

Welcome to the Maps and CMap Tutorial

Identify the location of a particular gene, trait, QTL or marker - and the grass species they have been mapped to - on genetic, QTL, physical, sequence, and deletion maps .

Use the CMap viewer to examine the co-linearity of a particular region in one chromosome or species to another; or infer which linkage group in one species is most conserved with a linkage group in another species. . .

Determine which maps are the best for making comparisons.

GMOD

CMap was originally written for the Gramene project (<http://www.gramene.org/>) and is now part of the GMOD (Generic Model Organism Database) Project (<http://www.gmod.org/>).

**For more assistance on cmap, visit
<http://www.gmod.org/cmap/>**



Tutorial Tips



If you are viewing this tutorial with Adobe Acrobat Reader, click the "bookmarks" on the left hand side of the Reader for easier navigation.

Note! Although we continually work to make Gramene compatible with all browsers, there are problems with some browser versions. If you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through Gramene Feedback.

Gramene Home Page

GRAMENE *A Resource for Comparative Grass Genomics* V24 (March 2007)

Search Genomes Species Download Resources About Help Feedback

Quick Search

Search a single module or all available modules plus online documentation.
Diversity, Pathways, BLAST and Mart not available in this search.

Have Questions...?

- Gramene now has [tutorials](#) for every module, also recommended for experienced users.
- Ask questions through [Feedback](#) or [Email](#).
- See [FAQ](#) for questions and answers.

Gramene Tip:

You can view/download Gramene's files. Use the [Download](#) and [FTP](#) pages.

- [Browse All Tips](#)

Navigation Menu:

- Genomes-Ensembl
- Maps-CMap**
- Markers
- QTL
- Diversity
- Genes
- Proteins
- Pathways
- Ontologies
- Literature
- Sequences-BLAST
- All-GrameneMart

Click here to open the Maps Home Page

Featured News

- [NEW](#) March 2007, V 24 release notes.
- [NEW](#) Gramene Jan/Feb Newsletter
- [Rice News Worldwide](#) from IRRI

Visit with us at

- March 15-18, 2007. [CSU Plant Genome meeting](#)
- March 22-25, 2007. [Mai Genetics Meeting](#)
- April 16-20, 2007. [ITMI](#)
- May 8-12, 2007. [Biology Genomes](#)
- July 7-11, 2007. [ASPB](#)

[View Previous Gramene Presentations Calendar](#)

TRAITS: Search the [Genes](#) or [QTL](#) database for important phenotype-related loci such as [Rice Genes](#), [Rice QTL](#), [Maize QTL](#). Don't forget to explore traits in [Ontologies](#).

GENETIC DIVERSITY: Search for SNP and SSR allelic variation on loci of [rice](#), [maize](#), and [wheat](#) germplasms.

BIOCHEMICAL PATHWAYS: Search for ALL the rice pathways on [starch biosynthesis](#) or get an overview of the [metabolic network](#). Compare [rice](#) and [Arabidopsis](#) pathway datasets.

LITERATURE: Search the literature for your friends and topics of interest.

SUBMISSION: Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

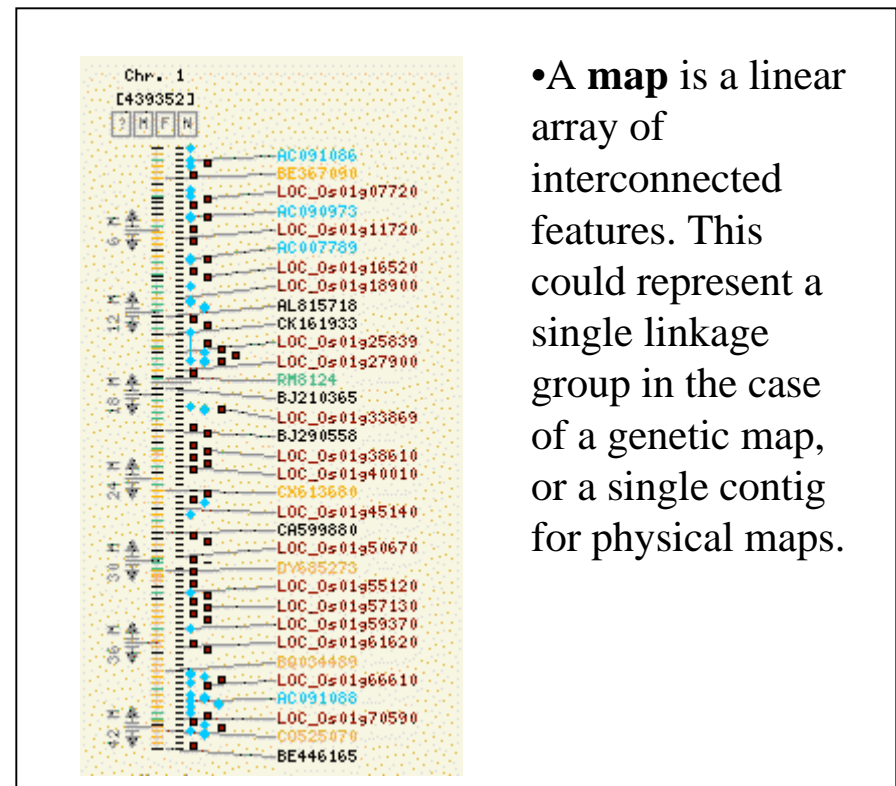
Gramene is a curated, open-source, web-accessible data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

Note! Although we continually work to make Gramene compatible with all browsers, if you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through [Gramene Feedback](#).

Concepts

Related maps are grouped into **map sets**. Generally, these are the result of a particular study, such as the set of linkage groups produced by a genetic mapping study.

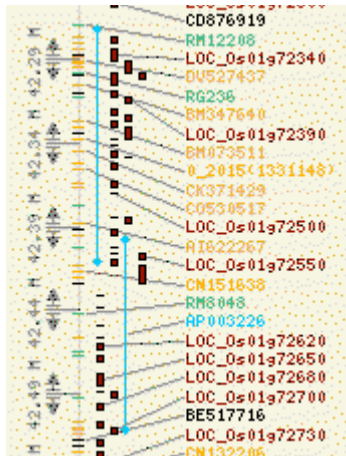
Map Set Name:	Gramene Annotated Nipponbare Sequence 2006
Abbreviated Name:	Gramene Annot Seq 2006
Accession ID:	gt0506
Species:	Oryza sativa (Rice)
Map Type:	Sequence
Map Units:	bp
Published On:	02 May, 2006
Maps:	Chr. 1 Chr. 2 Chr. 3 Chr. 4 Chr. 5 Chr. 6 Chr. 7 Chr. 8 Chr. 9 Chr. 10 Chr. 11 Chr. 12 Plastid Mitochondrion



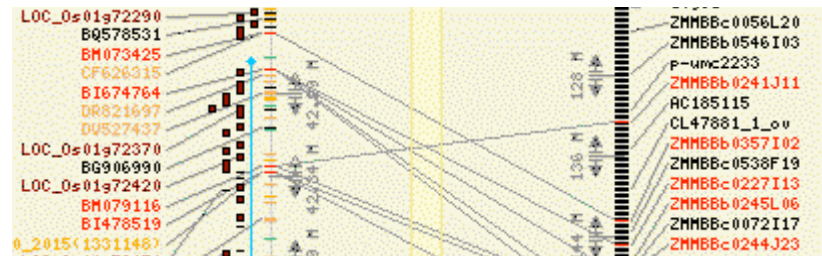
•A **map** is a linear array of interconnected features. This could represent a single linkage group in the case of a genetic map, or a single contig for physical maps.

Concepts, con't.

- Any item that is positioned on a map is called a **feature**. The position may be either a point or an interval. Different **feature types** are represented by different shapes or colors.



- The lines that connect features on one map to features on another map denote **correspondences**. These correspondences are assigned either automatically (based on feature name) or manually by the data curator to designate features on different maps that are equivalent in some manner. Different colors represent different **correspondence types**.



Concepts, con't.

- The data in Maps has been imported from the Gramene Markers DB. Use maps to find a feature on a map, but use the Markers DB to get specific data about the features.
- Not all the data in the Markers DB has been exported to CMap, only data that has correspondences has been imported into Maps.

Maps Home Page

Gramene - Maps

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Welcome to Gramene's Maps module where you can view genetic, physical, sequence, and QTL maps for many species of cereal crops. **CMap** — the Comparative Map Viewer — allows you to construct comparisons between different maps.

See the [release notes](#) for more information on any changes in the current release.

- **Maps:** View and compare maps
- **Map Search:** Search for a map by name
- **Feature Search:** Find a particular feature by name
- **Matrix:** See the number of correspondences among maps
- **Map Sets:** Get a description of one or all map sets
- **Feature Types:** Browse the feature types and their descriptions
- **Map Types:** Read descriptions of the different map types
- **Evidence Types:** Get a description of the different evidence types
- **Species:** Get a description of the species
- **Help:** Read the help
- **Tutorial:** How to use the map viewer to find and view maps and make comparisons
- **FAQ:** Frequently Asked Questions

Select “maps” to choose a starting map. You may later add comparative maps to the right or left.



Last modified: Thu May 4 11:54:35 2006

[Home](#) | [Site Map](#) | [About](#) | [Cite Gramene](#)

Maps: Select a Species

The screenshot shows the GRAMENE CMap website interface. The top navigation bar includes links for Search, Genomes, Species, Download, Resources, About, Help, and Feedback. A search box is located on the right. Below the navigation bar, the 'Maps' link in the main menu is circled in red. A dropdown menu is open, displaying a list of species. The 'Rice (Oryza sativa)' option is highlighted in blue. A 'Change Species' button is visible next to the dropdown. Two callout boxes provide instructions: one points to the 'Change Species' button, and the other points to the species list.

GRAMENE CMap

Find anything Search

Search Genomes Species Download Resources About Help Feedback

Maps Home **Maps** Map Search Feature Search Matrix Map Sets Feature Types Map Types Evidence Types Species Saved Links Help Tutorial FAQ

Ref. Species: --Select-- Change Species

--Select--

All Species

African rice (Oryza glaberrima)

Barley (Hordeum vulgare)

Foxtail millet (Setaria italica)

Maize (Zea mays)

Oat (Avena sativa)

Oryza alta (Oryza alta)

Oryza australiensis (Oryza australiensis)

Oryza brachyantha (Oryza brachyantha)

Oryza coarctata (Oryza coarctata)

Oryza granulata (Oryza granulata)

Oryza minuta (Oryza minuta)

Oryza nivara (Oryza nivara)

Oryza officinalis (Oryza officinalis)

Oryza punctata (Oryza punctata)

Oryza ridleyi (Oryza ridleyi)

Oryza rufipogon (Oryza rufipogon)

Oryza sativa x Oryza eichingeri (Oryza sativa x Oryza eichingeri)

Oryza sativa x Oryza longistaminata (Oryza sativa x Oryza longistaminata)

Oryza sativa x Oryza rufipogon (Oryza sativa x Oryza rufipogon)

Pearl Millet (Pennisetum glaucum)

Rice (Oryza sativa)

Rye (Secale cereale)

sorghum (Sorghum bicolor)

Tetraploid wheat (Triticum turgidum)

Wheat (Triticum aestivum)

Wild rice (Zizania palustris)

1. Select a species and click "Change Species".

You need to use the "reference menu" to select a species, map set and map that you will be able to compare other maps to later

Maps: Select a Map Set

Map type, species, and name are shown

Click here for more information on map sets (see slide 39).

Search | Matrix | Map Sets | Feature Types | Map Types | Evidence Types | Species | Saved Links | Help | Tutorial |

FAQ

Ref. Species: Rice (Oryza sativa) Change Species

Ref. Set: --Select-- Show Selected Set's Maps

The Maps Corner

Quick Start

To view a map:

1. Select a reference species
2. Select a reference map set
3. Select a map type
4. Select a map set

Please note: Java is required for this application.

SPECIES

Sequence : Rice - IRGSP Assm 2005
Genetic : Rice - M2000
Genetic : Rice - JFLP 2000
Genetic : Rice - IRGSP 2003
Genetic : Rice - IGDP 1998
Genetic : Rice - CIAT SSR 2006
Genetic : Rice - KRGRP 1998
Genetic : Rice - TTU CTIR 2000
Genetic : Rice - TTU IRIR 2000
Genetic : Rice - Niigata RFLP 2000
Genetic : Rice - Cornell SSR 2001
QTL : Rice - INDIR IR58025/O. rufipogon BC
QTL : Rice - HNAES MIL23/Aki RI QTL 2001
QTL : Rice - Aberdeen Bala/Azu QTL 2002
QTL : Rice - TTU IR58821/IR52561 QTL 2002
QTL : Rice - TKU Integrated QTL 2002
QTL : Rice - JNARC Noe29/Chu32 F3 QTL 2002
QTL : Rice - Brazil BG90-2/RS16 QTL 2002
QTL : Rice - JNIG W1944/Peik QTL 2002
QTL : Rice - JHPRC Rei/Yamd QTL 2002
QTL : Rice - CNRRI XeiB/Mil46 RI QTL 2002
QTL : Rice - CNNJAU Tai65/Bhad QTL 2002
QTL : Rice - CNRRI Zh97B/Mil46 RI QTL 2002
QTL : Rice - TTU IR64/Orufi RI QTL 2002
QTL : Rice - JRGP Nip/Kas F2 QTL 2002
QTL : Rice - CIRAD IR64/Azu DH QTL 2003
QTL : Rice - IRRI RD23/Olong F2 QTL 2003
QTL : Rice - IRRI Mil23/Aki RI QTL 2003
QTL : Rice - IRRI IR64/Azu DH QTL 2003
QTL : Rice - JNIR Aki/Kosh DH QTL 2003

Comparative maps to add to the left and/or right of the reference map

Map | About | Cite Gramene

2. Select a **reference map set**, and click “Show Selected Set’s Maps”

Reference Set Options will depend upon the reference species you have chosen. They are grouped by map types (sequence, genetic, etc). Displayed names may differ be abbreviated differently in different releases.

Maps: Select a Map

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [FAQ](#)

Ref. Species:
 Ref. Set:
 Ref. Map:

- 1 0.00-181.80
- 2 0.00-157.90
- 3 0.00-166.40
- 4 0.00-129.60
- 5 0.00-122.30
- 6 0.00-126.30
- 7 0.00-118.60
- 8 0.00-121.20
- 9 0.00-93.50
- 10 0.00-83.80
- 11 0.00-119.50
- 12 0.00-109.50

3a. Choose one or all of the **maps** from this set (use ctrl to make multiple selections).

d. Click "Draw Maps"

b. If you have selected only one map from the mapset, you may **select** area to view by entering coordinates, if known.

Ref Map Start:
 Ref Map End:

Feature Type Display:

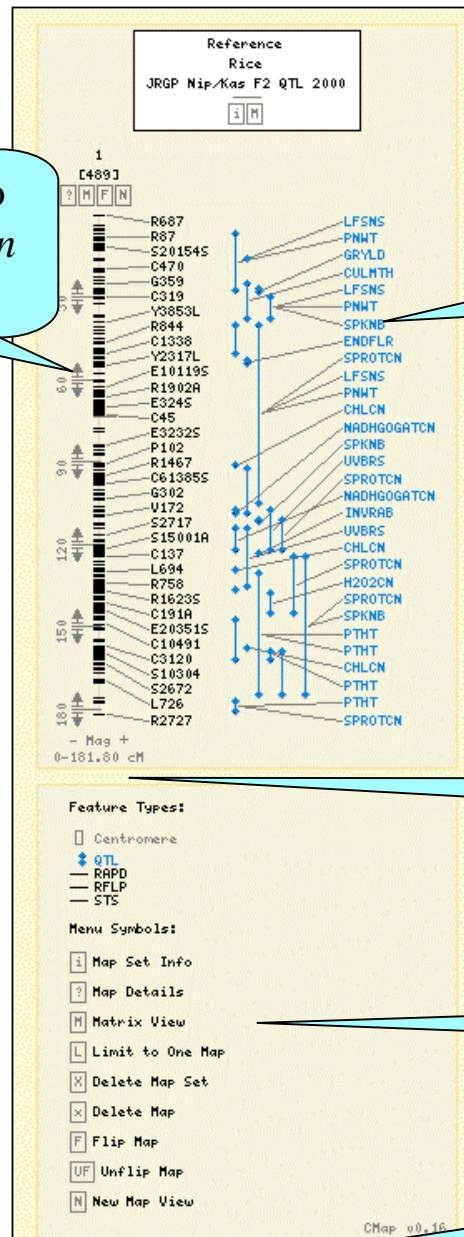
Feature	Ignore	Display if Correspondence	Always Display
Centromere	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Marker	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
RAPD	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
RFLP	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
STS	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Other	<input 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"/>

c. **Select** options. The "Other" value refers to feature types that are not on the current maps but may be on comparative maps.

Information on the Ref. Map Set will appear when one is selected.

Reference Map Set Info	
Map Set:	JRGP Nip/Kas F2 QTL 2000 (JRGP Nip/Kas F2 QTL 2000) [View More Info]
Species:	Rice (Oryza sativa) [View More Info]
Map Type:	QTL (cM) [View More Info]
Description:	This is an updated version of the map reported by Kurata et al. (1994) and Harushima et al. (1998) . It uses an F2 population of 186 plants from a cross between the cultivars Nipponbare (japonica) and

Maps: Viewing a map



Click arrow to crop map (as in slide 22)

Hover over a point for name and position, click for feature detail (see slide 13)

Change Magnification

Map Legend (see slide 29)

Scroll page for Map options – see slides 15-20

Bookmarks for this page will fail after this session expires. Use the "Save Link" button to create a permanent link (see slide 44)

Save Link*

3/22/07

*Bookmarks for this page will fail after this session expires. Use the "Save Link"

Viewing a Map - Feature Detail

Click here for Map Details (*see next slide*), as well as other information.

Feature Name:	SPKNB
Aliases:	CQN52 CQN52-SPKNB TO:0000456
Accession ID:	CQN52
Feature Type:	QTL
Map:	Species: Rice Map Set: JRGP Nip/Kas F2 QTL 2000 Map Name: 1
Start:	28.90 cM
Stop:	38.80 cM
Cross-references:	[View Oryza sativa QTL "CQN52" details]

[[Map Sets](#) | [Feature Types](#) | [Map Types](#)]

Feature "SPKNB"

[[View Alias Details](#)]

[[View Alias Details](#)]

[[View Alias Details](#)]

[[View Feature Type Info](#)]

[[View Map Details](#)]

Feature Alias Detail "CQN52"

Alias: CQN52

Feature Name: SPKNB [[View Feature](#)]

Feature Type Info

Display:

[[View All Feature Types](#)]

Items 1 to 1 of 1.

Feature Type:	QTL
Accession ID:	qtl
Color:	mediumpurple
Shape:	dumbbell

[[Search for All Features of This Type](#)]

Link to QTL information
(*See QTL tutorial*)

Correspondences

Feature	Accession	Map	Map Type	Aliases	Evidence Type	Actions		
CQN52-SPKNB	47074300	Rice-Gramene Annot Seq 2006-Chr. 1	Sequence	CQN52, SPKNB, TO:0000456	Marker Identity	[Correspondence Details]	[View On Map]	[Comparative View]
CQN52-SPKNB	OMAP47074300	Rice-OMAP Gramene Annot Seq 2006-Chr. 1	Sequence	CQN52, SPKNB, TO:0000456	Marker Identity	[Correspondence Details]	[View On Map]	[Comparative View]

Different features may offer different information and links to detail or map pages.

Map Detail

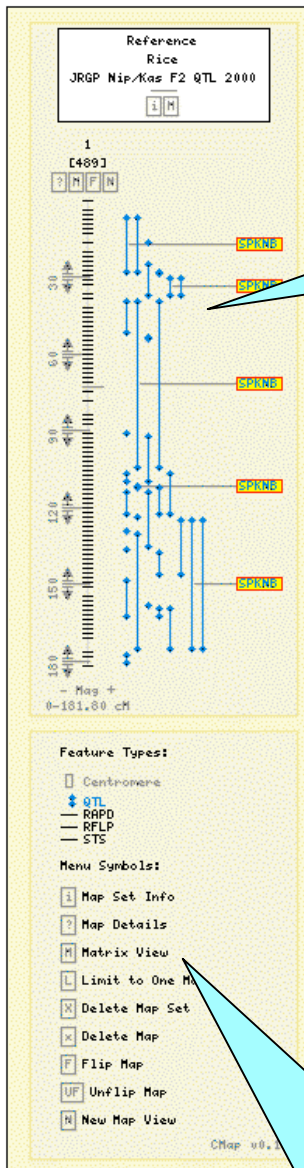
You now get a map with your features highlighted.

Note: "Map Details" will appear at the bottom of the page

Below the map and map options is your map Detail.

Map features presents a list of all features on this map.

Map Legend, see slide 29



Map Details

Map Type: QTL [[View Map Type Info](#)]
 Map Set Name: Rice - JRGF Nip/Kas F2 QTL 2000 [[View Map Set Info](#)]
 Map Name: 1
 Map Start: 0.00 cM
 Map Stop: 181.80 cM
 Features by Type:
 1 Centromere
 41 QTL
 11 RAPD
 429 RFLP
 7 STS
 489 Total

Map Features

Restrict by Map:

[\[Download Map Data \]](#)

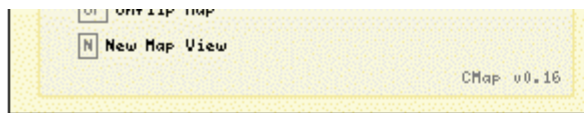
[\[Download Feature Correspondence Data \]](#)

Items 1 to 25 of 489.

Page of 20 | [Next](#)

Rice - JRGF Nip/Kas F2 QTL 2000 - 1 (Click headers to resort)			Comparative Maps					
Feature	Type	Position (cM)	Map	Feature	Type	Position	Evidence	Actions
RFLP		0.00	Rice - Gramene IRGSP Assm 2005 - Chr. 1	R687	RFLP	148,497.00 - 148,548.00 (bp)	Identity, Identity	View Maps
			Rice - OMAP Gramene Annot Seq 2006 - Chr. 1	R687	RFLP	146,436.00 - 146,544.00 (bp)	Identity	View Maps
			Rice - Gramene Annot Seq 2006 - Chr. 1	R687	RFLP	146,658.00 - 146,733.00 (bp)	Identity, Identity	View Maps
			Rice - OMAP Gramene Annot Seq 2006 - Chr. 1	R687	RFLP	146,953.00 - 147,124.00 (bp)	Identity	View Maps
			Rice - Gramene Annot Seq 2006 - Chr. 1	R687	RFLP	146,299.00 - 146,350.00 (bp)	Identity, Identity	View Maps
			Rice - OMAP Gramene Annot Seq 2006 - Chr. 1	R687	RFLP	146,299.00 - 146,350.00 (bp)	Identity	View Maps
			Rice - JRGF RFLP 2000 - 1	R687	RFLP	0.00 (cM)	Identity, Identity	View Maps

Options



Save Link*

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

- ☐ Map Options
- ☐ Feature Options
- ☐ Correspondence Options
- ☐ Display Options
- ☐ Advanced Options

*Save output for high-resolution printing only (no hyperlinks).

Print Preview Reset

Click [+] to open
the menus

*Below the map are
options menus. (Slides
15-20)*

Map Options

Defaults are to display entire chromosome at original magnification. You may customize these.

Use to compare maps, click the side (s) you wish to place them on. (see slide 24 and associated slides)

If multiple maps are displayed, this option displays them from top to bottom rather than left to right

Click to display map upside down from default view

Click to collapse (hide) map options.

Click to view another map or begin a new comparison

Click to add changes.

Map Options		Redraw	Reset
Map Set	Add Maps Left	Rice-JRGP Nip/Kas F2 QTL 2000 (Reference Set)	Add Maps Right
Min. Correspondences			
Stack Vertically		<input type="checkbox"/>	
Maps		1	
Start		0.00	
Stop		181.80	
Magnification		Original ▼	
Flipped		<input type="checkbox"/>	

hint: To save time, select the desired options before redrawing the map.

New Reference Maps

Redraw Reset (Hide Map Menu)

Feature Options

☐ Feature Options

Highlight Features: "SPKNB"

Feature Types:

Feature	Ignore	Display if Correspondence	Always Display
Centromere	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
QTL	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
RAPD	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
RFLP	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
STS	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Other	<input 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

(Hide Feature Menu)

Type in a feature name to highlight it on the map (as in slide 14).

Determine which feature types to include on the maps, and when to display them, by selecting the appropriate boxes.

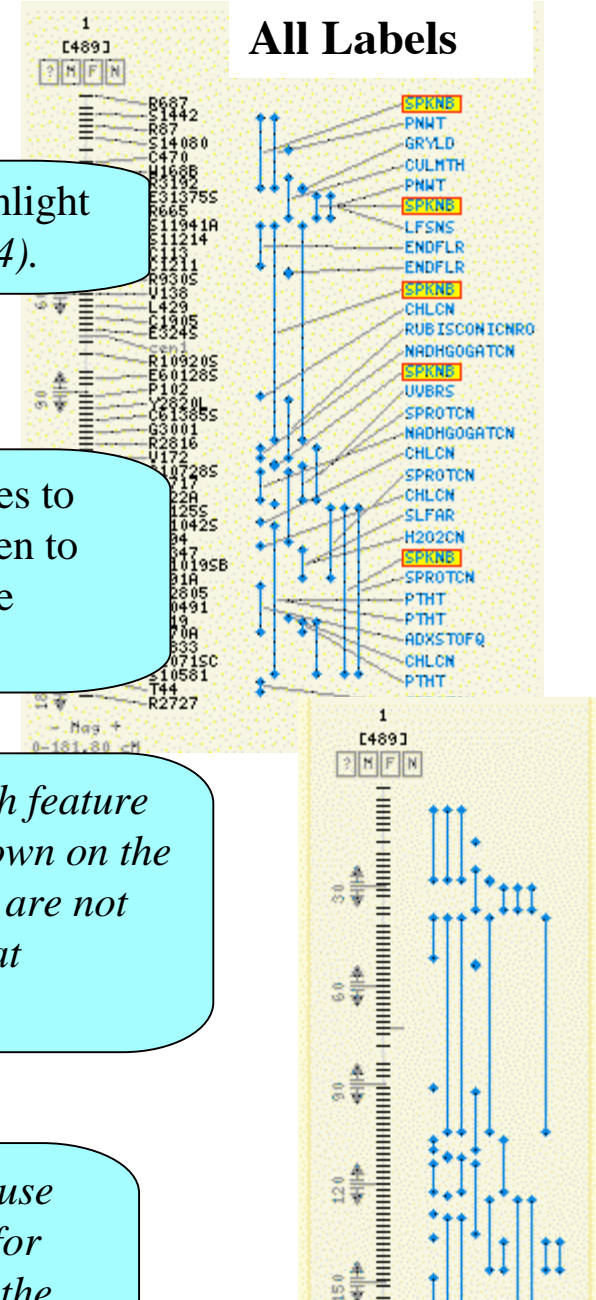
Determines which feature labels will be shown on the map. Landmarks are not currently active at Gramene.

Click to add changes.

Click to collapse (hide) feature options.

Determines whether to use one or multiple glyphs for features that span over the same coordinates. "yes" is recommended

All Labels



Features not overlapped

Correspondence Options

☐ Correspondence Options

Include Correspondence Types:

Evidence	Ignore	Use	Less Than Score	Greater Than Score	Score
Automated name-based	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
Marker Identity	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
SOG_OVERGO	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
Unknown	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
Wheat EST BI	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
Maize bin marker	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
Curated gene to QTL	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
dbest_poaceae	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
FPC loader	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
Gene model	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
gss_poaceae	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
OMAP synteny analysis 1	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0
OMAP synteny analysis 2	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	0

The “Correspondence Type” field allows restriction of correspondences by evidence type.

Click to add changes.

Correspondences: ☒ No ☐ 1 Line ☐ 2 Lines
 Correspondence lines drawn to: ☒ Feature ☐ Map
 View slot Correspondences: ☒ No ☐ yes
 Aggregate evidence types separately: ☒ No ☐ yes

(Hide Correspondence Menu)

Click to collapse (hide) correspondence options.

Display Options

Determines the vertical height of the image

Determines the size of the font

The screenshot shows a 'Display Options' menu with a title bar containing a collapse icon, the text 'Display Options', and 'Redraw' and 'Reset' buttons. The menu items are: 'Map Size:' with radio buttons for 'tiny', 'small' (selected), 'medium', 'large', and 'Custom' (with a text box containing '300'); 'Font Size:' with radio buttons for 'Small' (selected), 'Medium', and 'Large'; 'Image Type:' with radio buttons for 'PNG' (selected), 'JPEG', 'GIF', and 'SVG *'; and 'Clean View (no navigation buttons):' with radio buttons for 'No' (selected) and 'yes'. At the bottom of the menu are 'Redraw' and 'Reset' buttons, followed by the text '(Hide Display Menu)'. A callout points to the 'Custom' option and its text box, stating 'Select the desired image format.' Another callout points to the '(Hide Display Menu)' text, stating 'Click to collapse (hide) display options.'

Select the desired image format.

Click to collapse (hide) display options.

Click to add changes.

Advanced Options

Predefined Order: Maps are ordered in the selection menu based on that specified in the database

Number of Correspondences: Maps are ordered based on the number of correspondences with the reference map

Having too many clickable features may be problematic for some browsers. If the number of features to be displayed is too large during a sanity check, features will not be clickable in order to prevent these problems.

Click to collapse (hide) advanced options.

If “No” maps are drawn according to their specified length – If “Yes” maps are drawn to the same length

The screenshot shows a dialog box titled "Advanced Options" with a "Redraw" button and a "Reset" button. The options are as follows:

Option	Yes	No
Draw Maps Using Same Scale:	<input checked="" type="radio"/> Yes	<input type="radio"/> No
Clickable Image	<input checked="" type="radio"/> Other	<input type="radio"/> Omit Features <input type="radio"/> Omit All Buttons
Menu Order of Comparative Maps:	<input checked="" type="radio"/> Predefined Order	<input type="radio"/> Number of Correspondences
Ignore Image Map Sanity Check:	<input checked="" type="radio"/> No	<input type="radio"/> Yes

At the bottom, there are "Redraw" and "Reset" buttons, and a "(Hide Advanced Menu)" button.

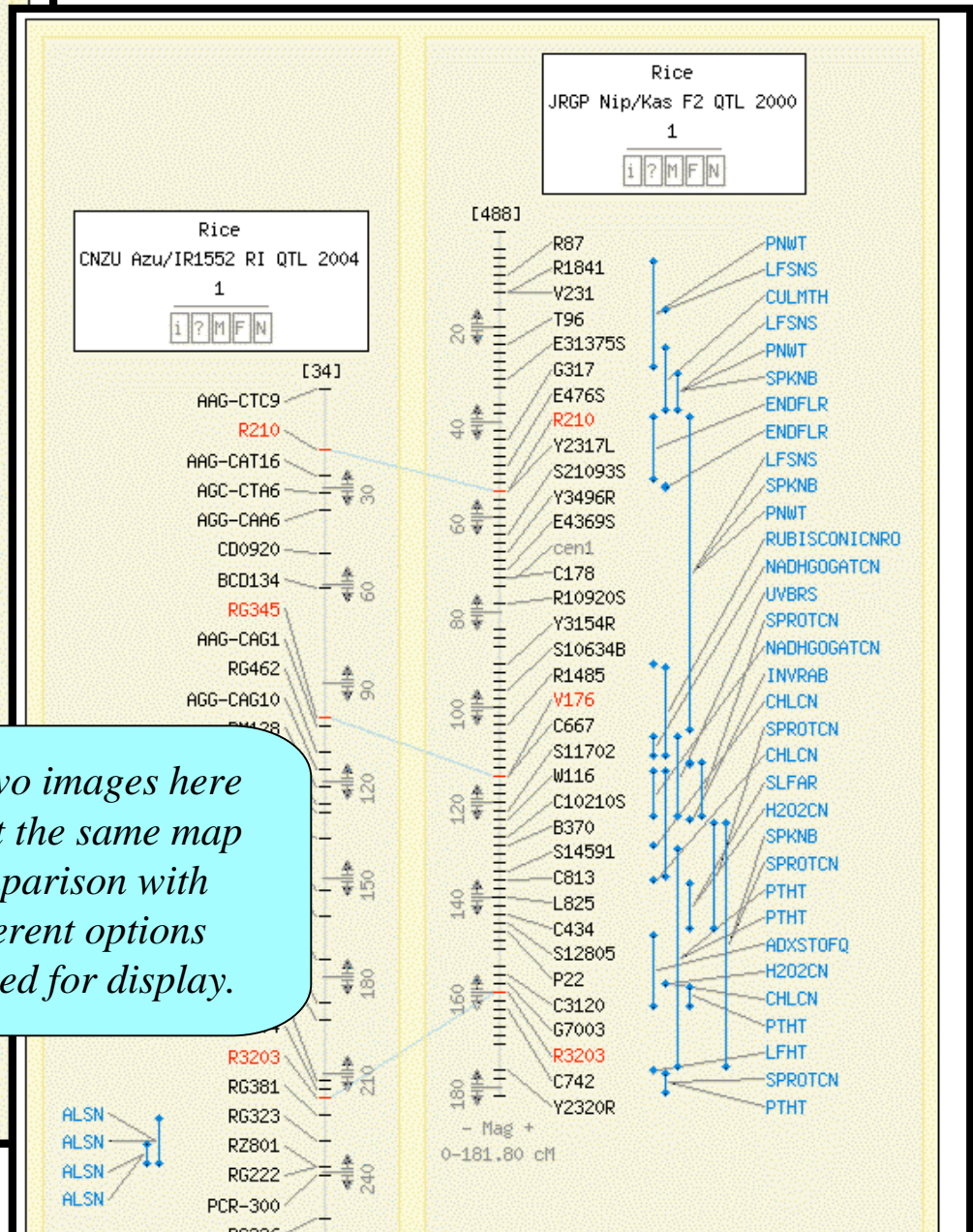
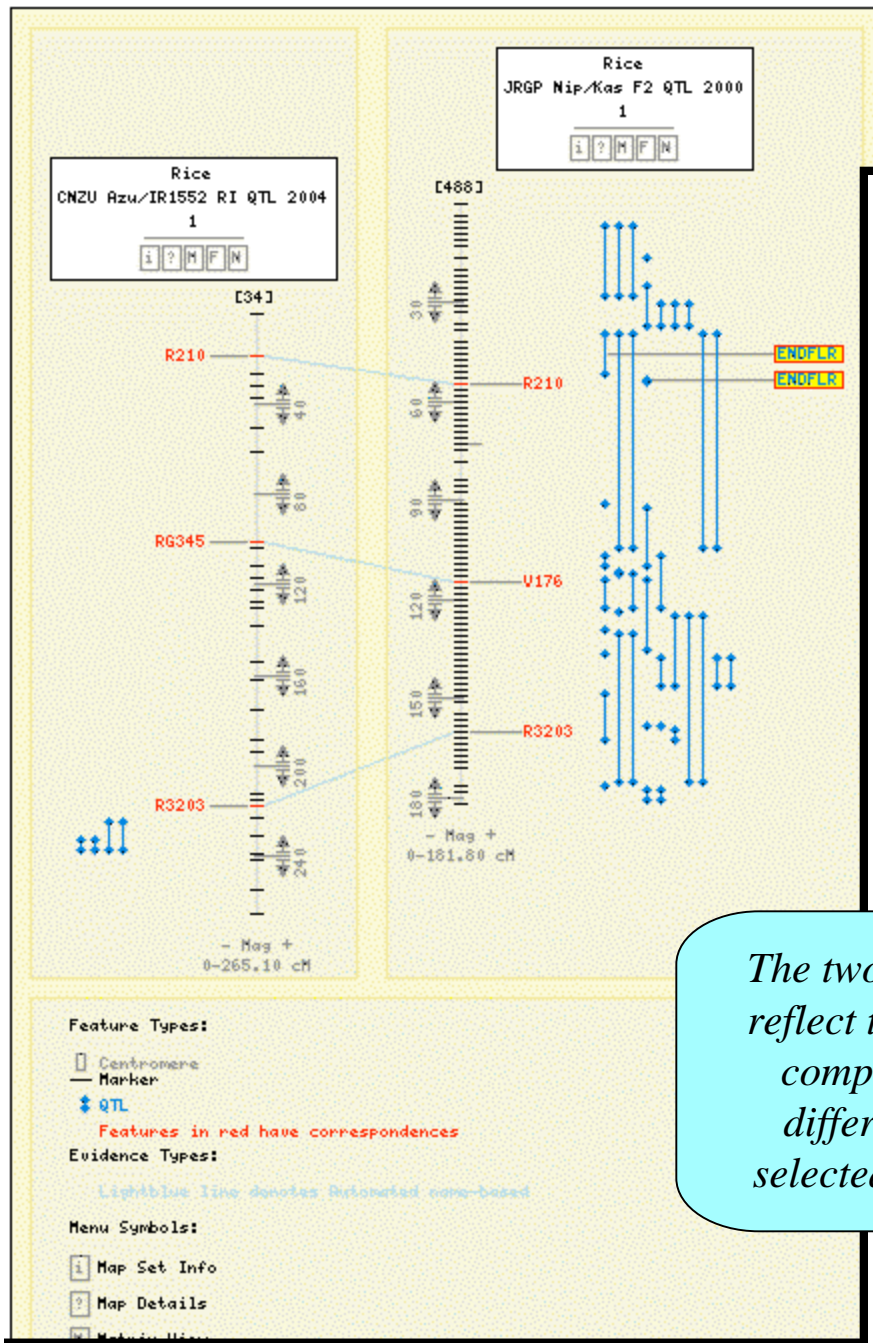
Click to add changes.

Other: Everything is clickable

Omit Features: Features and feature labels are not clickable. Speeds up image display.

Omit All Buttons: The little menu buttons on the image (e.g., [i], [?], [M]) are also removed as well as the crop arrows and magnification controls. Use this to generate a final image for publication.

The Same Maps: Displaying Different Options

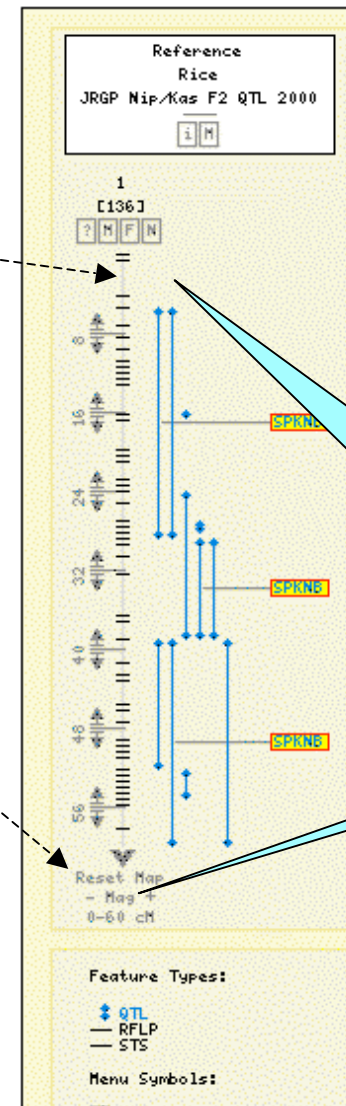
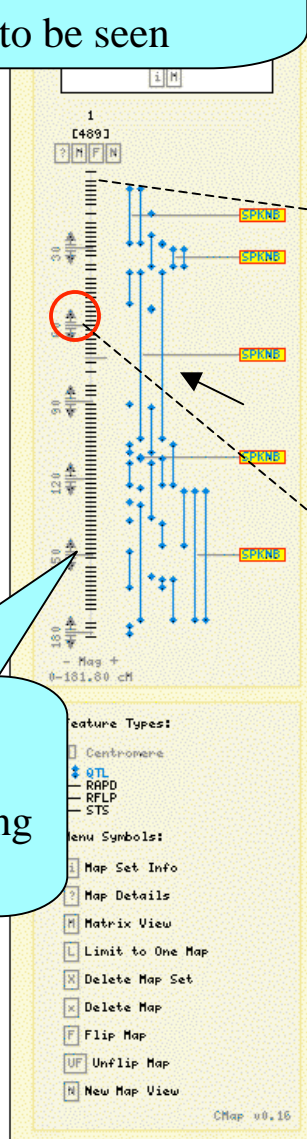


The two images here reflect the same map comparison with different options selected for display.

Zooming/Cropping

Zooming in on a map displays only a part of the entire maps and allows more features to be seen

Click arrow to zoom in onto section it is pointing to.

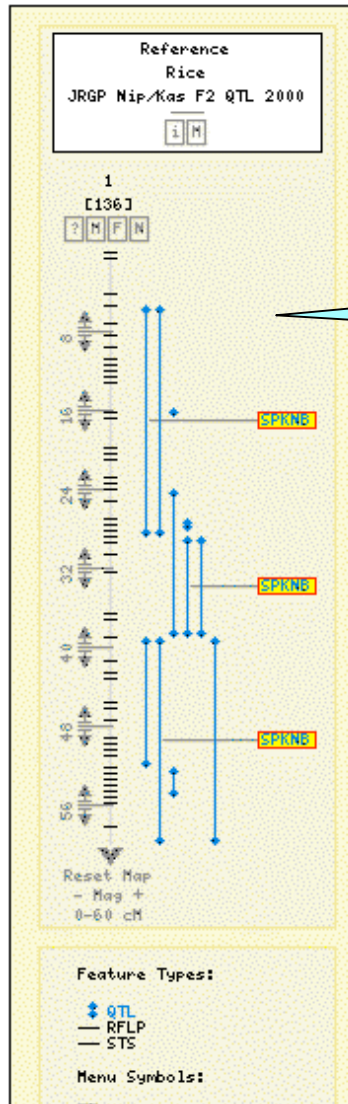


At the ends of the chromosome, the arrow indicates the chromosome continues, a solid bar indicates the end point

Compare Maps

- You may use the CMap viewer to compare maps.
- Start with a **reference map**, which will serve as the basis for any comparisons. (Often this is a well documented map.)
- Then select one or two **comparative maps**. These comparative maps may be added to both the left and the right of the reference map.

Select reference map



For simplicity we will use our currently loaded QTL map

Maps Home | Maps | Map Search | Feature Search | Matrix | Map Sets | Feature Types | Map Types | Evidence Types | Species | FAQ

Ref. Species: Rice (Oryza sativa)

Ref. Set: Sequence : Rice - Gramene Annot Seq 2006

Sequence : Rice - Gramene Annot Seq 2006

The Maps Comparison tool allows you to compare maps between and among species. See [help](#) for more information.

Quick Start

To view a map, select a species and a map set from the lists below.

1. Select a species
2. Select a map set
3. Select a map
4. Select a feature type

may compare maps between and among species.

Please note: Java is required for this tool.

SPECIES

- Genetic : Rice - JRGF RFLP 2000
- Genetic : Rice - IRMI 2003
- Genetic : Rice - IGCN 1998
- Genetic : Rice - CIAT SSR 2006
- Genetic : Rice - KRGF 1998
- Genetic : Rice - TTU CTIR 2000
- Genetic : Rice - TTU IRIR 2000
- Genetic : Rice - Niigata RFLP 2000
- Genetic : Rice - Cornell SSR 2001
- QTL : Rice - INDIR IR58025/O. rufipogon BC
- QTL : Rice - HNAES MIL23/Aki RI QTL 2001
- QTL : Rice - Aberdeen Bala/Azu QTL 2002

But. sequence maps are well documented and therefore are a good reference map for comparisons, so it is a good idea to start with a sequence map as the reference map when making multiple map comparisons

Cropping your reference map to the area of interest will limit the possible comparison maps to only those with correspondences to your area of interest.

Select comparative map

See slide 16 to see how to open comparative maps displays.

The number in brackets for the mapset indicates the number of corresponding maps

Map Op

Comparative Maps (Left Side)

QTL : Wheat - SynGene/MapMaker/MapMaker QT [1]

== ALL ==

4A [1,1]

Min. Correspondences: 0

Stack ☐

Refresh Menu Add Maps

Format:

Name [Total correspondences to slot, Max correspondences to single map]

Map Set	See Menu	Rice-JRGP N (Reference Set)
Min. Correspondences	Above	
Stack Vertically	<input type="checkbox"/>	
Maps	1	
Start	0.00	
Stop	60	
Magnification	Original	
Flipped	<input type="checkbox"/>	

hint: To save time, select the desired mapsets before redrawing the map.

New Reference Maps

Redraw Reset (Hide Map Menu)

Comparative Maps (Right Side)

Sequence : Rice - Gramene IRGSP Assm 2005 [1]

== ALL ==

Chr. 1 [197,197]

Chr. 2 [1,1]

Min. Correspondences: 0

Stack ☐

Refresh Menu Add Maps

Format:

Name [Total correspondences to slot, Max correspondences to single map]

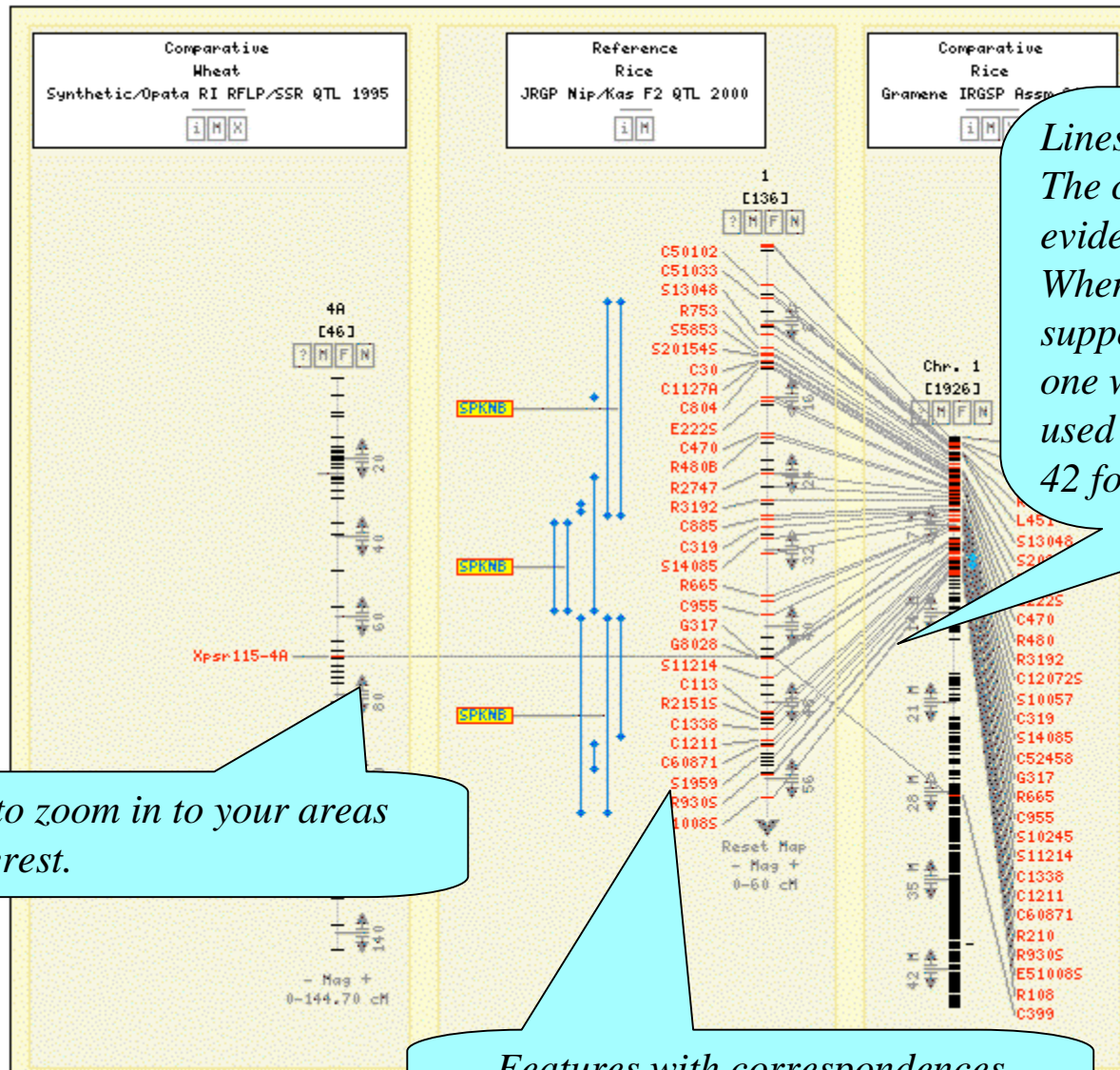
The number in brackets for a map indicates the number of correspondences to the reference map.

Select a map or maps to compare with your reference map, and click "Redraw" or "Add Maps"

You may determine the minimum number of correspondences that are desired from map to map.

You may place maps for comparison on the left and right of the reference map (and continuing on, ad infinitum).

Comparative Map Viewer



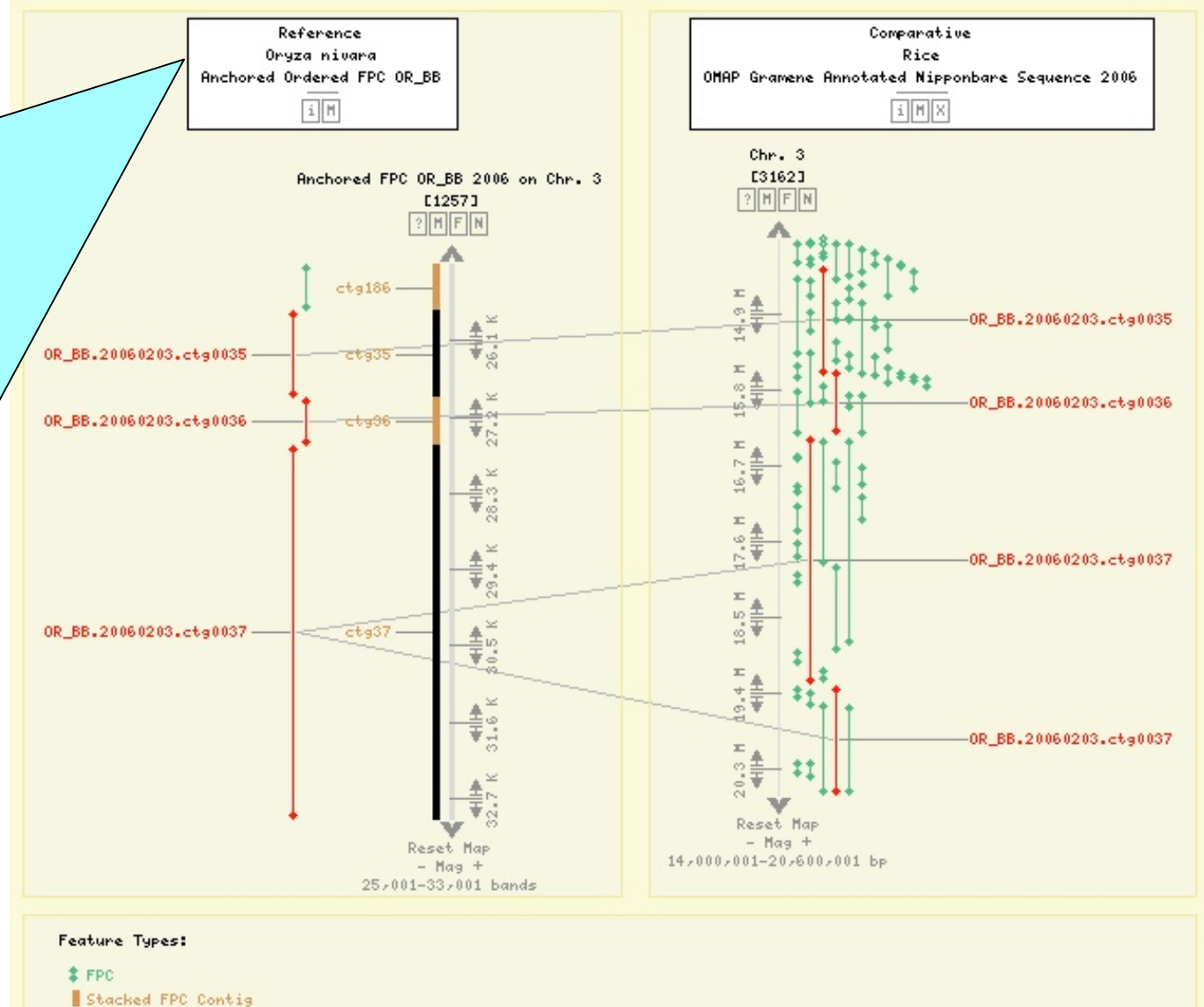
Lines show correspondences. The color of the line denotes evidence type (noted in legend). When multiple evidences support a correspondence, the one with the highest rank is used to color the line (see slide 42 for rankings).

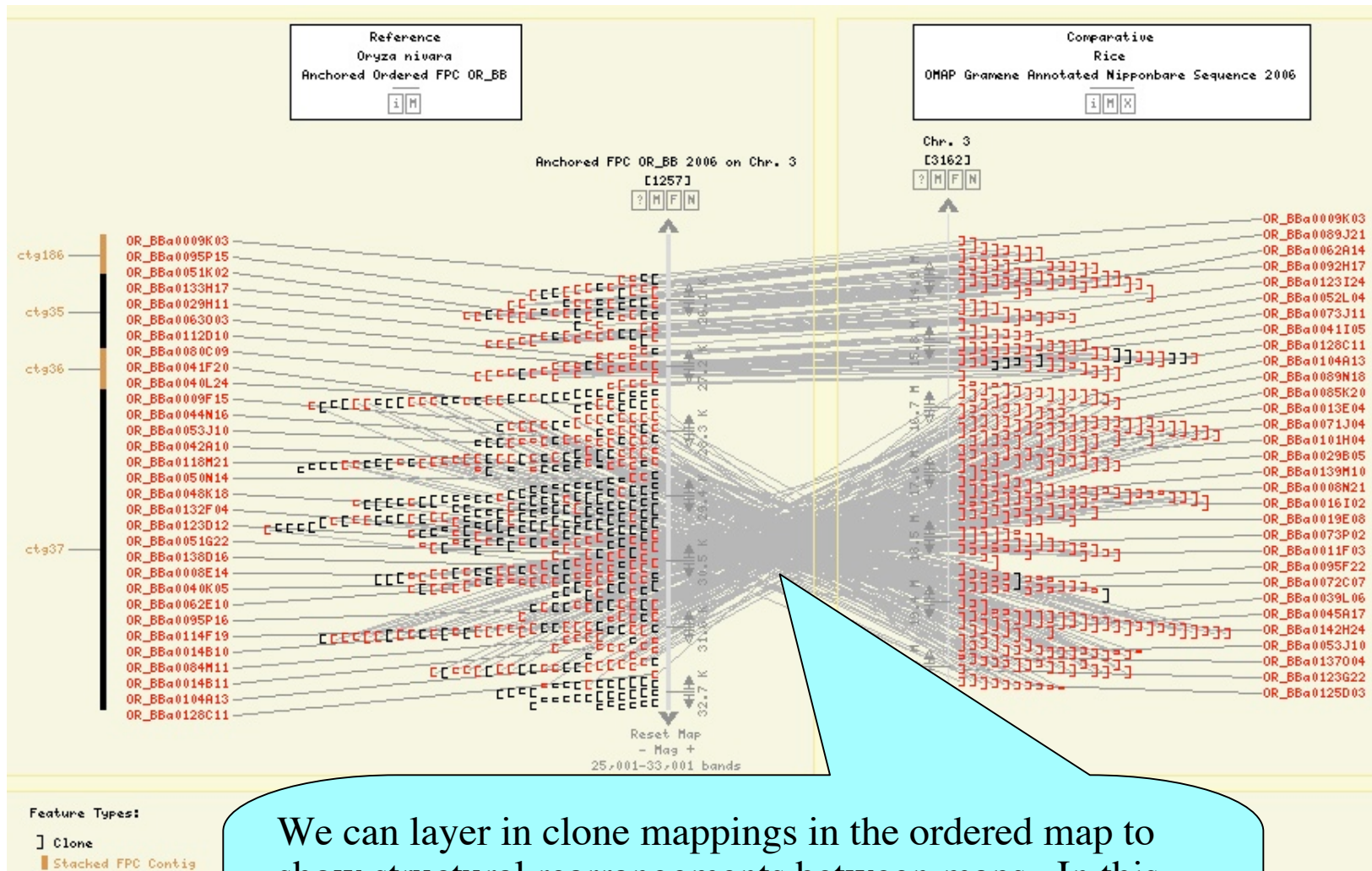
Crop to zoom in to your areas of interest.

Features with correspondences appear in red (noted in legend)

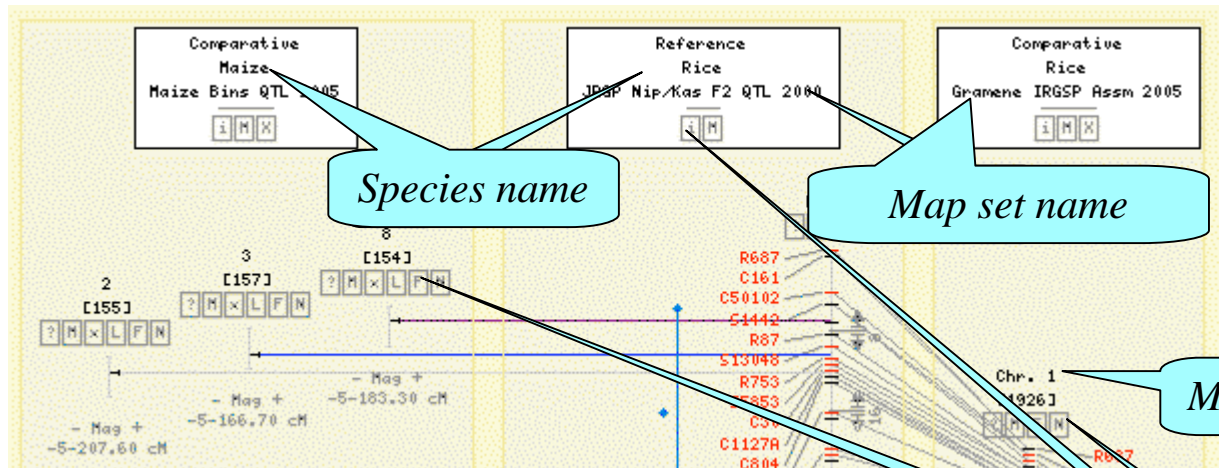
OMAP

The OMAP FPC maps are now available as ordered maps. These ordered maps offer faster rendering and a more compact arrangement, where contigs are displayed as a single map rather than as individual entities. The order of contigs on these ordered maps is based on correspondences to a reference map, namely the rice TIGR genome assembly. The user may view contig and clone mappings based on BAC end sequence alignments across a given chromosome.

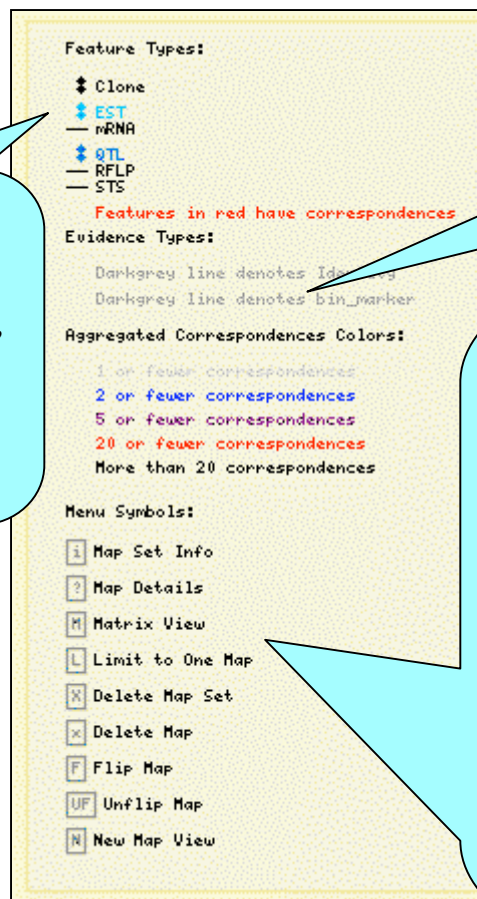




Map Legend



Listing of all the feature types found on the map, along with their corresponding glyphs



Legend at bottom of map explains options above. click on them to affect the display as described in the legend.

[i] Map set info –(slide 36)

[?] Map details (slide 13)

[M] Matrix View – (slide 32)

[L] Limit to one map – displayed when there is more than one map in the panel, select a single map by selecting [L] for the desired map.

[X] delete the map or mapset this symbol is associated with.

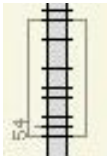
[F] Flip map – good for when most correspondences cross over each other.

[UF] Unflip map – displayed only when a map is flipped.

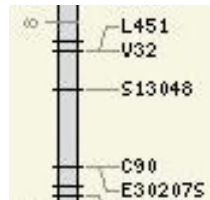
[N] New map view – limit the display to only this map.

Maps: Legend - Glyphs

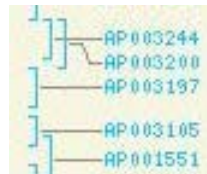
The following demonstrate some of the glyphs (shapes) that map features could appear as.



box



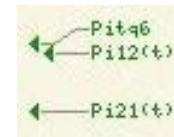
line



span



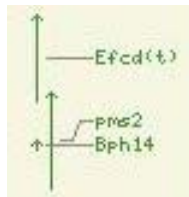
dumbbell



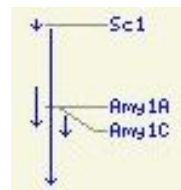
in-triangle



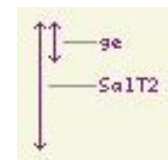
filled-box



up-arrow



down-arrow



double-arrow



out-triangle

Map Search

The screenshot shows the GRAMENE CMap website's Map Search interface. The top navigation bar includes links for Maps Home, Maps, Map Search (highlighted with a red circle), Feature Search, Matrix, Map Sets, Evidence Types, Map Types, Evidence Types, Species, Saved Links, Help, and Tutorial. A search bar at the top right contains the text 'Find anything' and a dropdown arrow. The main search form is titled 'Map Search' and includes the following fields:

- Ref. Species: A dropdown menu showing 'Rice (Oryza sativa)' with a 'Change Species' button to its right.
- Ref. Set: A dropdown menu showing '-Select-'.
- Name (optional): A text input field.
- Minimum Number of Related Maps: A text input field with the value '0'.
- Submit: A button.

Three callouts provide additional information:

- A callout pointing to the 'Ref. Species' dropdown: "Search maps in CMap by species."
- A callout pointing to the 'Ref. Set' dropdown: "Map sets available depend upon the species you selected."
- A callout pointing to the 'Name (optional)' field: "Name must match name in database, so it may be easier to leave this blank unless you know the exact name (Chr. 1)."

Map Search Results

The results give you information about the maps in matrix form. This information is sortable by hyperlinked column headings.

Map Search

Ref. Species:

Rice (Oryza sativa)

Change Species

Ref. Set:

Sequence : Rice - Gramene Annotated Nipponbare Sequence 2006

Name (optional):

Minimum Number of Related Maps:

0

Submit

Information about the maps is sortable by hyperlinked column headings.

Items 1 to 14 of 14.

Map Name	Related Maps	Related Maps per unit	Correspondences	Correspondences per unit	Start	Stop	GSS		Gene Model		Gene		QTL		mRNA		Centromere			
							total	per unit	total	per unit	total	per unit	total	per unit	total	per unit	total	per unit		
Chr. 1 (spider)	1135	26.04/M	31573	0.72/K	1.00	43594513.00	71	1.00	35924366.00	73	2.00	36345483.00	107	2.00	35244021.00	34	0.00	29874019.00	46	1.00
Chr. 2 (spider)	1044	29.06/M	23632	0.66/K	1.00	35924366.00	73	2.00	36345483.00	107	2.00	35244021.00	34	0.00	29874019.00	46	1.00	31242608.00	60	1.00
Chr. 3 (spider)	1116	30.71/M	32415	0.89/K	1.00	36345483.00	107	2.00	35244021.00	34	0.00	29874019.00	46	1.00	31242608.00	60	1.00	29678581.00	35	1.00
Chr. 4 (spider)	564	16.00/M	13988	0.40/K	1.00	35244021.00	34	0.00	29874019.00	46	1.00	31242608.00	60	1.00	29678581.00	35	1.00	28307495.00	25	0.00
Chr. 5 (spider)	699	23.40/M	21179	0.71/K	1.00	29874019.00	46	1.00	31242608.00	60	1.00	29678581.00	35	1.00	28307495.00	25	0.00	23011004.00	45	1.00
Chr. 6 (spider)	848	27.14/M	18071	0.58/K	1.00	31242608.00	60	1.00	29678581.00	35	1.00	28307495.00	25	0.00	23011004.00	45	1.00	22876596.00	15	0.00
Chr. 7 (spider)	561	18.90/M	15050	0.51/K	1.00	29678581.00	35	1.00	28307495.00	25	0.00	23011004.00	45	1.00	22876596.00	15	0.00	28459272.00	19	0.00
Chr. 8 (spider)	640	22.61/M	13792	0.49/K	1.00	28307495.00	25	0.00	23011004.00	45	1.00	22876596.00	15	0.00	28459272.00	19	0.00	27496040.00	28	1.00
Chr. 9 (spider)	604	26.25/M	13116	0.57/K	1.00	23011004.00	45	1.00	22876596.00	15	0.00	28459272.00	19	0.00	27496040.00	28	1.00	134481.00	0	0.00
Chr. 10 (spider)	511	22.34/M	13274	0.58/K	1.00	22876596.00	15	0.00	28459272.00	19	0.00	27496040.00	28	1.00	134481.00	0	0.00	457225.00	0	0.00
Chr. 11 (spider)	563	19.78/M	9608	0.34/K	1.00	28459272.00	19	0.00	27496040.00	28	1.00	134481.00	0	0.00	457225.00	0	0.00			
Chr. 12 (spider)	498	18.11/M	10918	0.40/K	1.00	27496040.00	28	1.00	134481.00	0	0.00	457225.00	0	0.00						
Chr. chloroplast (spider)	9	66.92/M	66	0.49/K	1.00	134481.00	0	0.00	457225.00	0	0.00									
Chr. mitochondrion (spider)	0	0/unit	0	0/unit	1.00	457225.00	0	0.00												

Matrix Form													
EST		Marker		Clone		RFLP		SSR		EST Cluster			
total	per unit	total	per unit	total	per unit	total	per unit	total	per unit	total	per unit	total	per unit
1679	38.51/M	315	7.23/M	6	0.14/M	729	16.72/M	2024	46.43/M	62	1.42/M		
1397	38.89/M	227	6.32/M	80	2.23/M	573	15.95/M	1732	48.21/M	75	2.09/M		
1986	54.64/M	385	10.59/M	28	0.77/M	759	20.88/M	1792	49.30/M	116	3.19/M		
910	25.82/M	157	4.45/M	27	0.77/M	417	11.83/M	1163	33.00/M	61	1.73/M		
1149	38.46/M	321	10.75/M	334	11.18/M	473	15.83/M	1239	41.47/M	92	3.08/M		
879	28.13/M	337	10.79/M	55	1.76/M	431	13.80/M	1212	38.79/M	31	0.99/M		
886	29.85/M	167	5.63/M	71	2.39/M	424	14.29/M	1034	34.84/M	26	0.88/M		
696	24.59/M	112	3.96/M	56	1.98/M	351	12.40/M	1168	41.26/M	43	1.52/M		
598	25.99/M	160	6.95/M	42	1.83/M	267	11.60/M	886	38.50/M	42	1.83/M		
495	21.64/M	104	4.55/M	72	3.15/M	255	11.15/M	855	37.37/M	46	2.01/M		
514	18.06/M	161	5.66/M	22	0.77/M	284	9.98/M	991	34.82/M	41	1.44/M		
665	24.19/M	95	3.46/M	26	0.95/M	308	11.20/M	997	36.26/M	45	1.64/M		
0	0	0	0	0	0	0	0	0	0	0	0		
0	0	0	0	0	0	0	0	0	0	0	0		

3/22/07

3/22/07

Search for a particular feature by name or accession ID, species, and feature type.

Feature Search

[Maps Home](#) | [Maps](#) | [Map Search](#) | **Feature Search** | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Feature Search

A feature is any element that can be mapped to a specific point or an interval.

Feature names:

Select species:

- Oryza rufipogon
- Oryza sativa x Oryza eichingeri
- Oryza sativa x Oryza longistaminata
- Oryza sativa x Oryza rufipogon
- Pearl Millet

Restrict feature types:

- All Feature Types-
- AFLP
- Breakpoint Interval
- Centromere
- Clone

Search field:

Separate with commas or whitespace. Use "" or "%" for wildcards. To find features with "abc 123."

2. Choose a species (optional)

1. Type the feature name(s) you wish to search for in CMap. Wildcards allow you to search partial names.

4. Search either the feature's name (and aliases) or accession ID

3. Choose a feature type (optional)

5. Click "Submit"

Feature Search Results

Found 61 features with a name or alias containing “YLD” in the species “Pearl Millet.”

Click on a hyperlinked column title to sort list by that column.

Select to view the “Feature Details” Page for this feature (see slide 13)

Items 1 to 25 of 61.

Page 1 of 3 | [Next](#)

Feature Name	Feature Type	Species	Map Set	Map Name	Position	Aliases		
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	0.00-7.80 cMAQES032, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cMAQEU025, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cMAQEU026, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cMAQES050, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	33.90-40.00 cMAQES017, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	19.50-62.00 cMAQES018, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	62.00-71.90 cMAQEU027, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	79.80-126.10 cMAQES051, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	24.30-34.40 cMAQEU030, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	24.30-34.40 cMAQEU029, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	24.30-34.40 cMAQEU028, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	9.10-24.30 cMAQES019, TO:0000327		View on Map	Feature Details
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	9.10-24.30 cMAQES069, TO:0000327		View on Map	Feature Details
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	0.00-7.80 cMAQES030, TO:0000388		View on Map	Feature Details
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	0.00-7.80 cMAQES047, TO:0000388		View on Map	Feature Details
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cMAQEU012, TO:0000388		View on Map	Feature Details
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	33.90-40.00 cMAQES013, TO:0000388		View on Map	Feature Details
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	3	21.30-22.90 cMAQES066, TO:0000388		View on Map	Feature Details
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	0.00-19.50 cMAQES067, TO:0000388		View on Map	Feature Details

Select to view the “Map Set Info” (see slide 39)

Select to view this feature highlighted on a map (as in slide 14)

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Correspondence Matrix

Select to view the **number of correspondences** among all maps and **choose a pair to display**

 [Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | **[Matrix](#)** | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Welcome to the Matrix

Each cell in the matrix shows the number of correspondences between a pair of maps. A correspondence is any relationship between two features.

Please use the form below to display the matrix. Note that not choosing any restrictions may result in a very large table.

Restrict Reference Sets By: ☒ Use Colors ☒ Hide Empty Rows

Similarly to comparing maps begin by selecting a reference set by type and species.

Options

Click "Submit"

Multiple Mapset Matrix

These are the available maps from your map type and species (Rice QTL)

The rest of the mapsets are those that have correspondences to the reference maps.

Continue to select from choices, or...

Simply click on the number of correspondences between the mapsets to view the matrix.

These two mapsets have 289 correspondences among 19 maps

		Rice						African					
		Gramene Annotated Nipponbare Sequence 2006	Gramene Annotated Nipponbare Sequence 2006	Class I SSR (93-11) 2005	Class I SSR (IRGSP) 2005	Class I SSR (TIGR) 2005	Gramene IRGSP Assm 2005	Curated FPC OG_BB Feb 2006	FPC Chr OG_BB Feb 2006	Curated FPC OG_BB Feb 2006	FPC Chr OG_BB Feb 2006	Curated FPC OG_BB Feb 2006	FPC Chr OG_BB Feb 2006
AGEBC KDM105/IRAT109 RI QTL 2000		301(29)	291(29)	14 (12)	19(14)	19(14)	208(26)	-	-	-	-	68	68
Aberdeen Bala/Azu DH QTL 2002		390(23)	428(26)	9(5)	9(5)	9(5)	173(22)	-	-	-	-	64	3
Brazil BG90-2/RS/6 QTL 2002		132(11)	132(11)	28 (10)	32(11)	32(11)	-	-	-	-	-	May 2006	May 2006
CAU IRAT109/YUEFU QTL 2004		366(26)	354(26)	30 (14)	31(15)	31(15)	204(19)	-	-	-	-	Oct 2004	FPC Oct 2004
CIRAD IR64/Azu DH QTL 2003		651(34)	790(42)	-	-	-	302(25)	76	87	76(10)	325	328	256
CNCAU Orufi/Gui2 BC1 QTL 2001		317(20)	307(20)	-	-	-	252(19)	-	-	-	61	61	61
CNHAU Zhen97/ H94 QTL 2005		289(19)	289(19)	113 (13)	129(13)	129 (13)	2(2)	-	-	-	-	-	-
CNHAU Zhenshan 97/IRAT109 QTL 2006		259(17)	259(17)	101 (14)	115(14)	115 (14)	1(1)	-	-	-	-	-	-
		44(4)	40(4)	-	-	-	42(4)	-	-	-	-	-	-
		39(3)	35(3)	-	-	-	38(3)	-	-	-	-	-	-
		25(2)	23(2)	-	-	-	10(2)	-	-	-	-	-	-

Two-MapSet Matrix

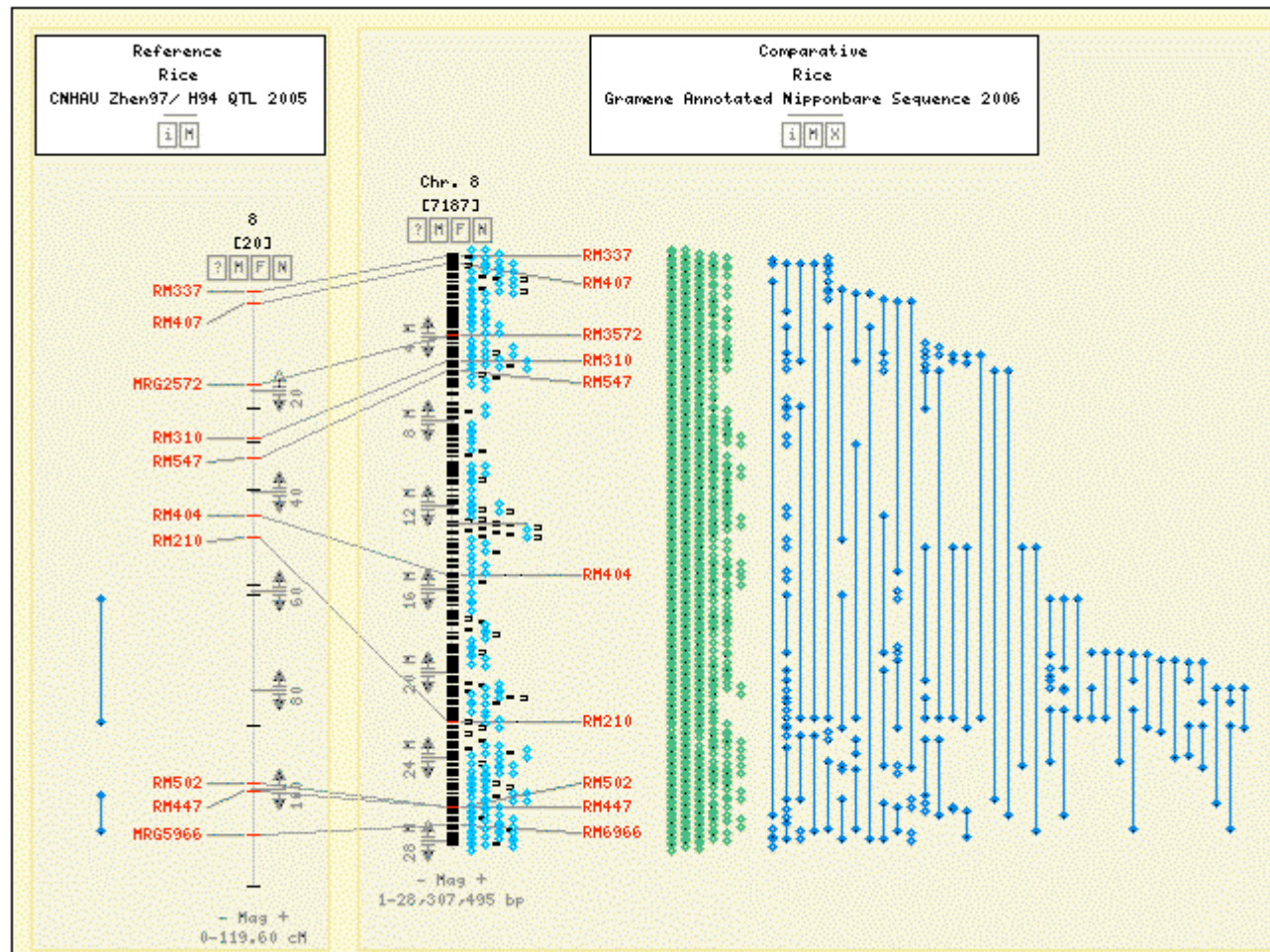
In this example, we have narrowed it down to two mapsets – the QTL mapset as the reference, and a Sequence mapset as the comparison.

Reference Set		Sequence												Reference Set			
		Rice															
		Gramene Annotated Nipponbare Sequence 2006															
		Chr. 1	Chr. 2	Chr. 3	Chr. 4	Chr. 5	Chr. 6	Chr. 7	Chr. 8	Chr. 9	Chr. 10	Chr. 11	Chr. 12				
QTL	Rice CNHAU Zhen97/ H94 QTL 2005	1	40(1)	-	1(1)	-	-	-	-	-	-	-	-	1	Rice CNHAU Zhen97/ H94 QTL 2005	QTL	
		2	-	29(1)	-	-	-	-	-	-	-	-	-	2			
		3	-	-	34(1)	-	-	-	-	-	-	-	-	3			
		4	-	-	-	20(1)	1(1)	-	-	-	-	-	-	4			
		5	-	-	-	-	29(1)	-	1(1)	-	-	-	-	5			
		6	-	-	-	-	-	28(1)	-	-	-	-	-	6			
		7	-	-	-	-	-	-	17(1)	-	-	-	-	7			
		8	-	-	-	-	-	-	-	19(1)	-	-	-	8			
		9	-	-	-	-	-	-	-	-	17(1)	-	-	9			
		10	-	-	-	-	-	-	-	-	-	10(1)	-	10			
		11	-	-	-	-	-	-	-	-	-	1(1)	18(1)	2(1)			11
													20(1)	12			
		Chr. 8	Chr. 9	Chr. 10	Chr. 11	Chr. 12											
		Gramene Annotated Nipponbare Sequence 2006															

Clicking on a number in a cell will take you to the Map Viewer

Clicking on a number in a cell will take you to the Map Viewer showing the comparisons of the two corresponding maps (see next slide).

Comparing 2 maps



Map Sets

[\[Home Page\]](#) [Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | **[Map Sets](#)** | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Map Set Info

Choose a species and/or a map type to filter your search.

Restrict by Species: Restrict by Map Type:

There are 202 map sets.

Items 1 to 25 of 202. Page of 9 | [Next](#)

Map Set Name:	Gramene Annotated Nipponbare Sequence 2006			[Show Only This Set]
Abbreviated Name:	Gramene Annot Seq 2006			[Download Map Set Data]
Accession ID:	gt0506			[View Map Set In Matrix]
Species:	Oryza sativa (Rice)			[View Species Info]
Map Type:	Sequence			[View Map Type Info]
Map Units:	bp			
Published On:	N/A			
Maps:	Chr. 1	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 2	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 3	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 4	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 5	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 6	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 7	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 8	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 9	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 10	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 11	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. 12	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. chloroplast	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
	Chr. mitochondrion	[Map Viewer]	[Map Details]	[Matrix Viewer] Download Map Data
[Display All Maps in Viewer]				
Cross-references:	• Map Set Details			

Follow links for more information.

Feature Type

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | **[Feature Types](#)** | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Feature Type Info

There are 23 feature types

Display:

Select a single feature

Items 1 to 24 of 24.

Feature Type:	AFLP
Accession ID:	afip
Color:	mediumseagreen
Shape:	line
Description:	Amplified Fragment Length Polymorphism [Search for All Features of This Type]

Feature Type:	Breakpoint Interval
Accession ID:	breakpoint-interval
Color:	deepskyblue
Shape:	dumbbell
Description:	Interval between chromosomal breakpoints [Search for All Features of This Type]

Feature Type:	Centromere
Accession ID:	centromere
Color:	gray
Shape:	box
Description:	Centromere [Search for All Features of This Type]

Feature Type:	Cloning Vector
Accession ID:	cloning-vector
Color:	black
Shape:	snare

These are the feature types used in Cmap – only features that have correlations to other features will be here.. Each feature type has a name, a color and a shape. The curator may additionally assign other attributes (such as a “Description”) and cross-references.

Map Type

These are the map types used to classify the maps. Listed are the map type name & accession ID, the map units, an indication as to whether maps of this type are “relational,” and an indication of how maps of this are normally drawn (though this can be overridden at the map set level).

[Matrix](#) | [Map Sets](#) | [Feature Types](#) | **Map Type** | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#)

Map Type Info

Display:

Items 1 to 6 of 6.

A deletion map of an organism is a type of low-resolution physical map. It is constructed using a "genome deletion panel" which consists of a set of mutant lines containing sub-chromosomal deletions and a reference wild-type line. Markers can be mapped onto the genome using this panel (by Southern hybridization or by PCR) based on the presence or absence of signal when comparing the banding pattern in the mutants lines with the pattern in the wild type. Linked markers (present in the same deleted region) share the same banding pattern (presence or absence) on the deletion panel.

[\[Show All Map Sets Of This Map Type \]](#)

Map Type: **Sequence**

Accession ID: sequence

Map Units: bp

Is Relational Only: No

Appearance: lightgrey I-beam

Description: The sequence map is a summarized representation of the contiguous, assembled genomic sequence of an organism in a linear map format.

[\[Show All Map Sets Of This Map Type \]](#)

Map Type: **QTL**

Accession ID: qtl

Map Units: cM

Is Relational Only: No

Appearance: lightgrey I-beam

Description: The QTL map is a type of genetic map which indicates the approximate location of a quantitative trait locus (QTL) within an interval delineated by two or more markers on a genetic map.

[\[Show All Map Sets Of This Map Type \]](#)

You may click to view all map sets of this map type

Correspondence Evidence Types

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | **[Evidence Types](#)** | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Evidence Type Info

Display:

Items 1 to 13 of 13.

Evidence Type:	OMAP synteny analysis 1
	synteny_bestaln
	2
	lightblue
	Marker Identity
	ID
	1
	lightblue
	marker (i.e., probe, primer, sequence, etc) was used to map the corresponding features.
	Curated gene to QTL
	curated_gene_to_qtl
	2
	lightblue
	Gene underlying a quantitative trait.
Evidence Type:	Automated name-based
Accession ID:	ANB
Rank:	4
Line Color:	lightblue

These define the evidence types used to support the correspondences. Each evidence has an accession ID, a rank relative to the other evidence types, and an assigned color for the line drawn on the map to differentiate the correspondence.

Species

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | **Species** | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

List of mapsets may be filtered by individual species.

Species Info

Display:

Items 1 to 25 of 26. Page 1 of 2 [Next](#)

Gramene currently has maps for 26 species.

Common Name: **African rice**

Full Name: *Oryza glaberrima*

Accession ID: glab

Map Sets (3):

Physical Maps

FPC Chr OG_BB Feb 2006

FPC OG_BB Feb 2006

FPC OG_BB Jul 2006

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

Common Name: **Barley**

Full Name: *Hordeum vulgare*

Accession ID: barley

Map Sets (13):

[\[Show Map Sets From This Species \]](#)

Genetic Maps

Barley consensus 2003

NABGMP SxM 1993

Barley consensus - 1995

Barley consensus 2 - 1996

Barley genes 2 - 1997

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

QTL Maps

Apex/H. spontaneum BC SSR QTL 2003

Galleon/Haruna nijo RFLP/AFLP/SSR QTL 2003

Steptoe/Morex DH RFLP QTL 2006

Tadmor/Er Aprm RI RFLP/AFLP/SSR QTL 1998

UMN Fred/Stan QTL 2003

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)

[View Map Set In Matrix](#)

[View Map Set Info](#)


[View Map Set In Matrix](#)

Species' common and full names along with any other attributes and cross-references the curators have created.

Gramene has over 100 mapsets for rice.

Follow links for map information

Saved Links

 [Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Saved Links

Display: CFW (1) ☐ Display Hidden Links

--Select a User Name--
CFW (1)
ricechr4 (1)
ricechr4vsZmchr2 (1)
Unknown Group (16)

to 1 of 1.

Saved Link ID	Group Name		Last Access	Comment	Permanent Link	Legacy Link	Actions
17	CFW	Rice 8 v Maize 10	2007-03-19	2007-03-19	Permanent Link	Legacy Link	edit

When someone creates a saved link (*see slide 12*) you can retrieve it here.

Maps Help

Maps Menu

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Saved Links](#) | **Help** | [Tutorial](#)

Help Sections: [Map Viewer](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Species](#) | [Map Details](#) | [Feature Details](#) | [Evidence Types](#) | [Correspondence Details](#) | **Saved Links** | [Feature Alias](#)

Saved Link Concepts

Link Group

*Maps Help
Menu*

This link has the session information stored in the server which makes it stable

Legacy Link

This link uses the legacy link parameters. The advantage is that it will be stable across different servers (with the same data). The disadvantages are that it can get longer than a browser (IE) can handle. It also has limitations such as minimum correspondences (which can be different for each map set added in the image).

Hidden

When there are a lot of saved links, the hidden links) but is still in the database to the saved link viewer (unless specifically looking for

When clicking on Help from the maps menu, you will be directed to the help page for the section of the Maps module that you were viewing.

For example, this page was accessed via the "saved links" page in the Maps module.

Creating Saved Link

Saving Links

- Links can be created using the "Save Link" button on the map viewer page.

Importing Links

- Links can be imported from xml file using the cmap_admin.pl script on the server.
- Ask you administrator to view the ADMINISTRATION document if you wish to utilize this feature.

Tutorial

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Imported Links](#) | [Help](#) | **Tutorial** | [FAQ](#)

Maps Tutorial

Select your preferred format:

- ◆ [PowerPoint](#)
- ◆ [Adobe PDF](#)

Release Notes

Tutorials are available in various formats.

Gramene Tutorials: [Navigation](#) | [Overview](#) | [Genomes](#) | [GrameneMart](#) | [BLAST](#) | **Maps** | [Mappings](#) | [Proteins](#) | [Ontologies](#) | [Genes](#) | [QTL](#) | [Diversity](#) | [Pathways](#) | [Literature](#)

Free associated software:



[PowerPoint viewer](#)

Download software for viewing tutorials.

Link to any of the Gramene tutorials.

FAQ

[Maps Home](#) | [Maps](#) | [Map Search](#) | [Feature Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Imported Links](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Click on FAQ, which will open a page where you can select your module of interest for FAQs.

GRAMENE *Cache*

[Search](#) [Genomes](#) [Species](#) [Download](#) [Resources](#) [About](#) [Help](#)


Gramene FAQ







- ♦ Moderator: cer17@cornell.edu
- ♦ Gramene FAQ's may be browsed by category or may be searched by keyword
- ♦ Subcategories:
 - [Maps and CMap](#)
 - [BLAST](#)
 - [Proteins](#)
 - [Ontologies](#)
 - [Genomes](#)
 - [Markers](#)
 - [QTL](#)
 - [Genes](#)
 - [Literature](#)
 - [Data Curation](#)
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Answers in this category:
[New Item](#)

♦ 2006-Aug-15 9:45am

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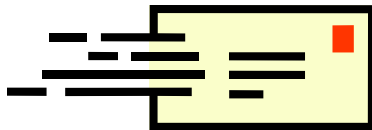
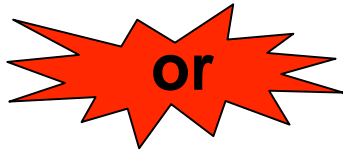
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