Flowering Time

Ken

GRAMENE *Home*

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Release #31

May 2010
Release notes

News

- Release#31 updates in Gramene Genetic Diversity
  Release #31 of Gramene brought new data sets and features in the Genetic Diversity module. Gramene...
- The Genomic Diversity and Phenotype Data Model (GDPDM) Database Schema Version 4.0
  Genome sequencing continues to become less expensive and faster which is great news for researchers...
- Gramene's new FastBit engine for DAS retrievals
  A while ago, Gramene instantiated a Distributed Annotation System (DAS) for serving some of our rice...

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Have Questions...?

- Quick Search Help
- Ask questions through **Feedback** or **Email**.
- See **FAQ**.

Outreach calendar

Explore Gramene

Quick Search

flowering time

Disable search suggestions

flowering time
flowering time control protein
Flowering time control protein FCA gamma-like
Flowering time control protein FCA-like protein
Flowering time control protein isoform rFCA-1
Flowering time control protein isoform rFCA-2
Flowering time control protein isoform rFCA-3

Pathways

Proteins

Genes

Ontologies

Markers

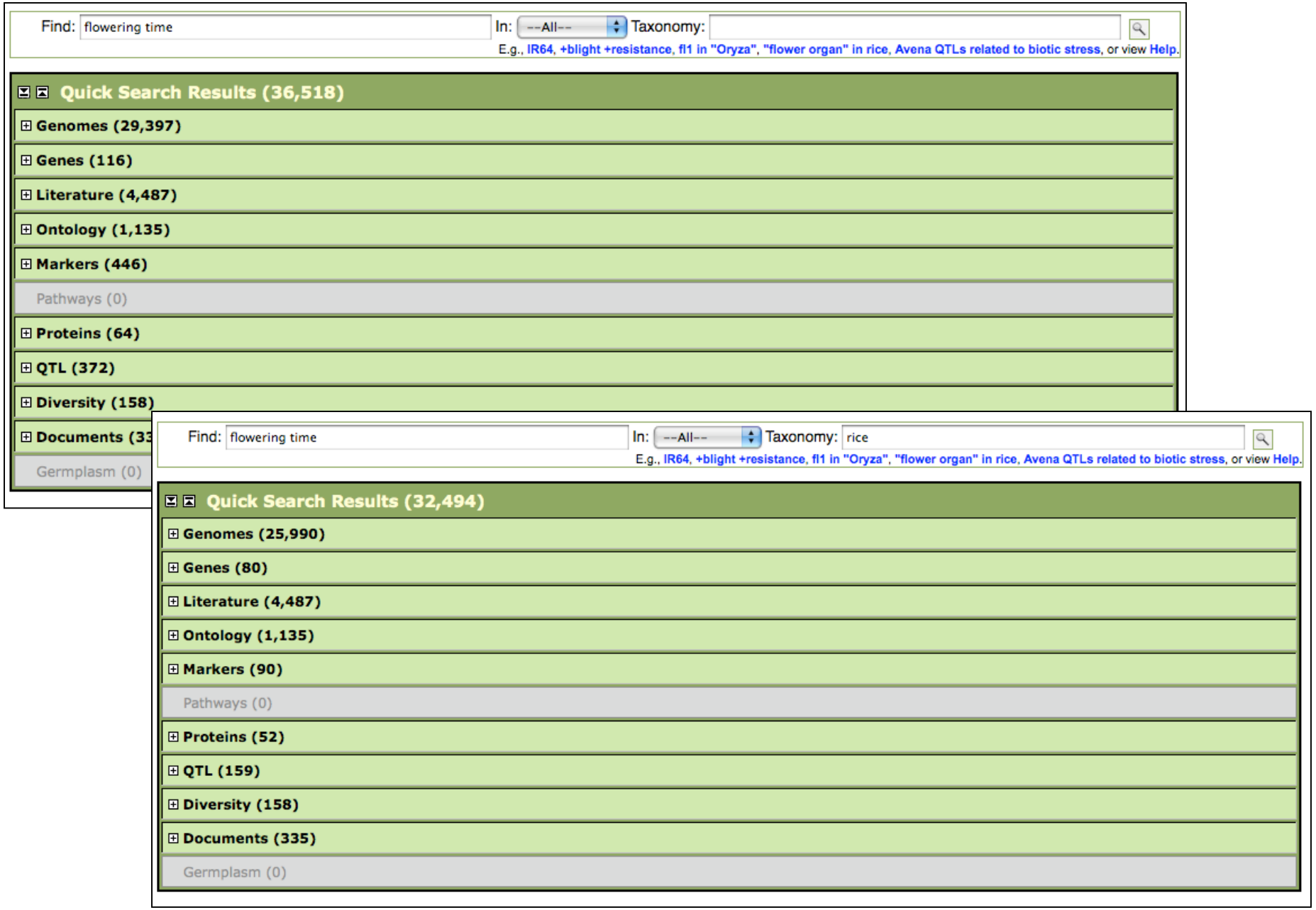
Comparative Maps

QTL

BLAST

Gramene Mart

Species Pages


Find: flowering time
In: --All--
Taxonomy:
E.g., IR64, +blight +resistance, fl1 in "Oryza", "flower organ" in rice, Avena QTLs related to biotic stress, or view Help.
Quick Search Results (36,518)
Genomes (29,397)
Genes (116)
Literature (4,487)
Ontology (1,135)
Markers (446)
Pathways (0)
Proteins (64)
QTL (372)
Diversity (158)
Documents (33
Germplasm (0)
Find: flowering time
In: --All--
Taxonomy: rice
E.g., IR64, +blight +resistance, fl1 in "Oryza", "flower organ" in rice, Avena QTLs related to biotic stress, or view Help.
Quick Search Results (32,494)
Genomes (25,990)
Genes (80)
Literature (4,487)
Ontology (1,135)
Markers (90)
Pathways (0)
Proteins (52)
QTL (159)
Diversity (158)
Documents (335)
Germplasm (0)

Oryza sativa QTL "AQHQ006" (days to flower)

QTL Accession ID	AQHQ006
Species	Oryza sativa (Rice) [GR_tax:013681]
Trait Symbol	DTFL
Trait Name	days to flower
Published Symbol	Dtf7a
Trait Synonym(s)	days to flowering; days to pollen; days to silk; flowering date; flowering duration
Trait Category	Development
Chromosome	7
Comments	The days to 50% flowering of each plant (3-5 panicles/plant) under 10 h day length condition was recorded to evaluate days to flowering.

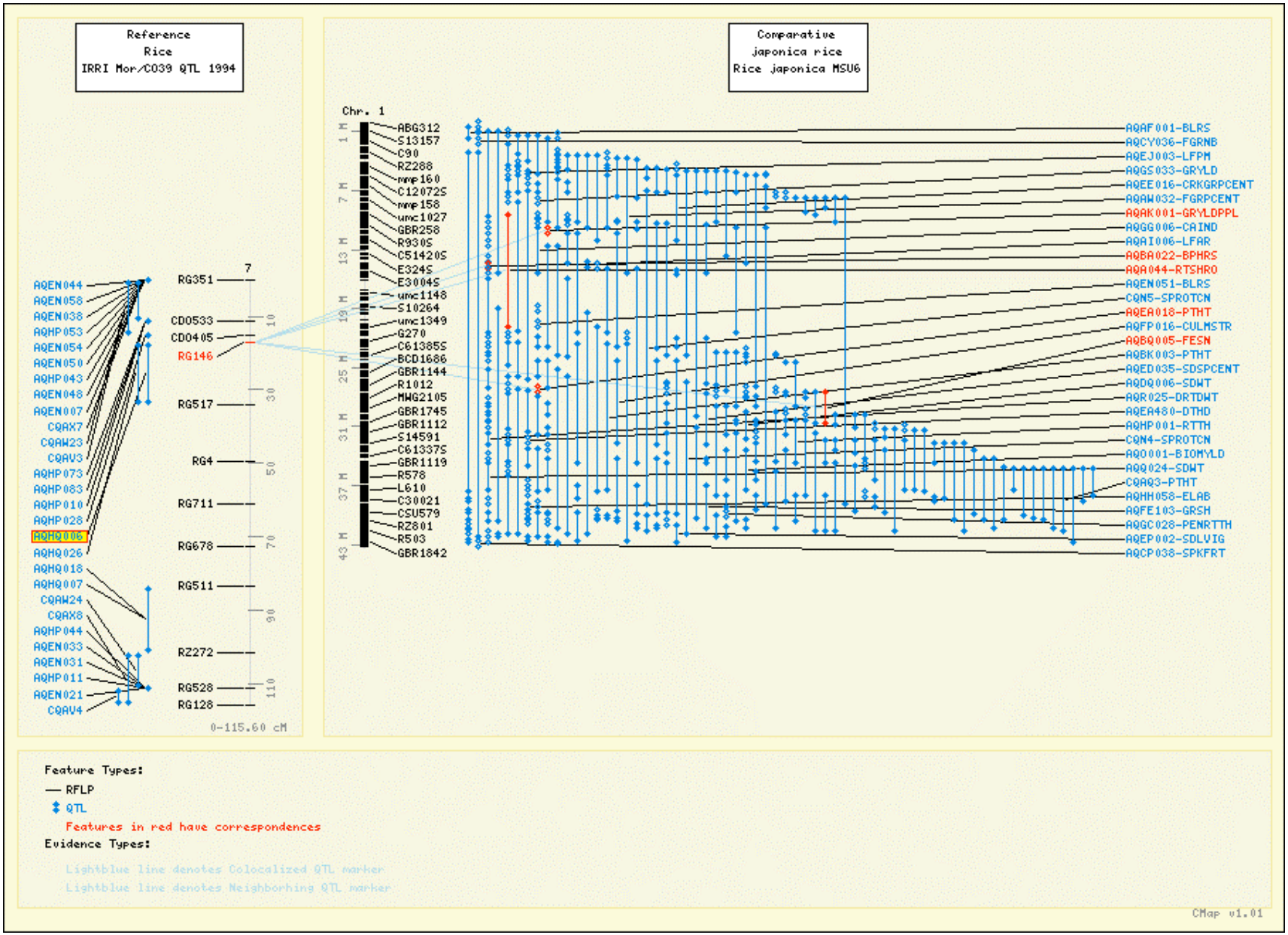
⊞ **Map Positions (2)**

⊞ **Associated Markers (4)**

Associated Genes (0)

⊞ **Associated Ontologies (2)**

⊞ **Database Cross-References (1)**


Reference
Rice
IRRI Mor/C039 QTL 1994
Comparative
japonica rice
Rice japonica MSU6
Chr. 1
AQEN044
AQEN058
AQEN038
AQHP053
AQEN054
AQEN050
AQHP043
AQEN048
AQEN007
CQAX7
CQAW23
CQAV3
AQHP073
AQHP083
AQHP010
AQHP028
AQHQ006
AQHQ026
AQHQ018
AQHQ007
CQAW24
CQAX8
AQHP044
AQEN033
AQEN031
AQHP011
AQEN021
CQAV4
RG351
CD0533
CD0405
RG146
RG517
RG4
RG711
RG678
RG511
RZ272
RG528
RG128
0-115.60 cM
ABG312
S13157
C90
RZ288
mwp160
C12072S
mwp158
umc1027
GBR258
R930S
C51420S
E324S
E3004S
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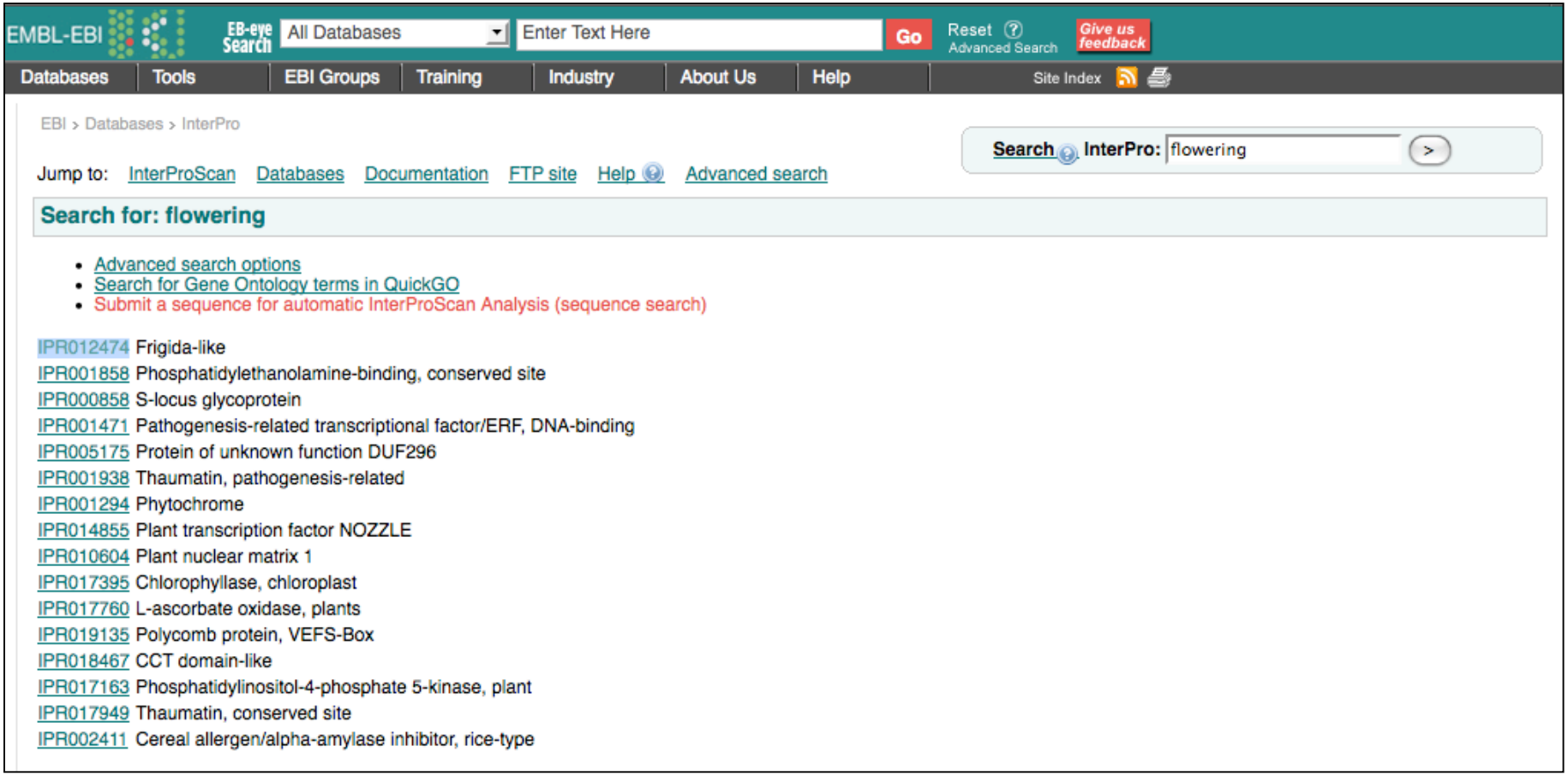
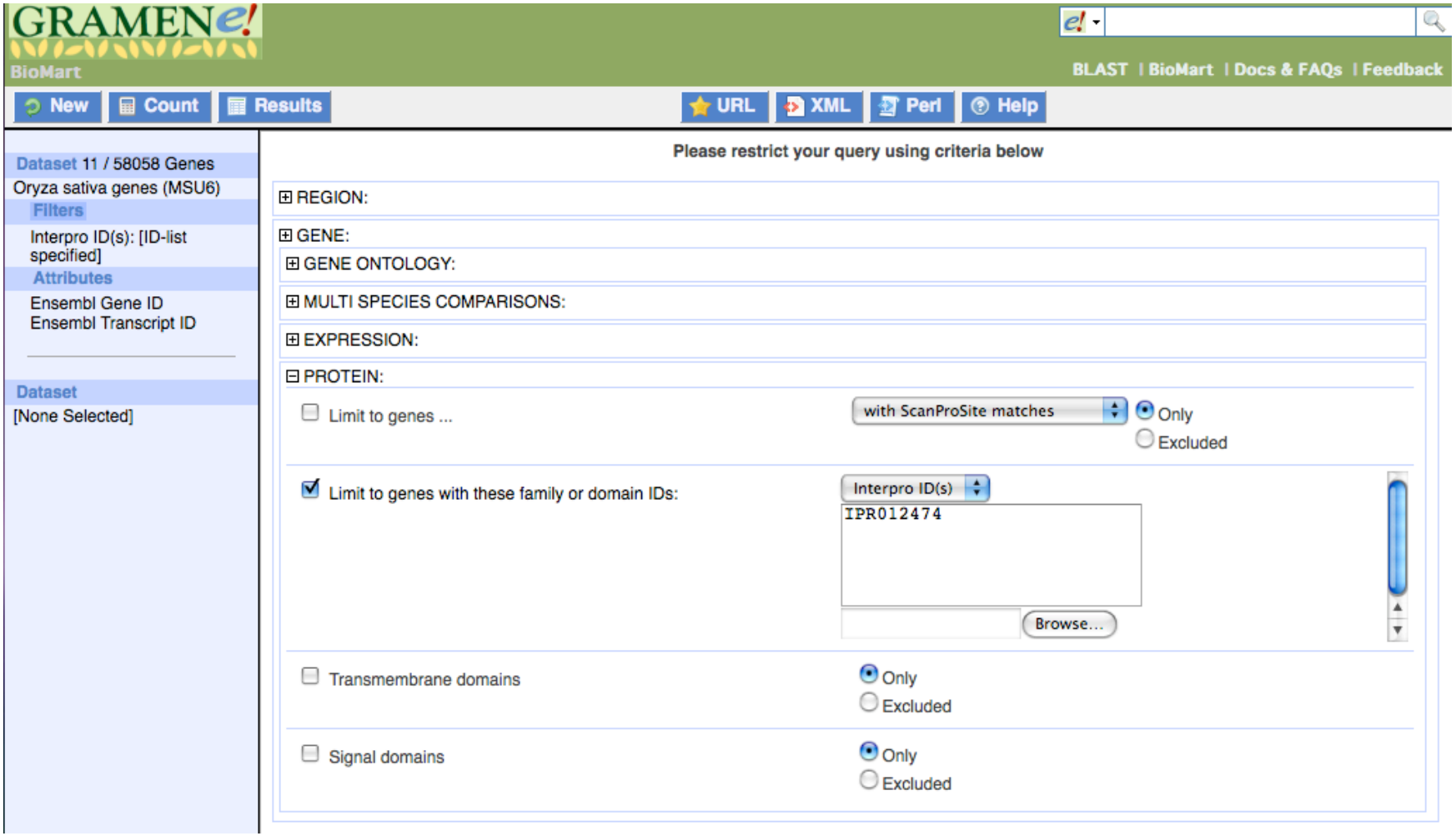
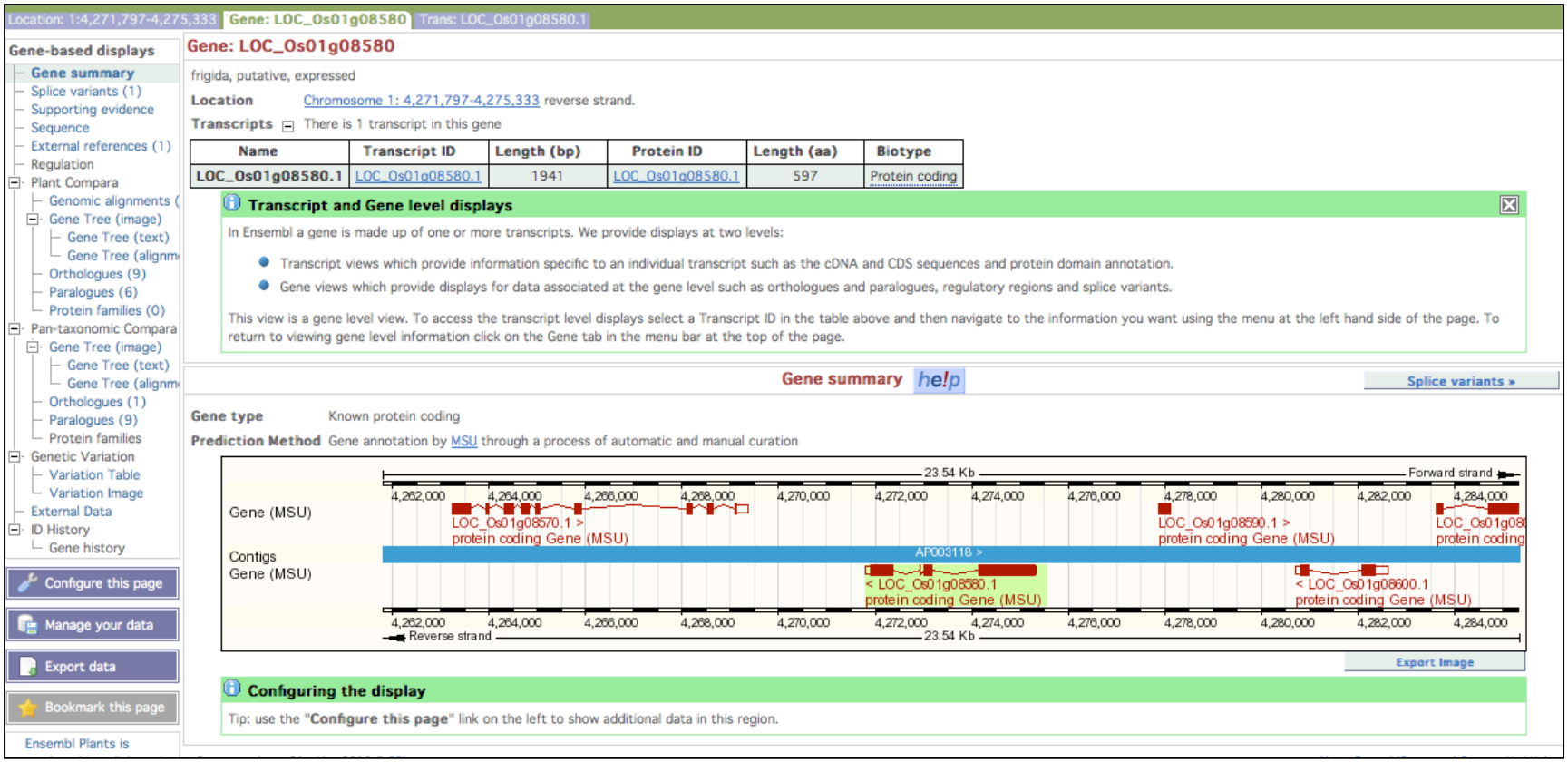
S10264
umc1349
G270
C61385S
BCD1686
GBR1144
R1012
MWG2105
GBR1745
GBR1112
S14591
C61337S
GBR1119
R578
L610
C30021
CSU579
RZ801
R503
GBR1842
AQAF001-BLRS
AQCY036-FGRNB
AQEJ003-LFPM
AQGS033-GRYLD
AQEE016-CRKGRPCENT
AQAW032-FGRPCENT
AQAK001-GRYLDPPL
AQGG006-CAIND
AQAI006-LFAR
AQBA022-BPHRS
AQA044-RTSHRO
AQEN051-BLRS
CQN5-SPROTCN
AQEA018-PTHT
AQFP016-CULMSTR
AQBQ005-FESN
AQBK003-PTHT
AQED035-SDSPCENT
AQDQ006-SDWT
AQR025-DRTDWT
AQEA480-DTHD
AQHP001-RTTH
CQN4-SPROTCN
AQO001-BIOMYLD
AQQ024-SDWT
CQAQ3-PTHT
AQHH058-ELAB
AQFE103-GRSH
AQGC028-PENRTTH
AQEP002-SDLVIG
AQCP038-SPKFRT
Feature Types:
RFLP
QTL
Features in red have correspondences
Evidence Types:
Lightblue line denotes Colocalized QTL marker
Lightblue line denotes Neighborhing QTL marker
CMap v1.01

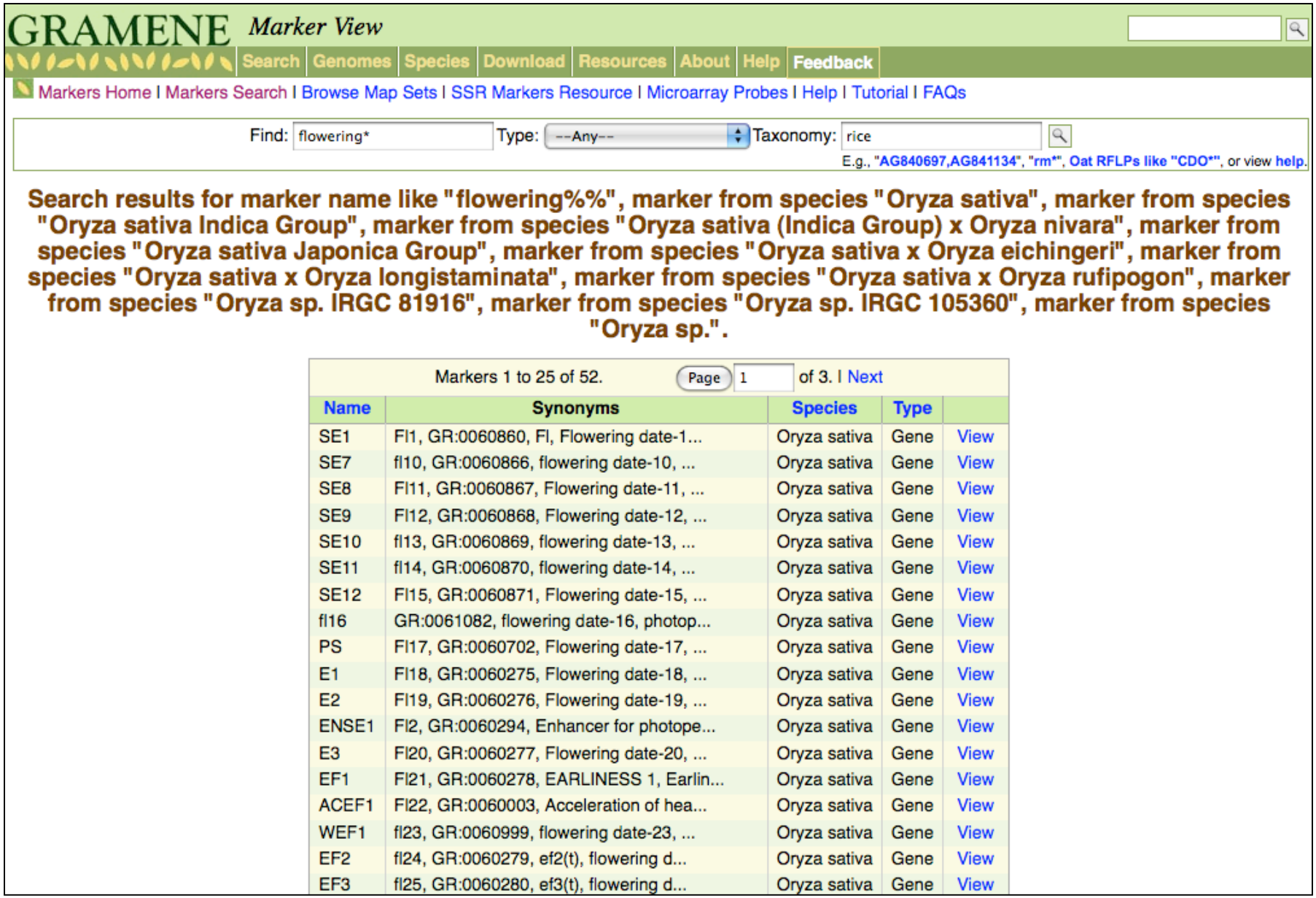

EMBL-EBI
EB-eye Search
All Databases
Enter Text Here
Go
Reset
Advanced Search
Give us feedback
Databases
Tools
EBI Groups
Training
Industry
About Us
Help
Site Index
EBI > Databases > InterPro
Search InterPro: flowering
Jump to: InterProScan Databases Documentation FTP site Help Advanced search
Search for: flowering
Advanced search options
Search for Gene Ontology terms in QuickGO
Submit a sequence for automatic InterProScan Analysis (sequence search)
IPR012474 Frigida-like
IPR001858 Phosphatidylethanolamine-binding, conserved site
IPR000858 S-locus glycoprotein
IPR001471 Pathogenesis-related transcriptional factor/ERF, DNA-binding
IPR005175 Protein of unknown function DUF296
IPR001938 Thaumatin, pathogenesis-related
IPR001294 Phytochrome
IPR014855 Plant transcription factor NOZZLE
IPR010604 Plant nuclear matrix 1
IPR017395 Chlorophyllase, chloroplast
IPR017760 L-ascorbate oxidase, plants
IPR019135 Polycomb protein, VEFS-Box
IPR018467 CCT domain-like
IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant
IPR017949 Thaumatin, conserved site
IPR002411 Cereal allergen/alpha-amylase inhibitor, rice-type


GRAMENE!
BioMart
BLAST | BioMart | Docs & FAQs | Feedback
New
Count
Results
URL
XML
Perl
Help
Dataset 11 / 58058 Genes
Oryza sativa genes (MSU6)
Filters
Interpro ID(s): [ID-list specified]
Attributes
Ensembl Gene ID
Ensembl Transcript ID
Dataset
[None Selected]
Please restrict your query using criteria below
REGION:
GENE:
GENE ONTOLOGY:
MULTI SPECIES COMPARISONS:
EXPRESSION:
PROTEIN:
Limit to genes ...
with ScanProSite matches
Only
Excluded
Limit to genes with these family or domain IDs:
Interpro ID(s)
IPR012474
Browse...
Transmembrane domains
Only
Excluded
Signal domains
Only
Excluded

View 20 rows as HTML

Ensembl Gene ID	Ensembl Transcript ID
LOC_Os01g08580	LOC_Os01g08580.1
LOC_Os03g58070	LOC_Os03g58070.1
LOC_Os03g39129	LOC_Os03g39129.1
LOC_Os03g39160	LOC_Os03g39160.1
LOC_Os03g63440	LOC_Os03g63440.1
LOC_Os03g09310	LOC_Os03g09310.1
LOC_Os03g09310	LOC_Os03g09310.2
LOC_Os03g39170	LOC_Os03g39170.1
LOC_Os07g07680	LOC_Os07g07680.1
LOC_Os07g40270	LOC_Os07g40270.1
LOC_Os09g07380	LOC_Os09g07380.1
LOC_Os09g07360	LOC_Os09g07360.2
LOC_Os09g07360	LOC_Os09g07360.3
LOC_Os09g07360	LOC_Os09g07360.1


Location: 1:4,271,797-4,275,333
Gene: LOC_Os01g08580
Trans: LOC_Os01g08580.1
Gene-based displays
Gene summary
Splice variants (1)
Supporting evidence
Sequence
External references (1)
Regulation
Plant Compara
Genomic alignments (
Gene Tree (image)
Gene Tree (text)
Gene Tree (alignm
Orthologues (9)
Paralogues (6)
Protein families (0)
Pan-taxonomic Compara
Gene Tree (image)
Gene Tree (text)
Gene Tree (alignm
Orthologues (1)
Paralogues (9)
Protein families
Genetic Variation
Variation Table
Variation Image
External Data
ID History
Gene history
Configure this page
Manage your data
Export data
Bookmark this page
Ensembl Plants is
Gene: LOC_Os01g08580
frigida, putative, expressed
Location
Chromosome 1: 4,271,797-4,275,333 reverse strand.
Transcripts
There is 1 transcript in this gene
Name
Transcript ID
Length (bp)
Protein ID
Length (aa)
Biotype
LOC_Os01g08580.1
LOC_Os01g08580.1
1941
LOC_Os01g08580.1
597
Protein coding
Transcript and Gene level displays
In Ensembl a gene is made up of one or more transcripts. We provide displays at two levels:
Transcript views which provide information specific to an individual transcript such as the cDNA and CDS sequences and protein domain annotation.
Gene views which provide displays for data associated at the gene level such as orthologues and paralogues, regulatory regions and splice variants.
This view is a gene level view. To access the transcript level displays select a Transcript ID in the table above and then navigate to the information you want using the menu at the left hand side of the page. To return to viewing gene level information click on the Gene tab in the menu bar at the top of the page.
Gene summary
help
Splice variants »
Gene type
Known protein coding
Prediction Method
Gene annotation by MSU through a process of automatic and manual curation
23.54 Kb
Forward strand
4,262,000
4,264,000
4,266,000
4,268,000
4,270,000
4,272,000
4,274,000
4,276,000
4,278,000
4,280,000
4,282,000
4,284,000
Gene (MSU)
LOC_Os01g08570.1 >
protein coding Gene (MSU)
LOC_Os01g08590.1 >
protein coding Gene (MSU)
Contigs
Gene (MSU)
AP003118 >
< LOC_Os01g08580.1
protein coding Gene (MSU)
< LOC_Os01g08600.1
protein coding Gene (MSU)
Reverse strand
23.54 Kb
Export Image
Configuring the display
Tip: use the "Configure this page" link on the left to show additional data in this region.



Name	Synonyms	Species	Type	
SE1	Fl1, GR:0060860, Fl, Flowering date-1...	Oryza sativa	Gene	View
SE7	fl10, GR:0060866, flowering date-10, ...	Oryza sativa	Gene	View
SE8	Fl11, GR:0060867, Flowering date-11, ...	Oryza sativa	Gene	View
SE9	Fl12, GR:0060868, Flowering date-12, ...	Oryza sativa	Gene	View
SE10	fl13, GR:0060869, flowering date-13, ...	Oryza sativa	Gene	View
SE11	fl14, GR:0060870, flowering date-14, ...	Oryza sativa	Gene	View
SE12	Fl15, GR:0060871, Flowering date-15, ...	Oryza sativa	Gene	View
fl16	GR:0061082, flowering date-16, photop...	Oryza sativa	Gene	View
PS	Fl17, GR:0060702, Flowering date-17, ...	Oryza sativa	Gene	View
E1	Fl18, GR:0060275, Flowering date-18, ...	Oryza sativa	Gene	View
E2	Fl19, GR:0060276, Flowering date-19, ...	Oryza sativa	Gene	View
ENSE1	Fl2, GR:0060294, Enhancer for photope...	Oryza sativa	Gene	View
E3	Fl20, GR:0060277, Flowering date-20, ...	Oryza sativa	Gene	View
EF1	Fl21, GR:0060278, EARLINESS 1, Earlin...	Oryza sativa	Gene	View
ACEF1	Fl22, GR:0060003, Acceleration of hea...	Oryza sativa	Gene	View
WEF1	fl23, GR:0060999, flowering date-23, ...	Oryza sativa	Gene	View
EF2	fl24, GR:0060279, ef2(t), flowering d...	Oryza sativa	Gene	View
EF3	fl25, GR:0060280, ef3(t), flowering d...	Oryza sativa	Gene	View

GRAMENE *Marker View*

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Find: SE1 Type: Gene Taxonomy: rice

E.g., "AG840697,AG841134", "rm*", Oat RFLPs like "CDO*", or view help.

Oryza sativa Gene "SE1"

ID	25516512
Name	SE1 (GENE SYMBOL)
Synonyms (10)	Fl — Flowering date-1 Hd1 — K Lf — Lm Photoperiod-sensitivity-1 — PHOTOSENSITIVITY 1 Rs — Se1
GENE SYMBOL	Fl1
GRAMENE GENE	GR:0060860
Type	Gene
Species	Oryza sativa (Oryza sativa) [GR_tax:013681]
Germplasm	Unknown
Analysis	• export-genes-to-mdb.pl
Description	Photoperiod sensitivity. Related to heading date and maturity in rice. Strong photoperiodic sensitivity is dominant over insensitivity.
Tags (0)	None

Source/Library

Details

Database Cross-References (0)

Sequences (0)

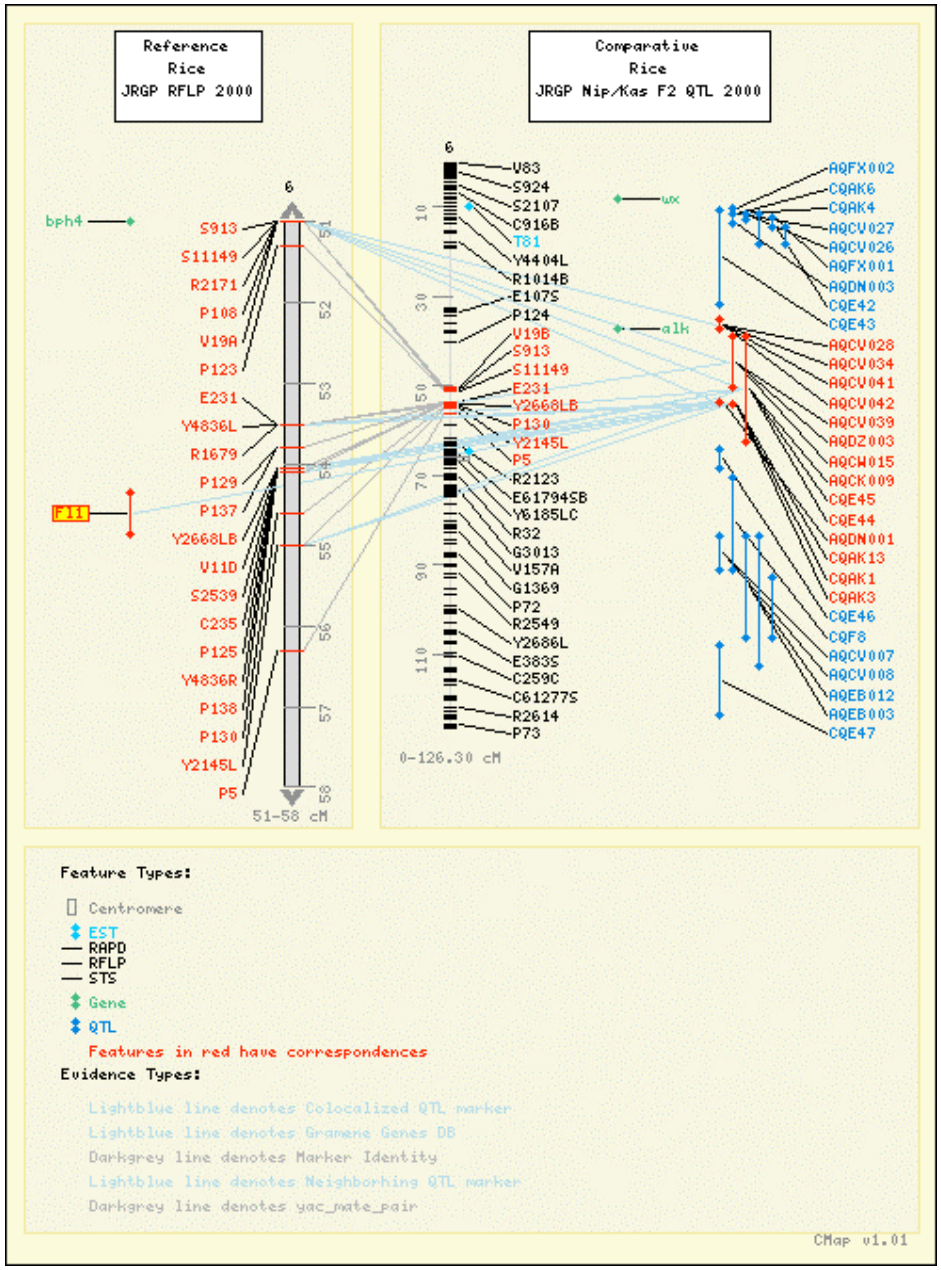
⊞ Map Positions (4)

⊟ Associations (11)

Direction	Name	Type	Species	Analysis	Assoc. Type
To	AB041837	Genomic DNA	Oryza sativa Japonica Group	export-genes-to-mdb.pl	ISS
To	AP003044	Genomic DNA	Oryza sativa Japonica Group	export-genes-to-mdb.pl	ISS
To	AB041838	mRNA	Oryza sativa Japonica Group	export-genes-to-mdb.pl	ISS
To	AB041841	Genomic DNA	Oryza sativa	export-genes-to-mdb.pl	ISS
To	AB041842	Genomic DNA	Oryza sativa	export-genes-to-mdb.pl	ISS
To	AB041839	Genomic DNA	Oryza sativa Indica Group	export-genes-to-mdb.pl	ISS
To	AB041840	Genomic DNA	Oryza sativa Japonica Group	export-genes-to-mdb.pl	ISS
To	LOC_Os06g16370	Gene Prediction	Oryza sativa Japonica Group	export-genes-to-mdb.pl	ISS
To	CQAK1 (DTHD, days to heading)	QTL	Oryza sativa	export-genes-to-mdb.pl	ISS
To	CQAK3 (DTHD, days to heading)	QTL	Oryza sativa	export-genes-to-mdb.pl	ISS
To	CQAK13 (DTHD, days to heading)	QTL	Oryza sativa	export-genes-to-mdb.pl	ISS

⊟ Associated Ontologies (23)

Term Type	Term Name	Term Accession	
Molecular Function	DNA binding	GO:0003677	Search
Molecular Function	transcription factor activity	GO:0003700	Search
Cellular Component	nucleus	GO:0005634	Search
Biological Process	biological_process	GO:0008150	Search
Molecular Function	zinc ion binding	GO:0008270	Search
Biological Process	photoperiodism	GO:0009648	Search
Biological Process	inflorescence development	GO:0010229	Search
Biological Process	long-day photoperiodism	GO:0048571	Search
Biological Process	short-day photoperiodism	GO:0048572	Search
Cereal Plant Growth Stage	06-heading stage	GRO:0007044	Search


Reference
Rice
JRGP RFLP 2000
Comparative
Rice
JRGP Nip/Kas F2 QTL 2000
6
bph4
S913
S11149
R2171
P108
V19A
P123
E231
Y4836L
R1679
P129
P137
Y2668LB
V11D
S2539
C235
P125
Y4836R
P138
P130
Y2145L
P5
F11
51
52
53
54
55
56
57
58
51-58 cM
6
10
30
50
70
90
110
V83
S924
S2107
C916B
T81
Y4404L
R1014B
E107S
P124
V19B
S913
S11149
E231
Y2668LB
P130
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P5
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Y6185LC
R32
G3013
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G1369
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R2549
Y2686L
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C61277S
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wx
alk
AQFX002
CQAK6
CQAK4
AQCV027
AQCV026
AQFX001
AQDN003
CQE42
CQE43
AQCV028
AQCV034
AQCV041
AQCV042
AQCV039
AQDZ003
AQCW015
AQCK009
CQE45
CQE44
AQDN001
CQAK13
CQAK1
CQAK3
CQE46
CQF8
AQCV007
AQCV008
AQEB012
AQEB003
CQE47
Feature Types:
Centromere
EST
RAPD
RFLP
STS
Gene
QTL
Features in red have correspondences
Evidence Types:
Lightblue line denotes Colocalized QTL marker
Lightblue line denotes Gramene Genes DB
Darkgrey line denotes Marker Identity
Lightblue line denotes Neighborhing QTL marker
Darkgrey line denotes yac_mate_pair
CMap v1.01