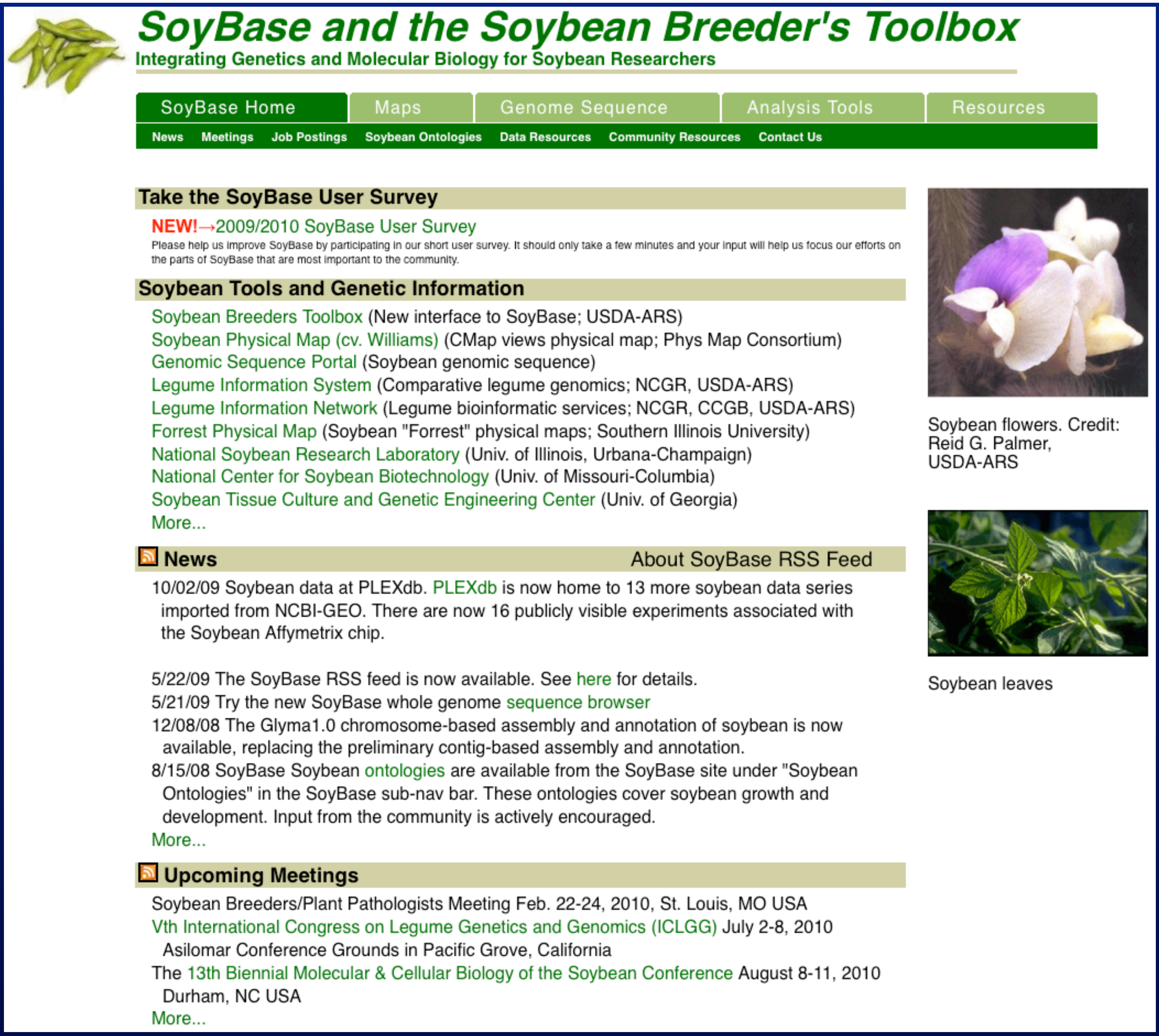
What’s New at SoyBase?

David Grant

Rex Nelson, Steven Cannon,
Nathan Weeks, Randy Shoemaker



SoyBase and the Soybean Breeder's Toolbox

Integrating Genetics and Molecular Biology for Soybean Researchers

Take the SoyBase User Survey

NEW!→2009/2010 SoyBase User Survey

Please help us improve SoyBase by participating in our short user survey. It should only take a few minutes and your input will help us focus our efforts on the parts of SoyBase that are most important to the community.

Soybean Tools and Genetic Information

Soybean Breeders Toolbox (New interface to SoyBase; USDA-ARS)
Soybean Physical Map (cv. Williams) (CMap views physical map; Phys Map Consortium)
Genomic Sequence Portal (Soybean genomic sequence)
Legume Information System (Comparative legume genomics; NCGR, USDA-ARS)
Legume Information Network (Legume bioinformatic services; NCGR, CCGB, USDA-ARS)
Forrest Physical Map (Soybean "Forrest" physical maps; Southern Illinois University)
National Soybean Research Laboratory (Univ. of Illinois, Urbana-Champaign)
National Center for Soybean Biotechnology (Univ. of Missouri-Columbia)
Soybean Tissue Culture and Genetic Engineering Center (Univ. of Georgia)
More...

News

About SoyBase RSS Feed

10/02/09 Soybean data at PLEXdb. PLEXdb is now home to 13 more soybean data series imported from NCBI-GEO. There are now 16 publicly visible experiments associated with the Soybean Affymetrix chip.

5/22/09 The SoyBase RSS feed is now available. See here for details.
5/21/09 Try the new SoyBase whole genome sequence browser
12/08/08 The Glyma1.0 chromosome-based assembly and annotation of soybean is now available, replacing the preliminary contig-based assembly and annotation.
8/15/08 SoyBase Soybean ontologies are available from the SoyBase site under "Soybean Ontologies" in the SoyBase sub-nav bar. These ontologies cover soybean growth and development. Input from the community is actively encouraged.
More...

Upcoming Meetings

Soybean Breeders/Plant Pathologists Meeting Feb. 22-24, 2010, St. Louis, MO USA
Vth International Congress on Legume Genetics and Genomics (ICLGG) July 2-8, 2010 Asilomar Conference Grounds in Pacific Grove, California
The 13th Biennial Molecular & Cellular Biology of the Soybean Conference August 8-11, 2010 Durham, NC USA
More...

Soybean flowers. Credit: Reid G. Palmer, USDA-ARS

Soybean leaves

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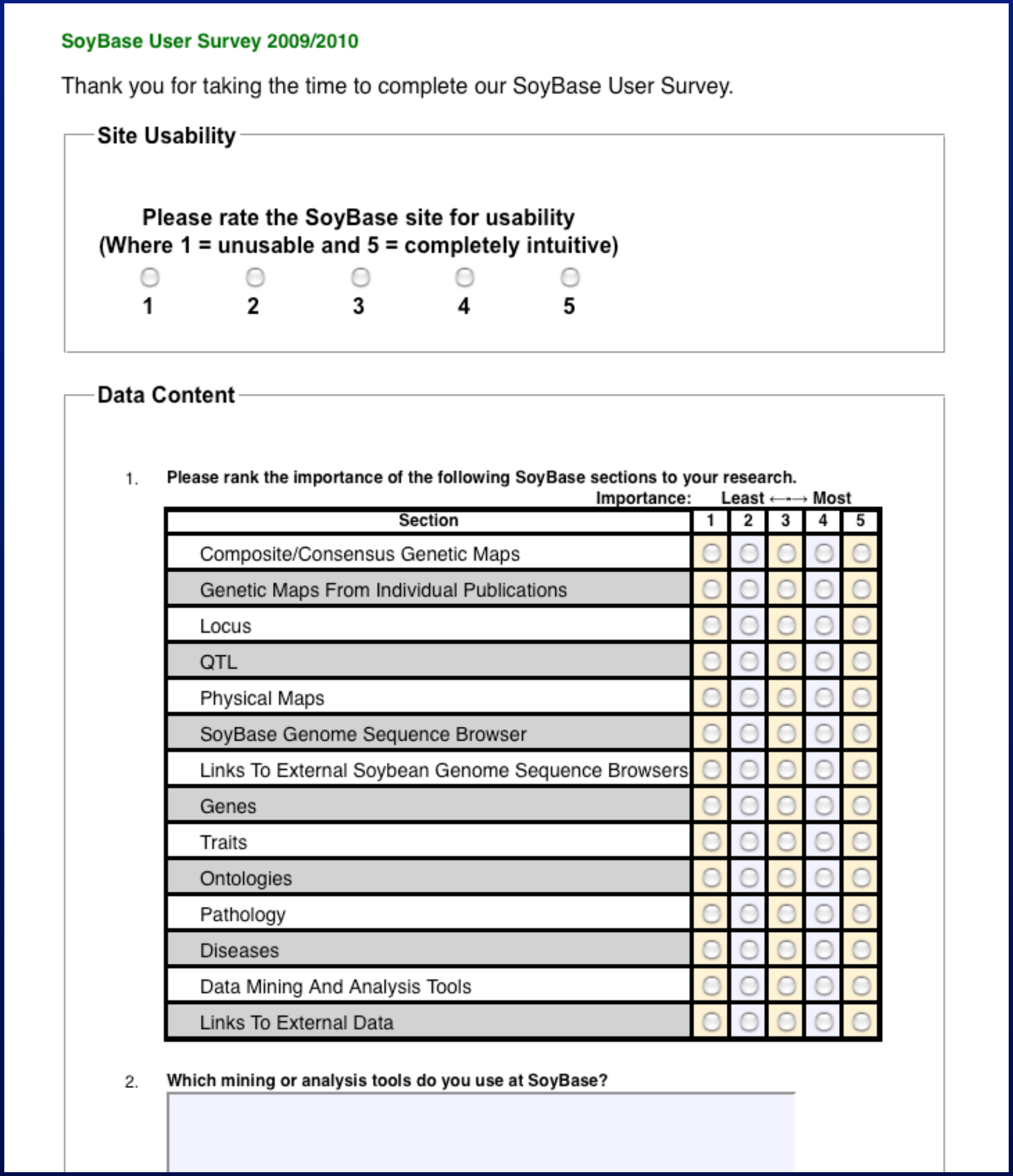
ars

SoyBase

SoyBase User Survey



SoyBase User Survey 2009/2010

Thank you for taking the time to complete our SoyBase User Survey.

Site Usability

Please rate the SoyBase site for usability
(Where 1 = unusable and 5 = completely intuitive)

○ 1 ○ 2 ○ 3 ○ 4 ○ 5

Data Content

1. **Please rank the importance of the following SoyBase sections to your research.**

Importance: Least ←-→ Most

Section	1	2	3	4	5
Composite/Consensus Genetic Maps	○	○	○	○	○
Genetic Maps From Individual Publications	○	○	○	○	○
Locus	○	○	○	○	○
QTL	○	○	○	○	○
Physical Maps	○	○	○	○	○
SoyBase Genome Sequence Browser	○	○	○	○	○
Links To External Soybean Genome Sequence Browsers	○	○	○	○	○
Genes	○	○	○	○	○
Traits	○	○	○	○	○
Ontologies	○	○	○	○	○
Pathology	○	○	○	○	○
Diseases	○	○	○	○	○
Data Mining And Analysis Tools	○	○	○	○	○
Links To External Data	○	○	○	○	○

2. **Which mining or analysis tools do you use at SoyBase?**

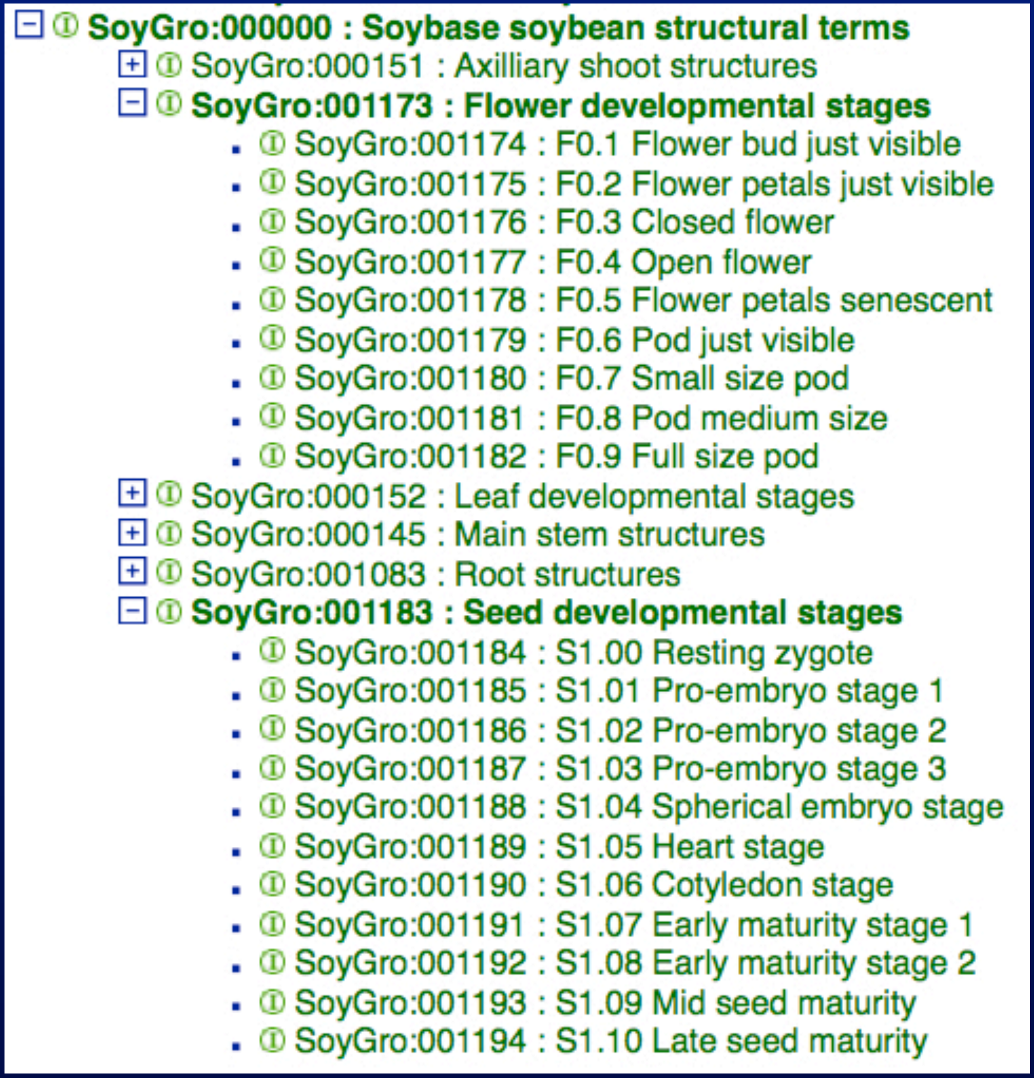
New QTL in SoyBase

- QTL for more than 100 traits from over 40 studies
- Confirmed QTL
  - cqOil-001
  - cqOil-002
  - cqOil-003
  - cqOil-004
  - cqPod mat-001
  - cqProt-001
  - cqPRO-003
  - cqSCN-001
  - cqSCN-002
  - cqSCN-003
  - cqSd wt-001
  - cqSd wt-002
  - cqSd wt-003
  - cqSd yld-001
  - cqSDS-001

SoyBase Soybean Ontologies

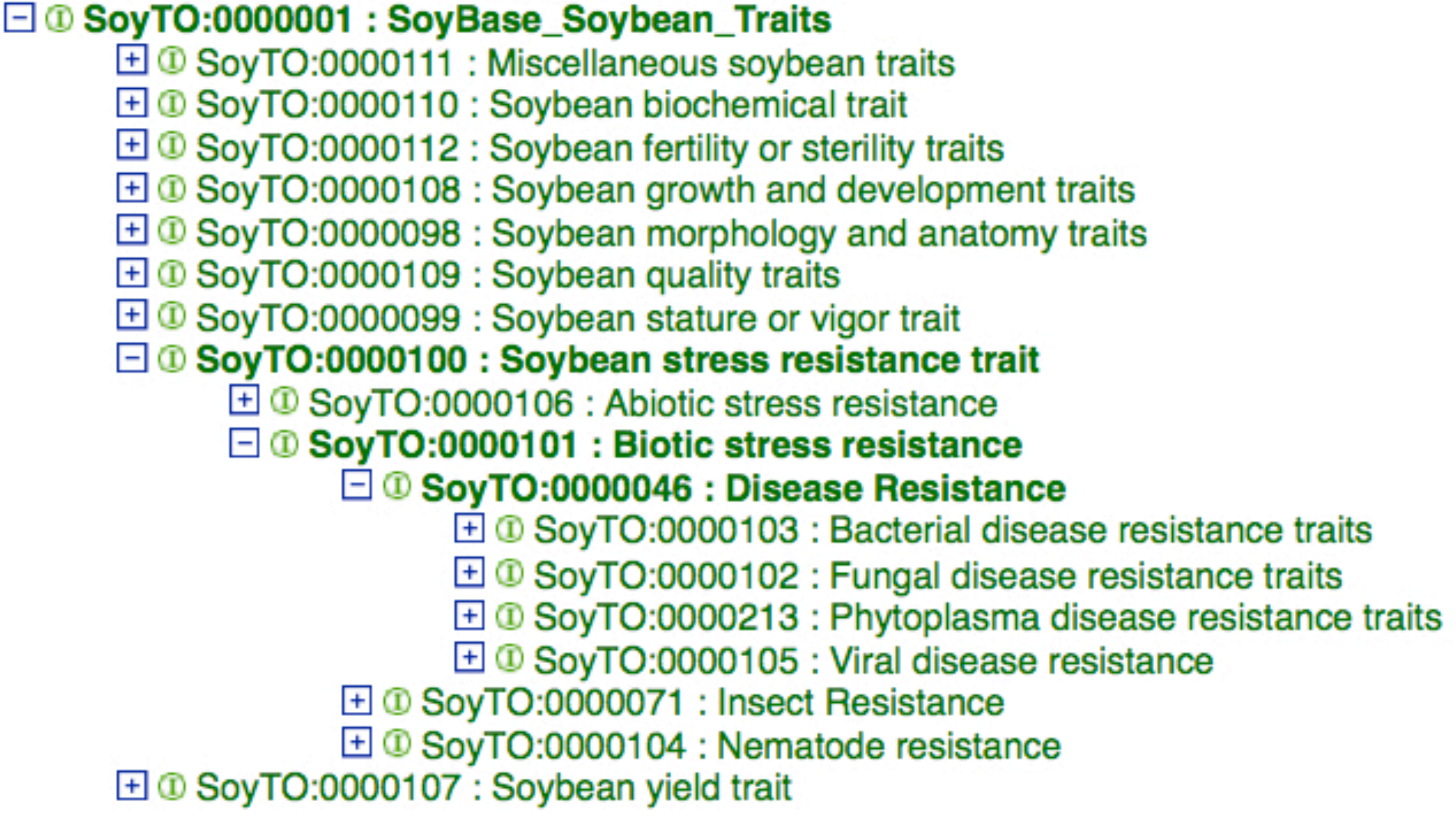
- Whole plant growth stages (SoyWGR)
  - Similar to the BBCH and Soybean Growth stages (ISU extension pub 1945) definitions
  - Links the BBCH scale to the soybean growth stages
- Growth and Development Stages (SoyGRO)
  - Describes in detail soybean growth and development
  - Links SoyGRO to the Plant Ontology
- Soybean Trait Ontology (SoyTO)
  - Incorporates the GRIN descriptors
  - Links soybean traits to the Plant Trait Ontology

Soybean Growth and Development Ontology (SoyGRO)



- ⊟ **SoyGro:000000 : Soybase soybean structural terms**
  - ⊞ SoyGro:000151 : Axilliary shoot structures
  - ⊟ **SoyGro:001173 : Flower developmental stages**
    - SoyGro:001174 : F0.1 Flower bud just visible
    - SoyGro:001175 : F0.2 Flower petals just visible
    - SoyGro:001176 : F0.3 Closed flower
    - SoyGro:001177 : F0.4 Open flower
    - SoyGro:001178 : F0.5 Flower petals senescent
    - SoyGro:001179 : F0.6 Pod just visible
    - SoyGro:001180 : F0.7 Small size pod
    - SoyGro:001181 : F0.8 Pod medium size
    - SoyGro:001182 : F0.9 Full size pod
  - ⊞ SoyGro:000152 : Leaf developmental stages
  - ⊞ SoyGro:000145 : Main stem structures
  - ⊞ SoyGro:001083 : Root structures
  - ⊟ **SoyGro:001183 : Seed developmental stages**
    - SoyGro:001184 : S1.00 Resting zygote
    - SoyGro:001185 : S1.01 Pro-embryo stage 1
    - SoyGro:001186 : S1.02 Pro-embryo stage 2
    - SoyGro:001187 : S1.03 Pro-embryo stage 3
    - SoyGro:001188 : S1.04 Spherical embryo stage
    - SoyGro:001189 : S1.05 Heart stage
    - SoyGro:001190 : S1.06 Cotyledon stage
    - SoyGro:001191 : S1.07 Early maturity stage 1
    - SoyGro:001192 : S1.08 Early maturity stage 2
    - SoyGro:001193 : S1.09 Mid seed maturity
    - SoyGro:001194 : S1.10 Late seed maturity

Soybean Trait Ontology (SoyTO)



- **SoyTO:0000001 : SoyBase_Soybean_Traits**
  - SoyTO:0000111 : Miscellaneous soybean traits
  - SoyTO:0000110 : Soybean biochemical trait
  - SoyTO:0000112 : Soybean fertility or sterility traits
  - SoyTO:0000108 : Soybean growth and development traits
  - SoyTO:0000098 : Soybean morphology and anatomy traits
  - SoyTO:0000109 : Soybean quality traits
  - SoyTO:0000099 : Soybean stature or vigor trait
  - **SoyTO:0000100 : Soybean stress resistance trait**
    - SoyTO:0000106 : Abiotic stress resistance
    - **SoyTO:0000101 : Biotic stress resistance**
      - **SoyTO:0000046 : Disease Resistance**
        - SoyTO:0000103 : Bacterial disease resistance traits
        - SoyTO:0000102 : Fungal disease resistance traits
        - SoyTO:0000213 : Phytoplasma disease resistance traits
        - SoyTO:0000105 : Viral disease resistance
      - SoyTO:0000071 : Insect Resistance
      - SoyTO:0000104 : Nematode resistance
  - SoyTO:0000107 : Soybean yield trait

Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean

Qijian Song, Gaofeng Jia, Youlin Zhu, David Grant,
Rex T. Nelson, Eun-Young Hwang,
David L. Hyten, Perry B. Cregan

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Agricultural Research Service

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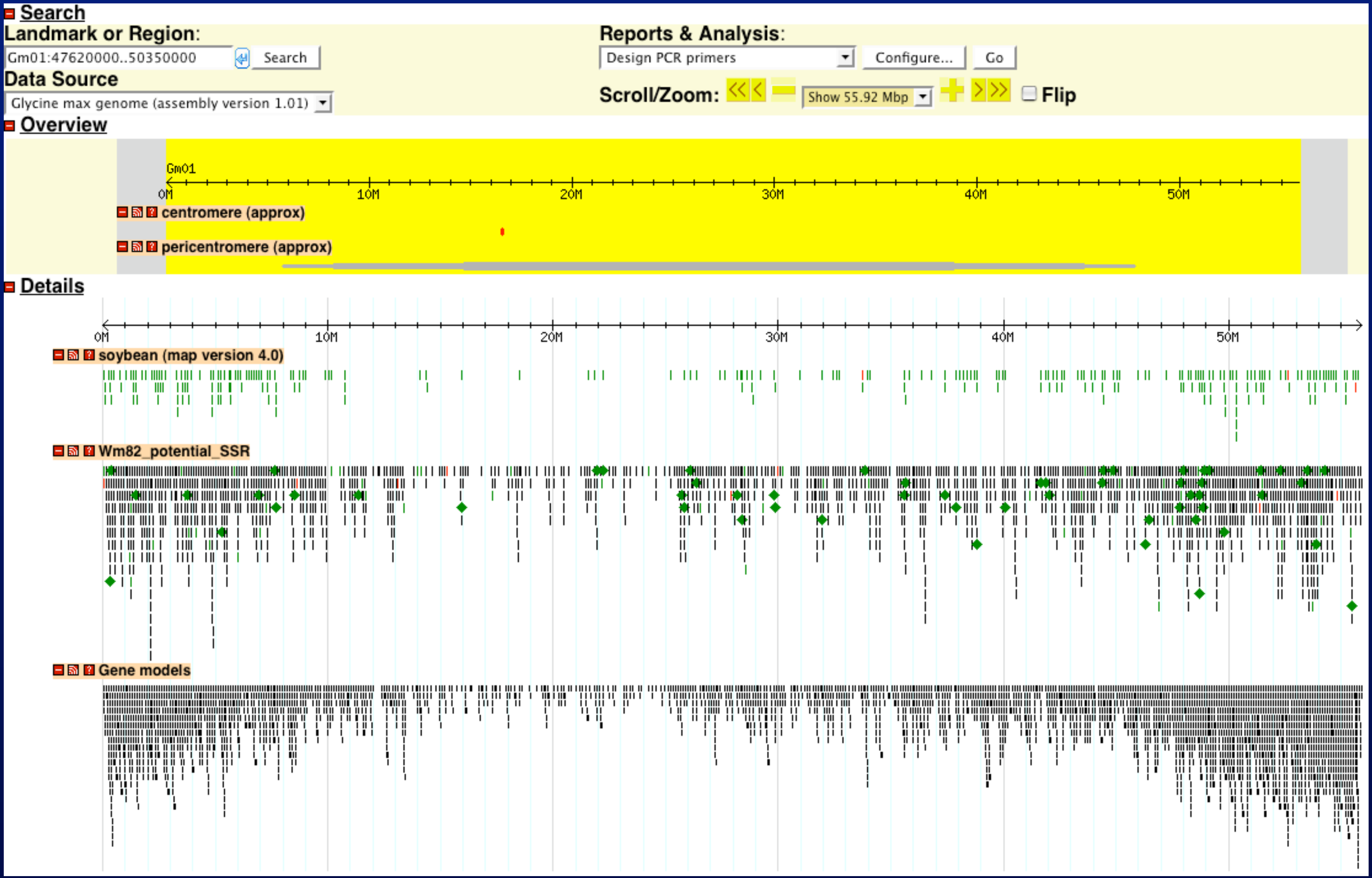
Potential SSRs in GBrowse



Landmark or Region: Gm01:47620000..50350000

Data Source: Glycine max genome (assembly version 1.01)

Reports & Analysis: Design PCR primers

Scroll/Zoom: Show 55.92 Mbp ☐ Flip

Search
Search
Configure...
Go
Overview
Gm01
0M
10M
20M
30M
40M
50M
centromere (approx)
pericentromere (approx)
Details
soybean (map version 4.0)
Wm82_potential_SSR
Gene models

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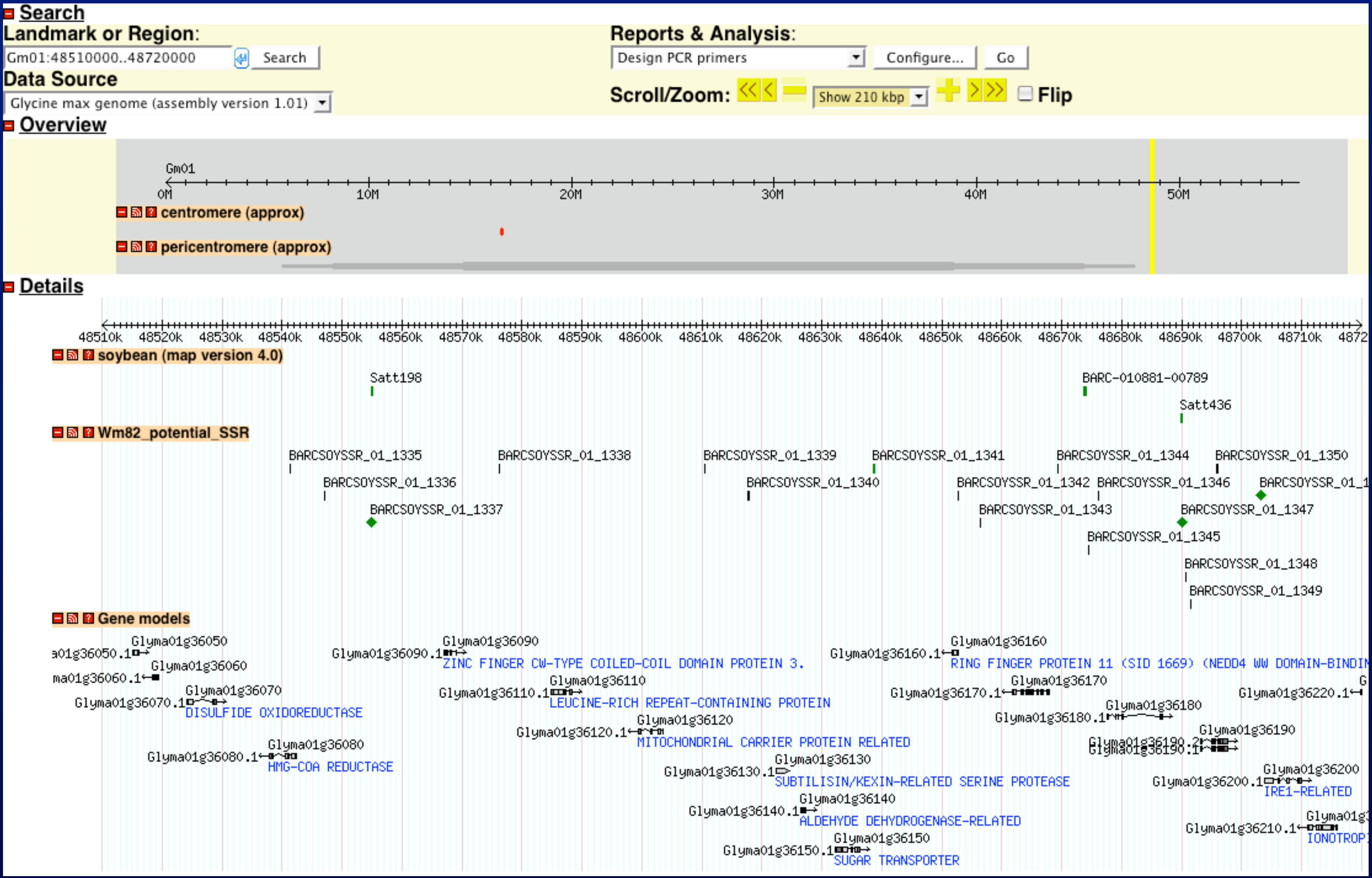
ars

SoyBase

Potential SSRs in GBrowse



Landmark or Region: Gm01:48510000..48720000

Data Source: Glycine max genome (assembly version 1.01)

Reports & Analysis: Design PCR primers

Scroll/Zoom: Show 210 kbp

☐ Flip

Search
Search
Configure...
Go
Overview
Gm01
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20M
30M
40M
50M
centromere (approx)
pericentromere (approx)
Details
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48520k
48530k
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48570k
48580k
48590k
48600k
48610k
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48630k
48640k
48650k
48660k
48670k
48680k
48690k
48700k
48710k
4872
soybean (map version 4.0)
Satt198
BARC-010881-00789
Satt436
Wm82_potential_SSR
BARCSOYSSR_01_1335
BARCSOYSSR_01_1336
BARCSOYSSR_01_1337
BARCSOYSSR_01_1338
BARCSOYSSR_01_1339
BARCSOYSSR_01_1340
BARCSOYSSR_01_1341
BARCSOYSSR_01_1342
BARCSOYSSR_01_1343
BARCSOYSSR_01_1344
BARCSOYSSR_01_1345
BARCSOYSSR_01_1346
BARCSOYSSR_01_1347
BARCSOYSSR_01_1348
BARCSOYSSR_01_1349
BARCSOYSSR_01_1350
BARCSOYSSR_01_1
Gene models
Glyma01g36050
a01g36050.1
Glyma01g36060
ma01g36060.1
Glyma01g36070
Glyma01g36070.1
DISULFIDE OXIDOREDUCTASE
Glyma01g36080
Glyma01g36080.1
HMG-COA REDUCTASE
Glyma01g36090
Glyma01g36090.1
ZINC FINGER CW-TYPE COILED-COIL DOMAIN PROTEIN 3.
Glyma01g36110
Glyma01g36110.1
LEUCINE-RICH REPEAT-CONTAINING PROTEIN
Glyma01g36120
Glyma01g36120.1
MITOCHONDRIAL CARRIER PROTEIN RELATED
Glyma01g36130
Glyma01g36130.1
SUBTILISIN/KEXIN-RELATED SERINE PROTEASE
Glyma01g36140
Glyma01g36140.1
ALDEHYDE DEHYDROGENASE-RELATED
Glyma01g36150
Glyma01g36150.1
SUGAR TRANSPORTER
Glyma01g36160
Glyma01g36160.1
RING FINGER PROTEIN 11 (SID 1669) (NEDD4 WW DOMAIN-BINDIN
Glyma01g36170
Glyma01g36170.1
Glyma01g36180
Glyma01g36180.1
Glyma01g36190
Glyma01g36190.2
Glyma01g36190.1
Glyma01g36200
Glyma01g36200.1
IRE1-RELATED
Glyma01g3
Glyma01g36210.1
IONOTROP
Glyma01g36220.1
G

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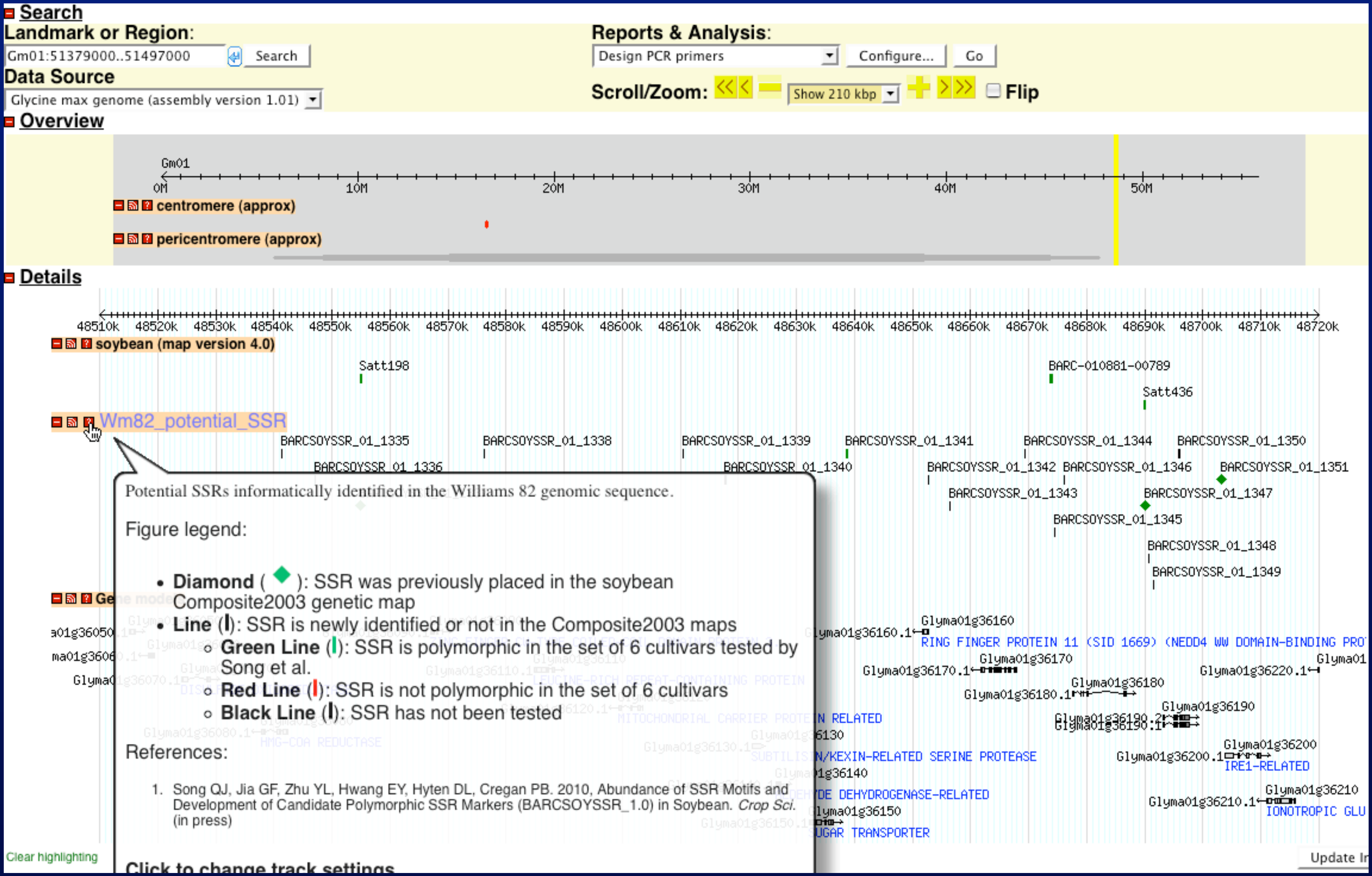
Potential SSRs in GBrowse



Search

Landmark or Region: Gm01:51379000..51497000

Data Source: Glycine max genome (assembly version 1.01)

Reports & Analysis: Design PCR primers

Scroll/Zoom: Show 210 kbp ☐ Flip

Search
Configure...
Go
Overview
Gm01
0M
10M
20M
30M
40M
50M
centromere (approx)
pericentromere (approx)
Details
48510k 48520k 48530k 48540k 48550k 48560k 48570k 48580k 48590k 48600k 48610k 48620k 48630k 48640k 48650k 48660k 48670k 48680k 48690k 48700k 48710k 48720k
soybean (map version 4.0)
Satt198
BARC-010881-00789
Satt436
Wm82_potential_SSR
BARCSOYSSR_01_1335
BARCSOYSSR_01_1336
BARCSOYSSR_01_1338
BARCSOYSSR_01_1339
BARCSOYSSR_01_1340
BARCSOYSSR_01_1341
BARCSOYSSR_01_1342
BARCSOYSSR_01_1343
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BARCSOYSSR_01_1345
BARCSOYSSR_01_1346
BARCSOYSSR_01_1347
BARCSOYSSR_01_1348
BARCSOYSSR_01_1349
BARCSOYSSR_01_1350
BARCSOYSSR_01_1351
Gene models
Glyma01g36160
RING FINGER PROTEIN 11 (SID 1669) (NEDD4 WW DOMAIN-BINDING PRO
Glyma01g36170
Glyma01g36180
Glyma01g36190
Glyma01g36200
IRE1-RELATED
Glyma01g36210
IONOTROPIC GLU
Glyma01g36220.1
MITOCHONDRIAL CARRIER PROTEIN RELATED
SUBTILISIN/KEXIN-RELATED SERINE PROTEASE
DEHYDE DEHYDROGENASE-RELATED
SUGAR TRANSPORTER
Clear highlighting
Update I

Potential SSRs informatically identified in the Williams 82 genomic sequence.

Figure legend:

- **Diamond** (◆): SSR was previously placed in the soybean Composite2003 genetic map
- **Line** (|): SSR is newly identified or not in the Composite2003 maps
  - **Green Line** (|): SSR is polymorphic in the set of 6 cultivars tested by Song et al.
  - **Red Line** (|): SSR is not polymorphic in the set of 6 cultivars
  - **Black Line** (|): SSR has not been tested

References:

1. Song QJ, Jia GF, Zhu YL, Hwang EY, Hyten DL, Cregan PB. 2010, Abundance of SSR Motifs and Development of Candidate Polymorphic SSR Markers (BARCSOYSSR_1.0) in Soybean. *Crop Sci.* (in press)

Click to change track settings

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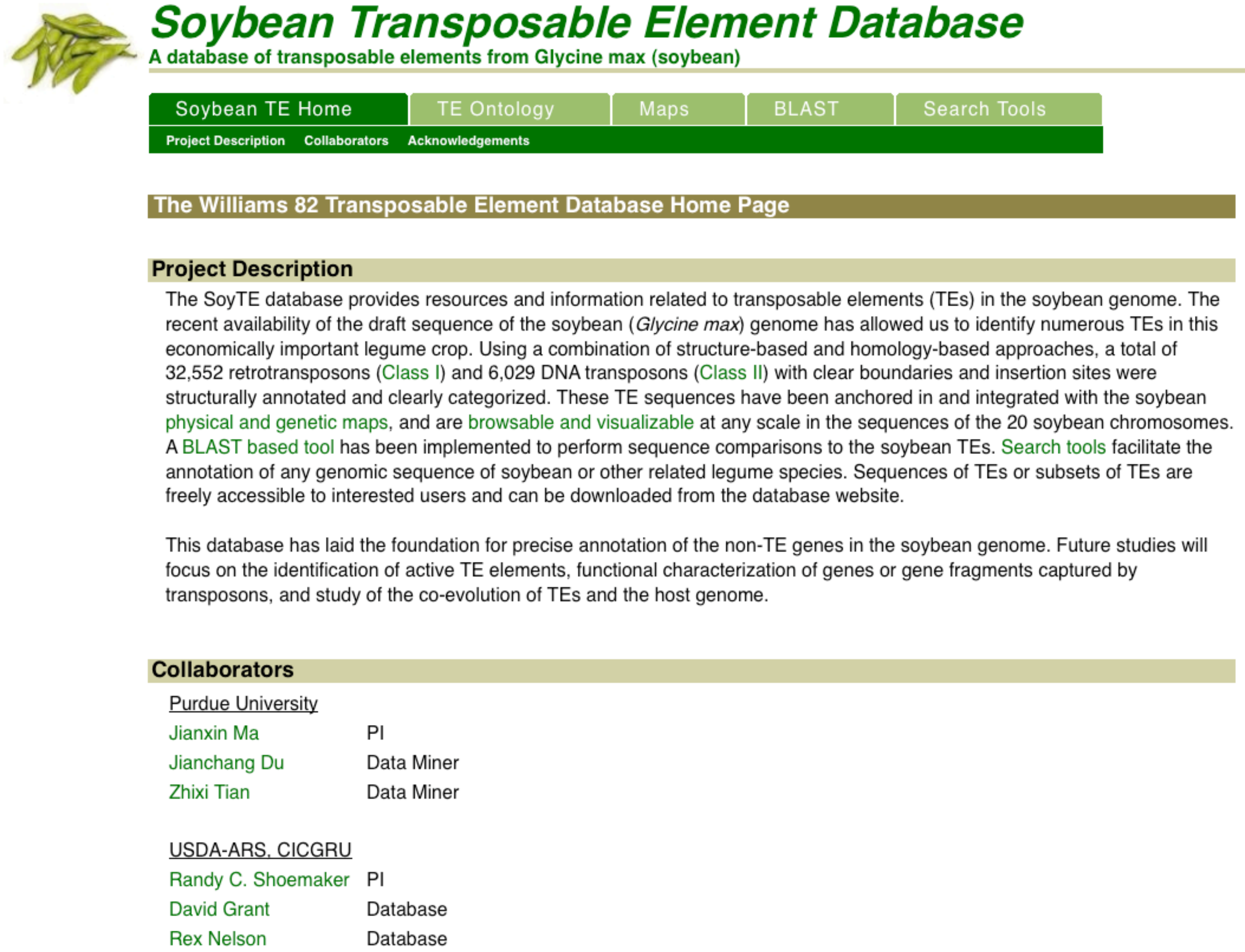
SoyBase



Soybean Transposable Element Database

A database of transposable elements from Glycine max (soybean)

The Williams 82 Transposable Element Database Home Page

Project Description

The SoyTE database provides resources and information related to transposable elements (TEs) in the soybean genome. The recent availability of the draft sequence of the soybean (*Glycine max*) genome has allowed us to identify numerous TEs in this economically important legume crop. Using a combination of structure-based and homology-based approaches, a total of 32,552 retrotransposons (Class I) and 6,029 DNA transposons (Class II) with clear boundaries and insertion sites were structurally annotated and clearly categorized. These TE sequences have been anchored in and integrated with the soybean physical and genetic maps, and are browsable and visualizable at any scale in the sequences of the 20 soybean chromosomes. A BLAST based tool has been implemented to perform sequence comparisons to the soybean TEs. Search tools facilitate the annotation of any genomic sequence of soybean or other related legume species. Sequences of TEs or subsets of TEs are freely accessible to interested users and can be downloaded from the database website.

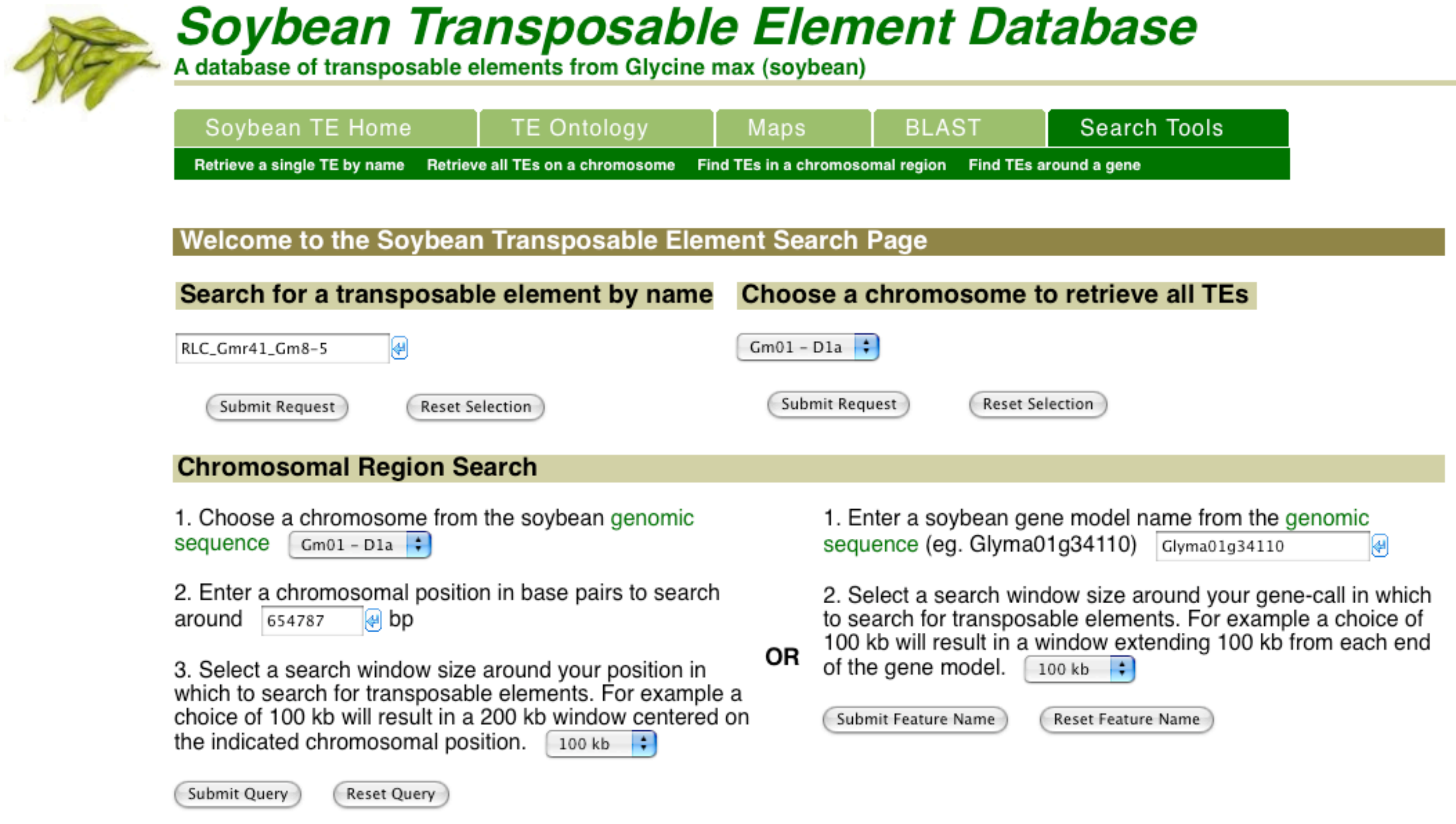
This database has laid the foundation for precise annotation of the non-TE genes in the soybean genome. Future studies will focus on the identification of active TE elements, functional characterization of genes or gene fragments captured by transposons, and study of the co-evolution of TEs and the host genome.

Collaborators

Purdue University	
Jianxin Ma	PI
Jianchang Du	Data Miner
Zhixi Tian	Data Miner

USDA-ARS, CICGRU	
Randy C. Shoemaker	PI
David Grant	Database
Rex Nelson	Database

Search Tools for SoyTEdb


Soybean TE Home
TE Ontology
Maps
BLAST
Search Tools
Retrieve a single TE by name
Retrieve all TEs on a chromosome
Find TEs in a chromosomal region
Find TEs around a gene
Submit Request
Reset Selection
Submit Request
Reset Selection
Submit Query
Reset Query
Submit Feature Name
Reset Feature Name

Soybean Transposable Element Database

A database of transposable elements from Glycine max (soybean)

Welcome to the Soybean Transposable Element Search Page

Search for a transposable element by name

RLC_Gmr41_Gm8-5

Choose a chromosome to retrieve all TEs

Gm01 - D1a

Chromosomal Region Search

1. Choose a chromosome from the soybean genomic sequence Gm01 - D1a

2. Enter a chromosomal position in base pairs to search around 654787 bp

3. Select a search window size around your position in which to search for transposable elements. For example a choice of 100 kb will result in a 200 kb window centered on the indicated chromosomal position. 100 kb

OR

1. Enter a soybean gene model name from the genomic sequence (eg. Glyma01g34110) Glyma01g34110

2. Select a search window size around your gene-call in which to search for transposable elements. For example a choice of 100 kb will result in a window extending 100 kb from each end of the gene model. 100 kb

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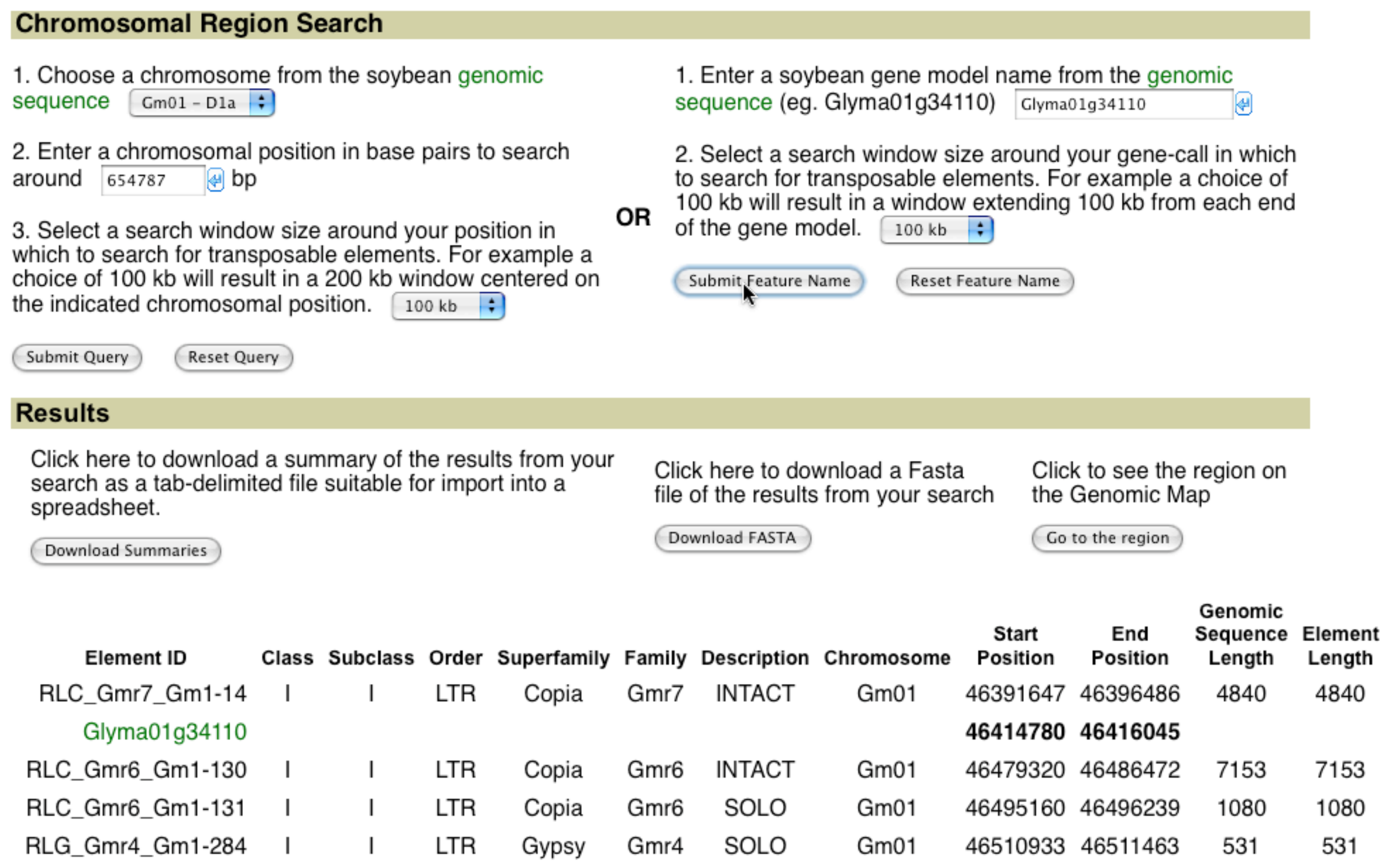
Search Tools for SoyTEdb



Chromosomal Region Search

1. Choose a chromosome from the soybean genomic sequence Gm01 - D1a

2. Enter a chromosomal position in base pairs to search around 654787 bp

3. Select a search window size around your position in which to search for transposable elements. For example a choice of 100 kb will result in a 200 kb window centered on the indicated chromosomal position. 100 kb

OR

1. Enter a soybean gene model name from the genomic sequence (eg. Glyma01g34110) Glyma01g34110

2. Select a search window size around your gene-call in which to search for transposable elements. For example a choice of 100 kb will result in a window extending 100 kb from each end of the gene model. 100 kb

Results

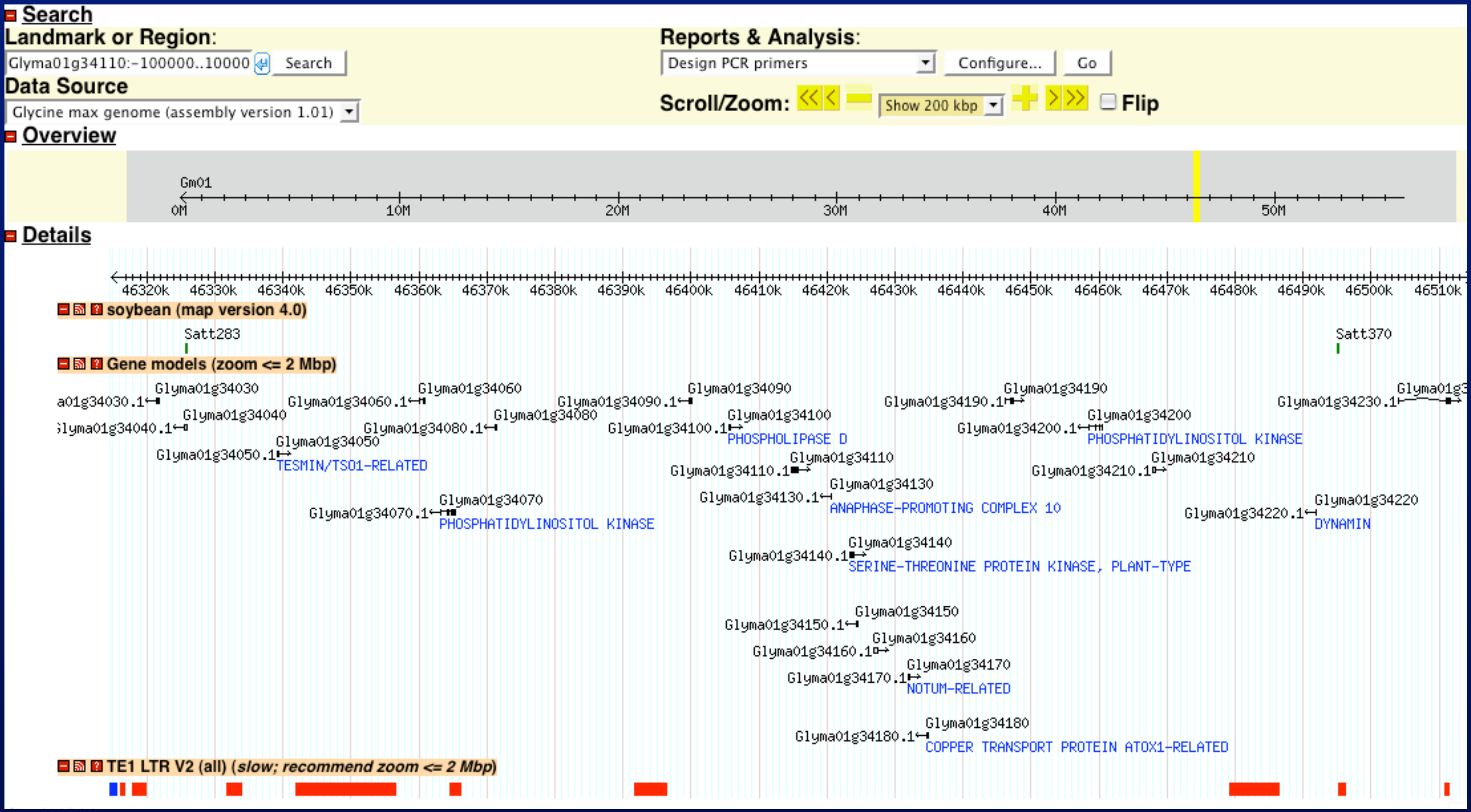
Click here to download a summary of the results from your search as a tab-delimited file suitable for import into a spreadsheet.

Click here to download a Fasta file of the results from your search

Click to see the region on the Genomic Map

Element ID	Class	Subclass	Order	Superfamily	Family	Description	Chromosome	Start Position	End Position	Genomic Sequence Length	Element Length
RLC_Gmr7_Gm1-14	I	I	LTR	Copia	Gmr7	INTACT	Gm01	46391647	46396486	4840	4840
Glyma01g34110								**46414780**	**46416045**		
RLC_Gmr6_Gm1-130	I	I	LTR	Copia	Gmr6	INTACT	Gm01	46479320	46486472	7153	7153
RLC_Gmr6_Gm1-131	I	I	LTR	Copia	Gmr6	SOLO	Gm01	46495160	46496239	1080	1080
RLG_Gmr4_Gm1-284	I	I	LTR	Gypsy	Gmr4	SOLO	Gm01	46510933	46511463	531	531

Search Tools for SoyTEdb



Search

Landmark or Region: Glyma01g34110:-100000..10000

Data Source: Glycine max genome (assembly version 1.01)

Reports & Analysis: Design PCR primers

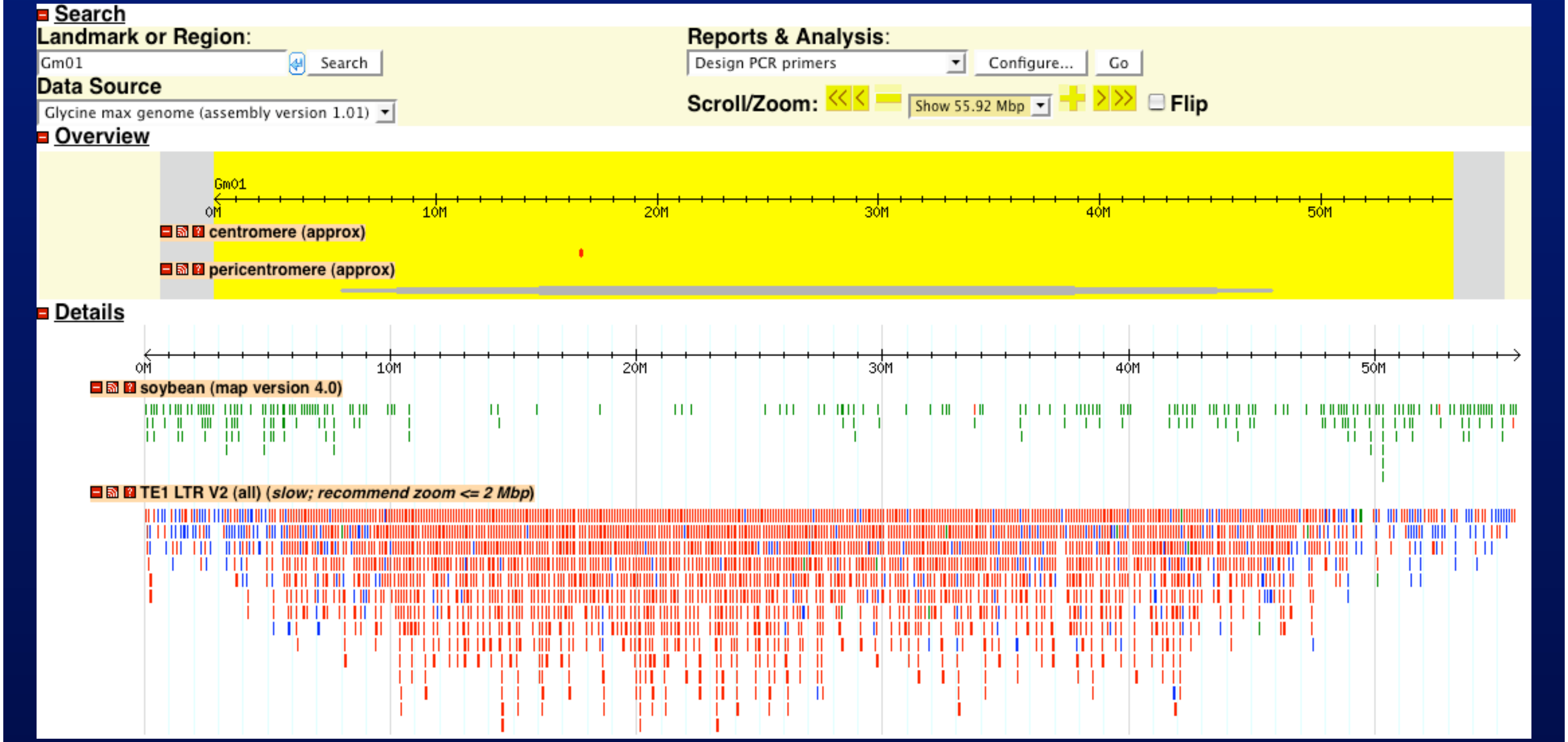
Scroll/Zoom: Show 200 kbp ☐ Flip

Overview

Details

Search
Configure...
Go
Gm01
0M
10M
20M
30M
40M
50M
46320k
46330k
46340k
46350k
46360k
46370k
46380k
46390k
46400k
46410k
46420k
46430k
46440k
46450k
46460k
46470k
46480k
46490k
46500k
46510k
soybean (map version 4.0)
Satt283
Satt370
Gene models (zoom <= 2 Mbp)
Glyma01g34030
Glyma01g34030.1
Glyma01g34040
Glyma01g34040.1
Glyma01g34050
Glyma01g34050.1
TESMIN/TSO1-RELATED
Glyma01g34060
Glyma01g34060.1
Glyma01g34070
Glyma01g34070.1
PHOSPHATIDYLINOSITOL KINASE
Glyma01g34080
Glyma01g34080.1
Glyma01g34090
Glyma01g34090.1
Glyma01g34100
Glyma01g34100.1
PHOSPHOLIPASE D
Glyma01g34110
Glyma01g34110.1
Glyma01g34130
Glyma01g34130.1
ANAPHASE-PROMOTING COMPLEX 10
Glyma01g34140
Glyma01g34140.1
SERINE-THREONINE PROTEIN KINASE, PLANT-TYPE
Glyma01g34150
Glyma01g34150.1
Glyma01g34160
Glyma01g34160.1
Glyma01g34170
Glyma01g34170.1
NOTUM-RELATED
Glyma01g34180
Glyma01g34180.1
COPPER TRANSPORT PROTEIN ATOX1-RELATED
Glyma01g34190
Glyma01g34190.1
Glyma01g34200
Glyma01g34200.1
PHOSPHATIDYLINOSITOL KINASE
Glyma01g34210
Glyma01g34210.1
Glyma01g34220
Glyma01g34220.1
DYNAMIN
Glyma01g34230.1
TE1 LTR V2 (all) (*slow; recommend zoom <= 2 Mbp*)

SoyTEdb Whole Chromosome Sequence View



Search

Landmark or Region: Gm01

Data Source Glycine max genome (assembly version 1.01)

Reports & Analysis: Design PCR primers

Overview

Details

Search
Configure...
Go
Scroll/Zoom:
Show 55.92 Mbp
☐ Flip
Gm01
0M
10M
20M
30M
40M
50M
centromere (approx)
pericentromere (approx)
soybean (map version 4.0)
TE1 LTR V2 (all) (*slow; recommend zoom <= 2 Mbp*)

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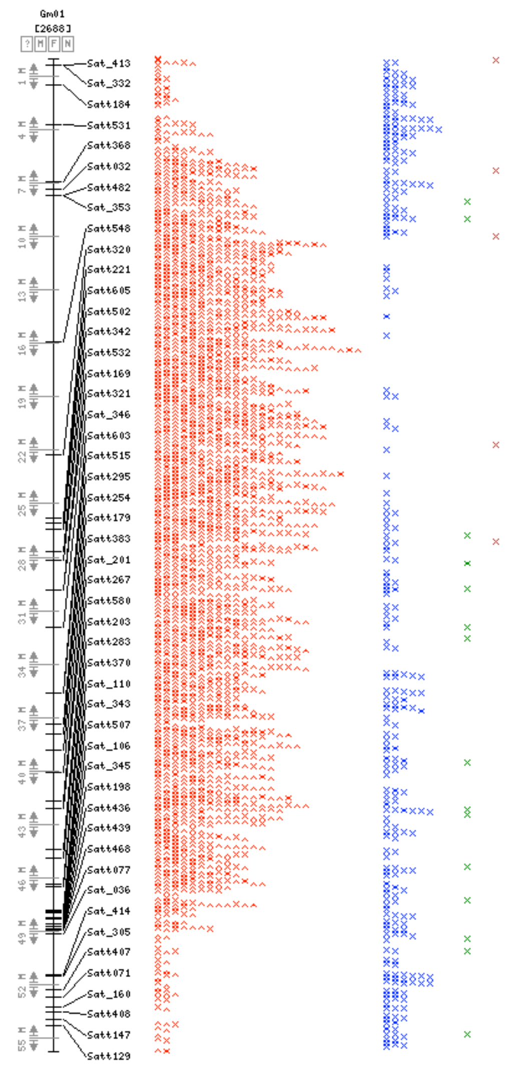
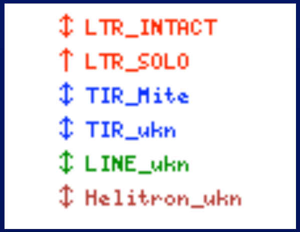
SoyTEdb Whole Chromosome Genetic Map View




LTR_INTACT
LTR_SOLO
TIR_Mite
TIR_ukn
LINE_ukn
Helitron_ukn

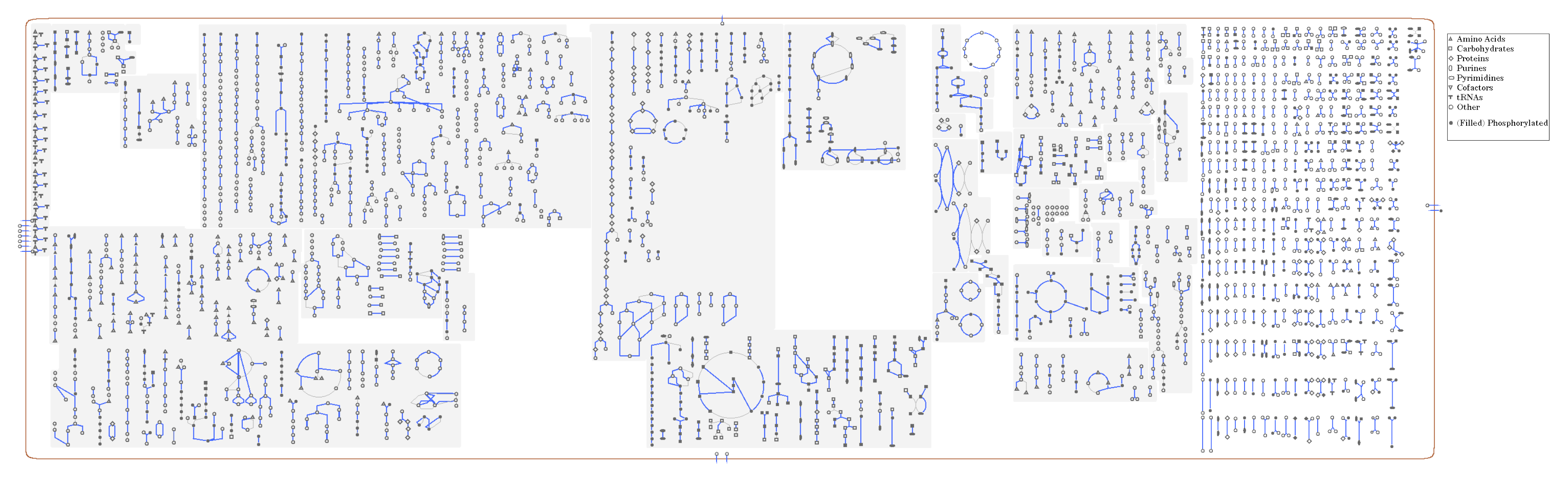
SoyCyc: A Soybean Metabolic Database and Data Exploration Tool

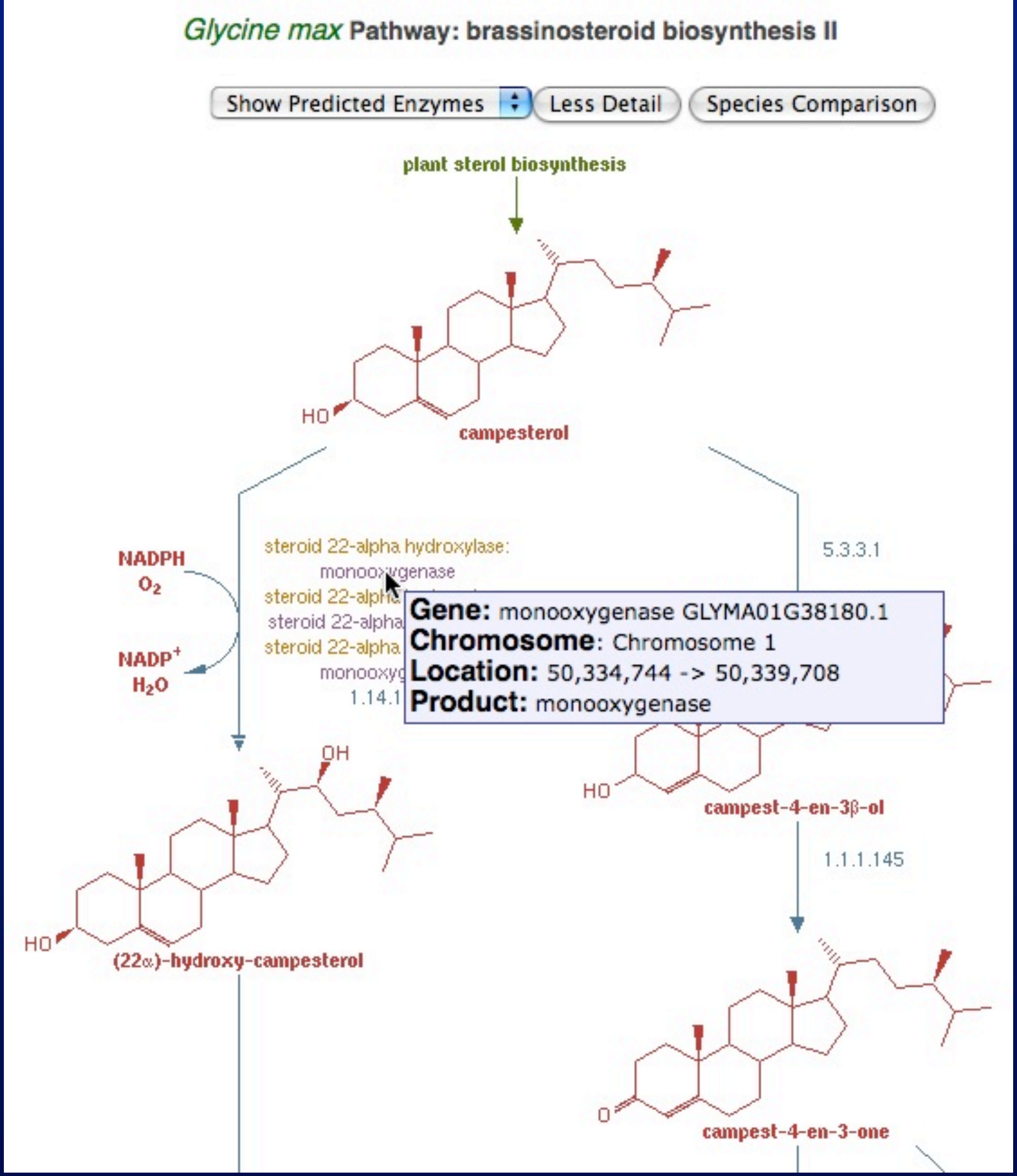
- Computationally predicted enzymatic functions for Wm82 Gm1.01 gene calls based on sequence similarity to known plant genes
  - Searchable by pathway, function, compound etc.

- Comparative
  - Allows the comparison of pathways shared between available taxa (*G. max*, *M. truncatula*, *A. thaliana*)

- Descriptive
  - Able to assign transcriptomic values to pathways to see what pathways have components up/down regulated

Identified Soybean Metabolic Pathways


△ Amino Acids
□ Carbohydrates
◇ Proteins
▯ Purines
▭ Pyrimidines
▽ Cofactors
T tRNAs
○ Other
● (Filled) Phosphorylated



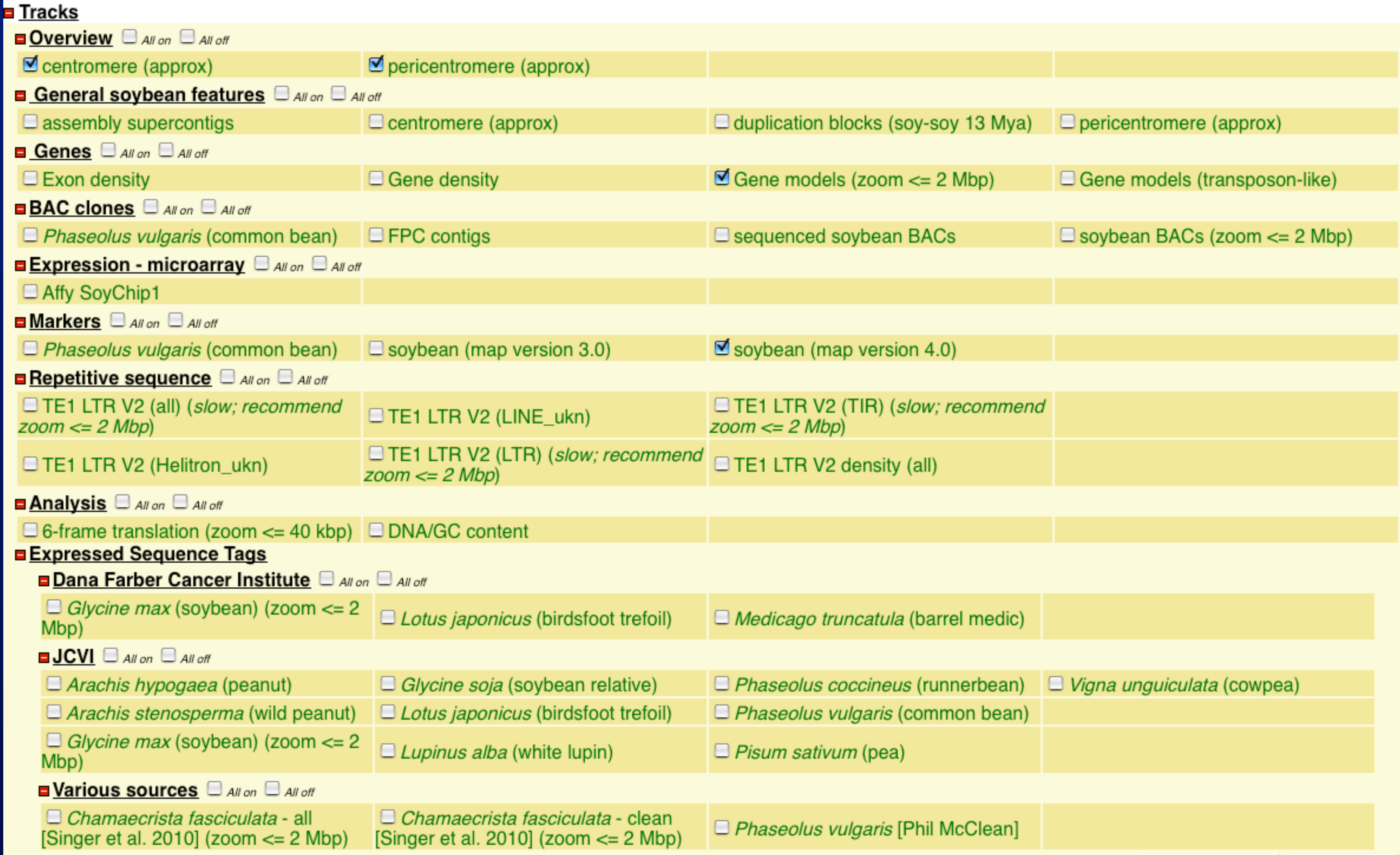
Glycine max **Pathway: brassinosteroid biosynthesis II**

Show Predicted Enzymes
Less Detail
Species Comparison
plant sterol biosynthesis
HO
campesterol
NADPH
O_2
$NADP^+$
H_2O
steroid 22-alpha hydroxylase:
monooxygenase
steroid 22-alpha
steroid 22-alpha
steroid 22-alpha
monooxyg
1.14.1
5.3.3.1
OH
HO
(22α)-hydroxy-campesterol
HO
campest-4-en-3β-ol
1.1.1.145
O
campest-4-en-3-one

Gene: monooxygenase GLYMA01G38180.1
Chromosome: Chromosome 1
Location: 50,334,744 -> 50,339,708
Product: monooxygenase

SoyCyc Pathway Information

Available Tracks for SoyBase Genomic Sequence Browser



Tracks

Overview ☐ *All on* ☐ *All off*

☑ centromere (approx)	☑ pericentromere (approx)		

General soybean features ☐ *All on* ☐ *All off*

☐ assembly supercontigs	☐ centromere (approx)	☐ duplication blocks (soy-soy 13 Mya)	☐ pericentromere (approx)

Genes ☐ *All on* ☐ *All off*

☐ Exon density	☐ Gene density	☑ Gene models (zoom <= 2 Mbp)	☐ Gene models (transposon-like)

BAC clones ☐ *All on* ☐ *All off*

☐ *Phaseolus vulgaris* (common bean)	☐ FPC contigs	☐ sequenced soybean BACs	☐ soybean BACs (zoom <= 2 Mbp)

Expression - microarray ☐ *All on* ☐ *All off*

☐ Affy SoyChip1			

Markers ☐ *All on* ☐ *All off*

☐ *Phaseolus vulgaris* (common bean)	☐ soybean (map version 3.0)	☑ soybean (map version 4.0)	

Repetitive sequence ☐ *All on* ☐ *All off*

☐ TE1 LTR V2 (all) (*slow; recommend zoom <= 2 Mbp*)	☐ TE1 LTR V2 (LINE_ukn)	☐ TE1 LTR V2 (TIR) (*slow; recommend zoom <= 2 Mbp*)	
☐ TE1 LTR V2 (Helitron_ukn)	☐ TE1 LTR V2 (LTR) (*slow; recommend zoom <= 2 Mbp*)	☐ TE1 LTR V2 density (all)	

Analysis ☐ *All on* ☐ *All off*

☐ 6-frame translation (zoom <= 40 kbp)	☐ DNA/GC content		

Expressed Sequence Tags

Dana Farber Cancer Institute ☐ *All on* ☐ *All off*

☐ *Glycine max* (soybean) (zoom <= 2 Mbp)	☐ *Lotus japonicus* (birdsfoot trefoil)	☐ *Medicago truncatula* (barrel medic)	

JCVI ☐ *All on* ☐ *All off*

☐ *Arachis hypogaea* (peanut)	☐ *Glycine soja* (soybean relative)	☐ *Phaseolus coccineus* (runnerbean)	☐ *Vigna unguiculata* (cowpea)
☐ *Arachis stenosperma* (wild peanut)	☐ *Lotus japonicus* (birdsfoot trefoil)	☐ *Phaseolus vulgaris* (common bean)	
☐ *Glycine max* (soybean) (zoom <= 2 Mbp)	☐ *Lupinus alba* (white lupin)	☐ *Pisum sativum* (pea)	

Various sources ☐ *All on* ☐ *All off*

☐ *Chamaecrista fasciculata* - all [Singer et al. 2010] (zoom <= 2 Mbp)	☐ *Chamaecrista fasciculata* - clean [Singer et al. 2010] (zoom <= 2 Mbp)	☐ *Phaseolus vulgaris* [Phil McClean]	

USDA United States Department Of Agriculture
Agricultural Research Service

SoyBase

SoyBase URLs

SoyBase	http://soybase.org
User Survey	http://soybase.org/survey/index.php
SoyOntologies	http://soybase.org/ontology.php
SoyTEdb	http://soytedb.org
SoyCyc	http://soybase.org/soycyc
Strategic Plan Survey	http://soybase.org/survey/new/index.php