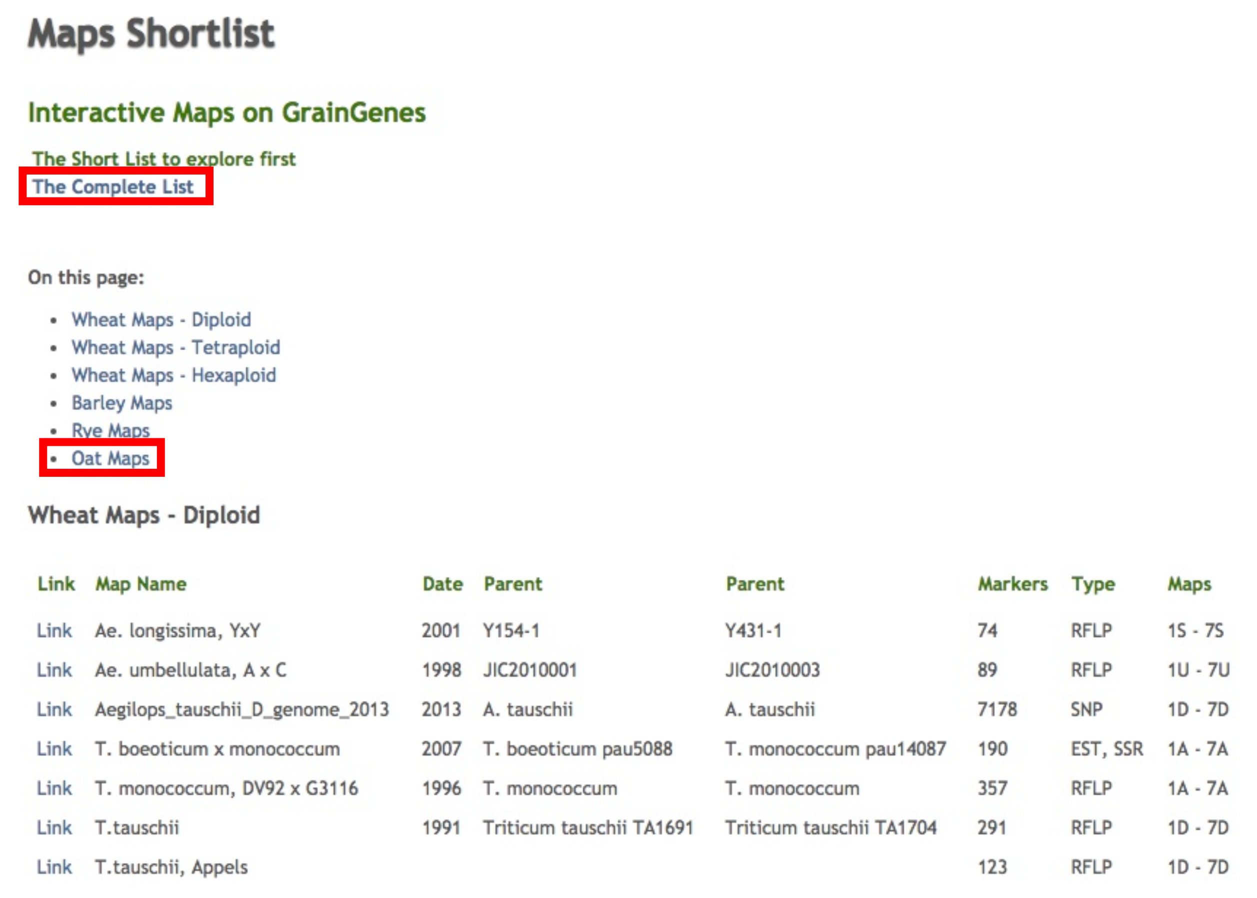
The International Wheat Genome Sequencing Consortium is pleased to announce that the first version of the reference sequence of the bread wheat variety Chinese Spring (IWGSC RefSeq v1.0) is now available with annotation of genes, non-coding RNAs and transposable elements at the IWGSC sequence repository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

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

GrainGenes Updates

- July 2017: Stripe Rust Genes and QTL
- June 2017: Wheat Landrace Consensus Map
- 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

more updates....



Maps Shortlist

Interactive Maps on GrainGenes

The Short List to explore first
The Complete List

On this page:

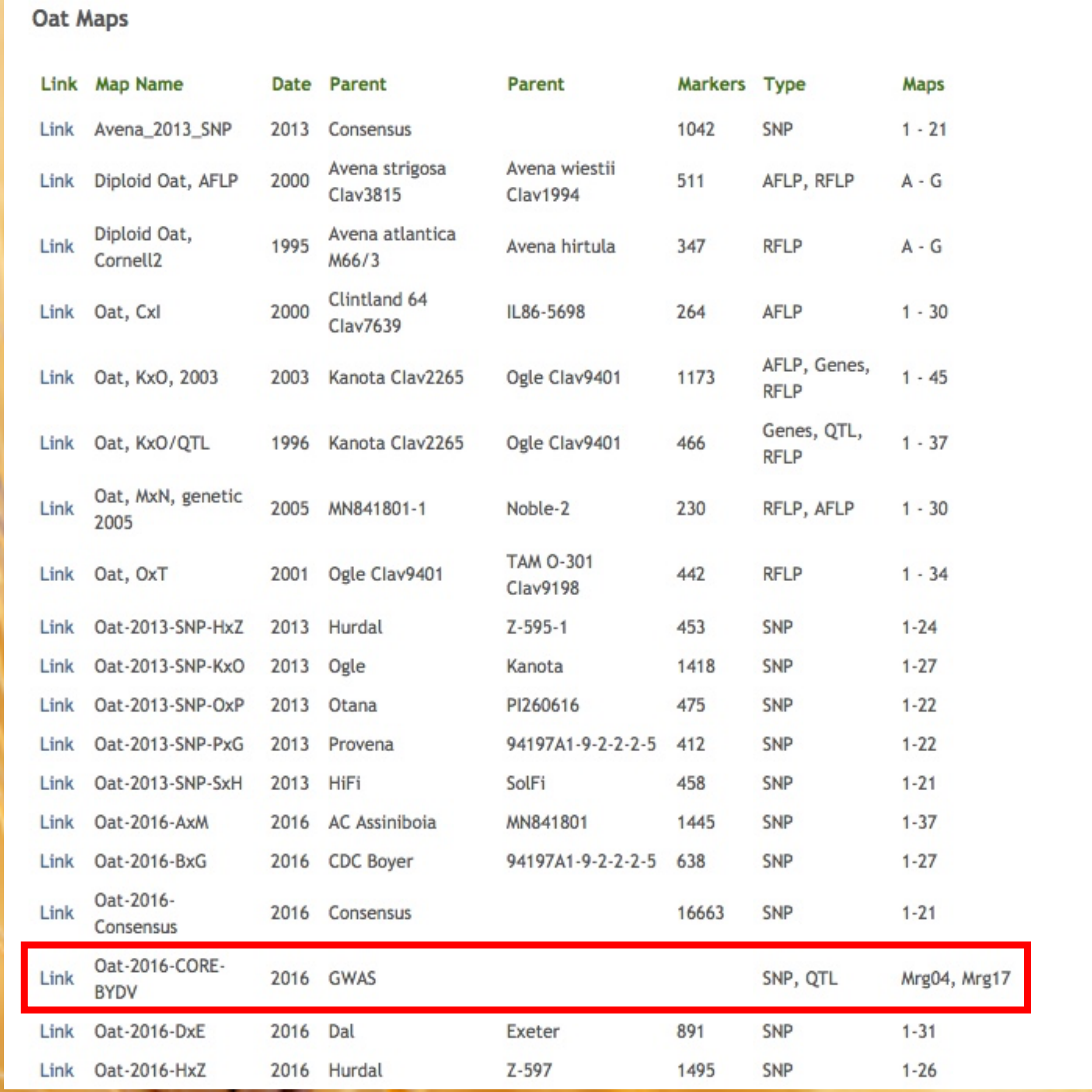
- Wheat Maps - Diploid
- Wheat Maps - Tetraploid
- Wheat Maps - Hexaploid
- Barley Maps
- Rye Maps
- Oat Maps

Wheat Maps - Diploid

Link	Map Name	Date	Parent	Parent	Markers	Type	Maps
Link	Ae. longissima, YxY	2001	Y154-1	Y431-1	74	RFLP	1S - 7S
Link	Ae. umbellulata, A x C	1998	JIC2010001	JIC2010003	89	RFLP	1U - 7U
Link	Aegilops_tauschii_D_genome_2013	2013	A. tauschii	A. tauschii	7178	SNP	1D - 7D
Link	T. boeoticum x monococcum	2007	T. boeoticum pau5088	T. monococcum pau14087	190	EST, SSR	1A - 7A
Link	T. monococcum, DV92 x G3116	1996	T. monococcum	T. monococcum	357	RFLP	1A - 7A
Link	T.tauschii	1991	Triticum tauschii TA1691	Triticum tauschii TA1704	291	RFLP	1D - 7D
Link	T.tauschii, Appels				123	RFLP	1D - 7D

The Maps Shortlist shows the major map sets available in GrainGenes sorted by species. For a complete list of map sets, click the link for The Complete List.

For this tutorial, we will look at an oat map set. Click Oat Maps to navigate down the page to the list of oat maps.

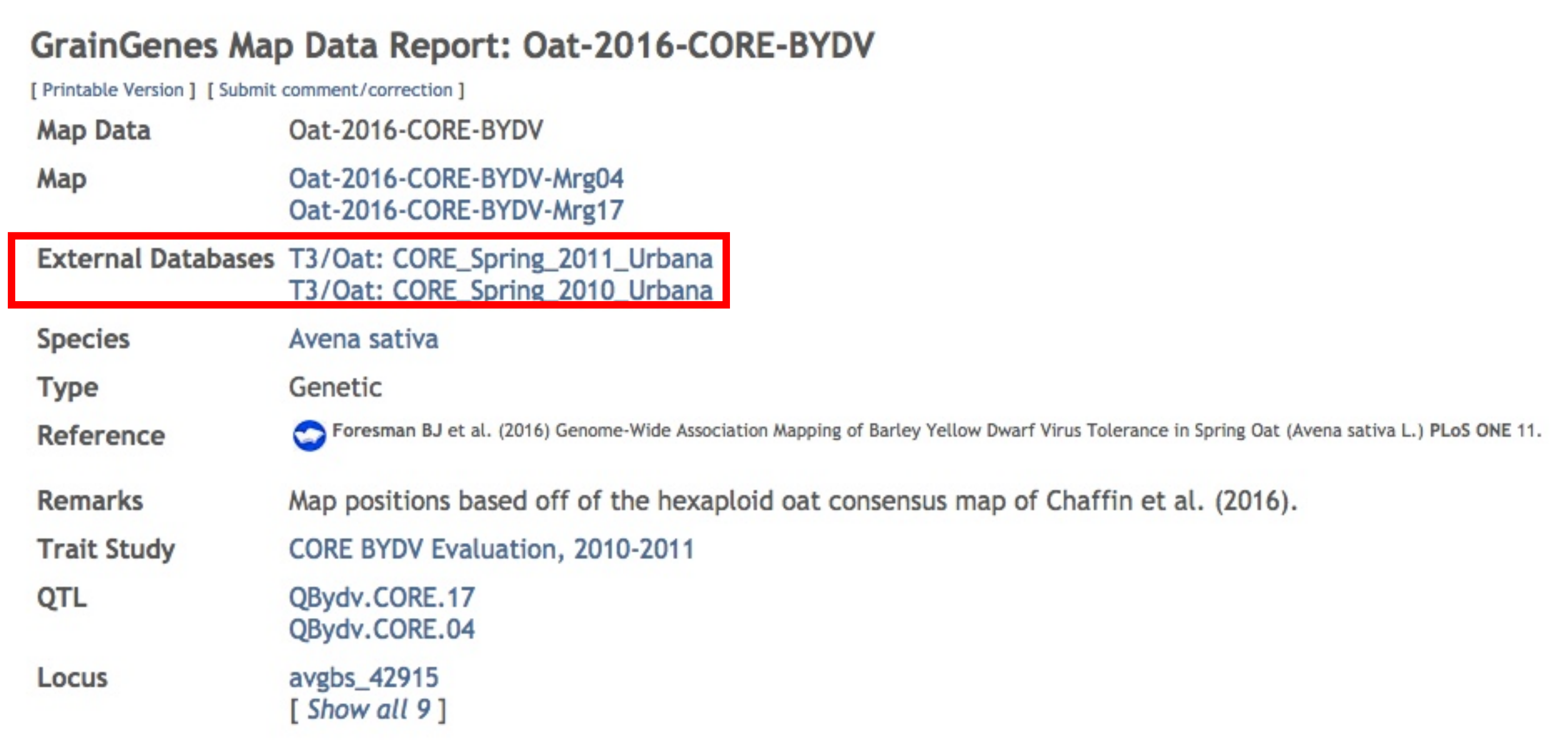


Oat Maps

Link	Map Name	Date	Parent	Parent	Markers	Type	Maps
Link	Avena_2013_SNP	2013	Consensus		1042	SNP	1 - 21
Link	Diploid Oat, AFLP	2000	Avena strigosa Clav3815	Avena wiestii Clav1994	511	AFLP, RFLP	A - G
Link	Diploid Oat, Cornell2	1995	Avena atlantica M66/3	Avena hirtula	347	RFLP	A - G
Link	Oat, CxI	2000	Clintland 64 Clav7639	IL86-5698	264	AFLP	1 - 30
Link	Oat, KxO, 2003	2003	Kanota Clav2265	Ogle Clav9401	1173	AFLP, Genes, RFLP	1 - 45
Link	Oat, KxO/QTL	1996	Kanota Clav2265	Ogle Clav9401	466	Genes, QTL, RFLP	1 - 37
Link	Oat, MxN, genetic 2005	2005	MN841801-1	Noble-2	230	RFLP, AFLP	1 - 30
Link	Oat, OxT	2001	Ogle Clav9401	TAM O-301 Clav9198	442	RFLP	1 - 34
Link	Oat-2013-SNP-HxZ	2013	Hurdal	Z-595-1	453	SNP	1-24
Link	Oat-2013-SNP-KxO	2013	Ogle	Kanota	1418	SNP	1-27
Link	Oat-2013-SNP-OxP	2013	Otana	PI260616	475	SNP	1-22
Link	Oat-2013-SNP-PxG	2013	Provena	94197A1-9-2-2-2-5	412	SNP	1-22
Link	Oat-2013-SNP-SxH	2013	HiFi	SolFi	458	SNP	1-21
Link	Oat-2016-AxM	2016	AC Assiniboia	MN841801	1445	SNP	1-37
Link	Oat-2016-BxG	2016	CDC Boyer	94197A1-9-2-2-2-5	638	SNP	1-27
Link	Oat-2016-Consensus	2016	Consensus		16663	SNP	1-21
Link	Oat-2016-CORE-BYDV	2016	GWAS			SNP, QTL	Mrg04, Mrg17
Link	Oat-2016-DxE	2016	Dal	Exeter	891	SNP	1-31
Link	Oat-2016-HxZ	2016	Hurdal	Z-597	1495	SNP	1-26

The Maps Shortlist provides a brief summary of each map set, including the year it was published, the number and types of markers, and the linkage groups for which there are maps. There is also a link provided to the Map Data Report Page for that map set.

As an example, we will look at a map set from a 2016 GWAS of barley yellow dwarf virus resistance in hexaploid oat, Oat-2016-CORE-BYDV. Click Link to go the the Map Data Report Page

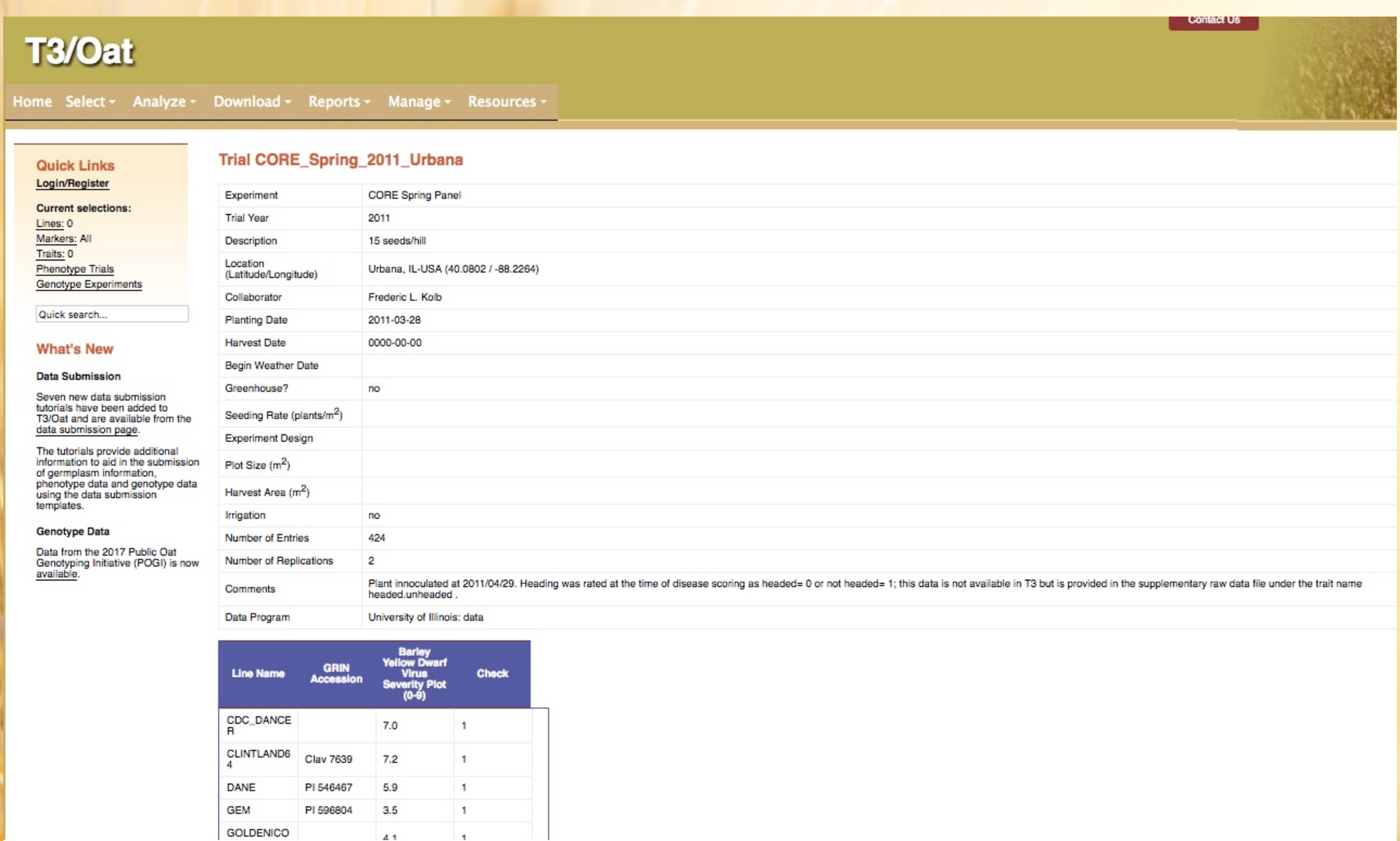


GrainGenes Map Data Report: Oat-2016-CORE-BYDV

[Printable Version] [Submit comment/correction]

Map Data	Oat-2016-CORE-BYDV
Map	Oat-2016-CORE-BYDV-Mrg04 Oat-2016-CORE-BYDV-Mrg17
External Databases	T3/Oat: CORE_Spring_2011_Urbana T3/Oat: CORE_Spring_2010_Urbana
Species	Avena sativa
Type	Genetic
Reference	Foresman BJ et al. (2016) Genome-Wide Association Mapping of Barley Yellow Dwarf Virus Tolerance in Spring Oat (Avena sativa L.) **PLoS ONE** 11.
Remarks	Map positions based off of the hexaploid oat consensus map of Chaffin et al. (2016).
Trait Study	CORE BYDV Evaluation, 2010-2011
QTL	QBydv.CORE.17 QBydv.CORE.04
Locus	avgbs_42915 [*Show all 9*]

The Map Data Report Page provides information on the map set, including the included maps, the publication it is from, loci in the map, and any QTLS that are inside the map.
For this particular GWAS data, there is phenotype data available in T3: The Triticeae Toolbox. By clicking on the links next to External Databases, we are brought to the location of the this data on the T3/Oat website.



Quick Links

Login/Register

Current selections:
Lines: 0
Markers: All
Traits: 0
Phenotype Trials
Genotype Experiments

What's New

Data Submission

Seven new data submission tutorials have been added to T3/Oat and are available from the data submission page.

The tutorials provide additional information to aid in the submission of germplasm information, phenotype data and genotype data using the data submission templates.

Genotype Data

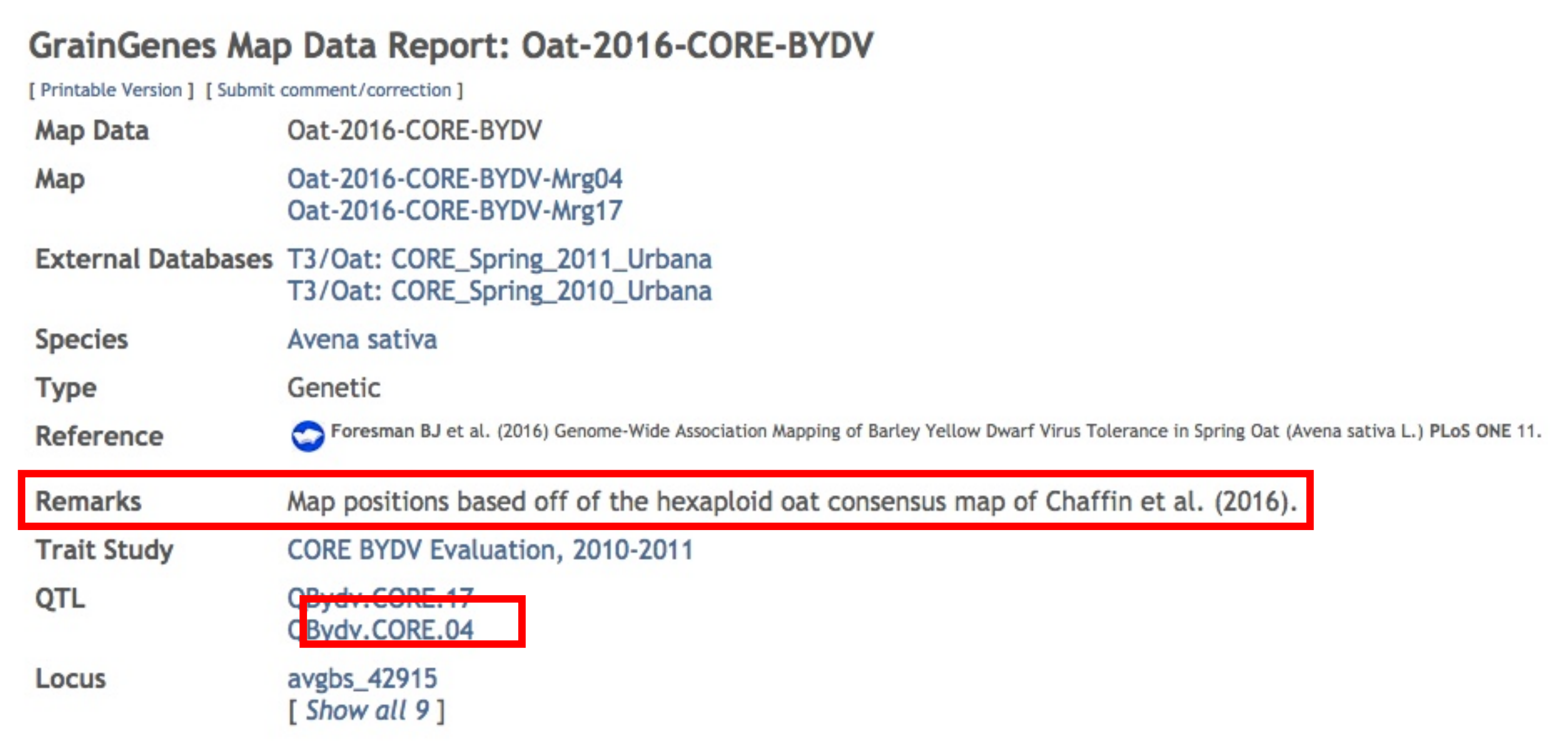
Data from the 2017 Public Oat Genotyping Initiative (POGI) is now available.

Trial CORE_Spring_2011_Urbana

Experiment	CORE Spring Panel
Trial Year	2011
Description	15 seeds/hill
Location (Latitude/Longitude)	Urbana, IL-USA (40.0802 / -88.2264)
Collaborator	Frederic L. Kolb
Planting Date	2011-03-28
Harvest Date	0000-00-00
Begin Weather Date	
Greenhouse?	no
Seeding Rate (plants/m^2)	
Experiment Design	
Plot Size (m^2)	
Harvest Area (m^2)	
Irrigation	no
Number of Entries	424
Number of Replications	2
Comments	Plant innoculated at 2011/04/29. Heading was rated at the time of disease scoring as headed= 0 or not headed= 1; this data is not available in T3 but is provided in the supplementary raw data file under the trait name headed.unheaded .
Data Program	University of Illinois: data

Line Name	GRIN Accession	Barley Yellow Dwarf Virus Severity Plot (0-9)	Check
CDC_DANCER		7.0	1
CLINTLAND64	Clav 7639	7.2	1
DANE	PI 546467	5.9	1
GEM	PI 596804	3.5	1
GOLDENICO		4.1	1

At T3/Oat we can find information on the germplasm used in GWAS and obtain phenotype scores for individual lines. This data is available for download and further analysis.



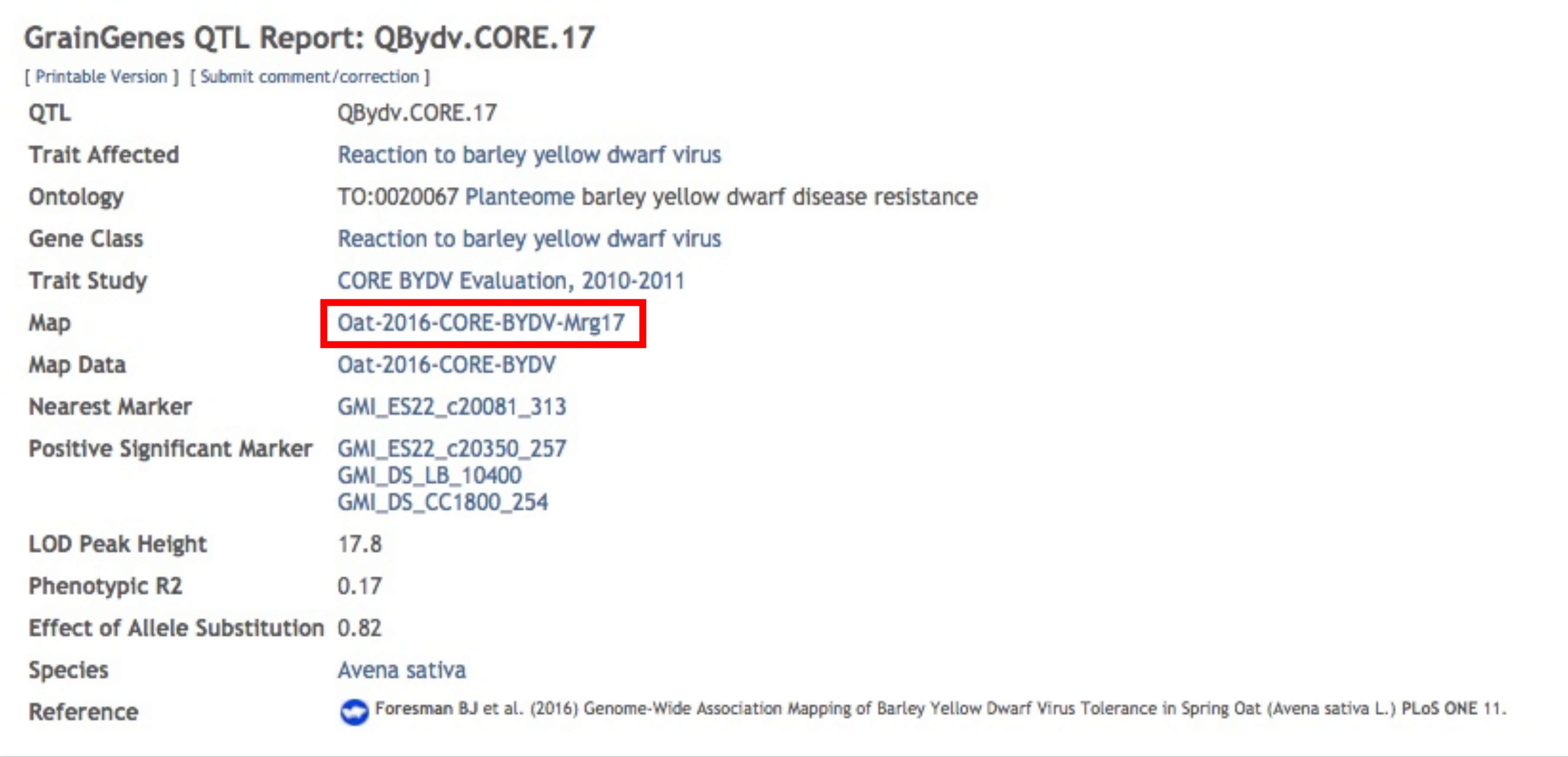
GrainGenes Map Data Report: Oat-2016-CORE-BYDV

[Printable Version] [Submit comment/correction]

Map Data	Oat-2016-CORE-BYDV
Map	Oat-2016-CORE-BYDV-Mrg04 Oat-2016-CORE-BYDV-Mrg17
External Databases	T3/Oat: CORE_Spring_2011_Urbana T3/Oat: CORE_Spring_2010_Urbana
Species	Avena sativa
Type	Genetic
Reference	Foresman BJ et al. (2016) Genome-Wide Association Mapping of Barley Yellow Dwarf Virus Tolerance in Spring Oat (Avena sativa L.) PLoS ONE 11.
Remarks	Map positions based off of the hexaploid oat consensus map of Chaffin et al. (2016).
Trait Study	CORE BYDV Evaluation, 2010-2011
QTL	QBydv.CORE.17 QBydv.CORE.04
Locus	avgbs_42915 [*Show all 9*]

For more information on the QTL found in this GWAS, we can click on the links to navigate to the QTL Report page for the individual QTL. There were two found in this study. In this tutorial, we will look at QBydv.CORE.17, which was located on linkage group Mrg17 from the Hexaploid Oat Consensus Map.

It is important to note that the map positions listed in this map set are relative and were based off of the Oat Consensus Map (Chaffin et al. 2016).



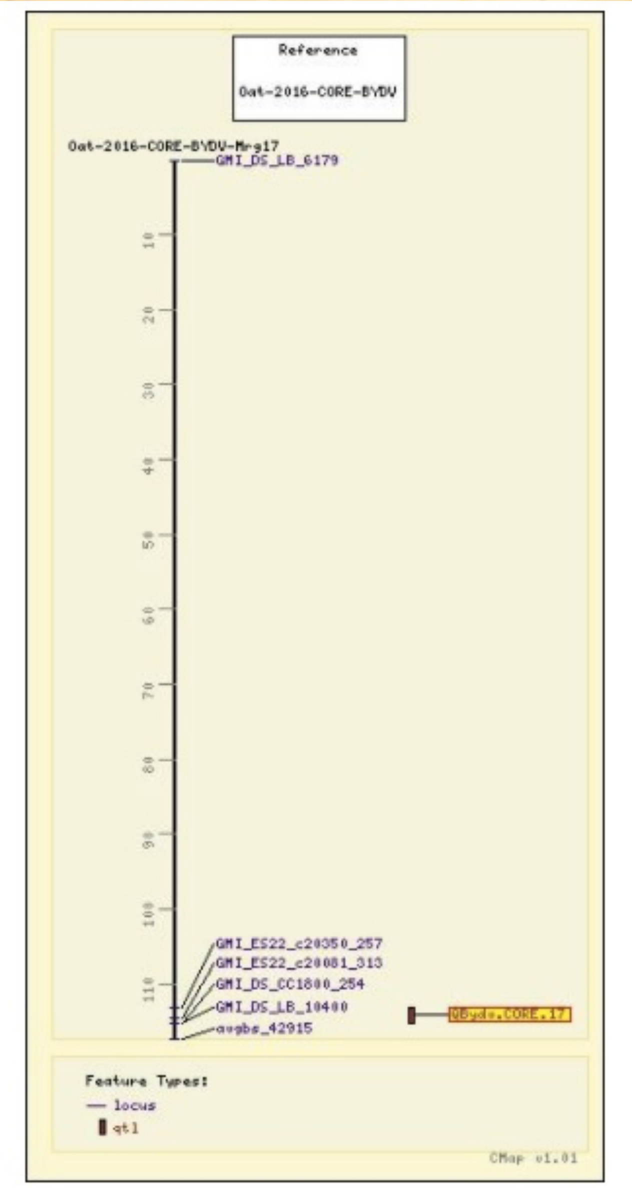
GrainGenes QTL Report: QBydv.CORE.17

[Printable Version] [Submit comment/correction]

QTL	QBydv.CORE.17
Trait Affected	Reaction to barley yellow dwarf virus
Ontology	TO:0020067 Planteome barley yellow dwarf disease resistance
Gene Class	Reaction to barley yellow dwarf virus
Trait Study	CORE BYDV Evaluation, 2010-2011
Map	Oat-2016-CORE-BYDV-Mrg17
Map Data	Oat-2016-CORE-BYDV
Nearest Marker	GMI_ES22_c20081_313
Positive Significant Marker	GMI_ES22_c20350_257 GMI_DS_LB_10400 GMI_DS_CC1800_254
LOD Peak Height	17.8
Phenotypic R2	0.17
Effect of Allele Substitution	0.82
Species	Avena sativa
Reference	Foresman BJ et al. (2016) Genome-Wide Association Mapping of Barley Yellow Dwarf Virus Tolerance in Spring Oat (Avena sativa L.) PLoS ONE 11.

The QTL Report Page provides details on the individual QTL, such as which trait is affected, its LOD score and phenotypic R-squared, as well as markers contained within the QTL.

In order to view the QTL in CMap, click the link next to Map, labelled Oat-2016-CORE-BYDV-Mrg17.



The map that is initially shown contains only the significant markers contained in QBydv.CORE.17, as well as two framing markers. By itself, this map is not particularly useful. As mentioned before, map positions were obtained from the Oat Consensus Map, so we must align the two maps to get a sense of this QTL's location on the linkage group.

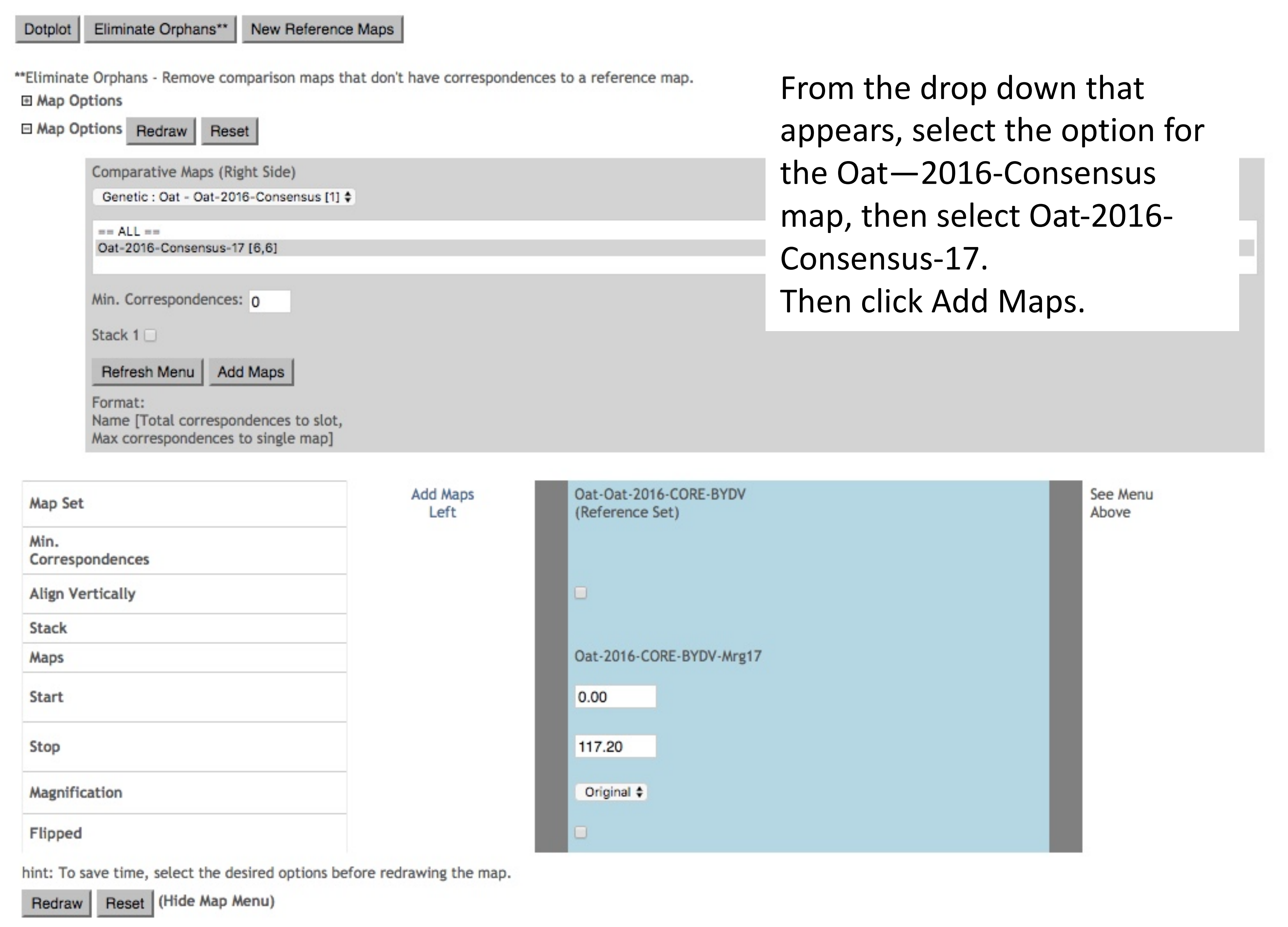
To do this, scroll down the page to an area with a light blue box. Then click Add Maps Right.

(For more information on how to use CMap, see the CMap Tutorial.)

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

Map Set	Oat-Oat-2016-CORE-BYDV (Reference Set)
Min. Correspondences	
Align Vertically	☐
Stack	
Maps	Oat-2016-CORE-BYDV-Mrg17
Start	0.00
Stop	117.20
Magnification	Original ⬍
Flipped	☐

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



Dotplot | Eliminate Orphans** | New Reference Maps

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

⊞ Map Options

⊟ Map Options | Redraw | Reset

Comparative Maps (Right Side)

Genetic : Oat - Oat-2016-Consensus [1]

== ALL ==
Oat-2016-Consensus-17 [6,6]

Min. Correspondences: 0

Stack 1 ☐

Refresh Menu | Add Maps

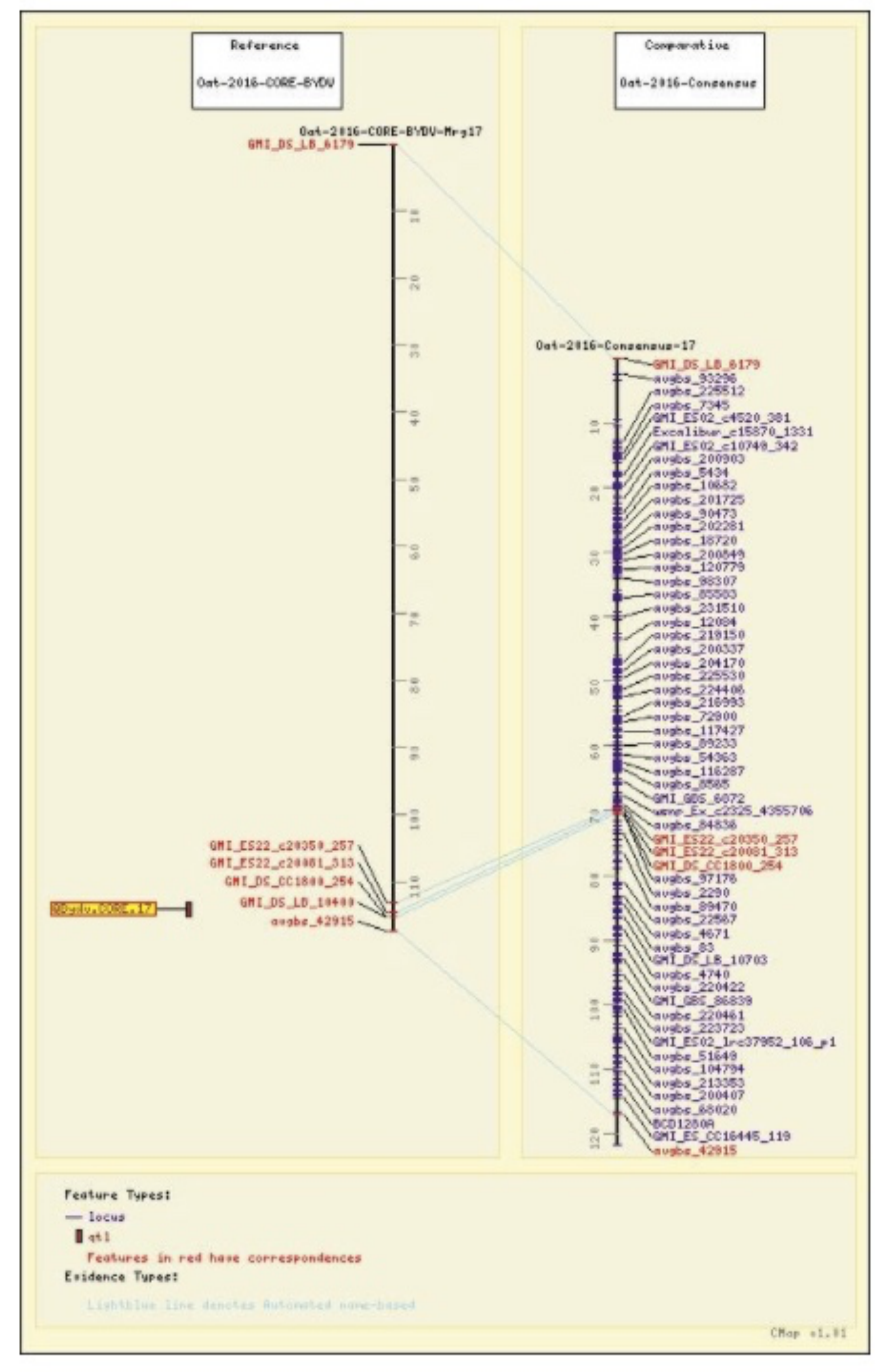
Format:
Name [Total correspondences to slot,
Max correspondences to single map]

Map Set	Add Maps Left	Oat-Oat-2016-CORE-BYDV (Reference Set)	See Menu Above
Min. Correspondences			
Align Vertically		☐	
Stack			
Maps		Oat-2016-CORE-BYDV-Mrg17	
Start		0.00	
Stop		117.20	
Magnification		Original	
Flipped		☐	

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

Redraw | Reset | (Hide Map Menu)

From the drop down that appears, select the option for the Oat—2016-Consensus map, then select Oat-2016-Consensus-17.
Then click Add Maps.



The resulting map shows the correspondences between the significant markers contained within the QTL to the full consensus map for linkage group Mrg17. The area highlighted in yellow, the QTL itself, now can be positioned relative to other markers in the map, and compared to data from other studies that use shared markers.