



SoyBase and the Soybean Breeder's Toolbox

Integrating Genetics and Molecular Biology for Soybean Researchers

- SoyBase
 - Maps
 - Genome
 - Analysis Tools
 - Resources
 - SoySeq
- Search News Meetings Job Postings Soybean Ontologies SoyCyc Data Resources Community Resources Gene Knockouts Contact Us

Sign Up [Here](#) To Receive SoyBase Update Emails

SoyBase Toolbox

SoyBase Search [HELP](#) [Advanced Search](#) →

Examples: BARC-013845-01256 Satt531
Oil Glyma12g10780 T

Quick Wm82 Genome BLAST [HELP](#) [Full BLAST](#) →

Select Output Format Select BLAST

NCBI BLAST report

Enter sequence below in FASTA format.

Or load it from disk

Or load an [Example Sequence](#).

[Clear Sequence](#)

SoyBean Breeder's Toolbox Quick Jump [HELP](#)

Genetic Map Viewer -OR- Genome Sequence Viewer

Linkage Group Chromosome

SoyCyc Search [HELP](#) [Advanced Metabolism Search](#) →

Examples: inosine ethanol gibberellin

SoyBase News

Soybean Genomics Research Strategic Plan Updates February 01 2012

Progress made by the soybean community on the 2012-2016 Soybean Genomics Research Strategic Plan is being compiled by George Graef, Katy Rainey and Rich Wilson. Please see the [Strategic Plan website](#) for details on how to contribute to the report.

[•Read More](#)

Soybean Mutant Finder Field Day January 05 2012

The 1st Soybean Mutant Finder Field Day will be held in late July, 2012 at the University of Minnesota. Participants will view fast neutron-derived mutant plants growing in the field and can request seed of those that may be of research interest. A tutorial on the gene knockout-related parts of SoyBase will be presented. Contact [Carroll Vance](#) or [Bob Stupar](#) for more information.

[•Read More](#)

Improved Genetic Maps Display November 14 2011

The number of QTL on the genetic maps has dramatically increased as the SoyBase staff continues to incorporate QTL experiments from the literature. This has resulted in displays that are increasingly crowded and potentially difficult to use. To address this we have split the QTL into 4 classes (seed composition & yield, disease & stress, plant architecture, and other traits) with each of these classes presented as a separate column in the CMap genetic map displays. We hope that this will enhance the useful...






Sign Up Page To Receive SoyBase Update Emails

The SoyBase staff frequently updates SoyBase with new data and additional or improved functionality. While notices about these changes are posted on the SoyBase home page, based on our interactions with the soybean community it appears that another venue for advertising these changes would be useful. To address this need we have decided to send out emails with a short description of recent changes and links to them when appropriate. There will not be a fixed schedule but we anticipate that there will be 1-3 emails a month.

The SoyBase update distribution list is an OPT-IN list. You must sign up using this page to receive these updates.

Use the form below to sign up for either or both of the email distribution list or the RSS feed.

Personal:

Name*:(first last)	<input type="text" value="David Grant"/>	
Organization:	<input type="text" value="USDA-ARS"/>	
Email*:	<input type="text" value="david.grant@ars.usda.gov"/>	

* Required Field


List Choices:

SoyBase Updates	<input checked="" type="checkbox"/>
SoyBase News	<input checked="" type="checkbox"/>

Subscribe to RSS Feed?

No	Yes
<input type="radio"/>	<input type="radio"/>

What is the value of the dice?*

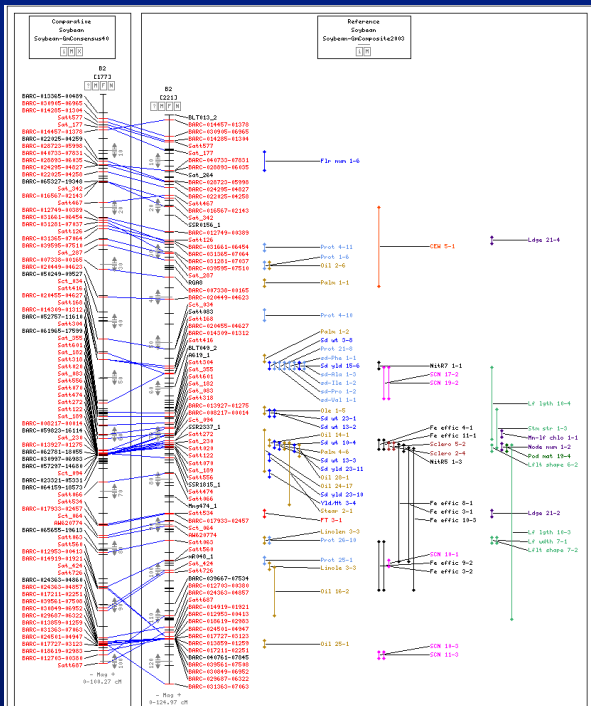
		<input type="text" value="6"/>
---	---	--------------------------------

Using SoyBase

- Customizing Genetic Map Views
- Searching
- SoyBase Ontologies

Using SoyBase

- Customizing Genetic Map Views
- Searching
- SoyBase Ontologies



Feature Types:

- Gene
- Marker
- RFPD
- RFLP
- SNP
- CSR
- QTL_oil
- QTL_protein
- QTL_reprod-period
- QTL_yield
- QTL_fungal
- QTL_inorganic
- QTL_insect
- QTL_nematode
- QTL_pod
- QTL_whole-plant

Features in red have correspondences

Evidence Types:

Blue line denotes Automated name-based

Menu Symbols:

- Map Set Info
- Map Details
- Matrix View
- Limit to One Map
- Delete Map Set
- Delete Map
- Flip Map
- Unflip Map
- New Map View

Save Link*

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

Dotplot | Eliminate Orphans** | New Reference Maps

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

Map Options | Redraw | Reset

Map Set	Add Maps Left	Soybean-Soybean-GmConsensus40 (Delete Set)	Soybean-Soybean-GmComposite2003 (Reference Set)	Add Maps Right
Min. Correspondences		0		
Align Vertically				
Stack				
Maps		B2	B2	
Start		0.00	0.00	
Stop		100.27	124.97	
Magnification		Original	Original	
Flipped				

Format: Name [Total correspondences to slot, Max correspondences to single map]
 hint: To save time, select the desired options before redrawing the map.

Redraw | Reset | (Hide Map Menu)

Feature Options | Correspondence Options | Display Options | Advanced Options

Feature Types:

- Gene
- Marker
- RFPD
- RFLP
- SNP
- CSR
- QTL_oil
- QTL_protein
- QTL_reprod-period
- QTL_yield
- QTL_fungal
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Magnification		Original	Original	
Flipped				

Format: Name [Total correspondences to slot, Max correspondences to single map]
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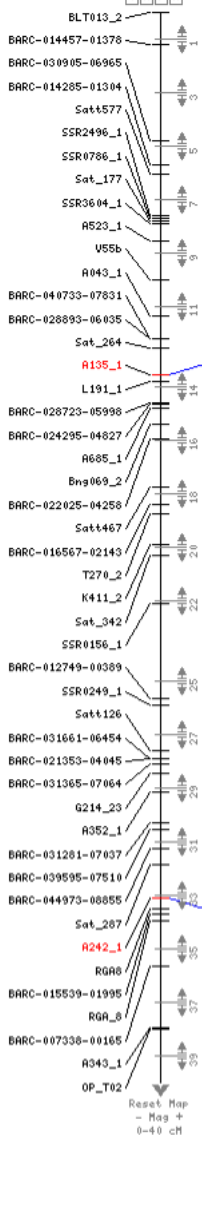
Redraw | Reset | (Hide Map Menu)

Feature Options | Correspondence Options | Display Options | Advanced Options

Reference Soybean
Soybean-GmComposite2003

1 2 3 4 5 6

B2 [54]



Flr num 1-6

Ldgc 21-4

CEW 5-1

Prot 4-11

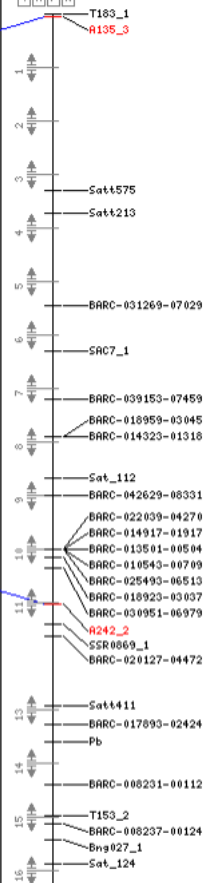
Oil 2-6
Prot 1-6

Palm 1-1

Comparative Soybean
Soybean-GmComposite2003

1 2 3 4 5 6

E [57]



Sd yld 16-4

CEW 6-1

P1 ht 18-5

Oil 2-5
Prot 1-5
Linolen 1-1

CEW 7-1

Lf 19th 3-1

Ole 1-4
Linole 1-4
Linolen 1-4

Ole 1-6
Linole 1-6
Oil 2-3

Reference
Soybean
Soybean-GmComposite2003

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

B2
[54]

BLT013_2
BARC-014457-01378
BARC-030905-06965
BARC-014285-01304
Satt4577
SSR2496_1
SSR0786_1
Sat_177
SSR3604_1
A523_1
V55b
R043_1
BARC-040733-07831
BARC-028893-06035
Sat_264
A135_1
L191_1
BARC-028723-05998
BARC-024295-04827
A685_1
Bng069_2
BARC-022025-04258
Satt4467
BARC-016567-02143
T270_2
K411_2
Sat_342
SSR0156_1
BARC-012749-00389
SSR0249_1
Satt126
BARC-031661-06454
BARC-021353-04045
BARC-031365-07064
G214_23
A352_1
BARC-031281-07037
BARC-039595-07510
BARC-044973-08855
Sat_267
A242_1
RGA6
BARC-015539-01995
RGA_8
BARC-007338-00165
A343_1
OP_T02

Flr num 1-6

Ldge 21-4



Prot 4-11

Oil 2-6
Prot 1-6

Palm 1-1

Comparative
Soybean
Soybean-GmComposite2003

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

E
[57]

T183_1
A135_3
1
2
3
Satt4575
Satt4213
4
5
BARC-031269-07029
6
SARC7_1
7
BARC-039153-07459
BARC-018959-03045
BARC-014323-01318
8
9
Sat_112
BARC-042629-08331
10
BARC-022039-04270
BARC-014917-01917
BARC-013501-00504
BARC-010543-00709
BARC-025493-06513
BARC-018923-03037
BARC-030951-06979
11
A242_2
SSR0869_1
BARC-020127-04472
12
13
Satt4411
BARC-017893-02424
Pb
14
BARC-008201-00112
15
T153_2
BARC-008207-00124
Bng027_1
16
Sat_124

Sd yld 16-4

CEM 6-1

P1 ht 18-5

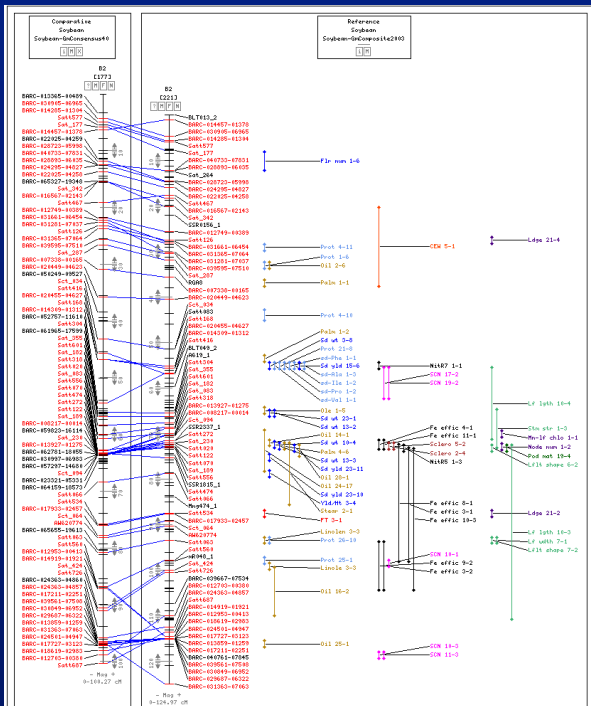
Oil 2-5
Prot 1-5
Linolen 1-1

CEM 7-1

Lf 19th 3-1

Ole 1-4
Linole 1-4
Linolen 1-4

Ole 1-6
Linole 1-6
Oil 2-3



Feature Types:

- Gene
- Marker
- RFPD
- RFLP
- SNP
- CSR
- QTL_oil
- QTL_protein
- QTL_reprod-period
- QTL_yield
- QTL_fungal
- QTL_inorganic
- QTL_insect
- QTL_nematode
- QTL_pod
- QTL_whole-plant

Features in red have correspondences

Evidence Types:

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Menu Symbols:

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- Unflip Map
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Dotplot | Eliminate Orphans** | New Reference Maps

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

Map Options | Redraw | Reset

Map Set	Add Maps Left	Soybean-Soybean-GmConsensus40 (Delete Set)	Soybean-Soybean-GmComposite2003 (Reference Set)	Add Maps Right
Min. Correspondences		0		
Align Vertically				
Stack				
Maps		B2	B2	
Start		0.00	0.00	
Stop		100.27	124.97	
Magnification		Original	Original	
Flipped				

Format: Name [Total correspondences to slot, Max correspondences to single map]
 hint: To save time, select the desired options before redrawing the map.

Redraw | Reset | (Hide Map Menu)

Feature Options
 Correspondence Options
 Display Options
 Advanced Options

Feature Types:

- Gene
- Marker
- RFPD
- RFLP
- SNP
- CSR
- QTL_oil
- QTL_protein
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Redraw | Reset | (Hide Map Menu)

Feature Options
 Correspondence Options
 Display Options
 Advanced Options

Map Options

Feature Options Redraw Reset

Highlight Features:

Feature Types:

Feature	Ignore	Display if Correspondence	Always Display
Gene	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Marker	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
PCR	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_fungal	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL_inorganic	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_insect	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL_leaf-stem	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_misc	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_nematode	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL_oil	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_pod	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_protein	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_reprod-period	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_whole-plant	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_yield	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
RAPD	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
RFLP	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
SNP	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
SSR	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Other	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
	<input type="button" value="Check All"/>	<input type="button" value="Check All"/>	<input type="button" value="Check All"/>

Show Labels: None Landmarks All

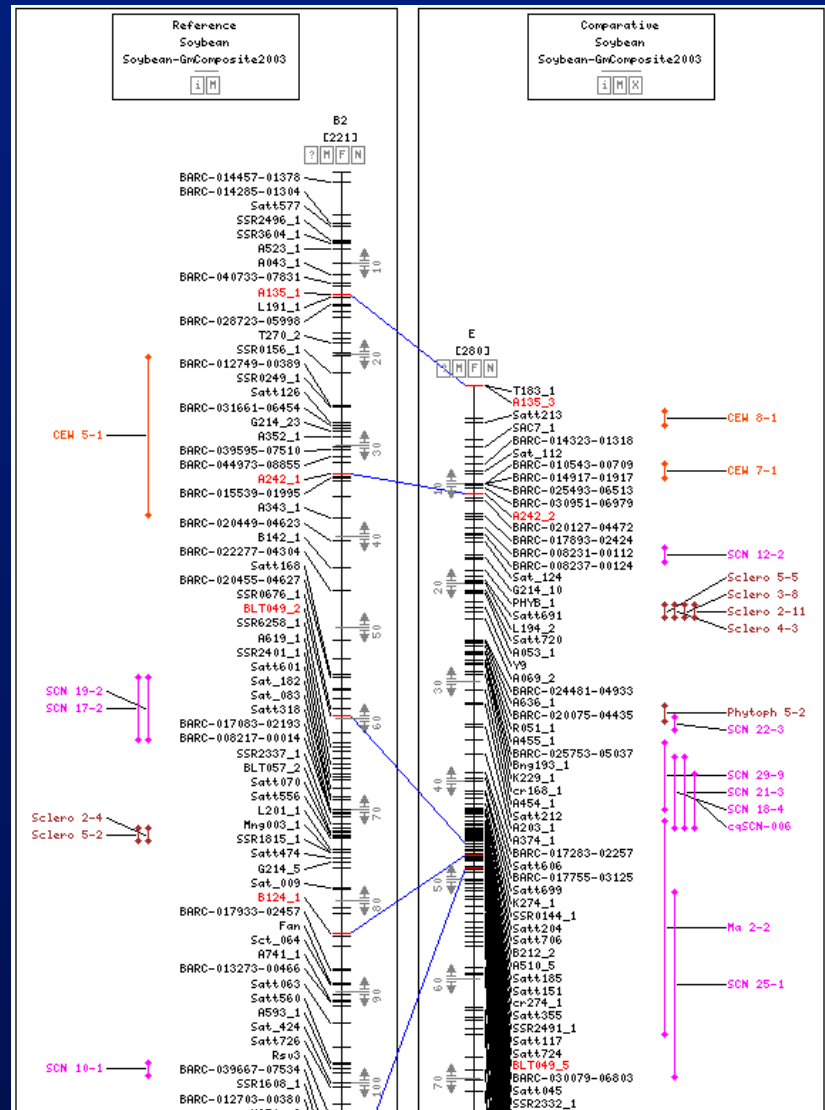
Collapse Overlapping Features: No Yes

Redraw Reset **(Hide Feature Menu)**

Correspondence Options

Display Options

Advanced Options



Map Options

Feature Options

Highlight Features:

Feature Types:

Feature	Ignore	Display if Correspondence	Always Display
Gene	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Marker	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
PCR	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_fungal	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_inorganic	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_insect	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_leaf-stem	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_misc	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_nematode	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_oil	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL_pod	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_protein	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL_reprod-period	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_whole-plant	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
QTL_yield	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
RAPD	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
RFLP	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
SNP	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
SSR	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Other	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
<input type="button" value="Check All"/>	<input type="button" value="Check All"/>	<input type="button" value="Check All"/>	

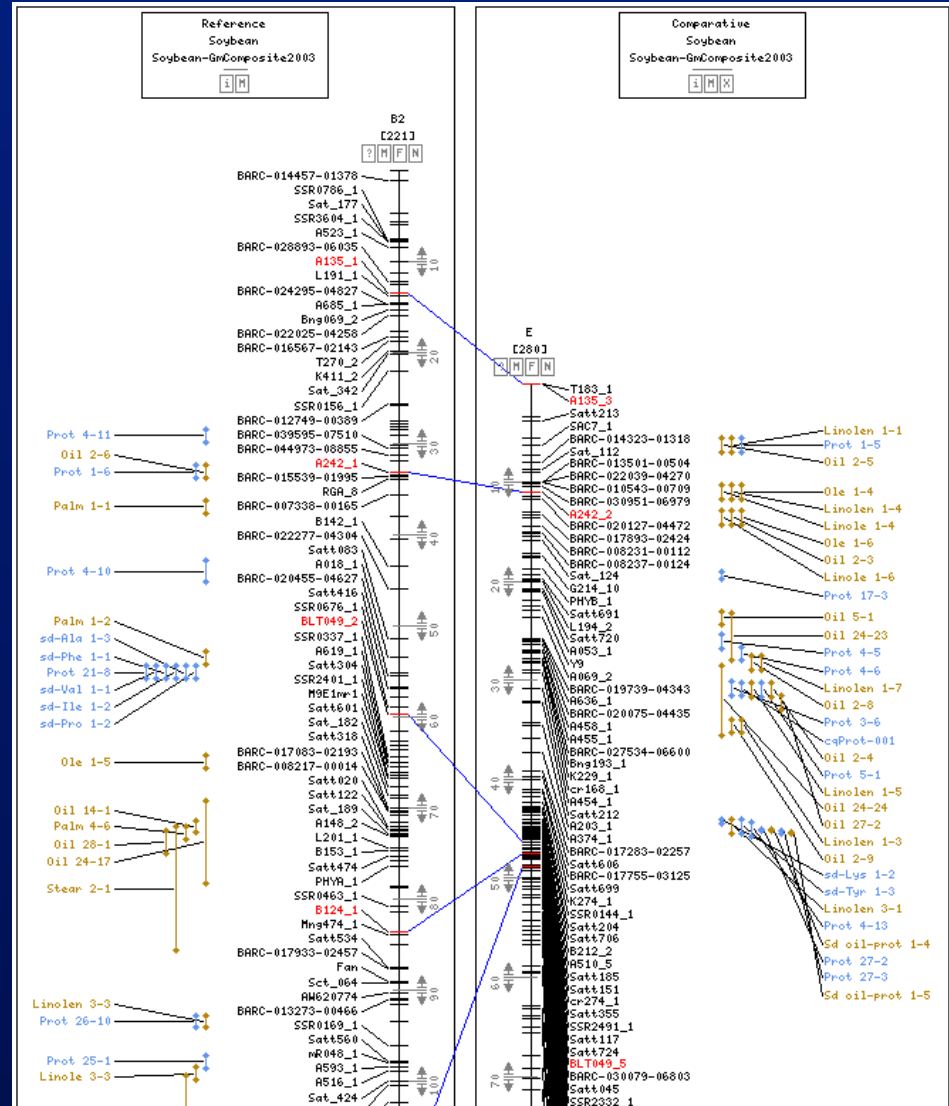
Show Labels: None Landmarks All

Collapse Overlapping Features: No Yes

Correspondence Options

Display Options

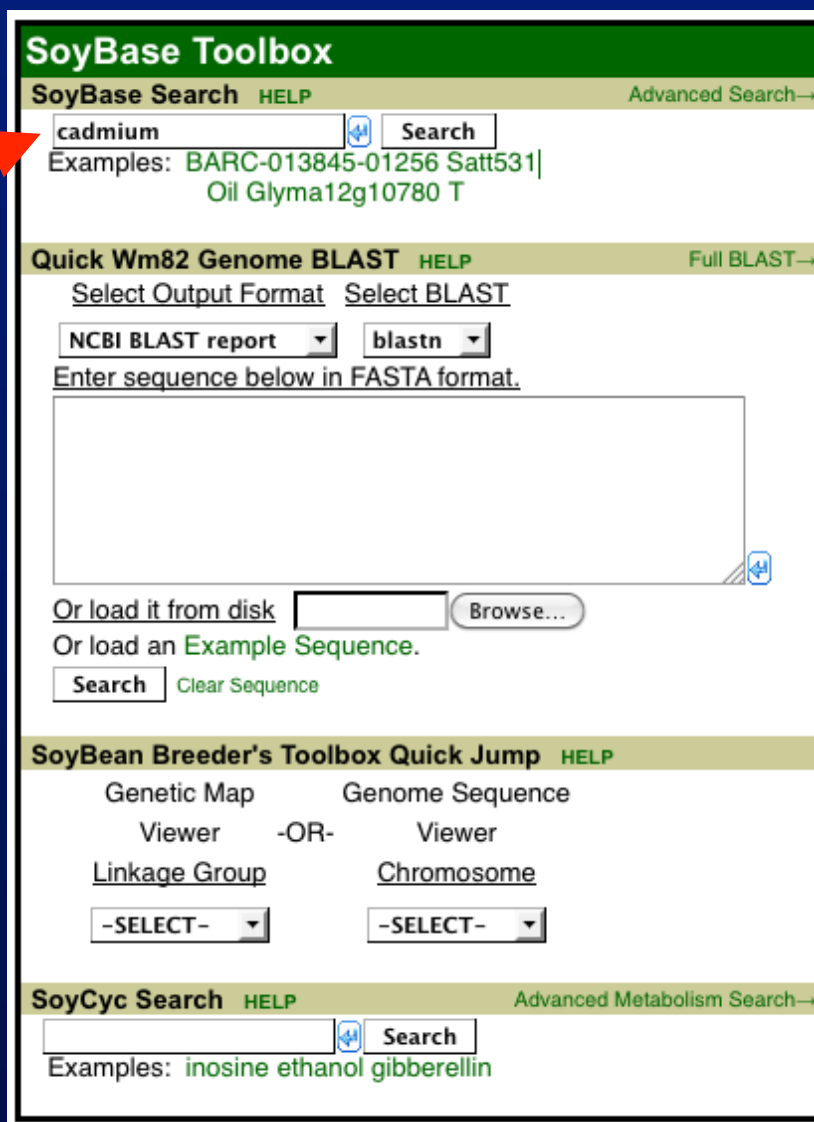
Advanced Options



Using SoyBase

- Customizing Genetic Map Views
- Searching
- SoyBase Ontologies

Search all of SoyBase for anything related to cadmium



SoyBase Toolbox

SoyBase Search [HELP](#) [Advanced Search](#)→

Examples: [BARC-013845-01256 Satt531](#)
[Oil Glyma12g10780 T](#)

Quick Wm82 Genome BLAST [HELP](#) [Full BLAST](#)→

[Select Output Format](#) [Select BLAST](#)

Enter sequence below in FASTA format.

Or load it from disk

Or load an [Example Sequence](#).

[Clear Sequence](#)

SoyBean Breeder's Toolbox Quick Jump [HELP](#)












Genetic Map Viewer -OR- Genome Sequence Viewer

[Linkage Group](#) [Chromosome](#)

SoyCyc Search [HELP](#) [Advanced Metabolism Search](#)→

Examples: [inosine](#) [ethanol](#) [gibberellin](#)

Results of Search

Search Domain	Query Term	Genetic Maps	Genomic Maps	Details Pages	Ontology Terms	Expression Data	Mutant Populations
Locus	<i>cadmium</i>	 1		 1			
QTL	<i>cadmium</i>	 1		 1	 4		
Gene Call	<i>cadmium</i>		 1	 1		 1	
Trait	<i>cadmium</i>			 1			
Gene	<i>cadmium</i>	 1		 1			

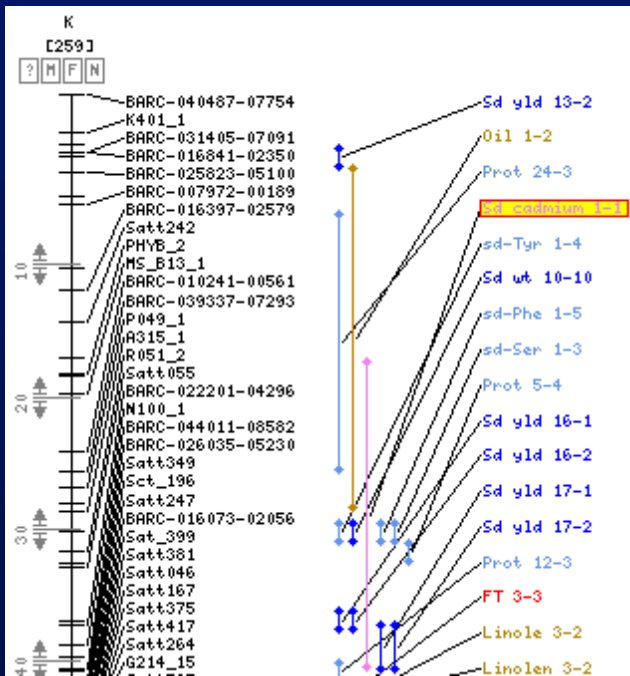
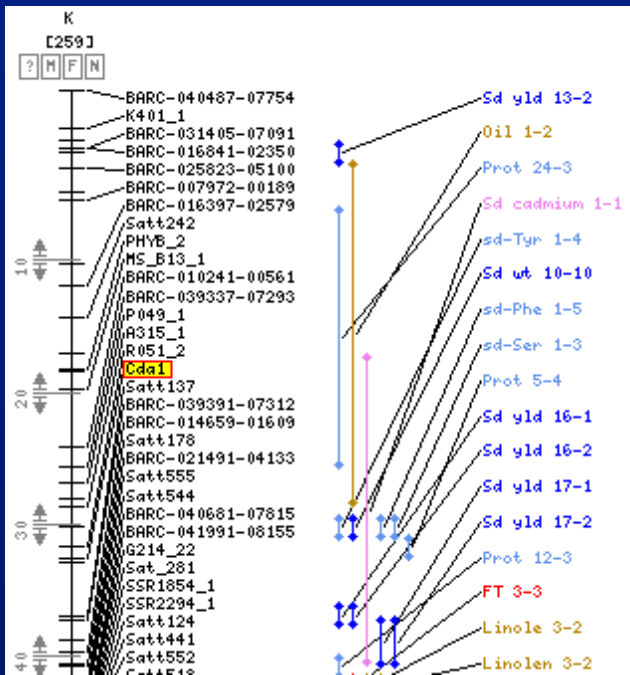
[Open In New Tabs](#)

This table summarizes the results of the search. The number in each column indicates the number of records of each data type that relate to the search term. Clicking on the number opens a page with additional details about these results.

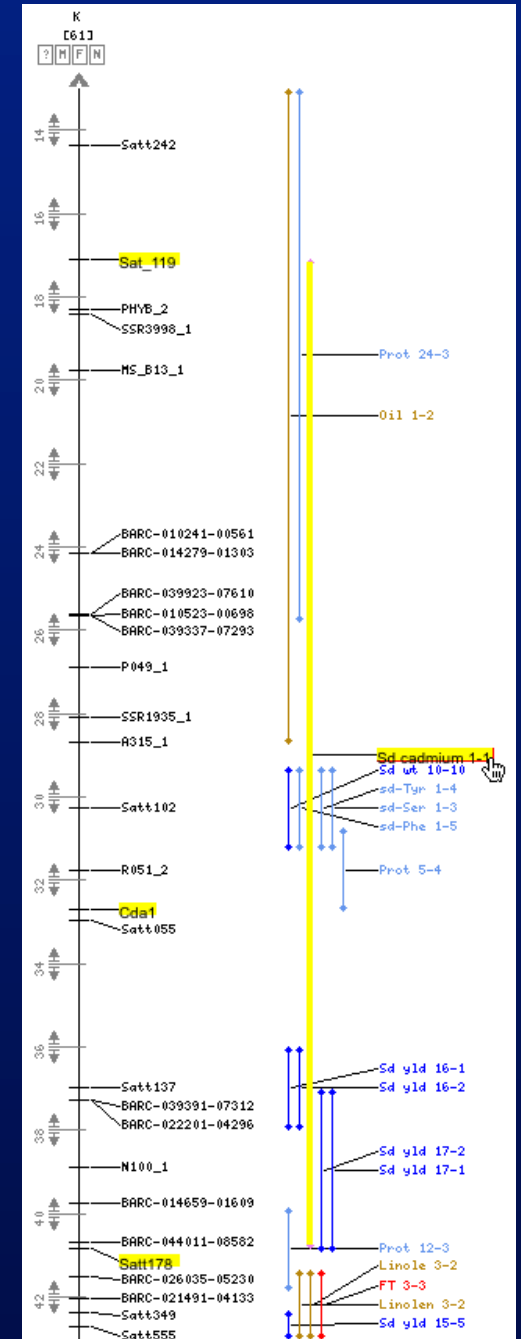
Search Domain	Query Term	Genetic Maps	Genomic Maps	Details Pages	Ontology Terms	Expression Data	Mutant Populations
Locus	<i>cadmium</i>	1		1			
QTL	<i>cadmium</i>	1		1	4		
Gene Call	<i>cadmium</i>		1	1		1	
Trait	<i>cadmium</i>			1			
Gene	<i>cadmium</i>	1		1			

[Open In New Tabs](#)

This table summarizes the results of the search. The number in each column indicates the number of records of each data type that relate to the search term. Clicking on the number opens a page with additional details about these results.



put cursor over either gene or QTL to see related map objects



Search Domain	Query Term	Genetic Maps	Genomic Maps	Details Pages	Ontology Terms	Expression Data	Mutant Populations
Locus	<i>cadmium</i>	1		1			
QTL	<i>cadmium</i>	1		1	4		
Gene Call	<i>cadmium</i>		1	1		1	
Trait	<i>cadmium</i>			1			
Gene	<i>cadmium</i>	1		1			

[Open In New Tabs](#)

This table summarizes the results of the search. The number in each column indicates the number of records of each data type that relate to the search term. Clicking on the number opens a page with additional details about these results.

Gene Report for Cda1

Gene Class: Seed composition

Loci for Cda1

Cda1

Controlled Vocabulary Terms for Cda1

Source	Accession
GO_function	GO:0055073
PO	PO:0009010
PO	PO:0001040
TO	TO:0006059
SOY	SOY:0001795

← links for info about these CV terms

Sequences associated with Cda1

Source Accession

JGI_V1 Glyma09g06170

← link for info about this gene model

References for Cda1

Benitez et al. 2010
A Major QTL Controlling Seed Cadmium Accumulation in Soybean
Crop Sci. 2010 50:1728-1734

Jegadeesan et al. 2010
Mapping and validation of simple sequence repeat markers linked to a major gene controlling seed cadmium accumulation in soybean [Glycine max (L.) Merr]
Theor. Appl. Genet. 2010, 121:283-294

← link to abstract and URL for paper

Benitez et al. 2012
Single-Base Substitution in P1B-ATPase Gene Is Associated with a Major QTL for Seed Cadmium Concentration in Soybean
J Hered 2012 103: 278-286

Comments for Cda1

Gene was mapped by Jegadeesan et al. 2010 using SSRs developed for this project and which are not on the SoyBase genetic maps. SoyBase genetic map location was approximated using reported linkage to SoyBase SSRs. The cadmium accumulation trait was also mapped by QTL analysis which identified a single QTL that explained 57.3% of the phenotypic variation and which mapped directly over Cda1.

A QTL in this region was identified by Benitez et al. 2010. Subsequently the underlying gene was identified as a H1b-ATPase (Glyma09g06170) by Benitez et al. 2012.

Using SoyBase

- Customizing Genetic Map Views
- Searching
- SoyBase Ontologies

What is a Controlled Vocabulary

- A way to ensure consistency and reduce the ambiguity inherent in normal human languages where the same concept can be given different names.
- Examples
 - MESH headings (NLM)
 - GO terms (Gene Ontology Consortium)
 - EC numbers (Enzyme Commission)

What a Controlled Vocabulary is Not

- A replacement for the official descriptors for a crop
 - A controlled vocabulary could and should include descriptors, but is not a replacement. They serve different purposes

Search Domain	Query Term	Genetic Maps	Genomic Maps	Details Pages	Ontology Terms	Expression Data	Mutant Populations
Locus	<i>cadmium</i>	1		1			
QTL	<i>cadmium</i>	1		1	4		
Gene Call	<i>cadmium</i>		1	1		1	
Trait	<i>cadmium</i>			1			
Gene	<i>cadmium</i>	1		1			



Open In New Tabs

This table summarizes the results of the search. The number in each column indicates the number of records of each data type that relate to the search term. Clicking on the number opens a page with additional details about these results.

Trait Report for Seed cadmium concentration

Trait Definition: Cadmium content of a seed

Comments on trait Seed cadmium concentration

Cadmium concentration in mg/kg dried seed.

QTL Associated with Seed cadmium concentration

Sd cadmium 1-1

Genes associated with Seed cadmium concentration

Cda1

Controlled Vocabulary Terms for Seed cadmium concentration

Source Accession

PO PO:0009010
PO PO:0001040
TO TO:0006059
SOY SOY:0001795
GO GO:0055073

References

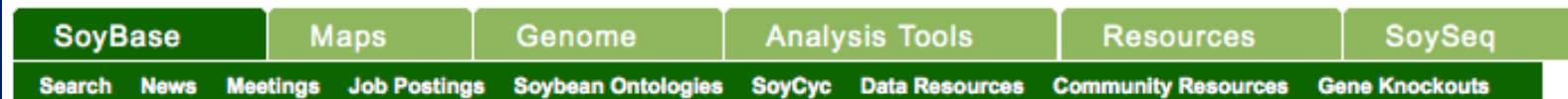
Title	Source
Mapping and validation of simple sequence repeat markers linked to a major gene controlling seed cadmium accumulation in soybean [Glycine max (L.) Merr]	Theor. Appl. Genet. 2010, 121:283-294
Single-Base Substitution in P1B-ATPase Gene Is Associated with a Major QTL for Seed Cadmium Concentration in Soybean	J. Hered. 2012 epub
A Major QTL Controlling Seed Cadmium Accumulation in Soybean	Crop Sci. 2010 50:1728-1734

SoyBase Soybean Ontology

- Four sections
 - Structure ontology
 - Enumerates the main structures of the root and shoot system. Useful for modeling the growth of a plant over time
 - Whole plant ontology
 - Describes the growth stages of a whole plant
 - Based on the widely used “Soybean Growth Stages” and is linked to the BBCH growth scale for soybean
 - Developmental ontology
 - Describes the stages of growth of individual plant parts such as leaves, flowers and pods/seeds
 - Trait ontology
 - Describes physical and biochemical traits of the plant or plant part

SoyBase and the Soybean Breeder's Toolbox

Integrating Genetics and Molecular Biology for Soybean Researchers



Soybean Whole Plant Growth Ontology

This ontology was developed to unite three different ontologies for soybean development, the BBCH scale, the more generic Plant Ontology Consortium's Whole Plant Growth Ontology and the Soybean Growth and Development growth stages as published in "Soybean Growth and Development" Iowa State University Extension publication PM 1945 [by Palle Pedersen](#).

[More ...](#)

[Browse and Search Soybean Whole Plant Growth Terms](#)

Soybean Structure Ontology

This ontology was developed to enumerate the parts of a soybean plant in order to follow the temporal development of individual plants. The ontology was modeled after the system described in [Bucciarelli et al. \(2006\) Plant Phys 142:207-219](#).

[More ...](#)

[Browse and Search Soybean Structure Terms](#)

Soybean Developmental Ontology

This ontology was developed to describe the growth and maturation of individual soybean tissues or organ systems. The structure was modeled on that of the greater Plant Ontology with modifications to accommodate soybean development.

[Browse and Search Developmental Terms](#)

Soybean Trait Ontology

This ontology was developed as a guide to describing soybean growth traits. These terms were developed from [GRIN Soybean Descriptors](#) and soybean traits and QTLs described in SoyBase as well as other publications.

[More ...](#)

[Browse and Search Soybean Trait Terms](#)

- [-] all : all
 - [+] ⓘ obsolete_soybean_structure : obsolete_soybean_structure
 - [+] ⓘ obsolete_soybean_trait : obsolete_soybean_trait
 - [+] ⓘ SOY:0000000 : Soybean Growth and Trait Ontology V1.0 rev 10
 - [+] ⓘ **SOY:0000099 : Soybean Trait Terms**



- [-] ⓘ **SOY:0000000 : Soybean Growth and Trait Ontology V1.0 rev 10**
 - [+] ⓘ SOY:0001650 : Soybean Development Stages
 - [+] ⓘ SOY:0000098 : Soybean Structure Terms
 - [-] ⓘ **SOY:0000099 : Soybean Trait Terms**
 - [+] ⓘ SOY:0001411 : Miscellaneous Soybean Traits
 - [+] ⓘ SOY:0001410 : Soybean Biochemical Traits
 - [+] ⓘ SOY:0001412 : Soybean Fertility or Sterility Traits
 - [+] ⓘ SOY:0001408 : Soybean Growth and Development Traits
 - [+] ⓘ SOY:0001398 : Soybean Morphology and Anatomy Traits
 - [+] ⓘ SOY:0001409 : Soybean Quality Traits
 - [+] ⓘ SOY:0001399 : Soybean Stature or Vigor Traits
 - [+] ⓘ SOY:0001400 : Soybean Stress Resistance Traits
 - [+] ⓘ SOY:0001407 : Soybean Yield Traits
 - [+] ⓘ SOY:0000097 : Soybean Whole Plant Growth Stages

Common names and synonyms are indicated here. Common names can be very misleading because they vary regionally

Mapping to the greater plant trait ontology (TO)

Accession: SOY:0001472

Ontology: soybean_trait

Synonyms:

Asian Soybean Rust

Malupa sojae

Soybean Rust

SoyTO:0000171 Reaction to Phakopsora pachyrhizi Infection

TO:0000439 fungal disease resistance

Definition:

Reaction of the plant or plant part to Phakopsora pachyrhizi infection.

Comment:

The anamorph of Phakopsora pachyrhizi is Malupa sojae. Disease severity scale is 1= no visible lesions, 2= few scattered lesions present, 3= moderate number of lesions on at least part of the leaf, 4= abundant number of lesions on part of the leaf, 5= prolific lesions over most of the leaf. Note, measurements taken on the first trifoliolate leaf but other leaf nodes have been used.

Taxonomic revisions to the causative organism and measurement values (from descriptors) are indicated here

Why Are Ontologies Important

- To orient new students to described soybean phenotypes
- To tag publications with accession numbers to aid in the curation process as well as make them machine readable.
 - “We measured the reaction of cultivar Raiden to soybean rust infection (SOY:0001472, TO: 0000171)”

Questions?