

How to use DAIZUbase: A unified soybean genome database

The screenshot displays the DAIZUbase website interface. The main header includes the DAIZUbase logo and navigation links: HOME, GBrowse, UnifiedMap, and BLAST. Below the header, a 'Keyword Search' section is visible, featuring a search form with fields for 'Keyword', 'Search Field' (set to 'id'), and 'Position' (set to 'chromosome (or scaffold)' with 'Gm01' selected). The 'Data Set' section includes checkboxes for 'marker', 'BAC_contig', 'BAC_end', 'Glyma1 annotation', 'Glyma1 TE annotation', and 'FLcDNA'. The 'search' and 'reset' buttons are at the bottom of the form.

Below the search form, a table of search results is shown. The table has three columns: 'Position', 'Description', and 'Link'. The results are as follows:

Position	Description	Link
1 : 27643 - 27978 (strand : -)		GBrowse UnifiedMap GeneViewer
1 : 51481 - 61502 (strand : -)		GBrowse UnifiedMap GeneViewer
1 : 61965 - 63428 (strand : -)		GBrowse UnifiedMap GeneViewer
1 : 70898 - 71210 (strand : -)		GBrowse UnifiedMap GeneViewer
Glyma01g00300.1	mRNA:Glyma1 Gm01 : 90693 - 94401 (strand : -)	GBrowse UnifiedMap GeneViewer
Glyma01g00300.2	mRNA:Glyma1 Gm01 : 94388 - 95580 (strand : -)	GBrowse UnifiedMap GeneViewer
Glyma01g00310.1	mRNA:Glyma1 Gm01 : 104684 - 106216 (strand : -)	GBrowse UnifiedMap GeneViewer
Glyma01g00320.1	mRNA:Glyma1 Gm01 : 116300 - 127990 (strand : +)	GBrowse UnifiedMap GeneViewer
Glyma01g00320.2	mRNA:Glyma1 Gm01 : 116300 - 127990 (strand : +)	GBrowse UnifiedMap GeneViewer

On the right side of the image, a 'UnifiedMap' view is shown, displaying a genomic map with various features and annotations. The map includes a 'physical Map' and a 'BLAST' section. The 'physical Map' shows a linear arrangement of markers and features, with a 'select: chr1:51481-61502' option. The 'BLAST' section shows a search result for the query 'Glyma01g00300.1'.

Outline

1. System overview
2. Top page
3. Browsers and viewer
 - 3.1 UnifiedMap
 - 3.2 GBrowse
 - 3.3 GeneViewer
4. Word search and sequence search
 - 4.1 An example of keyword search
 - 4.2 An example of sequence search

1. System overview

DAIZUbase is a unified soybean genome database with 2 map browsers and 1 gene viewer.

- * UnifiedMap : physical map and genetic linkage map with BAC contig, and BAC-ends for each chromosome.
- * GBrowse : genome annotation viewer based on GBrowse developed by GMOD.
- * GeneViewer : gene information viewer based on the gene viewer of RiceGAAS/KAIKOGAAS.

Top Page

DAIZUbase
HOME GBrowse UnifiedMap BLAST

Keyword Search

enter a keyword and choose from several parameters to delimit the search.

Keyword: Search Field

Position: chromosome (or scaffold)

Data Set:
☐ marker
☐ BAC_contig
☐ BAC_end
☐ Glyma1 annotation
☐ Glyma1 TE annotation
☐ FLCNA

Search Reset

Search Result

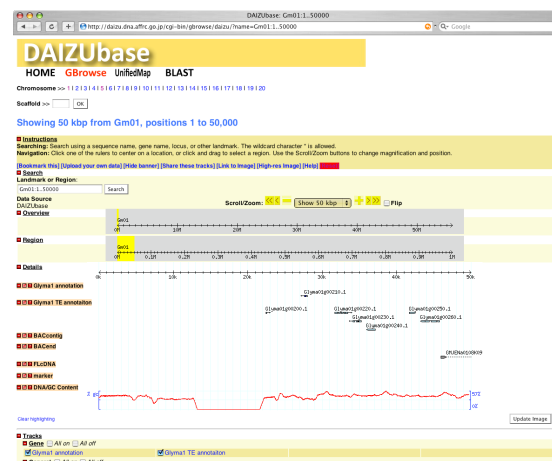
DAIZUbase
HOME GBrowse UnifiedMap BLAST

Keyword search result

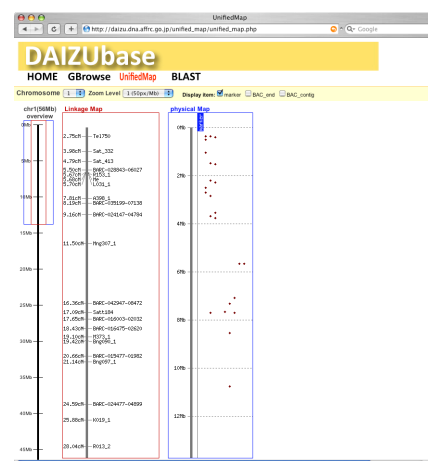
Number of hit: 3559

Data ID	Accession number	Data type	Position
Glyma01g00210.1		mRNA-Glyma1	Gm01 : 27643 - 27678
Glyma01g00270.1		mRNA-Glyma1	Gm01 : 51481 - 61302
Glyma01g00280.1		mRNA-Glyma1	Gm01 : 61965 - 63428 (strand -)
Glyma01g00290.1		mRNA-Glyma1	Gm01 : 70898 - 71210 (strand -)
Glyma01g00300.1		mRNA-Glyma1	Gm01 : 94603 - 94603 (strand -)

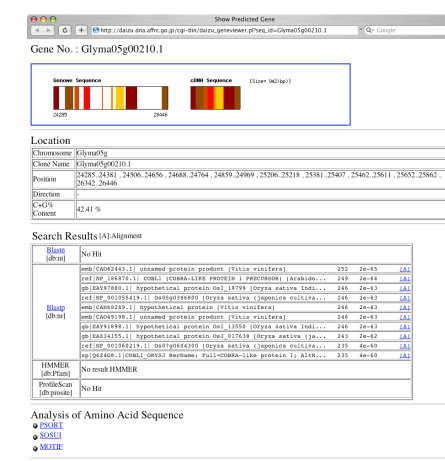
GBrowse



UnifiedMap



GeneViewer



2. Top page

The top page provides access to soybean genome (Williams82, ENREI) information.

- 1) Keyword Search: Input a keyword and choose from “Search Field”, “Search Chromosome”, and “Search Data Set” to delimit the search. The data sets include genes, FLcDNAs, markers, BAC ends, and BAC clones.
- 2) Sequence Search: Using the BLAST system with *Glycine max* (Williams82) and ENREI BACend sequence as a reference database. Nucleotide or amino acid sequence can be used as query. Upon clicking the “BLAST” link, a query input page is opened.

Keyword Search

DAIZUbase

HOME GBrowse UnifiedMap **BLAST**

DAIZUbase

The latest update on DAIZUbase (ver.1.1) is now available. [NEW](#) [\[Modification history\]](#)

DAIZUbase is an integrated soybean genome database and data mining tool, consists of 2 map browsers, a gene viewer, and BLAST search system. [more...](#)

Keyword Search

enter a keyword and choose from several parameters to delimit the search.

Keyword: Search Field:

Position: chromosome (or scaffold)

Data Set:

☐ marker ☐ BAC_contig ☐ BAC_end

☒ Glyma1 annotation ☐ Glyma1 TE annotation ☐ FLCDNA

Sequence Search (BLAST)

DAIZUbase

HOME GBrowse UnifiedMap **BLAST**

Program:

DataLib:

Your Query Comment:

Your Query:

or Upload File with FASTA Format Queries:
 ファイルが選択していません

Parameters:

Expect:	<input type="text"/>	Match:	<input type="text"/>
WordSize:	<input type="text"/>	Mismatch:	<input type="text"/>
Filter:	<input checked="" type="checkbox"/>	Gap Open:	<input type="text"/>
GI:	<input type="text"/>	Gap Extend:	<input type="text"/>
Gap Align:	<input checked="" type="checkbox"/>	DropOff:	<input type="text"/>
Descriptions:	<input type="text"/>	Extend Hit:	<input type="text"/>
Alignments:	<input type="text"/>		

A query input page

3. Browsers and viewer

3.1 UnifiedMap

3.2 GBrowse

3.3 GeneViewer

3.1 UnifiedMap

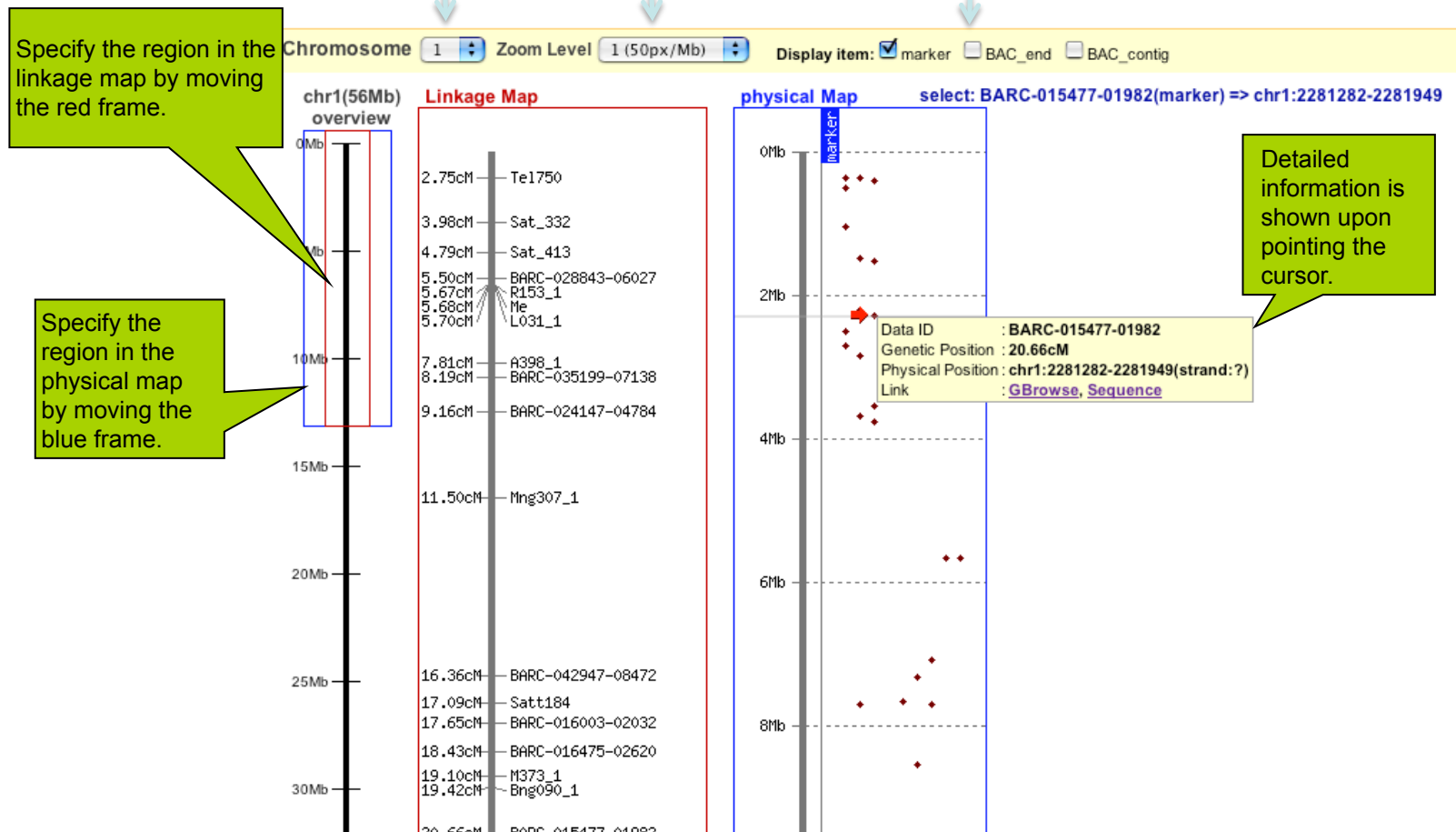
[Objective]

- linkage map and physical map showing Williams82 scaffolds, BAC contigs, BAC ends, and markers for each chromosome.

[Link]

- Choose designated region on the physical map and link to GBrowse or get to sequence.
 - Choose designated region on the linkage map. A red arrow appears on right side if marker information is available.

1. Select a chromosome
2. Specify the zooming level.
3. Check the desired items for display.



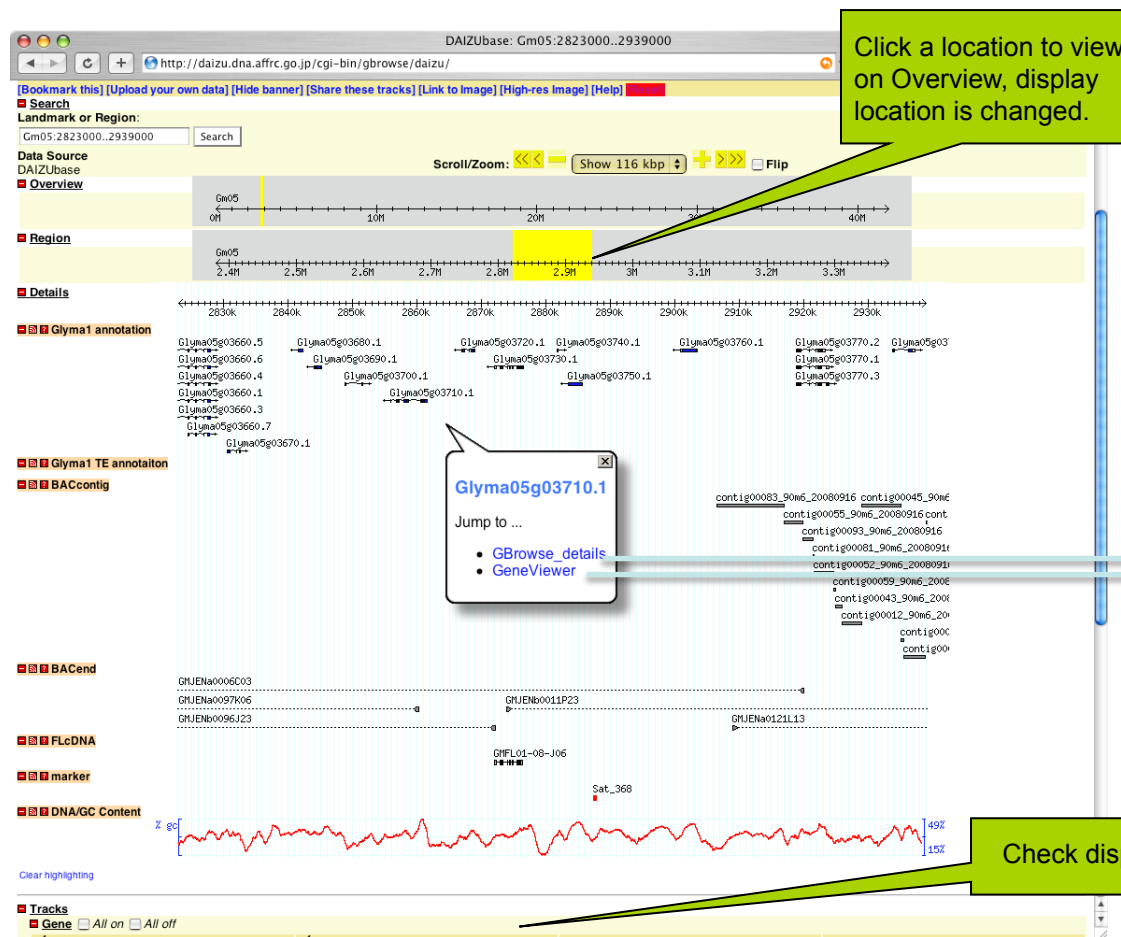
3.2 GBrowse

[Objective]

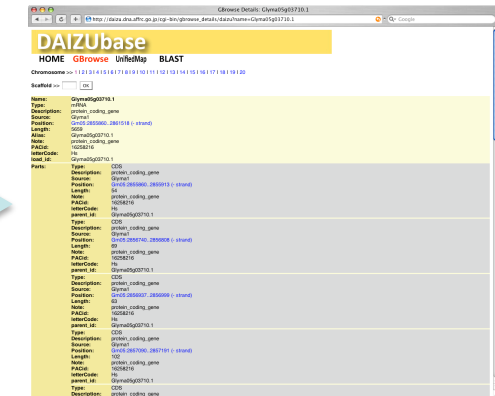
- Genome annotation viewer with a graphical representation of a section of a genome.

[Link]

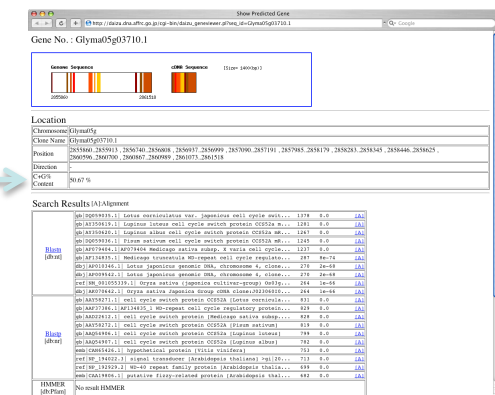
- Click designated region on Details and sequence and ID are displayed in another page.
- Click gene model on Details for link to GeneViewer.



GBrowse_details



GeneViewer



Check display items so display items are changed.

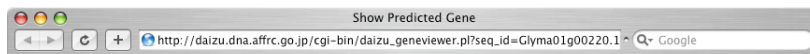
3.3 GeneViewer

[Objective]

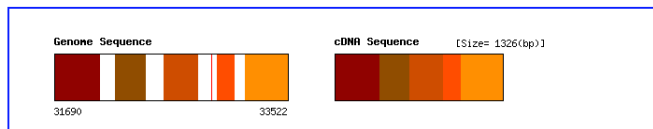
- Gene information viewer, showing the detailed information of the gene model.

[Link]

- “Search Results” links to results of homology search using BLASTn, BLASTp, HMMER and ProfileScan with corresponding alignments of the sequence.
- “Analysis of amino acid sequences” links to PSORT, SOSUI, MOTIF and Gene ontology (InterProScan).
- “Sequence” links to the nucleotide sequence, spliced nucleotide sequence and translated protein sequence of the predicted gene.



Gene No. : Glyma01g00220.1



Result of domain search against Pfam database.

Location

Chromosome	Glyma01g
Clone Name	Glyma01g00220.1
Position	31690..32043 , 32173..32407 , 32554..32819 , 32928..32929 , 32969..33104 , 33190..33522
Direction	+
C+G% Content	41.22 %

Detailed information of the predicted gene including chromosome number, clone name, position of exons and GC content.

Search Results [A]:Alignment

Blastn [db:nt]	No Hit
Blastp [db:nr]	emb CAN61586.1 hypothetical protein [Vitis vinifera] 192 7e-47 [A]
HMMER [db:Pfam]	No result HMMER
ProfileScan [db:prosite]	12..791 524 pos. 277 - 441 P550878 RT_POL Reverse transcriptase (RT) cat [A]

Results of homology search using BLASTn (top 3 ESTs), BLASTp (top 10 proteins), HMMER and ProfileScan with the corresponding alignments of the sequence.

Analysis of Amino Acid Sequence

- [PSORT](#)
- [SOSUI](#)
- [MOTIF](#)

Display the results of queries to amino acid analysis server/site such as PSORT, SOSUI, MOTIF and Gene ontology (InterProScan).

Sequence

- [Nucleotide Sequence](#)
- [Spliced Nucleotide Sequence](#)
- [Translated Protein Sequence](#)

Links to the nucleotide sequence, spliced nucleotide sequence and translated protein sequence of the predicted gene.

4. Keyword search and sequence search

4.1 An example of keyword search

4.2 An example of sequence search

4.1 An example of keyword search

Search for "00230" in gene data set on chromosome 5.

Enter "00230" in query box
Choose ID from pull-down menu

Choose "Gm5"

Click "Glyma1 annotation"

Click "Search" button.

DAIZUbase
HOME GBrowse UnifiedMap BLAST

DAIZUbase [\[How to use DAIZUbase\]](#)
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DAIZUbase is an integrated soybean genome database and data mining tool, consists of 2 map browsers, a gene viewer, and BLAST search system. [more...](#)

Keyword Search

Keyword Search
- enter a keyword and choose from several parameters to delimit the search.

Keyword:
00230 Search Field ID

Position:
chromosome (or scaffold) Gm05

Data Set:
☐ marker ☐ BAC_contig ☐ BAC_end
☒ Glyma1 annotation ☐ Glyma1 TE annotation ☐ FLcDNA

search reset

Result of keyword search

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Keyword search result

Number of hit : 1 [Download as an Excel file](#)

Data ID	Accession number	Data type	Position	Description	Link
Glyma05g00230.1		mRNA:Glyma1	Gm05 : 42358 - 42873 (strand : +)		GBrowse UnifiedMap GeneViewer

4.2 An example of sequence search

Choose Blastn and Williams82

Upload query sequence file

Set parameters

Search for location of a nucleotide sequence on Williams82.

DAIZUbase: DAIZU sequence database BLAST search

Program: Blastn -- [Query] Nucleotide [DB] Nucleotide

DataLib: Williams82 Scaffold (Glyma1)

Your Query Comment: Glyma1_cds
Glyma1_TE_cds
ENREI BAC end

Your Query:

or Upload File with FASTA Format Queries:

Choose File Glyma05g00...DNA.fasta

Search Reset

Parameters:

Expect: 100 Match: 100

Word size: 12 Mismatch: 12

Filter: [x] 12 Gap Open: 5

GI: 12 Gap Extend: 2

Gap Align: [x] 12 DropOff: 12

Descriptions: 100 Extend Hit: 12

Alignments: 100

Click "Search" button

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HOME GBrowse UnifiedMap BLAST

Thanks!

Now your search request is accepted.

Program: Blastn
Data Library: Glyma1_cds
Descriptions: 100
Alignments: 100
Filter: T
Gap Open: 5
Gap Extend: 2
GI: F
Gap Align: T

Begin
-CGTAA5g00239.1
TTATACAGT CAGAGAGAA GTTGTGTTG TGTAAATAC TTGGAGAAA
ATTGGGCTT TTATATATG TGAAGGAAA TTGCACTCT ATTGGAAT
TAGAGATGA TTGAGTGTG ATAAATGTT TAAAGGAAA TTTGTGTTG
ACCTTGTAT TTGAGCTAA TGGAGAAA GTTATATG AGCACTGTG
GATTTTCA GCTTCAGAT CAAGTGTG AAGAGCTT GTAAAGTGTG
ATTGAGCAT TGTACAGAT GATGTGTG GATTTGTG GTAAAGTGTG
GAGATGAT TATGTATCT ACTGAGAAA TTTGTTAA ATGAGTGTG
GTAAAGTGTG GATGTGTG GATTTGTG T

Please check following URL.
<http://daizu.dna.affrc.go.jp/blast/resulta/Blastn044671250142be811c83209402a55.html>

If you have any trouble with this server, please let us know.
We will fix your problem.

This URL allows the user to redisplay the result of for a certain period.

Result of sequence search

DAIZUbase

HOME GBrowse UnifiedMap BLAST

Result.

No.	query ID	Hit Query Position	Hit Length (Hit Rate)	e-value (score)	Hit Chromosome/Scaffold ID	Hit Chromosome/Scaffold Position	Link
1	Glyma05g00239.1	1-204	204 (100.00%)	5e-111 (404)	Gm05	42358-42361	Browse UnifiedMap
1	Glyma05g00239.1	241-381	141 (100.00%)	2e-73 (285)	Gm05	42733-42873	Browse UnifiedMap
1	Glyma05g00239.1	204-241	38 (100.00%)	5e-12 (75.8)	Gm05	42611-42648	Browse UnifiedMap
1	Glyma05g00239.1	176-193	18 (100.00%)	4.5 (36.2)	Gm05	1302948-1302949	Browse UnifiedMap
1	Glyma05g00239.1	39-56	18 (100.00%)	4.5 (36.2)	Gm05	16485670-16485687	Browse UnifiedMap
2	Glyma05g00239.1	256-362	107 (90.45%)	3e-29 (133)	Gm17	6505142-6505036	Browse UnifiedMap
2	Glyma05g00239.1	204-241	38 (97.37%)	3e-09 (67.9)	Gm17	6505284-6505247	Browse UnifiedMap
2	Glyma05g00239.1	348-358	19 (100.00%)	1.1 (38.2)	Gm17	18825444-18825462	Browse UnifiedMap
2	Glyma05g00239.1	324-341	18 (100.00%)	4.5 (36.2)	Gm17	4605112-4605129	Browse UnifiedMap
2	Glyma05g00239.1	95-116	22 (95.45%)	4.5 (36.2)	Gm17	19395446-19395487	Browse UnifiedMap
2	Glyma05g00239.1	95-116	22 (95.45%)	4.5 (36.2)	Gm17	24311041-24311040	Browse UnifiedMap
2	Glyma05g00239.1	95-116	22 (95.45%)	4.5 (36.2)	Gm17	24418680-24418701	Browse UnifiedMap