What's New at SoyBase

August 2014

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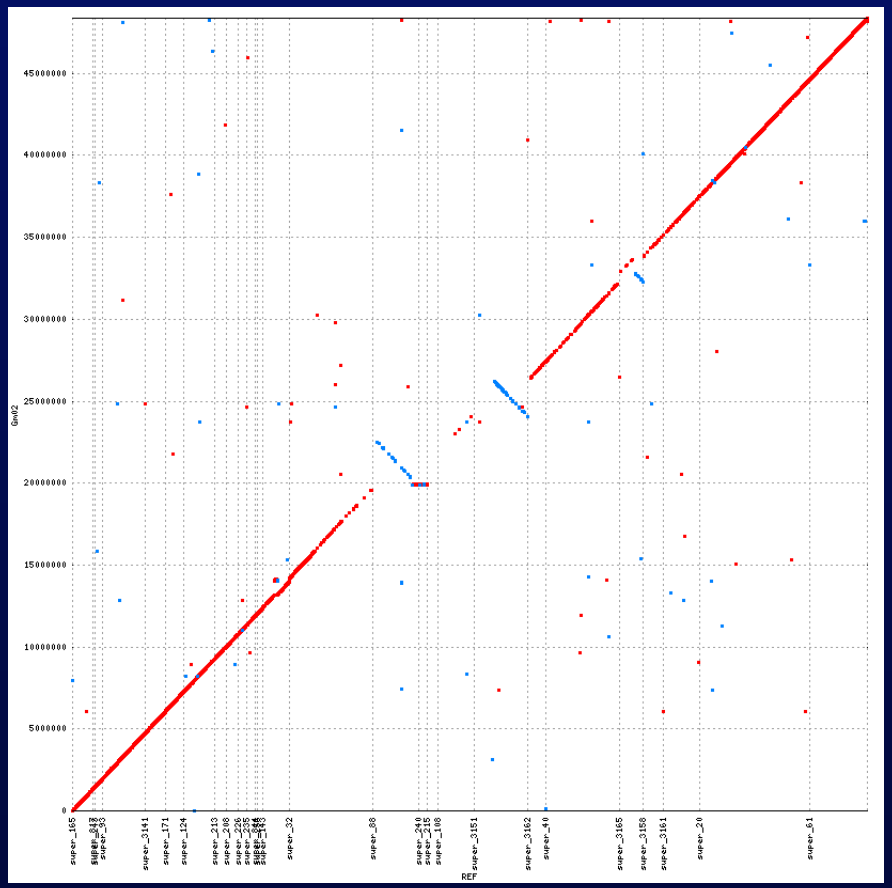
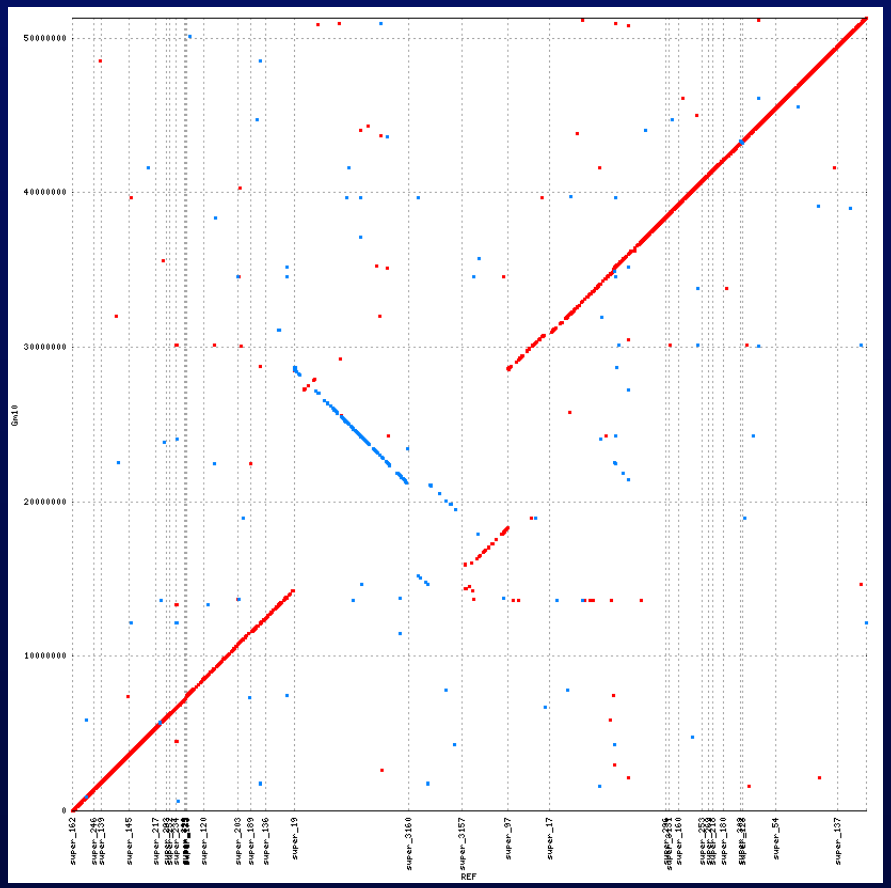
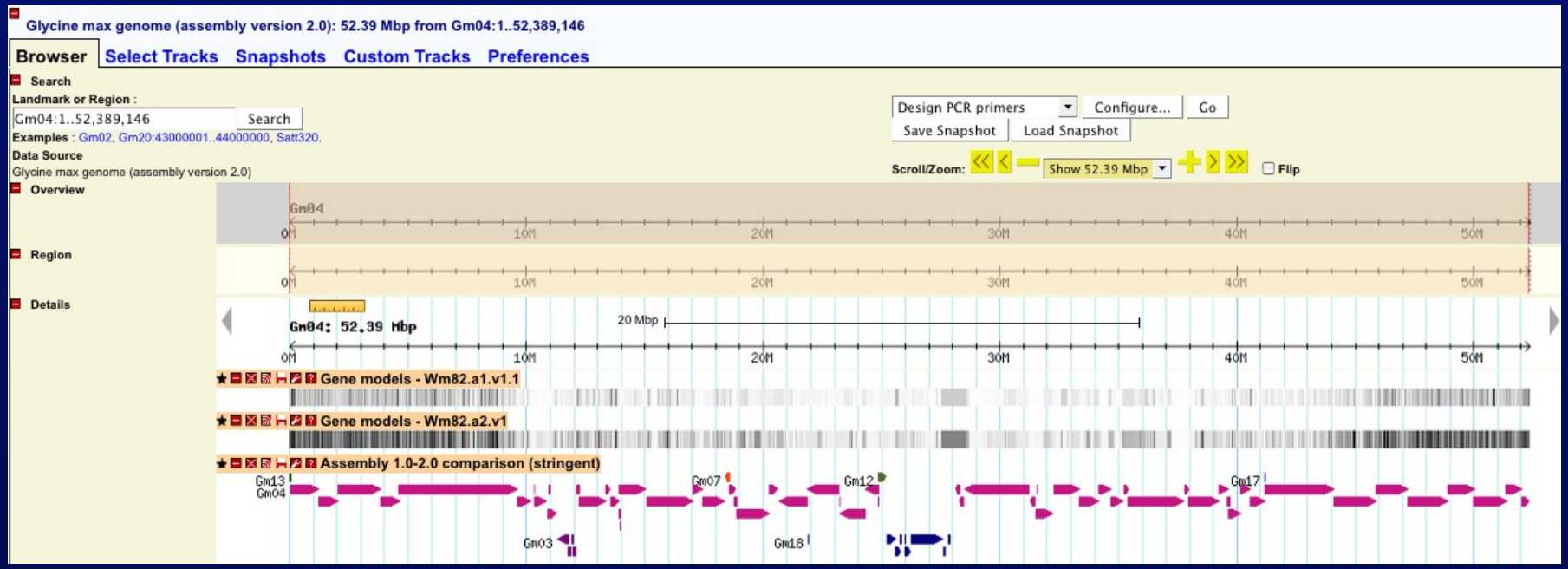
Overview

- Wm82.a2.v1 genome sequence
- Fast Neutron-induced indels and Transposable Element insertions
- SoySNP50K haplotypes
- SoyMap2 genome browser
- improved QTL names
- SoyBase and community-provided tutorials
- GWAS QTL

Comparison of Wm82.a1 and Wm82.a2 Genome Assemblies







New Wm82 genome assembly from JGI

- corrects known problems with the v1 assembly
- incorporates additional transcript data resulting in improved gene predictions
- revised gene model and annotation nomenclature

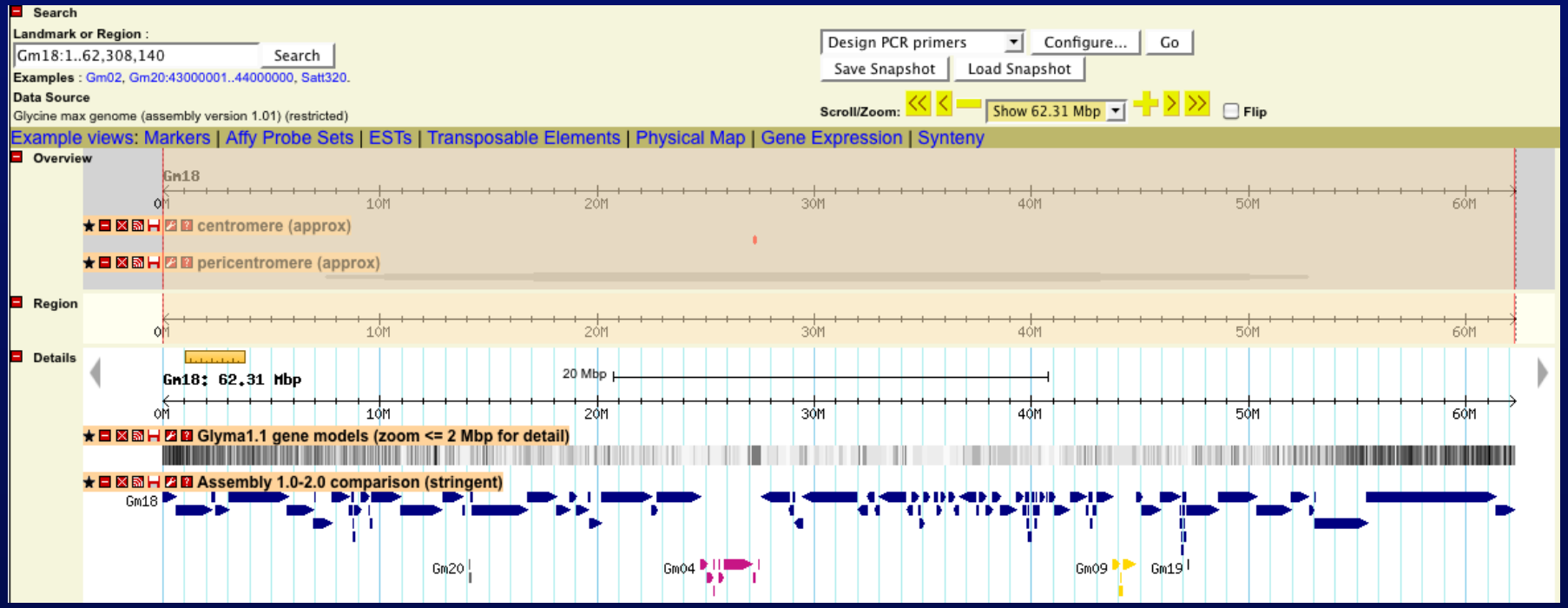
locus: Glyma.01g000100

transcript: Glyma.01g000100.1

for annotation version Wm82.a2.v1

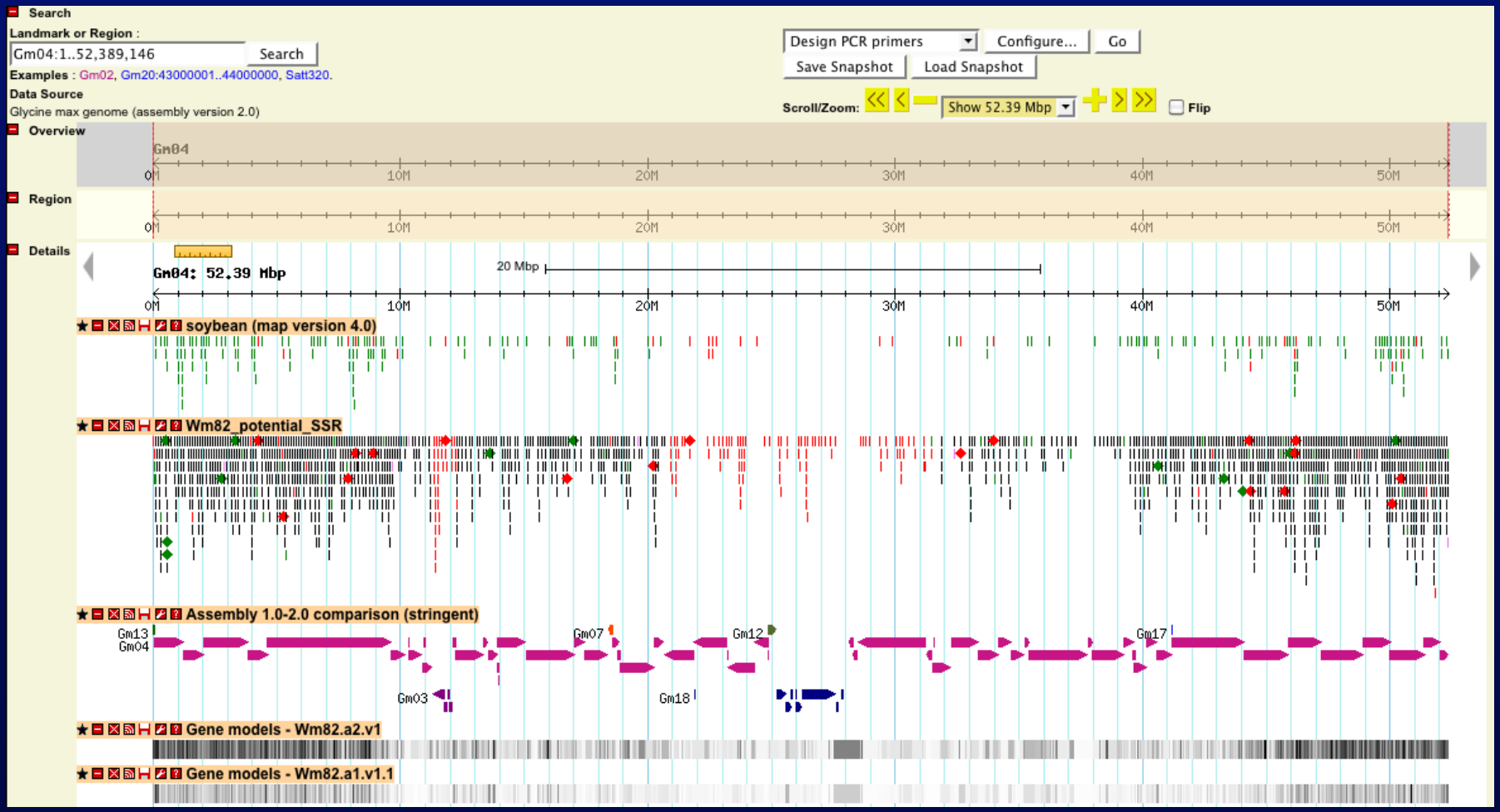
locus ID: Glyma.01g000100.Wm82.a2.v1

transcript ID: Glyma.01g000100.1.Wm82.a2.v1



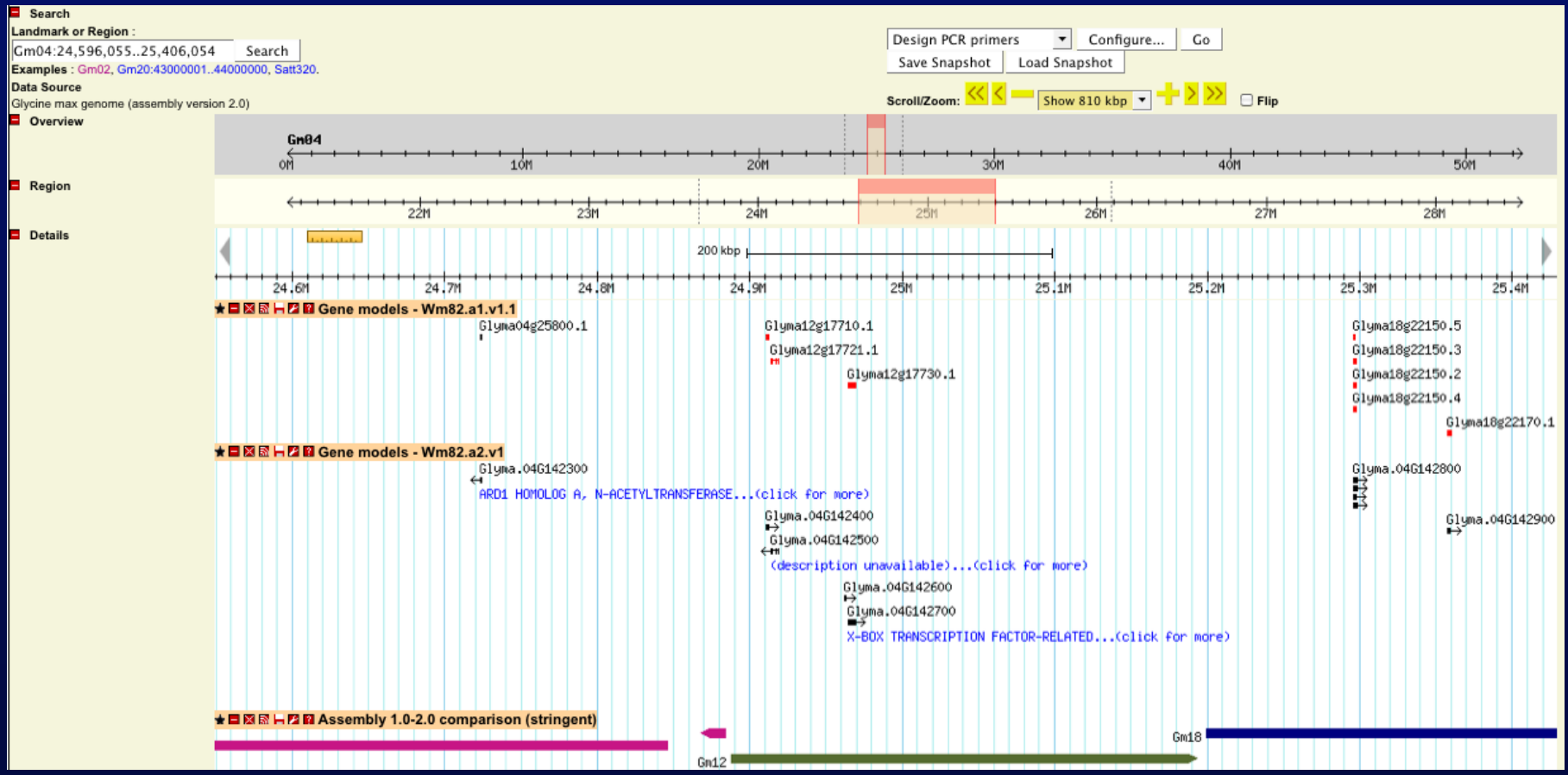
The current sequence browser now has a track showing synteny between the v1 and v2 assemblies.

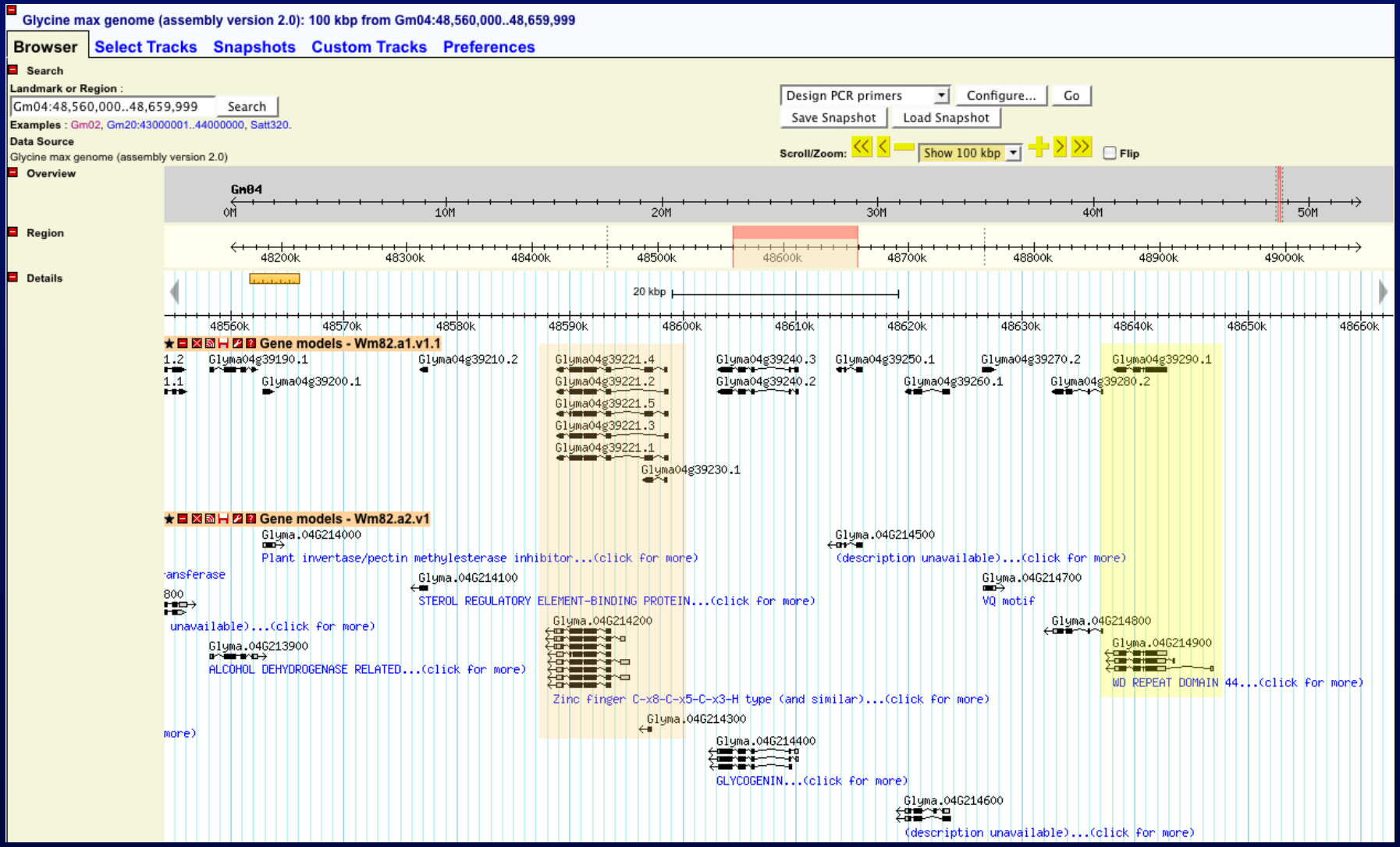
The v1 and v2 synteny tracks are reciprocal for shared regions.



Wm82.a1.v1.1 gene models and markers mapped onto new assembly when possible.

Markers and gene models with different chromosomal locations or DNA strand between the two assemblies are indicated in red.


Search
Landmark or Region :
Gm04:24,596,055..25,406,054
Search
Examples : Gm02, Gm20:43000001..44000000, Satt320.
Data Source
Glycine max genome (assembly version 2.0)
Design PCR primers
Configure...
Go
Save Snapshot
Load Snapshot
Scroll/Zoom:
Show 810 kbp
Flip
Overview
Gm04
0M
10M
20M
30M
40M
50M
Region
22M
23M
24M
25M
26M
27M
28M
Details
200 kbp
24.6M
24.7M
24.8M
24.9M
25M
25.1M
25.2M
25.3M
25.4M
Gene models - Wm82.a1.v1.1
Glyma04g25800.1
Glyma12g17710.1
Glyma12g17721.1
Glyma12g17730.1
Glyma18g22150.5
Glyma18g22150.3
Glyma18g22150.2
Glyma18g22150.4
Glyma18g22170.1
Gene models - Wm82.a2.v1
Glyma.04G142300
ARD1 HOMOLOG A, N-ACETYLTRANSFERASE...(click for more)
Glyma.04G142400
Glyma.04G142500
(description unavailable)...(click for more)
Glyma.04G142600
Glyma.04G142700
X-BOX TRANSCRIPTION FACTOR-RELATED...(click for more)
Glyma.04G142800
Glyma.04G142900
Assembly 1.0-2.0 comparison (stringent)
Gm18
Gm12


Glycine max genome (assembly version 2.0): 100 kbp from Gm04:48,560,000..48,659,999
Browser
Select Tracks
Snapshots
Custom Tracks
Preferences
Search
Landmark or Region :
Gm04:48,560,000..48,659,999
Search
Examples : Gm02, Gm20:43000001..44000000, Satt320.
Data Source
Glycine max genome (assembly version 2.0)
Design PCR primers
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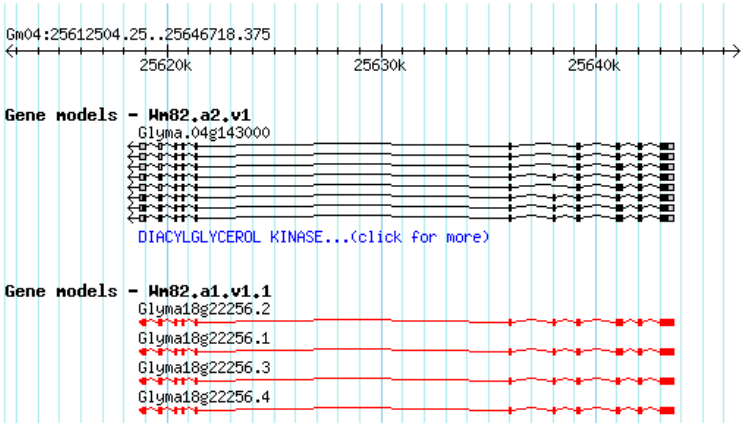
Scroll/Zoom:
Show 100 kbp
Flip
Overview
Region
Details
Gm04
0M
10M
20M
30M
40M
50M
48200k
48300k
48400k
48500k
48600k
48700k
48800k
48900k
49000k
20 kbp
48560k
48570k
48580k
48590k
48600k
48610k
48620k
48630k
48640k
48650k
48660k
Gene models - Wm82.a1.v1.1
Glyma04g39190.1
Glyma04g39210.2
Glyma04g39221.4
Glyma04g39240.3
Glyma04g39250.1
Glyma04g39270.2
Glyma04g39290.1
Glyma04g39200.1
Glyma04g39221.2
Glyma04g39240.2
Glyma04g39260.1
Glyma04g39280.2
Glyma04g39221.5
Glyma04g39221.3
Glyma04g39221.1
Glyma04g39230.1
Gene models - Wm82.a2.v1
Glyma.04G214000
Plant invertase/pectin methylesterase inhibitor...(click for more)
Glyma.04G214500
(description unavailable)...(click for more)
Glyma.04G214100
STEROL REGULATORY ELEMENT-BINDING PROTEIN...(click for more)
Glyma.04G214700
VQ motif
Glyma.04G214200
Glyma.04G214800
Glyma.04G213900
ALCOHOL DEHYDROGENASE RELATED...(click for more)
Glyma.04G214900
WD REPEAT DOMAIN 44...(click for more)
Zinc finger C-x8-C-x5-C-x3-H type (and similar)...(click for more)
Glyma.04G214300
Glyma.04G214400
GLYCOGENIN...(click for more)
Glyma.04G214600
(description unavailable)...(click for more)

Report for Sequence Feature Glyma.04g143000

Feature Type: gene_model
Chromosome: Gm04
Start: 25618725
stop: 25643608
Source: JGI
Version: Glyma2.0
High confidence: yes



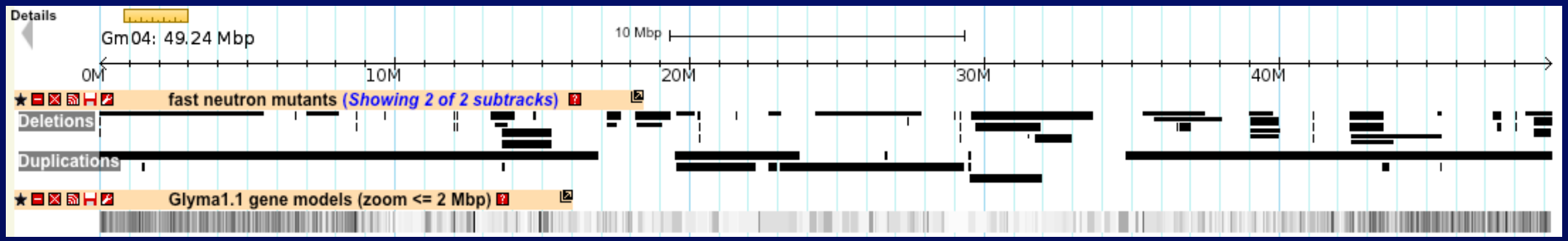
A previous version of this gene model can be found here: See Previous Version

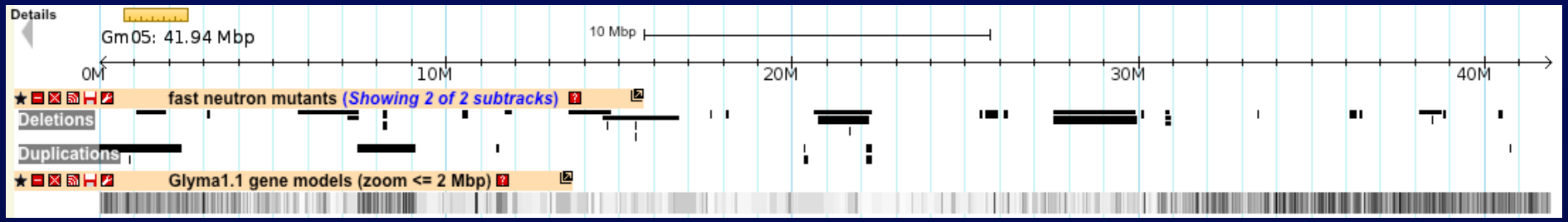
Annotations for Glyma.04g143000

Database ID	Annotation Type	Annotation Description	Annotation Source	Match Score	Evidence Code
AT2G18730.1	AT	diacylglycerol kinase 3	JGI	N/A	IEA
AT4G30340.1	AT	diacylglycerol kinase 7	JGI	N/A	IEA
AT5G57690.1	AT	diacylglycerol kinase 4	JGI	N/A	IEA
GO:0004143	GO	diacylglycerol kinase activity	JGI	N/A	IEA
GO:0007205	GO	protein kinase C-activating G-protein coupled receptor signaling pathway	JGI	N/A	IEA
KOG1169	KOG	Diacylglycerol kinase	JGI	N/A	IEA
PTHR11255	Panther	DIACYLGLYCEROL KINASE	JGI	N/A	IEA
PTHR11255:SF32	Panther	DIACYLGLYCEROL KINASE BETA	JGI	N/A	IEA
PF00609	PFAM	Diacylglycerol kinase accessory domain	JGI	N/A	IEA
PF00781	PFAM	Diacylglycerol kinase catalytic domain	JGI	N/A	IEA

Gene model name correspondences to Glyma.04g143000 Gene Call Version Glyma2.0

Corresponding Name	Annotation Version	Evidence	Comments
Glyma18g22256	Glyma 1.1	IGC	As supplied by JGI





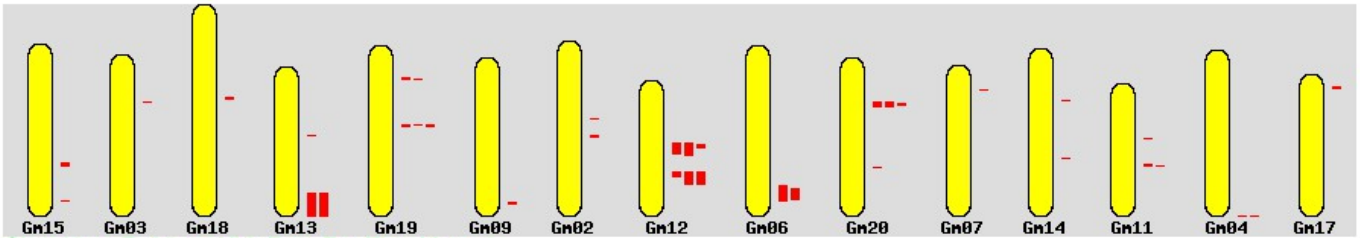
Newly identified Fast Neutron-induced deletions and duplications placed on genome sequence.

http://www.soybase.org/mutants/index.php

Sample Information

Mutant Name	FN0110332
Genus species	Glycine max
Cultivar	M92-220
Seed Availability	Unknown
Experiment ID	FN1.09
Laboratory	USDA-ARS & UMN: Bolon/Vance
Mutagen	fast neutron
Mutagenesis Date	9/2008

Genomic Analysis



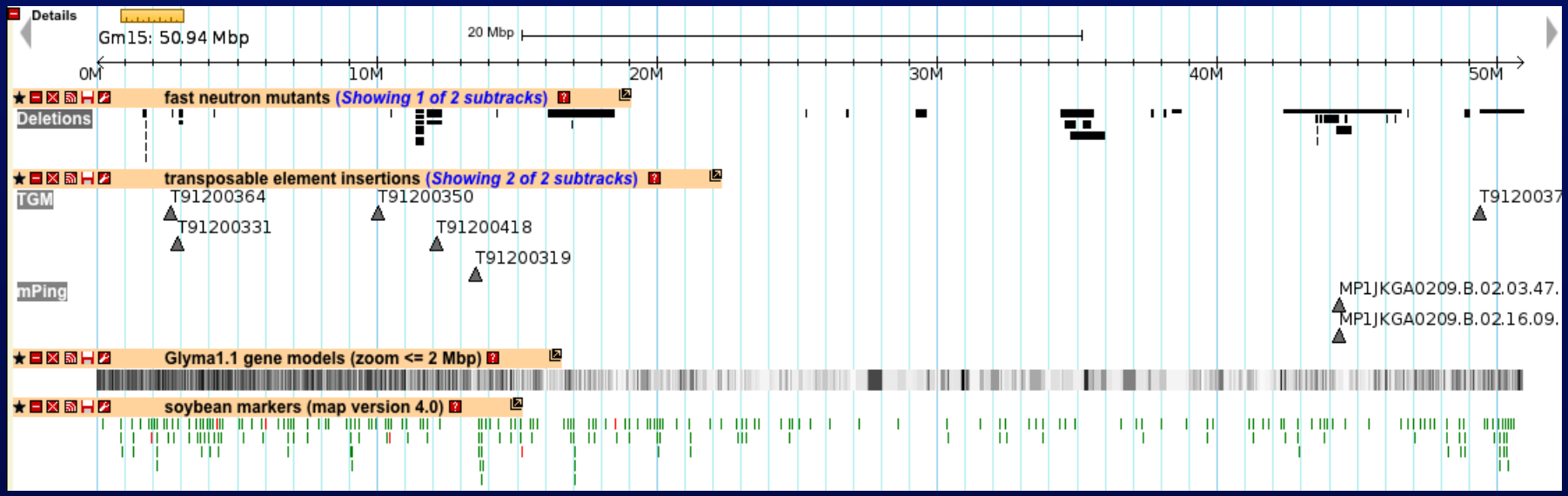
Click Here To View All InDels For This Mutant

Phenotype and Seed Composition

M2 Name	FN0110332
SSD Generation	M2
Plant Description	spindly
Photo(s)	Image Type: whole_plant Filename: 1R03C32CMN09NSFBV_1.jpg

Trait	Method	Value	Method	Value
Ash	NIR,DM	5.65		
Fiber	NIR,DM	7		

All indels for a M2-derived mutant family now viewable in the genome browser.



Transposable Element insertions and Fast Neutron-induced indels displayed in genome browser.

SoyBase and the Soybean Breeder's Toolbox

Integrating Genetics and Molecular Biology for Soybean Researchers

SoyBase | Maps | Genome | Analysis Tools | Resources | SoySeq

About the Sequence Map | SoyBase Browser | Transposable Elements | Soybean at Phytozome (JGI) | PlantGDB Browser | Download Data

SoyBase Soybean Sequence Map Resources

SoyBase browser

Choose a Chromosome

Chromosome Number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Linkage Group	D1a	D1b	N	C1	A1	C2	M	A2	K	O	B1	H	F	B2	E	J	D2	G	L	I

View the JGI Gma1.01 WGS soybean genomic sequence, as pseudomolecules, integrating features from the soybean composite genetic and physical maps with the genomic sequence. Links from GBrowse features (BACs, markers) to locations in the SoyBase genetic and physical maps are available from a contextual menu. The preliminary 7x assembly is still available here.

View or download a list of markers or other sequence map features by chromosomes here.

Download gene call sequences from the Williams 82 genomic sequence.

Search for Sequence Features and Annotations

SoyBase Search
Perform searches of our entire data set.

See haplotype data for 19,652 cultivars analyzed with the SoySNP50K chip

View or download a list of genetic markers or other features by linkage group.

SoySNP50K iSelect BeadChip

An Illumina Infinium BeadChip containing over 50,000 SNPs from soybean (Glycine max L. Merr.) has been developed (Song et al. 2013). A total of 498,921,777 reads 35-45 bp in length were obtained from DNA sequence analysis of reduced representation libraries from several soybean accessions which included six cultivated and two wild soybean (G. soja Sieb. et Zucc.) genotypes. These reads were mapped to the soybean whole genome sequence and 209,903 SNPs were identified. After applying several filters, a total of 146,161 SNPs were determined to be candidates for Illumina Infinium II BeadChip design. To equalize the distance between selected SNPs, increase assay success rate, and minimize the number of SNPs with low minor allele frequency, an iteration algorithm based on a selection index was developed and used to select 60,800 SNPs for Infinium BeadChip design. Of the 60,800 SNPs, 50,701 were targeted to euchromatic regions and 10,000 to heterochromatic regions of the 20 soybean chromosomes. In addition, 99 SNPs were targeted to unanchored sequence scaffolds. Of the 60,800 SNPs, a total of 52,041 passed Illumina's manufacturing phase to produce the SoySNP50K iSelect BeadChip. Validation of the SoySNP50K chip with 96 landrace genotypes, 96 elite cultivars and 96 wild soybean accessions showed that 47,337 SNPs were polymorphic and generated successful SNP allele calls. In addition, 40,841 of the 47,337 SNPs (86%) had minor allele frequencies >10% among the landraces, elite cultivars and the wild soybean accessions.

Search SoyBase for a specific SoySNP50K SNP

Search

Examples: ss715578909 or BARC_1.01_Gm01_29091115_A_G

Note: Searches covering the original BARC SNPs can be done on this page.

View SoySNP50K SNPs in SoyBase Genome Browser

– Select a Chromosome – Go

Download SNP Data

The SoySNP50K iSelect BeadChip has been used to genotype the USDA Soybean Germplasm Collection (Song et al. in preparation) and the data generously provided by the authors before publication. The complete data set for 19,652 G. max and G. soja accessions genotyped with 52,041 SNPs is available here (approx. 170 Mb compressed with GZIP) .

SoySNP50K haplotypes for a user-selected subset of the genotyped cultivars can be downloaded from this page.

Download SoySNP50K haplotypes for a subset of the cultivars

Paste a list of cultivar names, one per line, into the box below or use the Browse button to navigate to a plain text file on your computer that contains a list of cultivar names.

The submit button will initiate a download to your computer of the SoySNP50K haplotypes for the cultivars you provide.

```
PI086046
PI090208
PI219698
PI253651A
PI347550A
PI398807
PI408055A
PI408069
```

Browse...

Submit Load Examples

Or use our shopping cart tool to select cultivars of interest from the complete list of cultivars haplotyped by Song et al.

Readme Text:
(Included in download)

Including this READ ME there are four files returned for a cultivar-haplotype search. All data are in plain text files with tab delimiters between columns.

NOTE:
We have observed that on some computers opening these files directly in Excel results in each line being placed in a single cell rather than 1 cell per tab-separated column. This can be solved by opening the file in Word or another text editor and using copy/paste to put the data into Excel.

Downloaded Data Files:

cultivar_snps

This is a 2 column tab-delimitted file, 1 line per cultivar.

Cultivar Name	Cultivar Haplotype
PI442007B	TAATTAACTAAAGTAGTAAATAACCCAGGA.....

snp_id_and_position

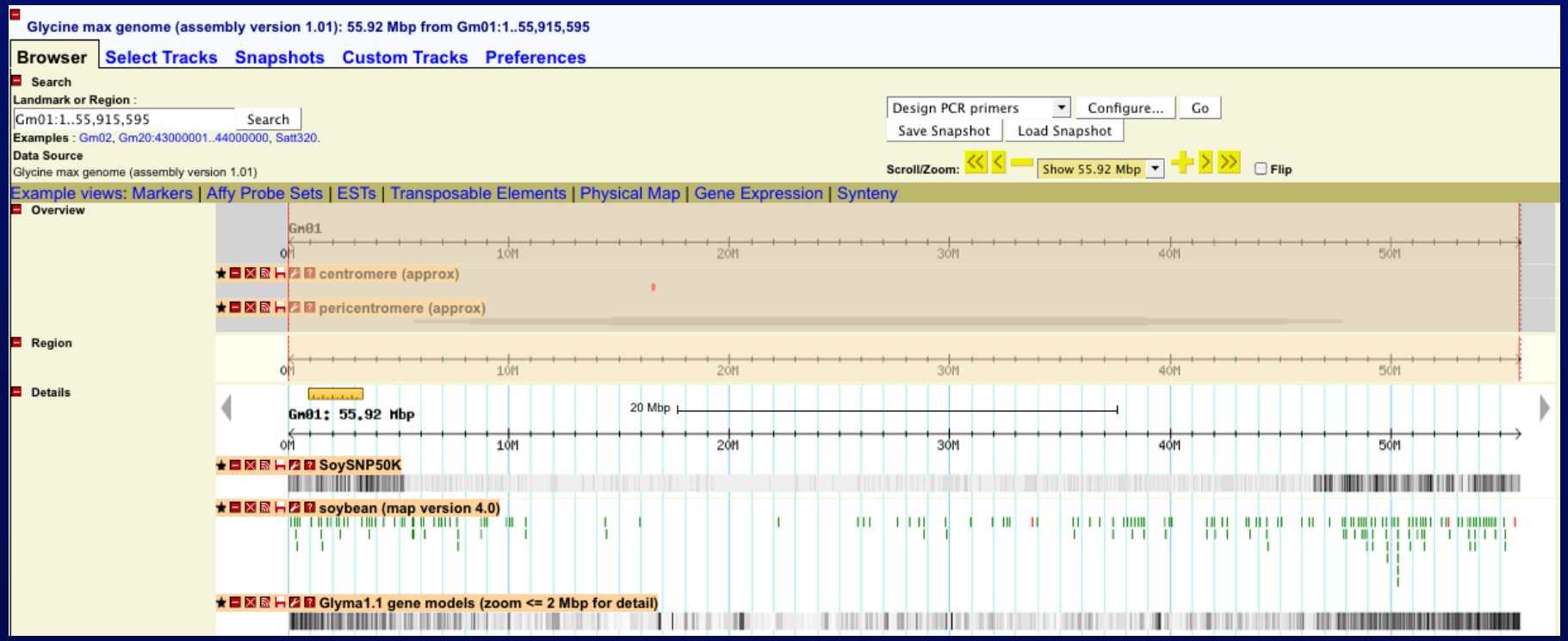
This file contains what amounts to the column header information for 'cultivar_snps'. It is provided as a separate file so that the haplotype data in 'cultivar_snps' doesn't need to have tabs between each SNP allele value.

SNP Name	ss715578401	ss715578402	ss715578403	ss715578404	ss715578405
Chromosome	Gm01	Gm01	Gm01	Gm01	Gm01
Position	10015701	10052330	1006696	10074809	1009248

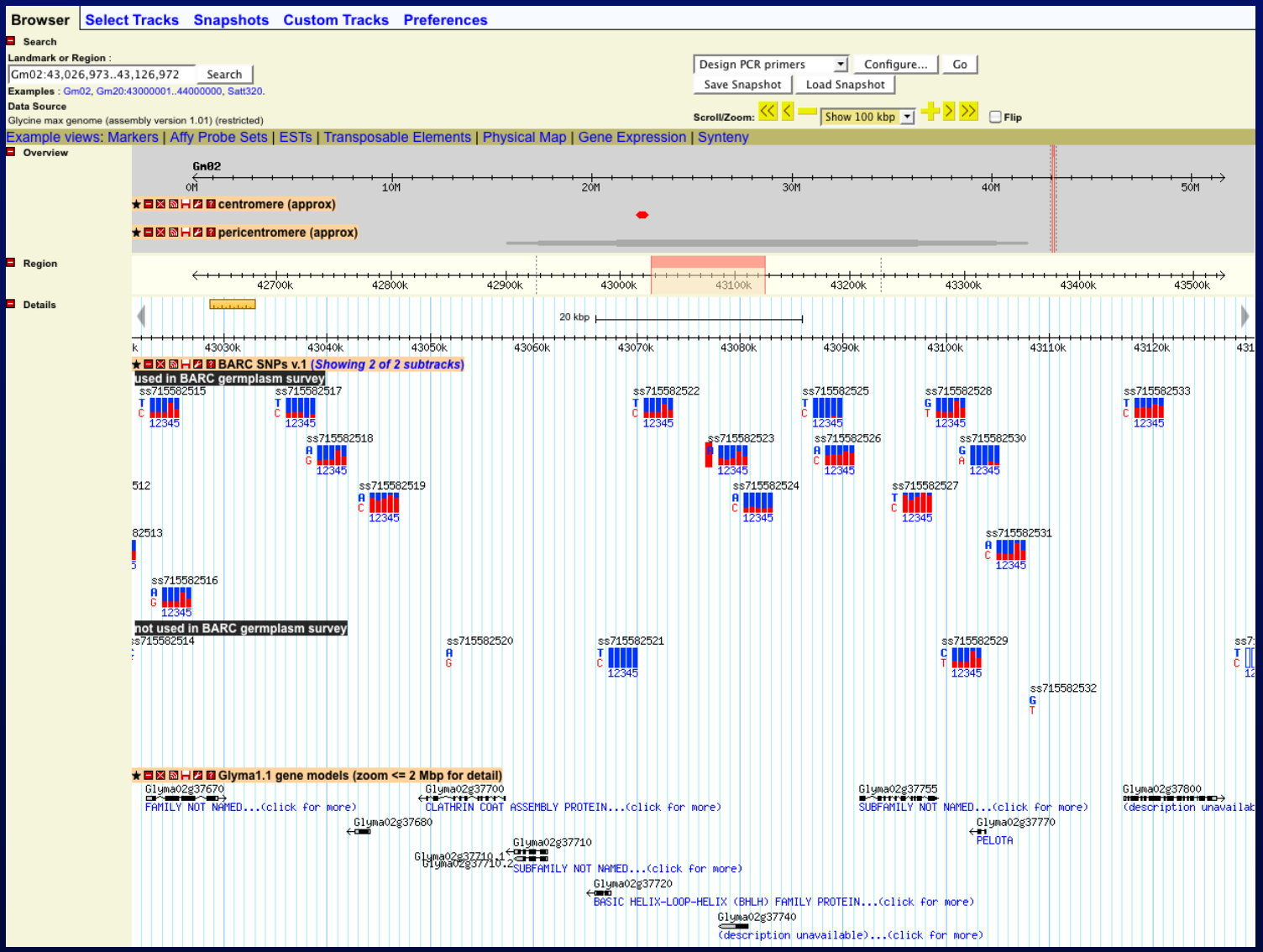
snp_id_position_and_value

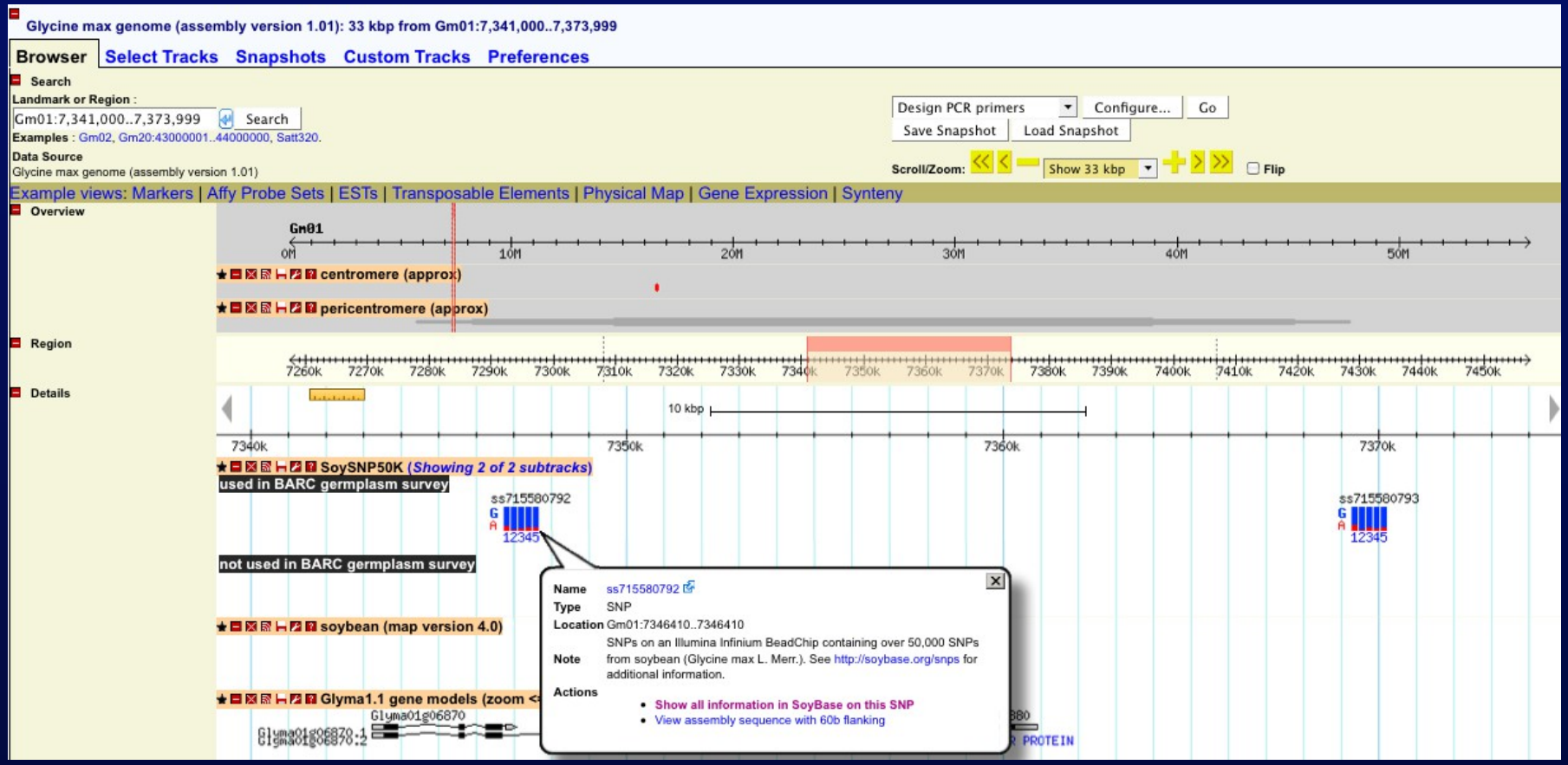
This is a more human readable version that includes both the haplotype data and the SNP descriptions. The order of SNP lines is the same as the order of SNP allele values in 'cultivar_snps'.

SNP ID	Chromosome	Position	PI442007B	PI365426	PI587703A	PI228064
ss715578401	Gm01	10015701	A	A	A	A
ss715578402	Gm01	10052330	C	C	C	C



SoySNP50K data currently only on genome assembly Wm82.a1.v1.1 (Wm82.a2.v1 coming soon).


Browser
Select Tracks
Snapshots
Custom Tracks
Preferences
Search
Landmark or Region :
Gm02:43,026,973..43,126,972
Search
Examples : Gm02, Gm20:43000001..44000000, Satt320.
Data Source
Glycine max genome (assembly version 1.01) (restricted)
Design PCR primers
Configure...
Go
Save Snapshot
Load Snapshot
Scroll/Zoom:
Show 100 kbp
Flip
Example views: Markers | Affy Probe Sets | ESTs | Transposable Elements | Physical Map | Gene Expression | Synteny
Overview
Gm02
centromere (approx)
pericentromere (approx)
Region
Details
20 kbp
BARC SNPs v.1 (Showing 2 of 2 subtracks)
used in BARC germplasm survey
not used in BARC germplasm survey
Glyma1.1 gene models (zoom <= 2 Mbp for detail)
Glyma02g37670
FAMILY NOT NAMED...(click for more)
Glyma02g37700
CLATHRIN COAT ASSEMBLY PROTEIN...(click for more)
Glyma02g37680
Glyma02g37710
SUBFAMILY NOT NAMED...(click for more)
Glyma02g37720
BASIC HELIX-LOOP-HELIX (BHLH) FAMILY PROTEIN...(click for more)
Glyma02g37740
(description unavailable)...(click for more)
Glyma02g37755
SUBFAMILY NOT NAMED...(click for more)
Glyma02g37770
PELOTA
Glyma02g37800


Glycine max genome (assembly version 1.01): 33 kbp from Gm01:7,341,000..7,373,999
Browser
Select Tracks
Snapshots
Custom Tracks
Preferences
Search
Landmark or Region :
Gm01:7,341,000..7,373,999
Search
Examples : Gm02, Gm20:43000001..44000000, Satt320.
Data Source
Glycine max genome (assembly version 1.01)
Design PCR primers
Configure...
Go
Save Snapshot
Load Snapshot
Scroll/Zoom:
Show 33 kbp
Flip
Example views: Markers | Affy Probe Sets | ESTs | Transposable Elements | Physical Map | Gene Expression | Synteny
Overview
Gm01
centromere (approx)
pericentromere (approx)
Region
Details
10 kbp
SoySNP50K (Showing 2 of 2 subtracks)
used in BARC germplasm survey
ss715580792
ss715580793
not used in BARC germplasm survey
Name ss715580792
Type SNP
Location Gm01:7346410..7346410
Note SNPs on an Illumina Infinium BeadChip containing over 50,000 SNPs from soybean (Glycine max L. Merr.). See http://soybase.org/snps for additional information.
Actions
Show all information in SoyBase on this SNP
View assembly sequence with 60b flanking
soybean (map version 4.0)
Glyma1.1 gene models (zoom <
Glyma01g06870
Glyma01g06870.1
Glyma01g06870.2

Report for ss715578909

Locus type: SNP
Organism: Glycine max
dbSNP name: ss715578909
Alternname name: BARC_1.01_Gm01_29091115_A_G

Genomic sequence information

Chromosome: Gm01
SNP position: 29091115
SNP alleles: A/G
Location in gene: intergenic
Genomic context: **Start:** 29091055
End: 29091175

Sequence:
```
GTCCGAGATCGTAGTTTTACTGGAACAAGTTTTGGAGAGGAAGAAGGGAGAATGAATTTG
[A/G]GAGGAAGAGAGGGTGTACAAACATAACATATCTTAAATGTAAAACATGGACCTAA
TATGT
```
Select All

Genome Assembly Version: Glyma1.0

Allele frequency

Population	Minor Allele	Minor Allele Frequency
96 G. max landraces	G	0.427
96 G. max elite cultivars	G	0.431
Gmax192 G. max landrace + elite	G	0.429
96 G. soja accessions	G	0.219
ALL288 G. max landrace + elite cultivars + G. soja	G	0.359

Allele distribution

Accession	Allele
Wm82	A

The allelic composition for the 19,652 cultivars and accessions used in the BARC Germplasm Survey can be downloaded here.

Data source

Data provided by: Cregan, Perry and Song, Qijian
Reference: Song et al. 2013a
Assay Information: Illumina Infinium BeadChip

SoyMap2 Diversity Browser

About

The resources below are part of the NSF project **SoyMap II: Leveraging untapped genetic diversity in soybean**, 0822258-DFBI. This project is determining important parts of the genome sequences of seven wild relatives of soybean, in order to better understand how these wild relatives have been are able to adapt to the harsh conditions where they grow - and to understand how this group of species has evolved over the several million years since they separated from their common ancestor.

This page gives access to the survey sequencing from the project, and to the twelve focus regions in the project, which are being sequenced and studied in detail. Also please see these project sites: Hudson-Alpha Intitute sequencing, Project resources for download, and Project outreach.

[More about the resources on this page ↓]

Example configurations

- Main BAC-end tracks; assembly v. 1; Gm03, 1 Mb window.
- Main BAC-end tracks; assembly v. 2; Gm03, 1 Mb window.

- Main BAC-end tracks; assembly v. 1; Gm02 entire; with exon and repeat densities.
- Main BAC-end tracks; assembly v. 2; Gm02 entire; showing correspondence between assembly versions.

- "Long" BAC-end tracks; assembly v. 1; Gm11 entire; with likely rearrangements among species.
- BAC-end tracks on assembly v. 2; Gm11 entire; showing rearrangements between assemblies 1 and 2.

Data repository for this project

All publicly-available data for this project are at http://soybase.org/data_distribution/soymap/
along with sequence- and alignment statistics, and methods. Additional data for this project will be available later in 2014, including assembled sequences for the "Regions of Interest", and transcriptome assemblies for each species.

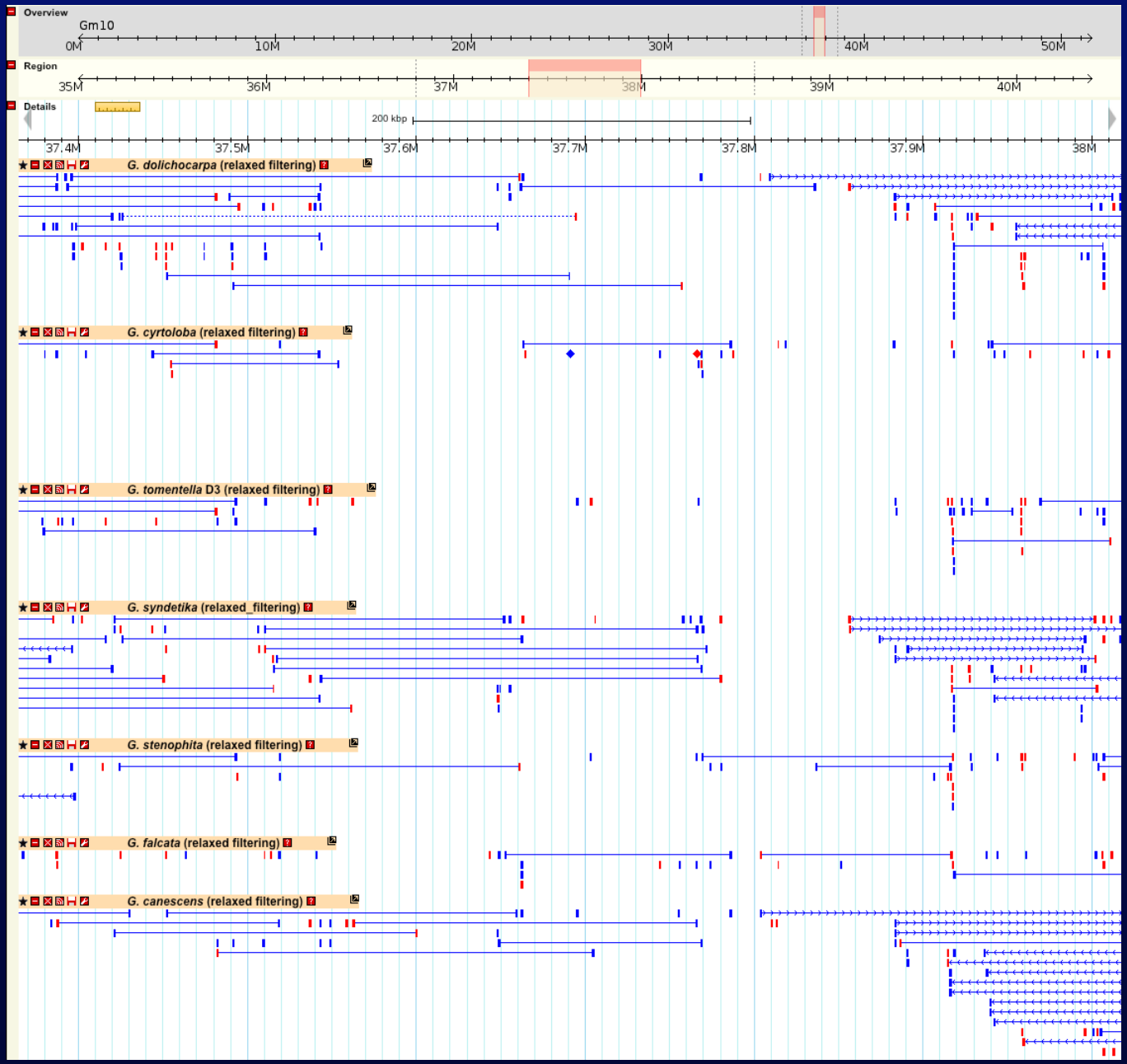
Regions of Interest - assembly v1.0

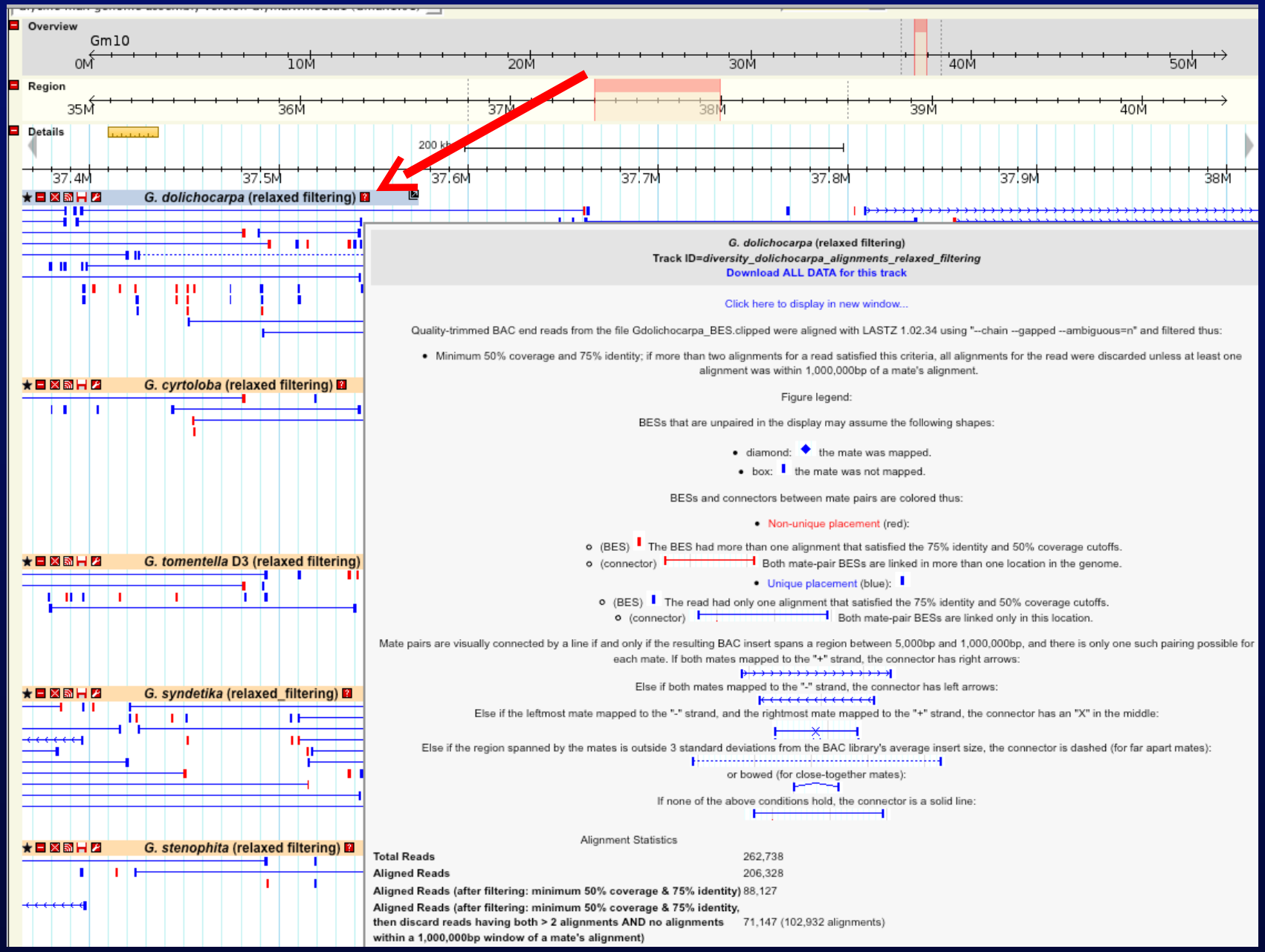
Region-Pair Nickname	Region Interest	chrA	start	end	chrB	start	end
SCN1 & SCN2	nematode resistance	Gm18	1,666,025	2,000,234	Gm11	37,055,905	37,388,911
seed protein	seed composition	Gm20	32,200,000	32,500,000	Gm10	37,095,000	37,395,000
LG E & A2	structural traits	Gm15	49,548,981	49,854,667	Gm08	12,210,798	12,633,244
Dt1 & Dt2	morphological	Gm19	44,829,743	45,129,743	Gm03	42,384,079	42,684,079
Rpp1 & Rpp2	ASR resistance	Gm18	55,655,000	55,955,000	Gm09	44,900,000	45,200,000
isoflavone synthase	seed composition	Gm07	37,114,977	37,414,977	Gm13	27,401,000	27,701,000

Regions of Interest - assembly v2.0

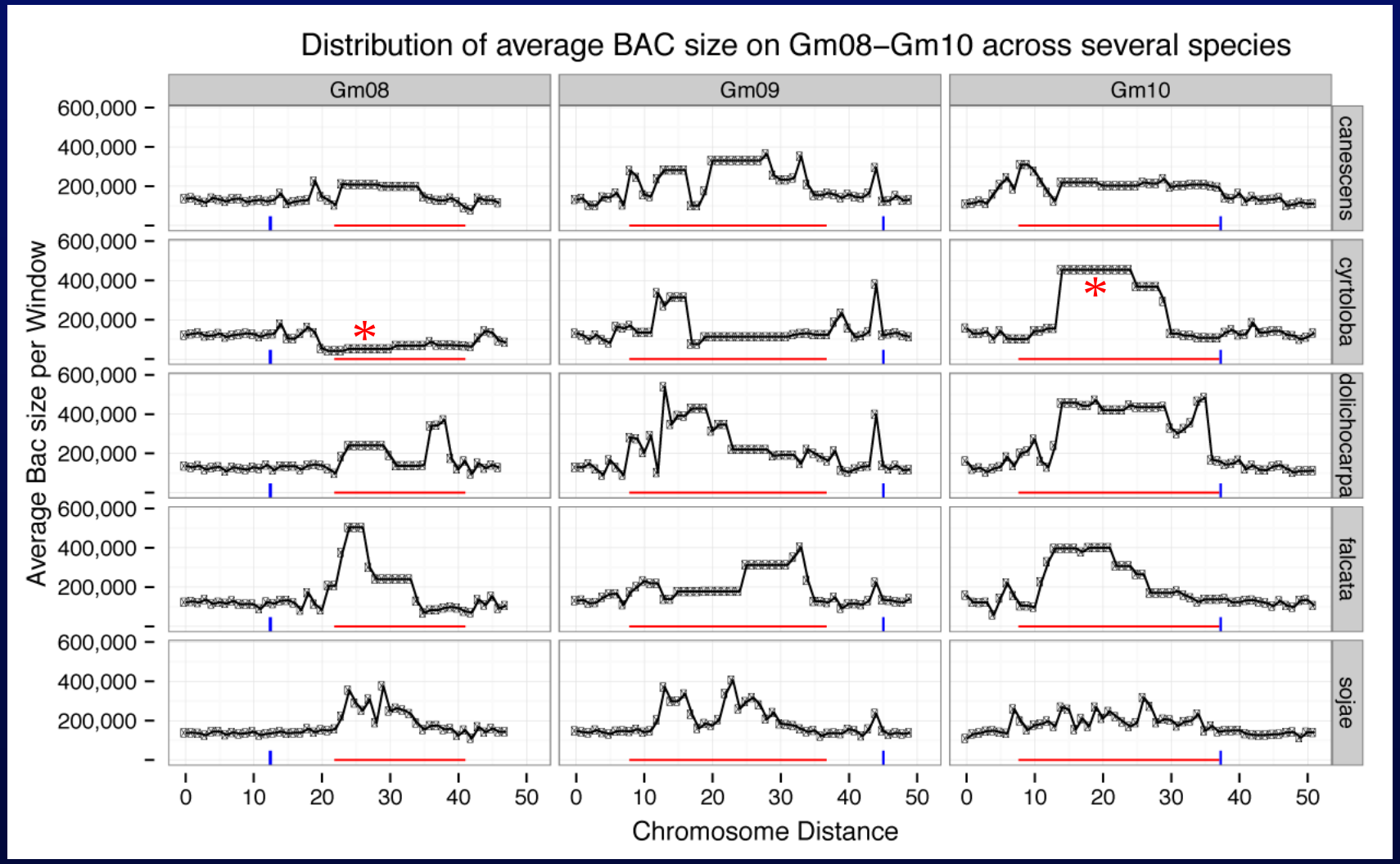
Region-Pair Nickname	Region Interest	chrA	start	end	chrB	start	end
SCN1 & SCN2	nematode resistance	Gm18	1,666,460	2,000,762	Gm11	32,603,866	32,940,400
seed protein	seed composition	Gm20	33,343,658	33,641,332	Gm10	37,621,924	37,921,195
LG E & A2	structural traits	Gm15	50,347,696	50,653,388	Gm08	12,128,367	12,550,870
Dt1 & Dt2	morphological	Gm19	45,033,356	50,013,023	Gm03	40,372,379	40,668,152
Rpp1 & Rpp2	ASR resistance	Gm18	51,379,854	51,682,831	Gm09	48,099,948	48,398,414
isoflavone synthase	seed composition	Gm07	37,011,571	37,320,614	Gm13	28,594,532	28,895,103

http://soybase.org/soymap2


Overview
Gm10
0M
10M
20M
30M
40M
50M
Region
35M
36M
37M
38M
39M
40M
Details
200 kbp
37.4M
37.5M
37.6M
37.7M
37.8M
37.9M
38M
G. dolichocarpa (relaxed filtering)
G. cyrtoloba (relaxed filtering)
G. tomentella D3 (relaxed filtering)
G. syndetika (relaxed_filtering)
G. stenophita (relaxed filtering)
G. falcata (relaxed filtering)
G. canescens (relaxed filtering)


Overview
Gm10
0M
10M
20M
30M
40M
50M
Region
35M
36M
37M
38M
39M
40M
Details
200 kb
37.4M
37.5M
37.6M
37.7M
37.8M
37.9M
38M
G. dolichocarpa (relaxed filtering)
G. cyrtoloba (relaxed filtering)
G. tomentella D3 (relaxed filtering)
G. syndetika (relaxed_filtering)
G. stenophita (relaxed filtering)
G. dolichocarpa (relaxed filtering)
Track ID=diversity_dolichocarpa_alignments_relaxed_filtering
Download ALL DATA for this track
Click here to display in new window...
Quality-trimmed BAC end reads from the file Gdolichocarpa_BES.clipped were aligned with LASTZ 1.02.34 using "--chain --gapped --ambiguous=n" and filtered thus:
Minimum 50% coverage and 75% identity; if more than two alignments for a read satisfied this criteria, all alignments for the read were discarded unless at least one alignment was within 1,000,000bp of a mate's alignment.
Figure legend:
BESs that are unpaired in the display may assume the following shapes:
diamond: the mate was mapped.
box: the mate was not mapped.
BESs and connectors between mate pairs are colored thus:
Non-unique placement (red):
(BES) The BES had more than one alignment that satisfied the 75% identity and 50% coverage cutoffs.
(connector) Both mate-pair BESs are linked in more than one location in the genome.
Unique placement (blue):
(BES) The read had only one alignment that satisfied the 75% identity and 50% coverage cutoffs.
(connector) Both mate-pair BESs are linked only in this location.
Mate pairs are visually connected by a line if and only if the resulting BAC insert spans a region between 5,000bp and 1,000,000bp, and there is only one such pairing possible for each mate. If both mates mapped to the "+" strand, the connector has right arrows:
Else if both mates mapped to the "-" strand, the connector has left arrows:
Else if the leftmost mate mapped to the "-" strand, and the rightmost mate mapped to the "+" strand, the connector has an "X" in the middle:
Else if the region spanned by the mates is outside 3 standard deviations from the BAC library's average insert size, the connector is dashed (for far apart mates):
or bowed (for close-together mates):
If none of the above conditions hold, the connector is a solid line:
Alignment Statistics
Total Reads 262,738
Aligned Reads 206,328
Aligned Reads (after filtering: minimum 50% coverage & 75% identity) 88,127
Aligned Reads (after filtering: minimum 50% coverage & 75% identity, then discard reads having both > 2 alignments AND no alignments within a 1,000,000bp window of a mate's alignment) 71,147 (102,932 alignments)

Comparison of BAC Sizes Among Representative Glycines



Improved QTL Names

Asian Soybean Rust	Asian Soybean Rust
Branching	Branching
BSR	BSR
Cnpy ht	Canopy height
Cnpy wdth	Canopy width
CID	Carbon isotope discrimination
CWP	Cellwall polysacch composition
CES	Chlorimuron sensitivity
CCW	Common cutworm
CEW	Corn earworm
Lf ł chlorophyll	Leaf łet chlorophyll
Lf lgth	Leaf łet length
Specif ċ lf ł N	Leaf łet N, specif ċ
Lf Phos	Leaf łet P
Lf ł shape	Leaf łet shape
TRG(DW)	Leaf łet trigonelline, dry
TRG(FW)	Leaf łet trigonelline, fresh
Lf wdth	Leaf łet width
NitR7	Seed N at R7
Sd num	Seed number
Oil	Seed oil
Sd wt/plant	Seed weight per plant
Sd yld	Seed yield
Yld/Ht	Seed yield/Plant height
Yld/SW	Seed yield/Seed weight
R5	Seed, beginning

SoyBase and the Soybean Breeder's Toolbox

Integrating Genetics and Molecular Biology for Soybean Researchers

SoyBase | Maps | Genome | Analysis Tools | Resources | SoySeq

Search | Data | Tools | SoyCyc | Legume Research Programs | Soybean Breeders Workshop | Download Data | Submit Your Data | Contact Us

Community Resources and Communications

Tutorials

SoyBase Video Tutorials

- SoyBase Genetic Map Tutorials
- SoyBase Sequence Map Tutorials
- SoyBase Database Searching Tutorials

YouTube Videos

- Soybean Growth and Development
- Soybean Diseases
- Soybean Pests
- Methods and Protocols

Making Crosses with Soybean
Harvesting Research Plots

YouTube and MP4 Tutorials

Table of Contents

Clicking on the table of contents below will take you to the YouTube and MP4 links. Click the title to view a YouTube video or click the "MP4" to download an MP4 version of the YouTube video. Mousing over the title will produce a thumbnail of the video and an expanded description.

- **SoyBase Tutorials**
  - *SoyBase Genetic Map Tutorials*
  - *SoyBase Sequence Map Tutorials*
  - *SoyBase Database Searching Tutorials*

- **YouTube Videos of Note**
  - *Soybean Growth and Development Videos*
  - *Soybean Disease Videos*
  - *Soybean Pest Videos*
  - *Methods and Protocol Videos*

SoyBase Genetic Map Tutorials

- How to zoom into a region on the genetic map
  (3:10, 118 Mb MP4)
- How to flip genetic maps to resolve corresponding marker positions
  (1:44, 57 Mb MP4)
- Turning QTL classes off/on
  (3:08, 78 Mb MP4)
- Removing and adding genetic maps
  (4:27, 115 Mb MP4)
- How to quickly bring up a genetic or sequence map at SoyBase
  (1:18, 28 Mb MP4)
- How do I find markers on a genetic map that are not visible
  (2:00, 57 Mb MP4)
- How do I compare the genetic marker order to the sequence marker order
  (3:45, 113 Mb MP4)

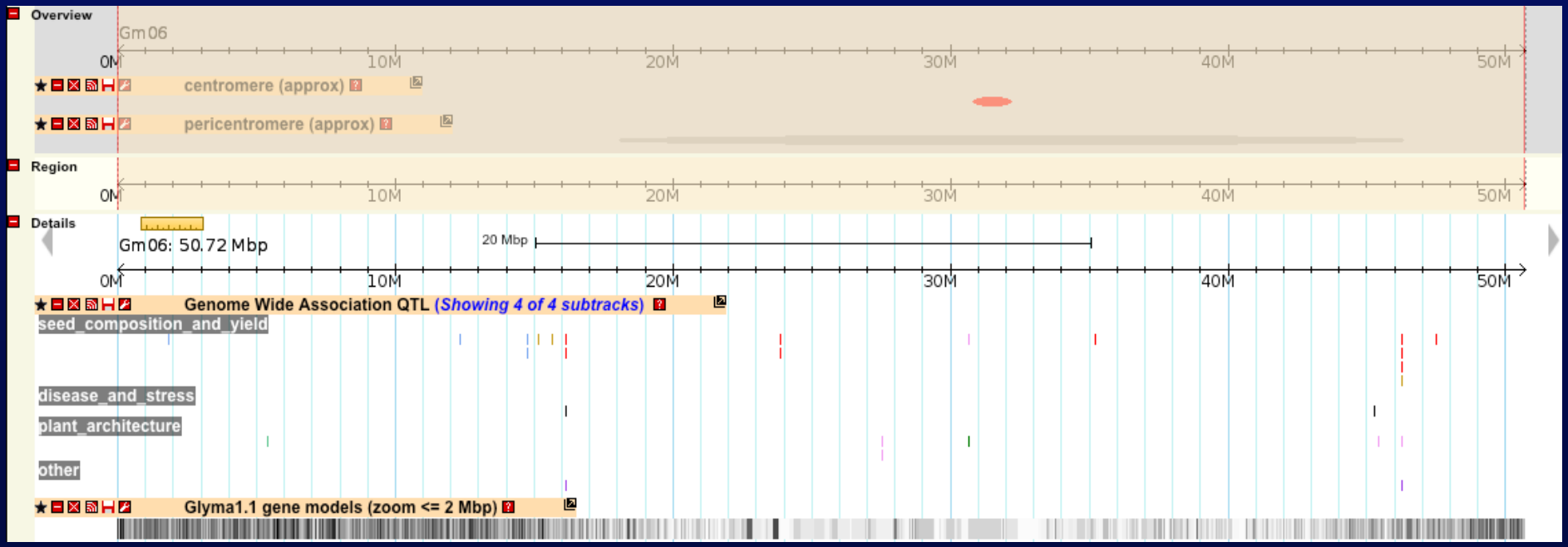
Sequence Map Tutorials

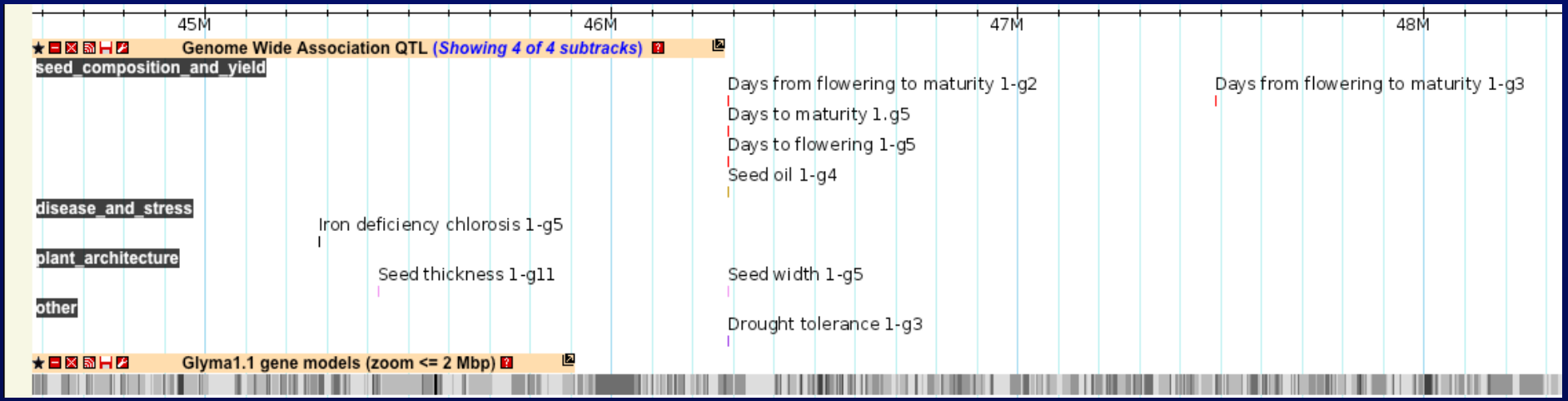
- How to move tracks in the SoyBase sequence viewer
  (0:56, 31 Mb MP4)
- How to find information on tracks in the SoyBase sequence viewer
  (2:01, 35 Mb MP4)
- Modifying tracks on the SoyBase sequence viewer
  (1:12, 41 Mb MP4)
- Zooming into a region on the SoyBase sequence map
  (2:04, 44 Mb MP4)
- How to visualize the approximate genetic position of a gene call on the genetic map
  (2:19, 62 Mb MP4)

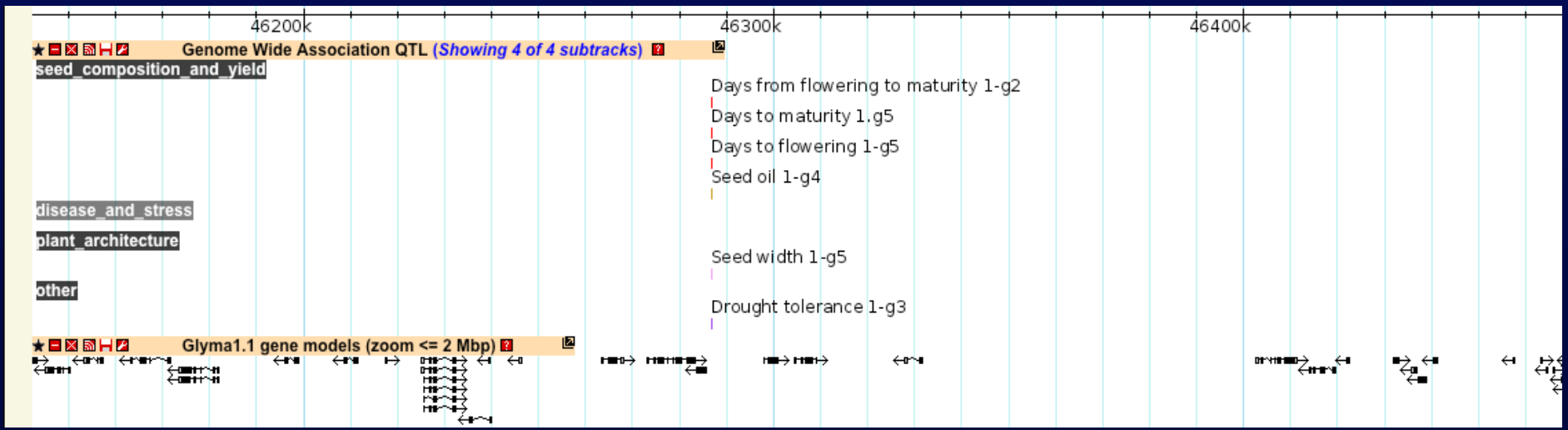
SoyBase Searching Tutorials

- How to do a quick BLAST against the soybean genome sequence
  (1:45, 46 Mb MP4)
- Advanced BLAST analysis at SoyBase
  (4:07, 95 Mb MP4)
- How to perform a quick search of SoyBase
  (3:17, 79 Mb MP4)
- How to perform a SoyCyc quick search
  (2:01, 44 Mb MP4)
- How to quickly get a list of all loci at SoyBase
  (2:10, 80 Mb MP4)
- How do I get a list of all QTL in SoyBase
  (3:08, 79 Mb MP4)
- How to search the Fast Neutron Mutant collection using a trait value
  (1:51, 44 Mb MP4)
- Explanation of a Fast Neutron search report
  (4:07, 120 Mb MP4)

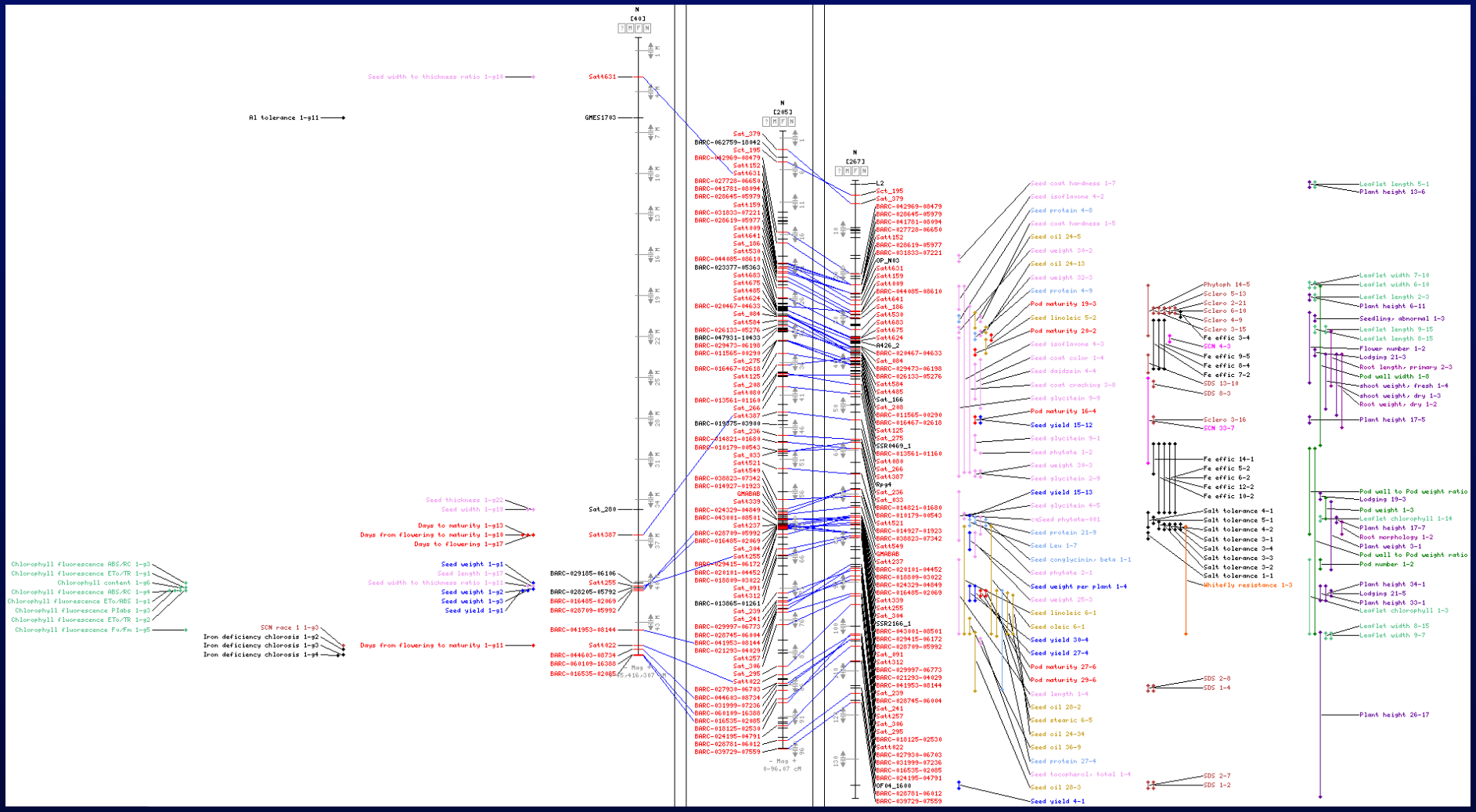
Trait Associated Markers Shown on the Genome Sequence




45M
46M
47M
48M
Genome Wide Association QTL (Showing 4 of 4 subtracks)
seed_composition_and_yield
Days from flowering to maturity 1-g2
Days from flowering to maturity 1-g3
Days to maturity 1.g5
Days to flowering 1-g5
Seed oil 1-g4
disease_and_stress
Iron deficiency chlorosis 1-g5
plant_architecture
Seed thickness 1-g11
Seed width 1-g5
other
Drought tolerance 1-g3
Glyma1.1 gene models (zoom <= 2 Mbp)

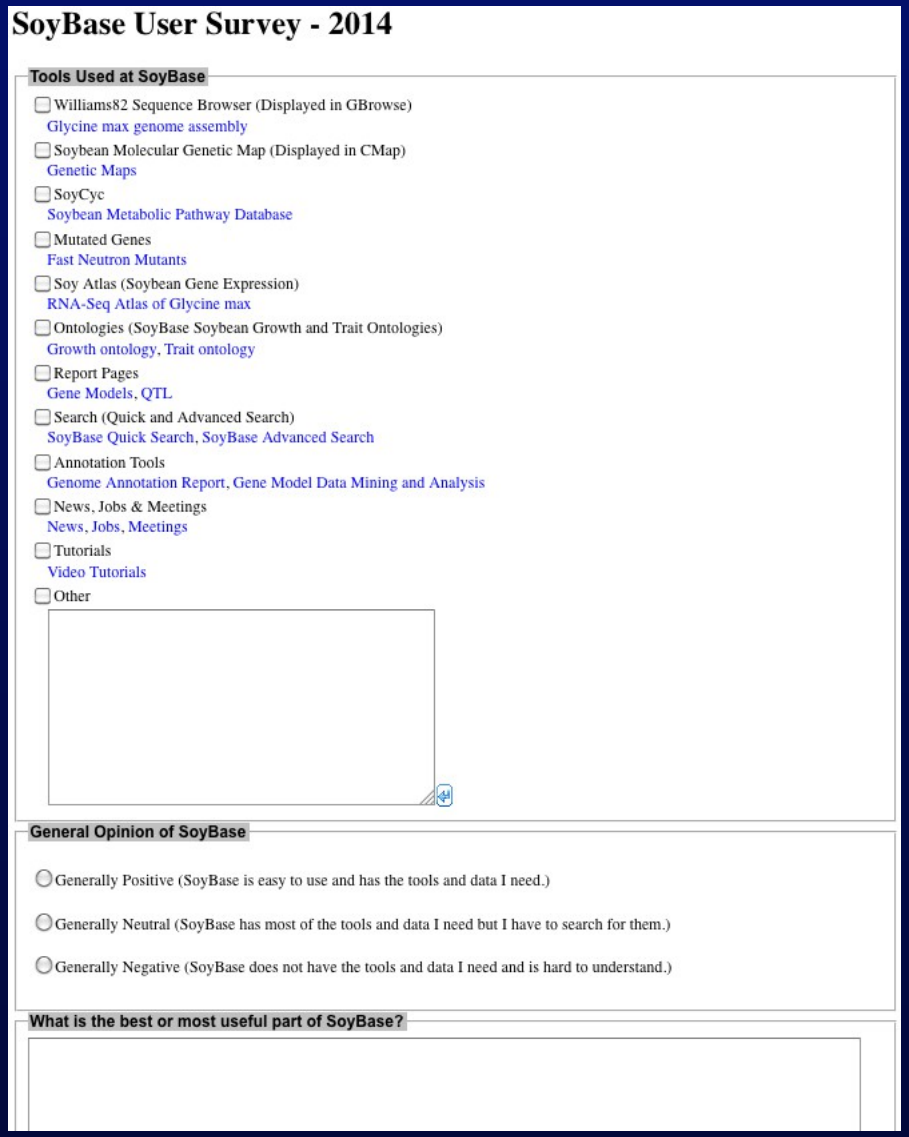

46200k
46300k
46400k
Genome Wide Association QTL (Showing 4 of 4 subtracks)
seed_composition_and_yield
Days from flowering to maturity 1-g2
Days to maturity 1.g5
Days to flowering 1-g5
Seed oil 1-g4
disease_and_stress
plant_architecture
Seed width 1-g5
other
Drought tolerance 1-g3
Glyma1.1 gene models (zoom <= 2 Mbp)

Trait Associated Markers Shown on the Genetic Map



USDA United States Department Of Agriculture Agricultural Research Service

SoyBase



SoyBase User Survey - 2014

Tools Used at SoyBase

- Williams82 Sequence Browser (Displayed in GBrowse)
  Glycine max genome assembly
- Soybean Molecular Genetic Map (Displayed in CMap)
  Genetic Maps
- SoyCyc
  Soybean Metabolic Pathway Database
- Mutated Genes
  Fast Neutron Mutants
- Soy Atlas (Soybean Gene Expression)
  RNA-Seq Atlas of Glycine max
- Ontologies (SoyBase Soybean Growth and Trait Ontologies)
  Growth ontology, Trait ontology
- Report Pages
  Gene Models, QTL
- Search (Quick and Advanced Search)
  SoyBase Quick Search, SoyBase Advanced Search
- Annotation Tools
  Genome Annotation Report, Gene Model Data Mining and Analysis
- News, Jobs & Meetings
  News, Jobs, Meetings
- Tutorials
  Video Tutorials
- Other

General Opinion of SoyBase

- Generally Positive (SoyBase is easy to use and has the tools and data I need.)
- Generally Neutral (SoyBase has most of the tools and data I need but I have to search for them.)
- Generally Negative (SoyBase does not have the tools and data I need and is hard to understand.)

What is the best or most useful part of SoyBase?

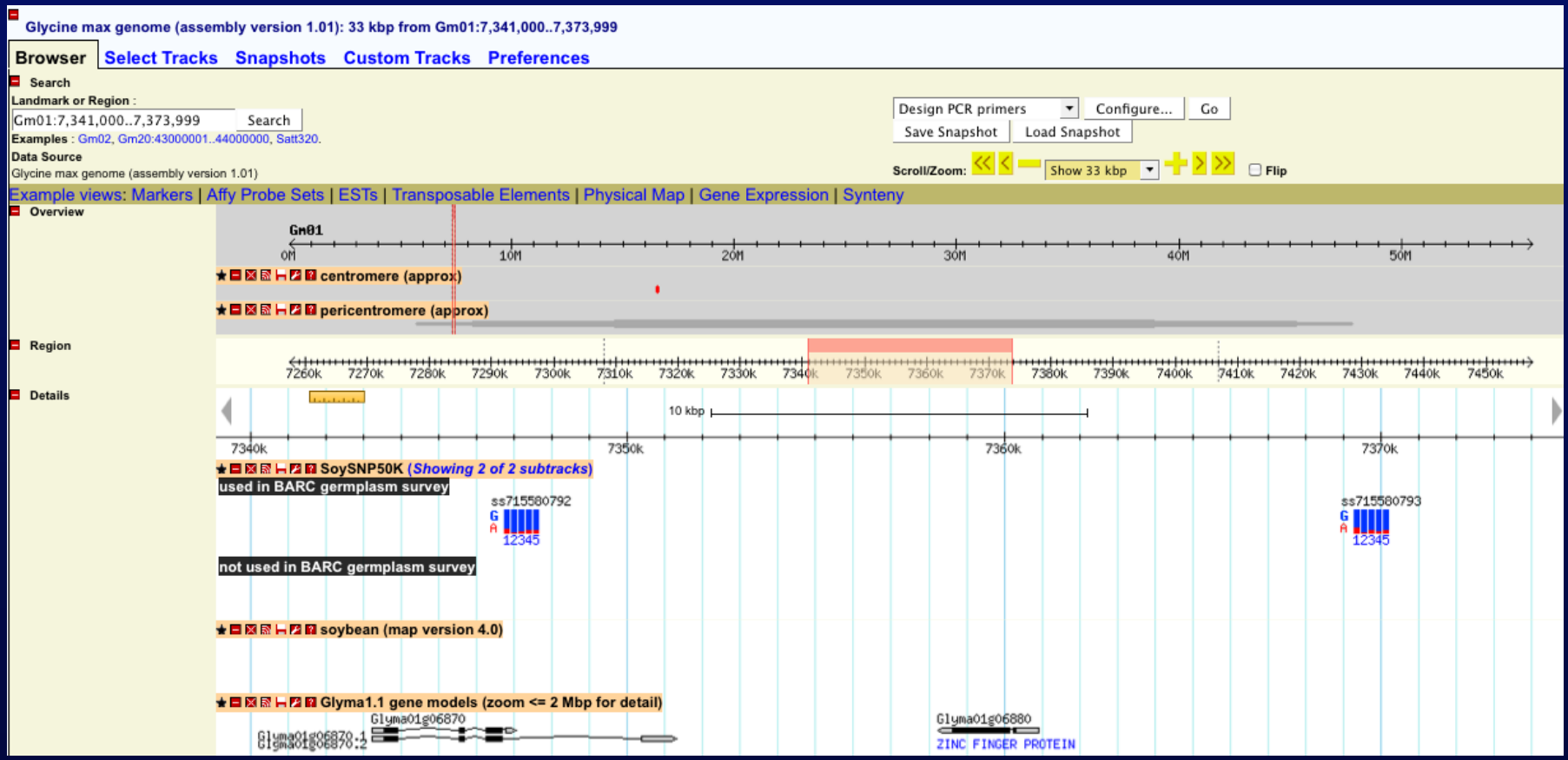
Please take the SoyBase survey

http://soybase.org/survey

Also linked from SoyBase home page

Questions?

http://soybase.org


Glycine max genome (assembly version 1.01): 33 kbp from Gm01:7,341,000..7,373,999
Browser
Select Tracks
Snapshots
Custom Tracks
Preferences
Search
Landmark or Region :
Gm01:7,341,000..7,373,999
Search
Examples : Gm02, Gm20:43000001..44000000, Satt320.
Data Source
Glycine max genome (assembly version 1.01)
Design PCR primers
Configure...
Go
Save Snapshot
Load Snapshot
Scroll/Zoom:
Show 33 kbp
Flip
Example views: Markers | Affy Probe Sets | ESTs | Transposable Elements | Physical Map | Gene Expression | Synteny
Overview
Gm01
0M
10M
20M
30M
40M
50M
centromere (approx)
pericentromere (approx)
Region
7260k
7270k
7280k
7290k
7300k
7310k
7320k
7330k
7340k
7350k
7360k
7370k
7380k
7390k
7400k
7410k
7420k
7430k
7440k
7450k
Details
10 kbp
7340k
7350k
7360k
7370k
SoySNP50K (Showing 2 of 2 subtracks)
used in BARC germplasm survey
ss715580792
G
A
12345
ss715580793
G
A
12345
not used in BARC germplasm survey
soybean (map version 4.0)
Glyma1.1 gene models (zoom <= 2 Mbp for detail)
Glyma01g06870
Glyma01g06870.1
Glyma01g06870.2
Glyma01g06880
ZINC FINGER PROTEIN

Conceptual Haplotype Viewer Using A Condensed Graphical Form