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.

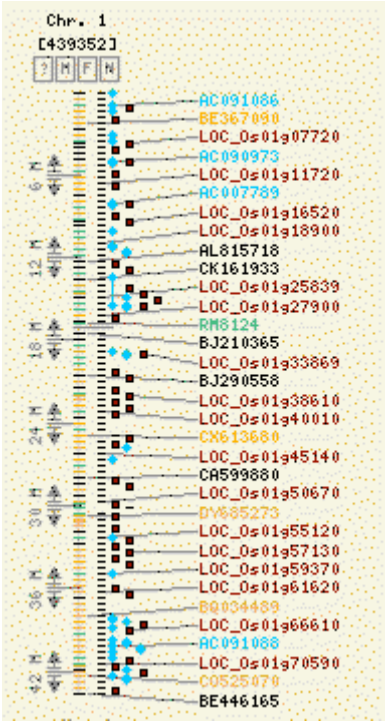
Note! Although we continually work to make Gramene compatible with all browsers, there are problems with some browser versions. If you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through Gramene Feedback.

Gramene Home Page

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.

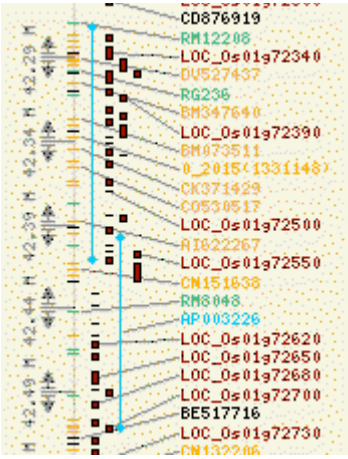
Map Set Name:	**Gramene Annotated Nipponbare Sequence 2006**
Abbreviated Name:	Gramene Annot Seq 2006
Accession ID:	gt0506
Species:	Oryza sativa (Rice)
Map Type:	Sequence
Map Units:	bp
Published On:	02 May, 2006
Maps:	Chr. 1
	Chr. 2
	Chr. 3
	Chr. 4
	Chr. 5
	Chr. 6
	Chr. 7
	Chr. 8
	Chr. 9
	Chr. 10
	Chr.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



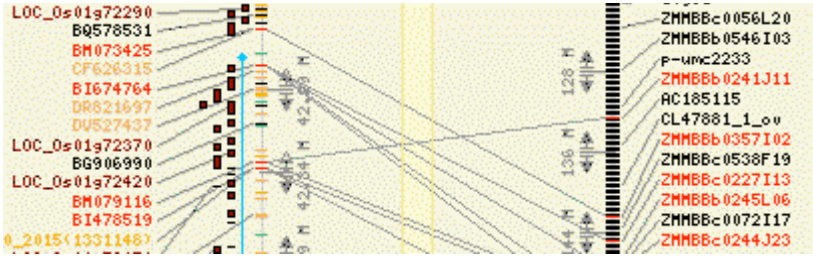
•A **map** is a linear array of interconnected features. This could represent a single linkage group in the case of a genetic map, or a single contig for physical maps.

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 and map sets.
- Not all the data in the Markers DB has been exported to CMap, only data that has correspondences has been imported into Maps. Some data, such as the OMAP stacked maps will be found only in Maps, and not in Markers.

Module Home-Page layout

Module home pages provide the following information:

- **Searching/Browsing –** links to different types of searches.
- **Other Tools –** if applicable, links to different tools used in this module.
- **Help –** links to help pages, tutorials, release notes, FAQ and other helpful documentation.
- **Download –** information on where to download the database.
- **Feedback –** How to contact Gramene
- **Acknowledgements –** Other programs that contribute to this data.
- **Quicklinks and external links –** when appropriate these links are provided.

Maps Home Page

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

Gramene Maps Database

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. All data (map sets, maps, features, and correspondences) in the Maps Module are built from the Markers Module. Users are encouraged to consult the Markers Module for primary information about markers and their mappings. The Maps Module should be considered to be primarily a visualization tool

Search or Browse Options

Maps	Browse, 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

Help

Map Sets	Get a description of the 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 correspondence evidence types
Species	Get a description of the species
Help	Presents an overview on how to use the Genes and Alleles data
Tutorial	More in-depth than the help pages, use the tutorial for an example datasets, and get tips to increase your data search efficiency.
FAQs	Frequently Asked Questions - see what questions users have
Release Notes	For more information about the most recent release.

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

Collaborative Projects

- OMap Data at Gramene - To faciliate comparison with Sequence. This map set includes features not exported maps are also available as ordered maps. These ordered single map rather than individual contigs. The ordered TIGR genome contig

Access OMAP data *(see slide 28)*

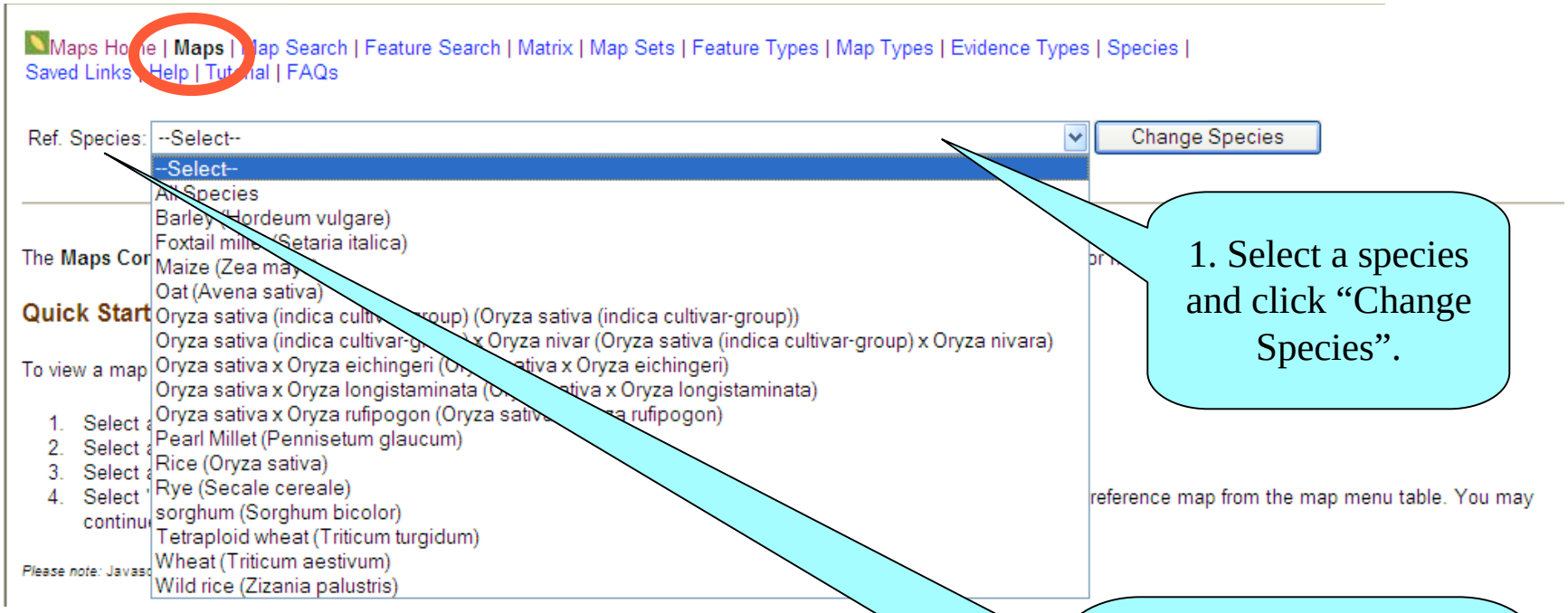
Download

The Comparative Maps are maps that only contain features original maps with all their features, see the Markers

Acknowledgements

Gramene uses CMap. GMOD's CMap - CMap is a web-based tools for curating map data. For a list of data contributors, p

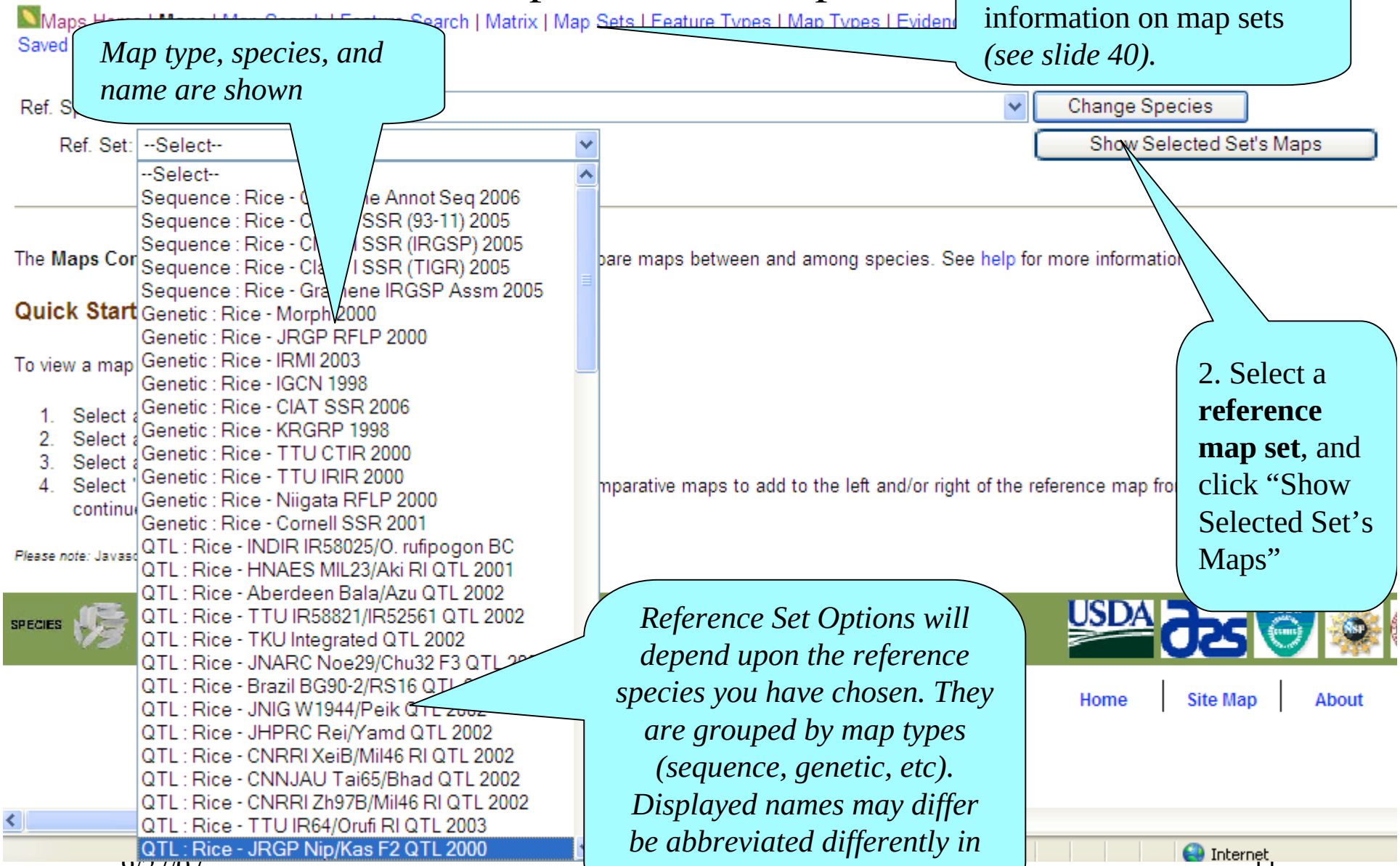
Maps: Select a Species



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 40).*

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 | Help | Tutorial | FAQs

Ref. Species: Rice (Oryza sativa) — Change Species

Ref. Set: QTL : Rice - JRGP Nip/Kas F2 QTL 2000 — Show Selected Set's Maps

Ref. Map: Draw Maps

- -All- -
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"

Ref Map Start:

Ref Map End:

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

Feature Type Display:

Feature	Ignore	Display if Correspondence	Always Display
Centromere	○	○	◉
Marker	○	○	◉
QTL	○	○	◉
RAPD	○	○	◉
RFLP	○	○	◉
STS	○	○	◉
Other	○	○	○
	Check All	Check All	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.

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]

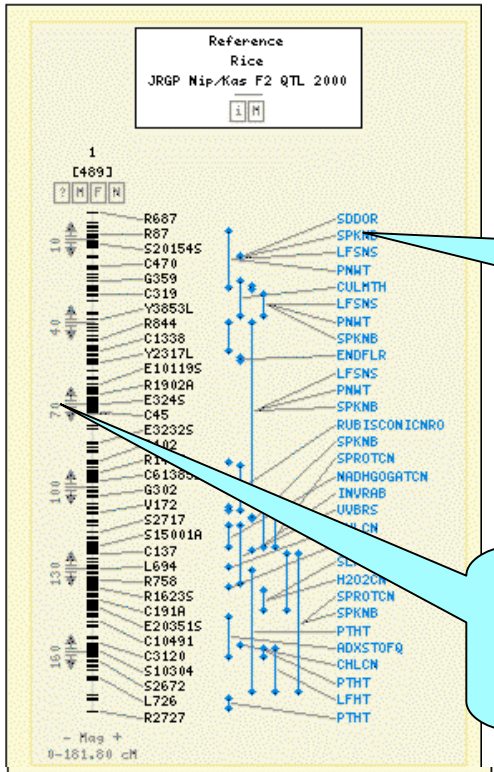
Map Type: QTL (cM) [View More Info]

Description: This is an updated version of the map reported by Kurata et al. (1994) and Harushima et al. [illegible] uses an F2 population of 186 plants from a cross between the cultivars Nip[illegible] (japonica) and Kasalath (indica). A total of 3267 markers were located covering 1530.4 cM. Marker names ending with the letter 'S' indicate that the 3' UTR of a cDNA fragment was used as a probe rather than the whole insert. The centromere position of chromosome 10 has been updated to reflect the new estimate given by Cheng et al. (2001).

Cross-references:
- Map Set Details

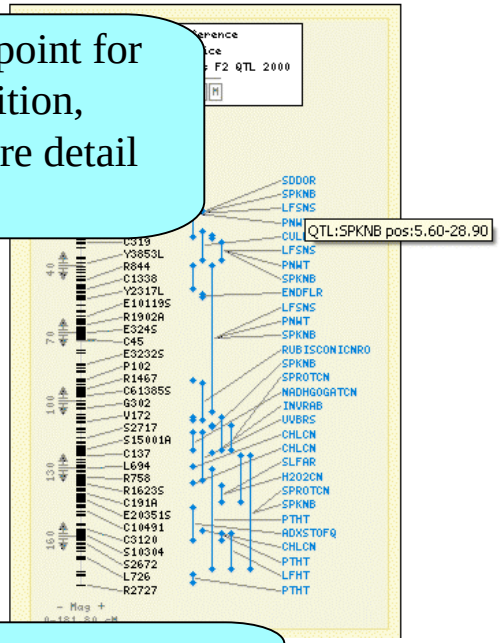
Information on the Ref. Map Set will appear when one is selected.

Maps: Viewing a map

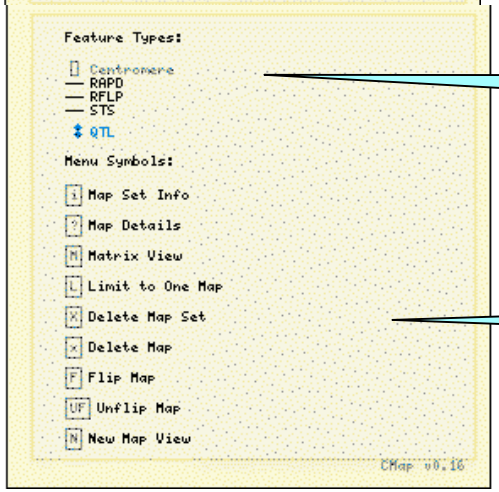


Hover over a point for name and position, click for feature detail *(see slide 14)*

Click arrow to crop map *(as in slide 23)*



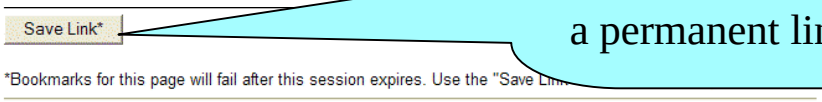
Change Magnification



Map Legend (see slide 30)

Scroll page for **Map options** – *see slides 16-21*

Bookmarks for this page will fail after this session expires. Use the "Save Link" button to create a permanent link *(see slide 45)*



Viewing a Map - Feature Detail

Click here for Map Details *(see slide 15)*, as well as other information.

Feature Alias Detail "CQN52"

Alias: CQN52
Feature Name: SPKNB [View Feature]

ap Sets | Feature Types | Map Types | Ev

Feature "SPKNB"

Feature Name:	SPKNB
Aliases:	CQN53 [View Alias Details] CQN53-SPKNB [View Alias Details] TO:0000456 [View Alias Details]
Accession ID:	CQN53
Feature Type:	QTL [View Feature Type Info]
Map:	Species: Rice Map Set: JRGP Nip/Kas F2 QTL 2000 [View Map Details] Map Name: 1
Start:	5.60 cM
Stop:	28.90 cM
Cross-references:	[View Oryza sativa QTL "CQN53" details]

Feature Type Info

Display: QTL Submit

[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)*

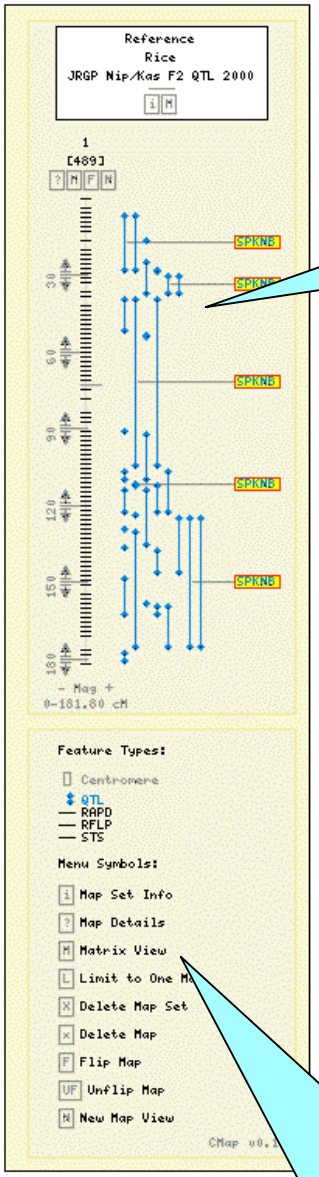
Correspondences

Feature	Accession	Map	Map Type	Aliases	Evidence Type	Actions		
CQN53-SPKNB	gt0506-1-CQN53-1	Rice-Gramene Annot Seq 2006-Chr. 1	Sequence	CQN53, 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

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



When clicking "Map Detail" from previous slide you now get a map with your features highlighted.

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 30

Map Details

Map Type:	QTL [View Map Type Info]
Map Set Name:	Rice - JRGP Nip/Kas F2 QTL 200
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

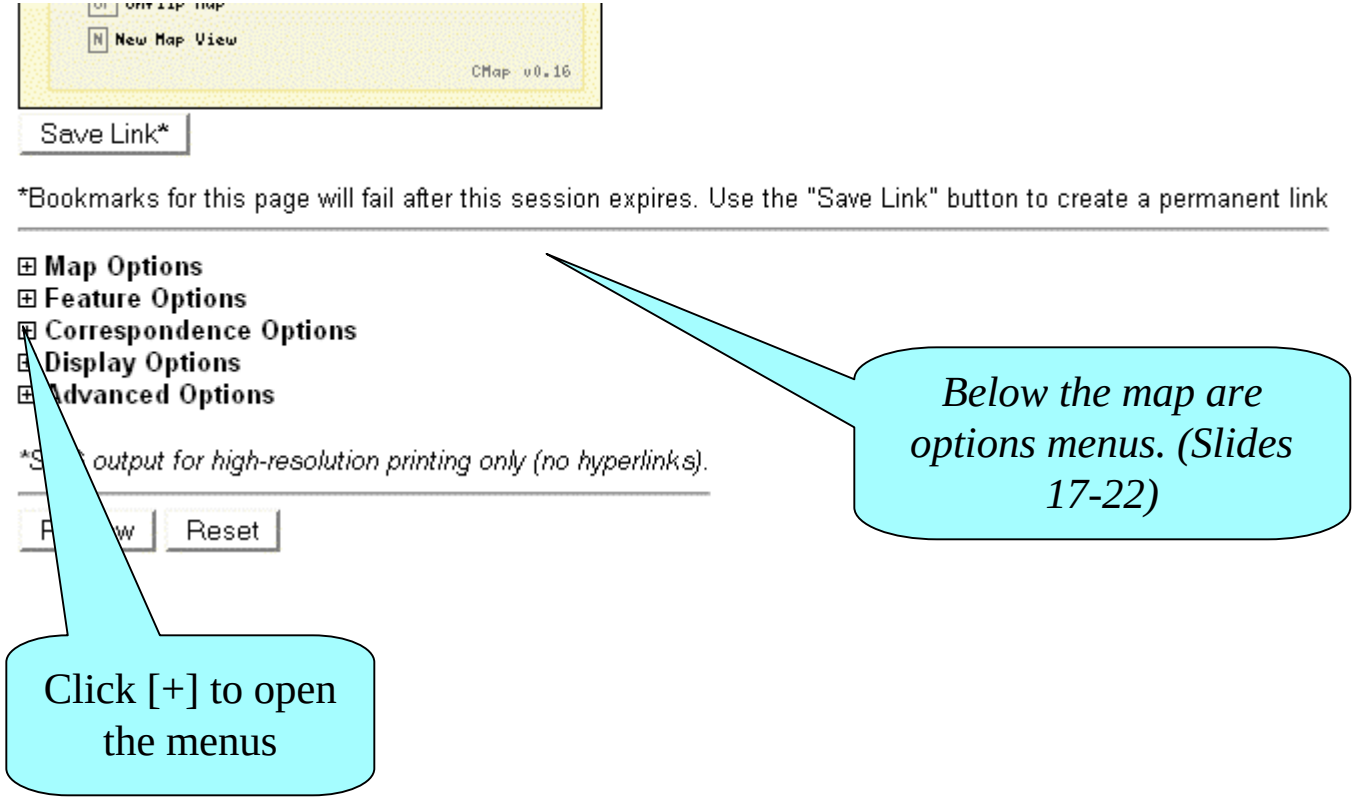
Restrict by Map: --All-- Submit

[Download Feature Correspondence Data]

Items 1 to 25 of 489. Page 1 of 20 | Next

Rice - JRGP Nip/Kas F2 QTL 2000 - 1 (Click headers to resort)			Comparative Maps					
Feature	Type	Position (cM)	Map	Feature	Type	Position	Evidence	Actions
			Rice - JRGP RFLP 2000 - 1	R687	RFLP	0.00 (cM)	Marker Identity	View Maps
			Rice - Gramene IRGSP Assm 2005 - Chr. 1	R687	RFLP	148,634.00 - 148,742.00 (bp)	Marker Identity	View Maps
			Oryza sativa (indica cultivar-group) - - Chr. 1	D23969	EST	163,289.00 - 163,460.00 ()	RFLP Sequence	View Maps
			Rice - Gramene Annot Seq 2006 - Chr. 1	R687	RFLP	146,299.00 - 146,350.00 (bp)	Marker Identity	View Maps
			Oryza sativa (indica cultivar-group) - - Chr. 1	D23969	EST	162,635.00 - 162,686.00 ()	RFLP Sequence	View Maps
			Oryza sativa (indica cultivar-group) - - Chr. 1	D23969	EST	162,994.00 - 163,069.00 ()	RFLP Sequence	View Maps
R687	RFLP	0.00	Rice - Gramene IRGSP Assm 2005 - Chr. 1	R687	RFLP	148,497.00 - 148,548.00 (bp)	Marker Identity	View Maps
			Oryza sativa (indica cultivar-group) - - Chr. 1	D23969	EST	162,772.00 - 162,880.00 ()	RFLP Sequence	View Maps

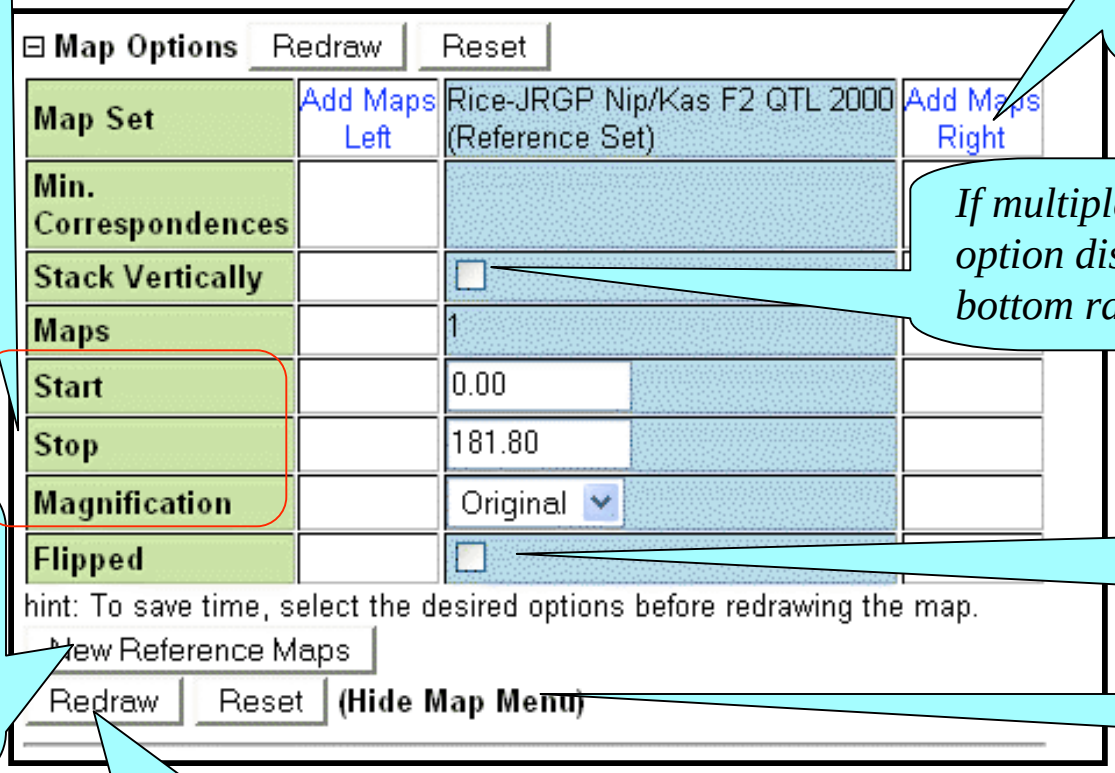
Options


New Map View
CMap v0.16
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
output for high-resolution printing only (no hyperlinks).
Reset
Below the map are options menus. (Slides 17-22)
Click [+] to open the menus

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 view another map or begin a new comparison

Click to collapse (hide) map options.

Click to add changes.

Feature Options

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

⊟ **Feature Options** Redraw Reset

Highlight Features: "SPKNB"

Feature Types:

Feature	Ignore	Display if Correspondence	Always Display
Centromere	○	○	◉
QTL	○	○	◉
RAPD	○	○	◉
RFLP	○	○	◉
STS	○	○	◉
Other	○	○	○
	Check All	Check All	Check All

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

Show Labels: ○ None ◉ Landmarks ○ All

Collapse Overlapping Features: ○ No ◉ Yes

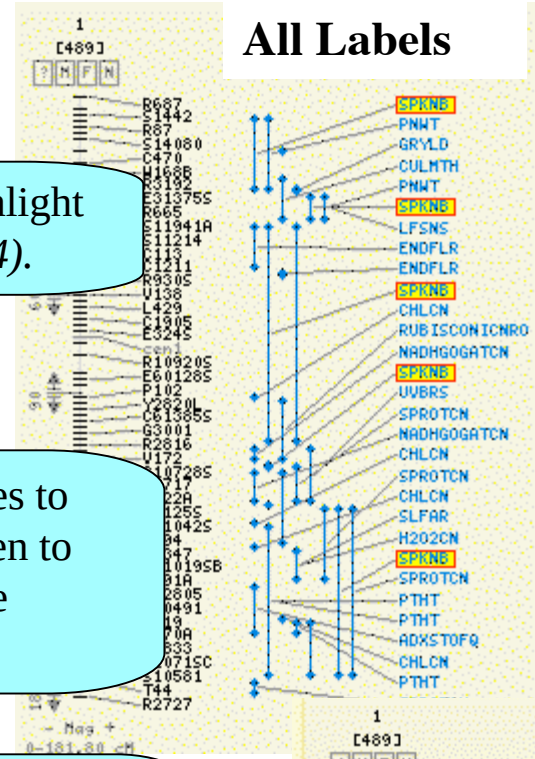
Redraw Reset **(Hide Feature Menu)**

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

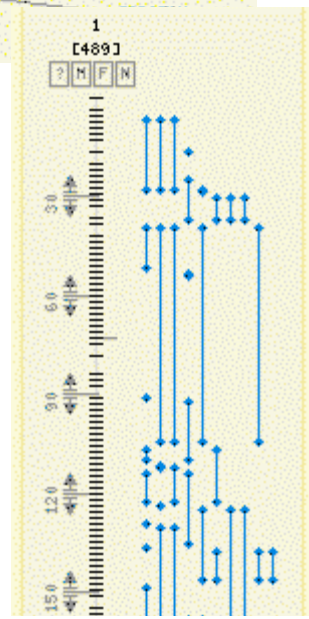
Click to add changes.

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 Redraw Reset

Include Correspondence Types:

Evidence	Ignore	Use	Less Than Score	Greater Than Score	Score
Automated name-based	○	◉	○	○	0
Marker Identity	○	◉	○	○	0
SOG_OVERGO	○	◉	○	○	0
Unknown	○	◉	○	○	0
Wheat EST BI	○	◉	○	○	0
Maize bin marker	○	◉	○	○	0
Curated gene to QTL	○	◉	○	○	0
dbest_poaceae	○	◉	○	○	0
FPC loader	○	◉	○	○	0
Gene model	○	◉	○	○	0
gss_poaceae	○	◉	○	○	0
Maize cytogenetic map	○	◉	○	○	0
OMAP synteny analysis 2	○	◉	○	○	0
RFLP Sequence	○	◉	○	○	0
SOG Overgo	○	○	○	○	0
OMAP synteny analysis 2	○	◉	○	○	0
Unknown	○	○	○	○	0
			○	○	0

eck All

Aggre rrespondences: ◉ No ○ 1 Line ○ 2 Lines

Corre ence lines drawn to: ◉ Feature ○ Map

View a-Slot Correspondences: ◉ No ○ yes

Aggre gate evidence types separately: ◉ No ○ yes

Redraw Reset **(Hide Correspondence Menu)**

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

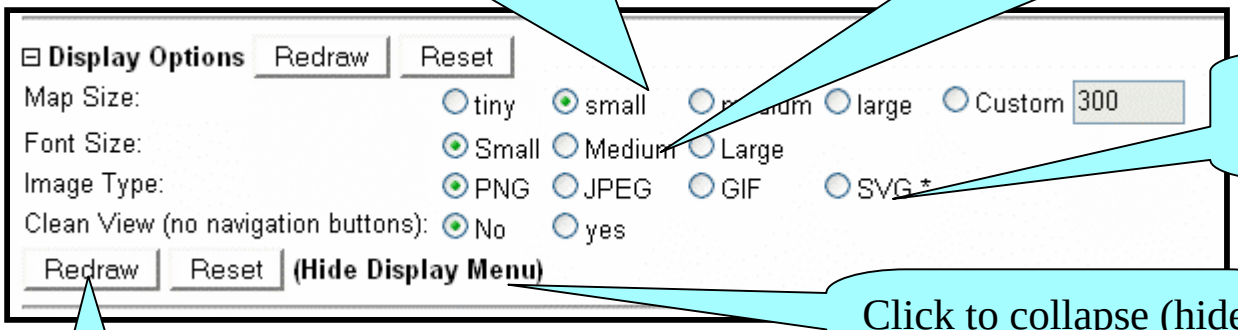
Click to add changes.

Click to collapse (hide) correspondence options.

Display Options

Determines the vertical height of the image

Determines the size of the font



Select the desired image format.

Click to collapse (hide) display options.

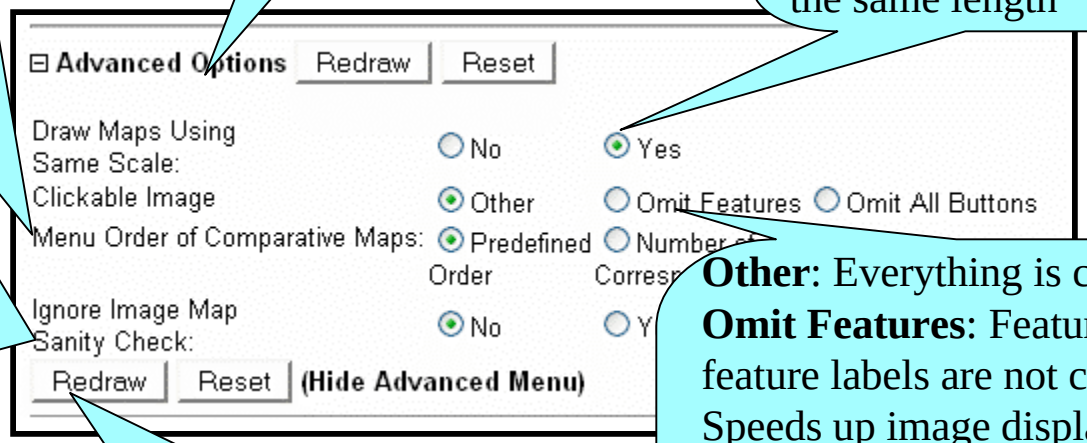
Click to add changes.

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

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

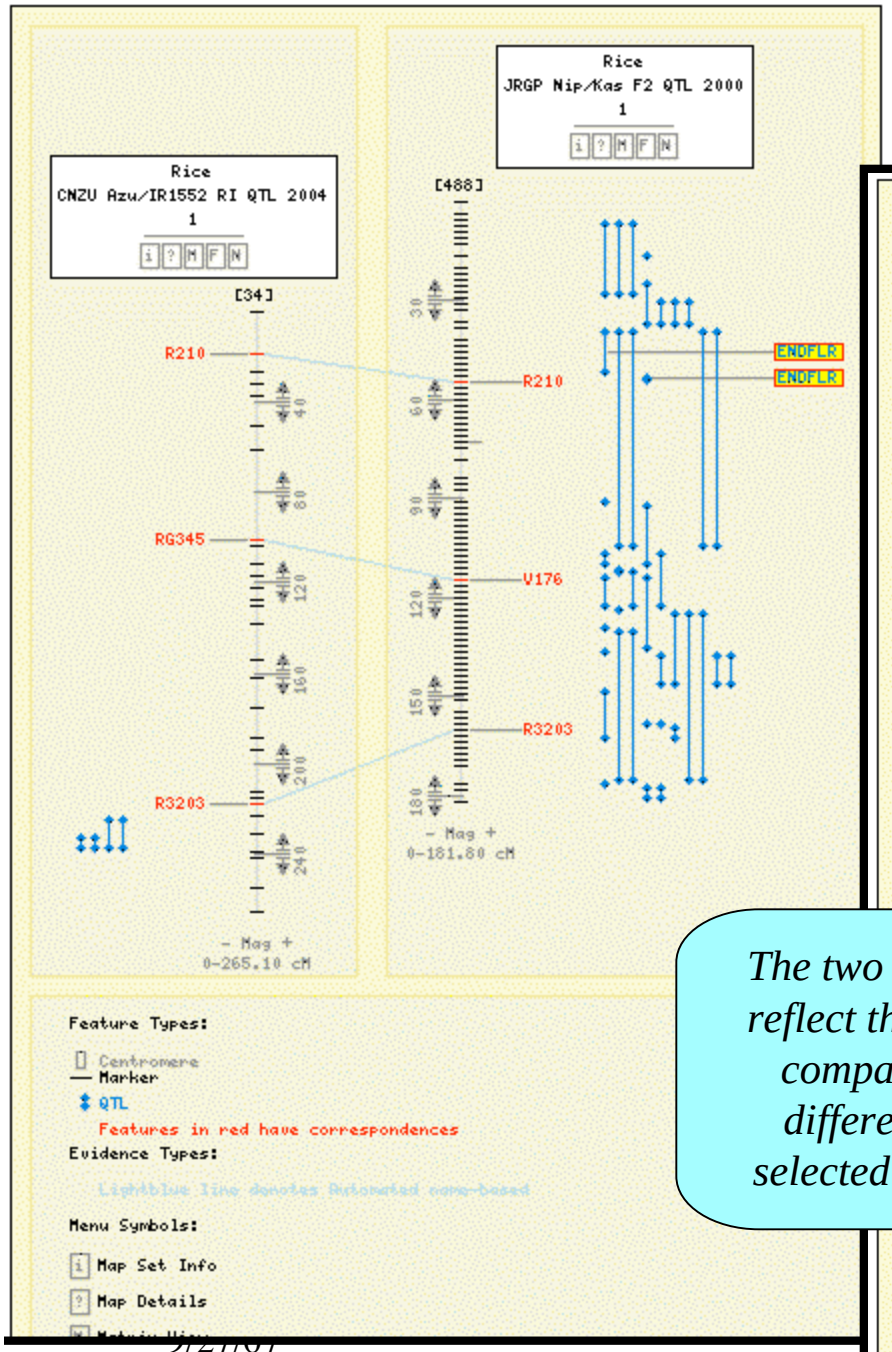


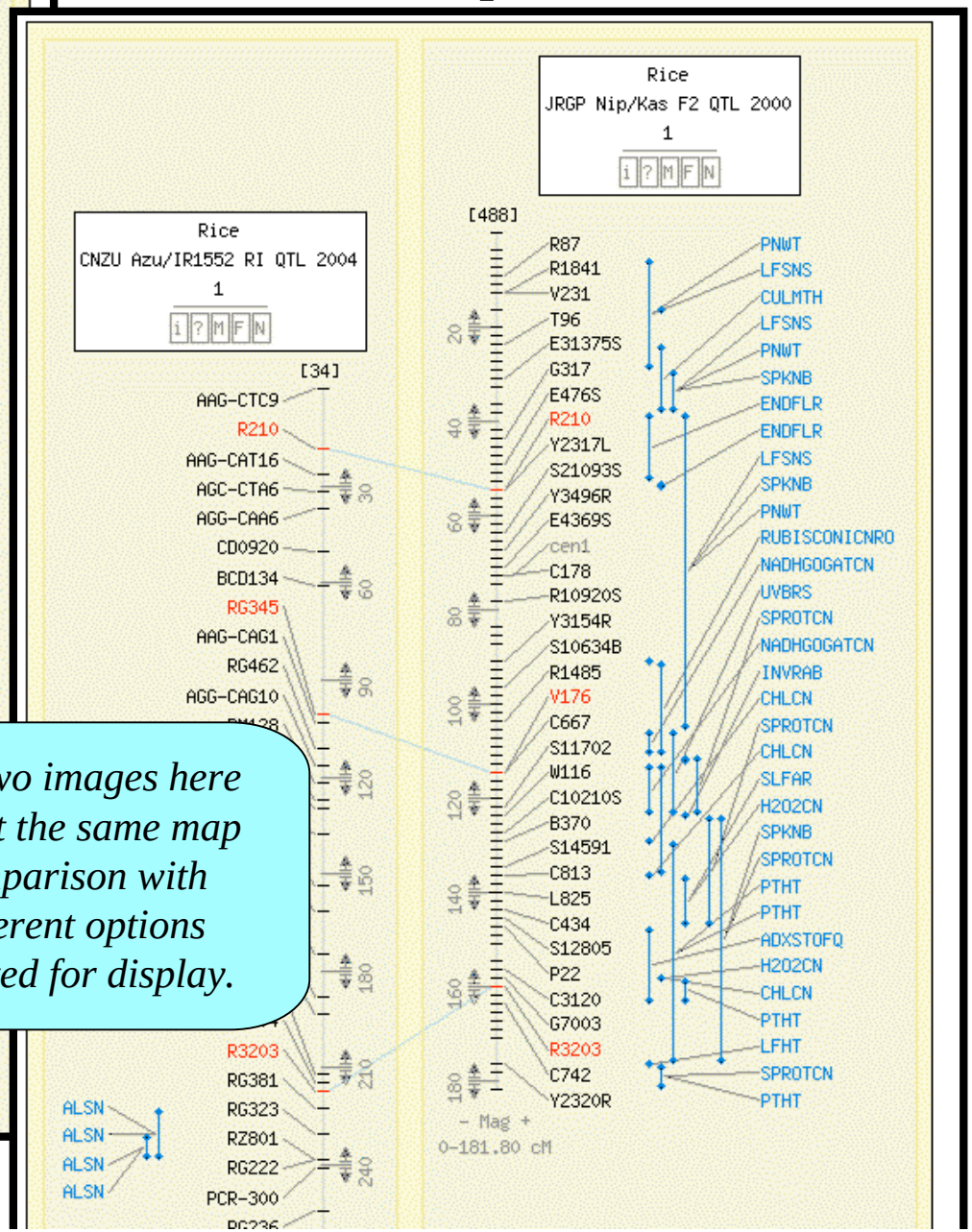
Having too many clickable features may be problematic for some browsers. If the number of features to be displayed is too large during a sanity check, features will not be clickable in order to prevent these problems.

Click to 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

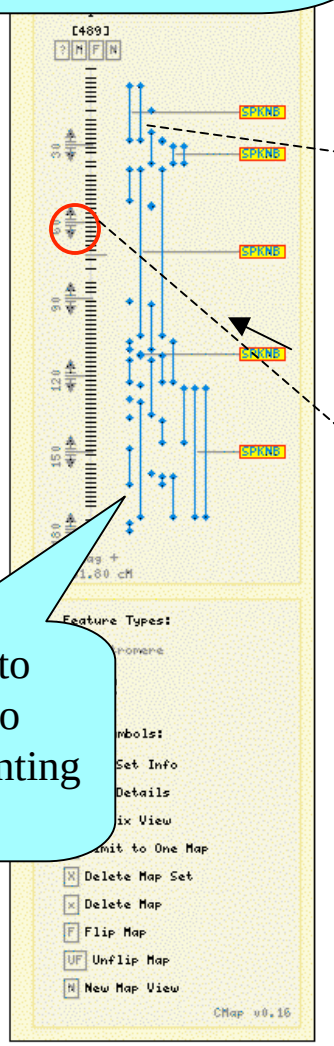




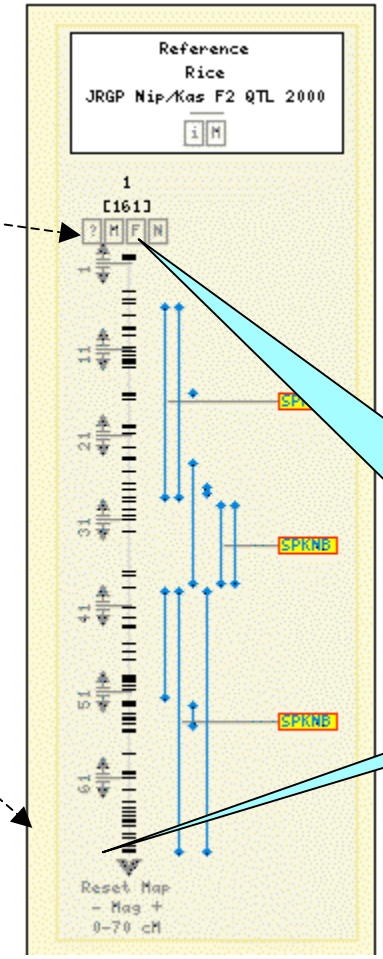
The two images here reflect the same map comparison with different options selected for display.

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.

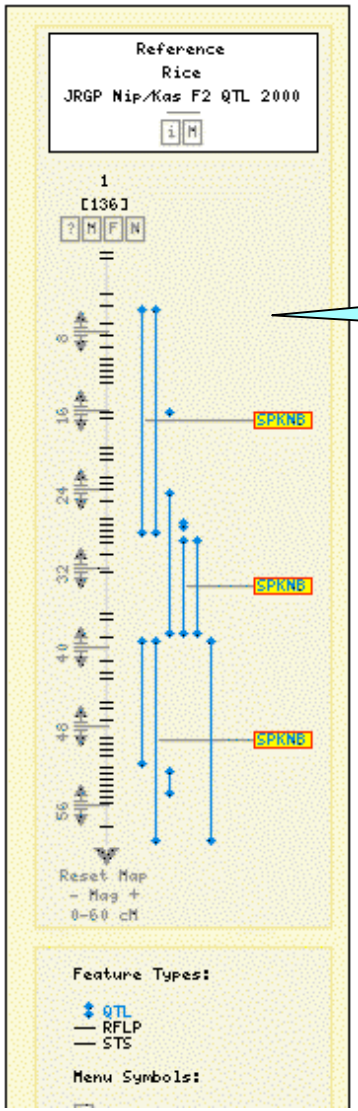


At the ends of the chromosome, the arrow indicates the chromosome continues, a solid bar indicates the end point

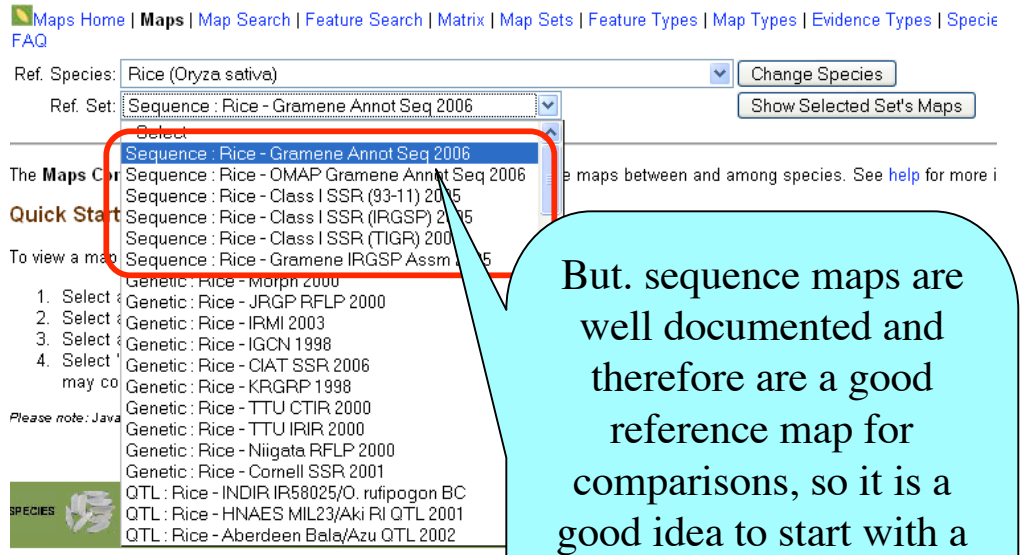
Compare Maps

- 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



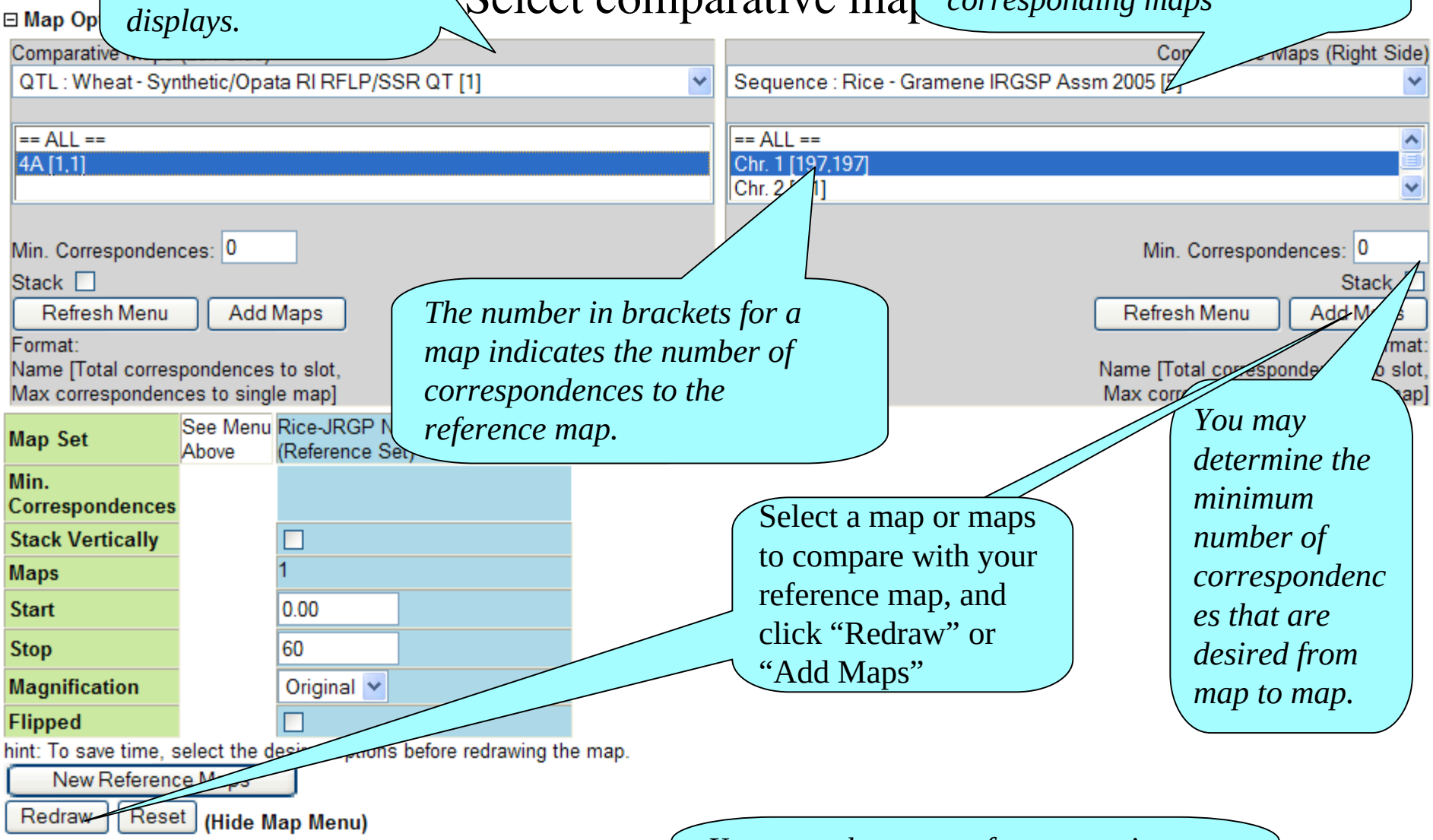
But. sequence maps are well documented and therefore are a good reference map for comparisons, so it is a good idea to start with a sequence map as the reference map when making multiple map comparisons

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 maps

See slide 17 to see how to open comparative maps displays.

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



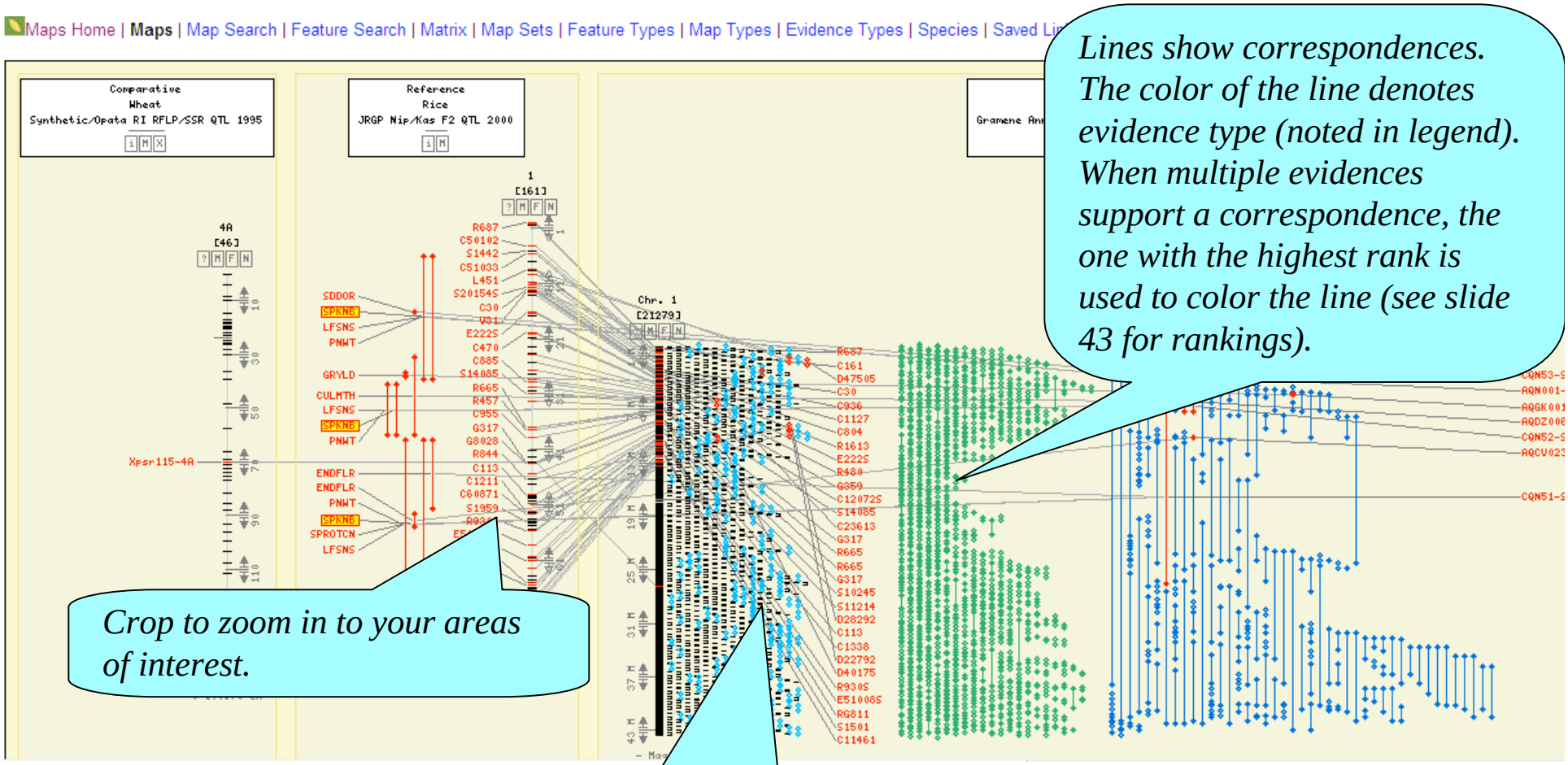
The number in brackets for a map indicates the number of correspondences to the reference map.

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



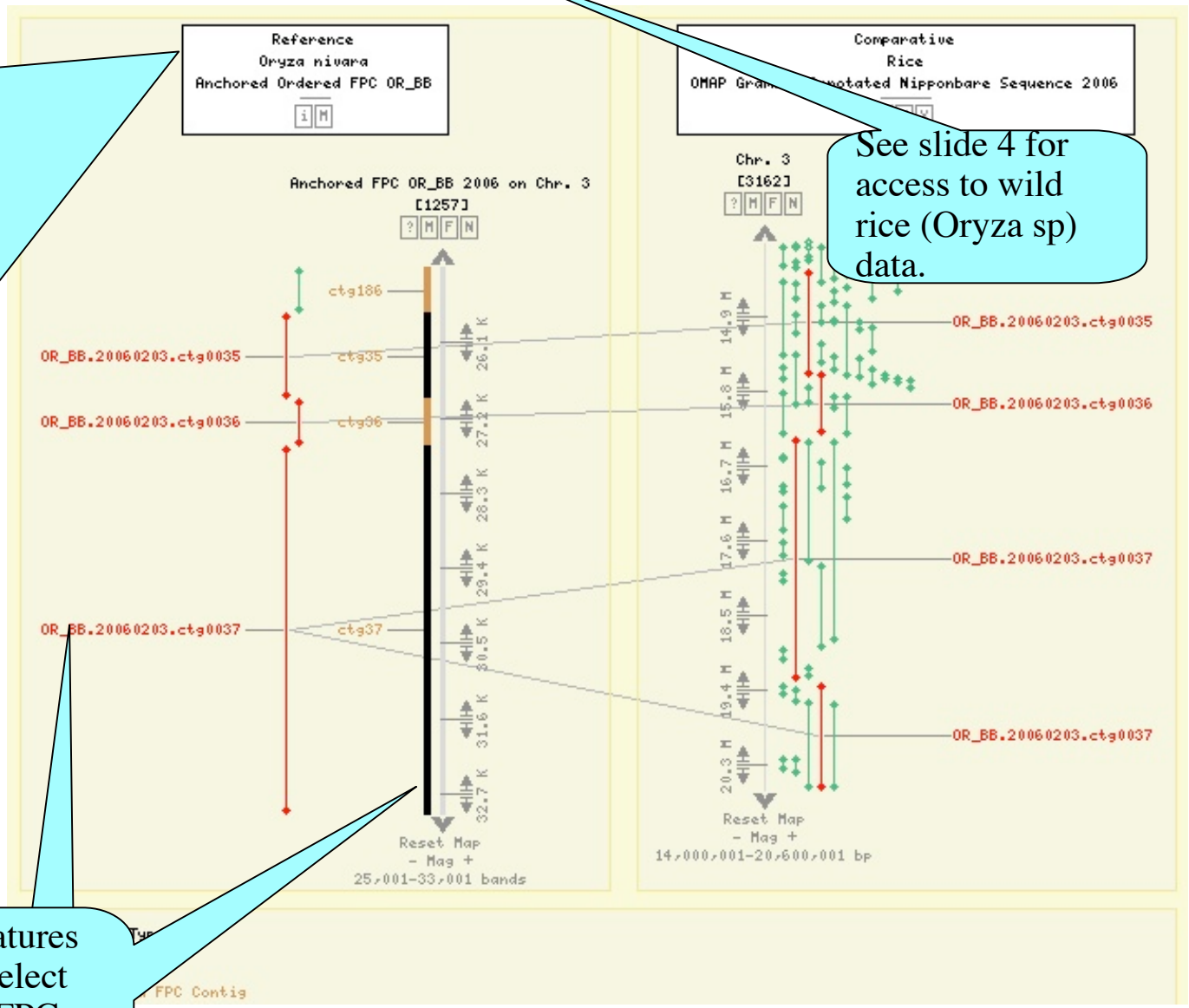
Lines show correspondences. The color of the line denotes evidence type (noted in legend). When multiple evidences support a correspondence, the one with the highest rank is used to color the line (see slide 43 for rankings).

Crop to zoom in to your areas of interest.

Features with correspondences appear in red (noted in legend)

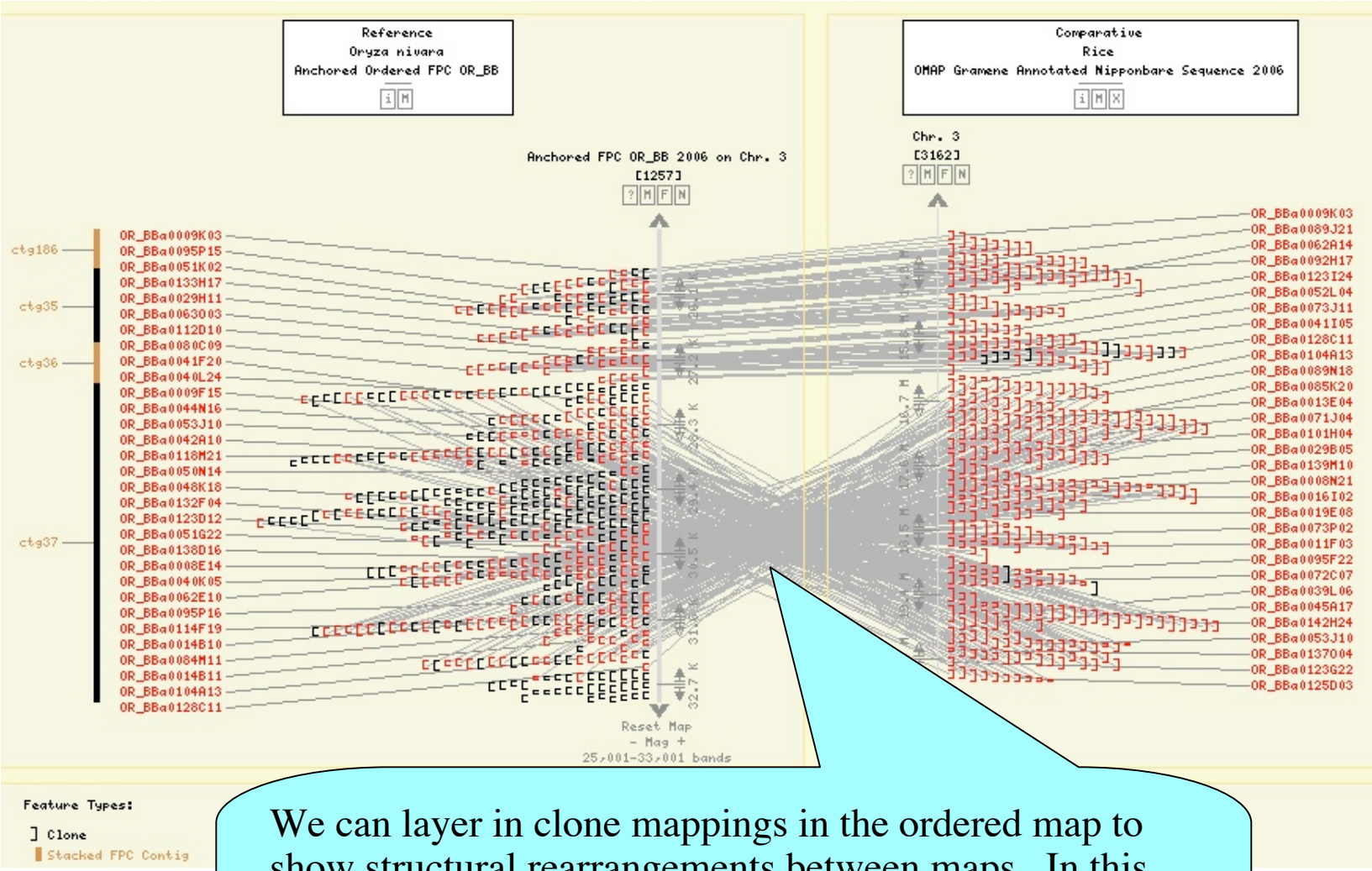
OMAP

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.



See slide 4 for access to wild rice (Oryza sp) data.

Using Features options, select "stacked FPC contigs" and "FPC"



We can layer in clone mappings in the ordered map to show structural rearrangements between maps. In this example, we see a large scale inversion between O. nivara and O. sativa. This is shown using evidence from the clone mapping in the ordered O. nivara FPContig as compared to the O. sativa TIGR V4 assembly.

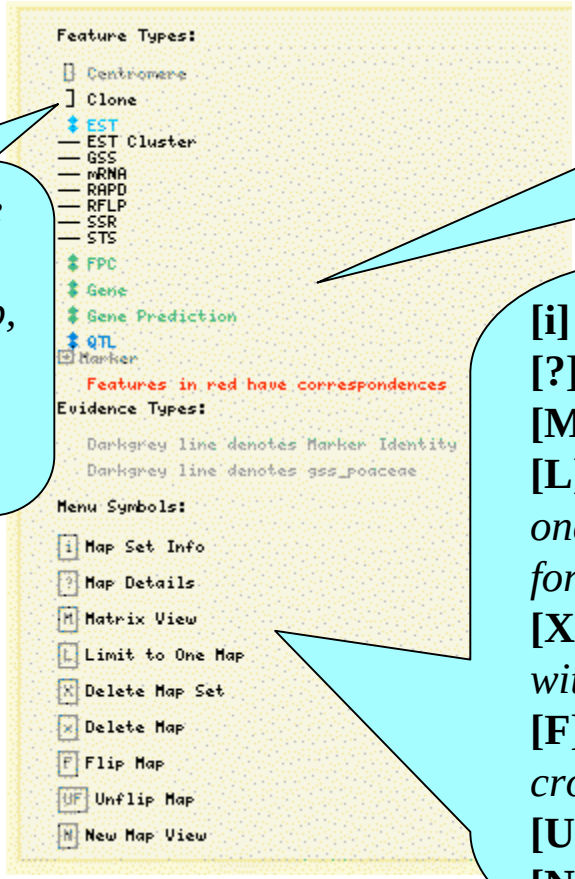
Map Legend

Species name

Map set name

Map name

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

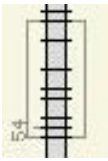


Listing of all the feature types found on the map, along with their corresponding glyphs

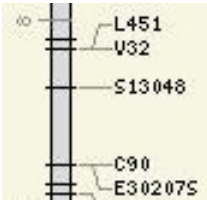
[i] *Map set info –(slide 40)*
[?] *Map details (slide 14)*
[M] *Matrix View – (slide 36)*
[L] *Limit to one map – displayed when there is more than one map in the panel, select a single map by selecting [L] for the desired map.*
[X] *delete the map or mapset this symbol is associated with.*
[F] *Flip 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

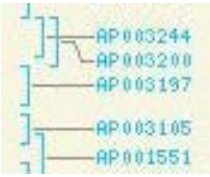
The following demonstrate some of the glyphs (shapes) that map features could appear as.



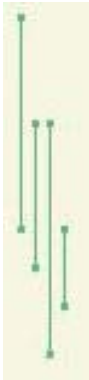
box



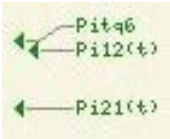
line



span



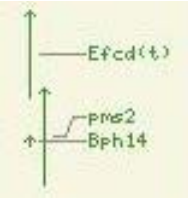
dumbbell



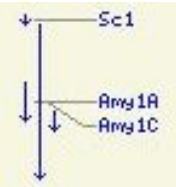
in-triangle

filled-box

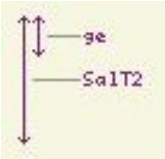
out-triangle



up-arrow



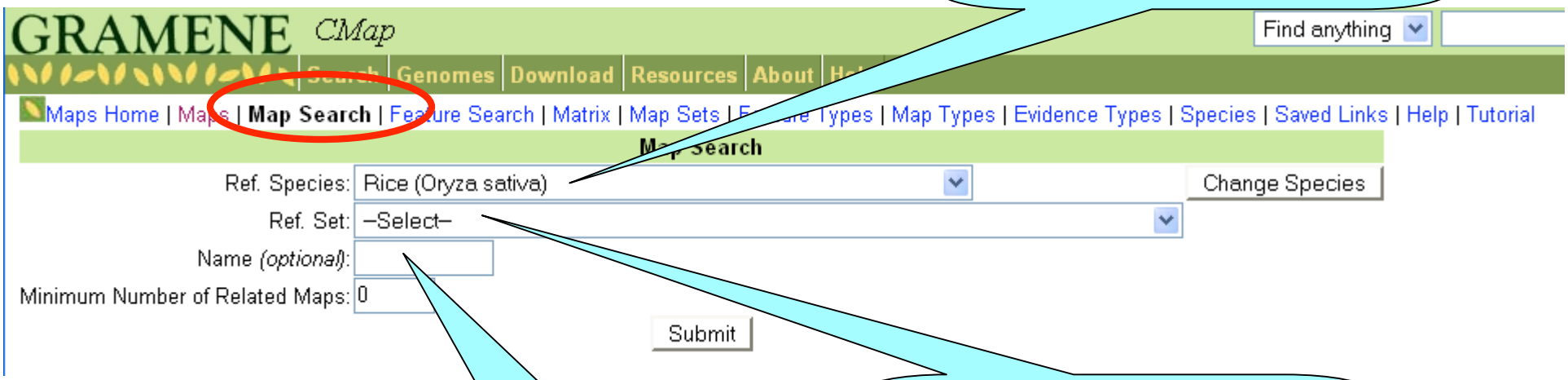
down-arrow



double-arrow

Map Search

Search maps in CMap by species.



Map sets available depend upon the species you selected.

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 Spec

Ref. Set: Sequence : Rice - Gramene Annotated Nipponbare Sequence 2006

Name *(optional)*:

Minimum Number of Related Maps: 0

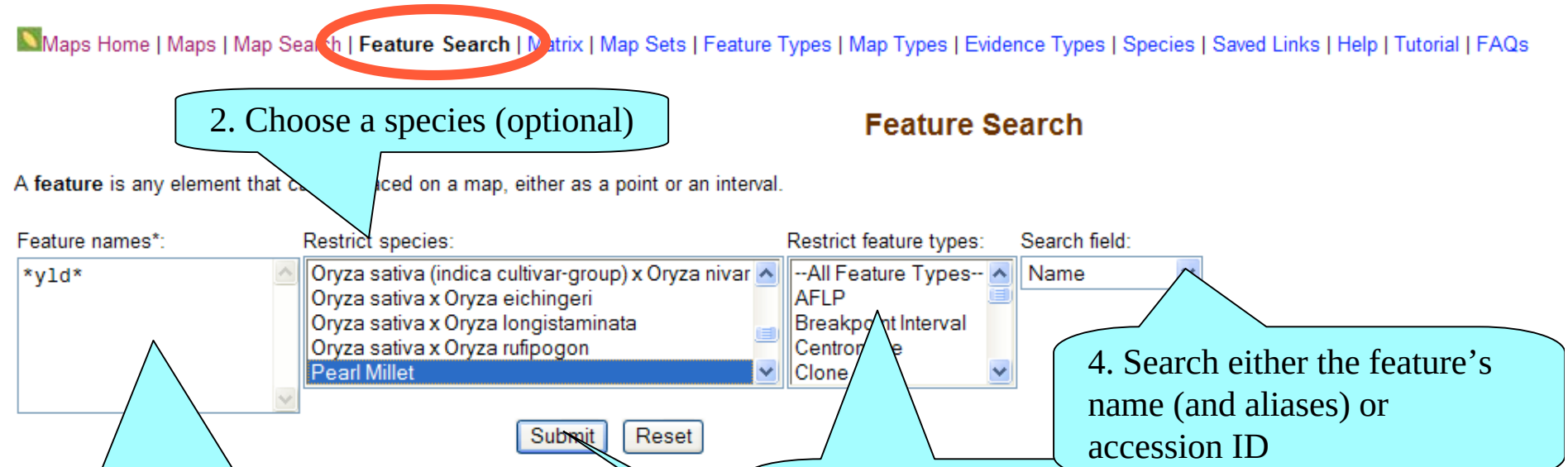
Submit

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		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	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.											1679	38.51/M	315	7.23/M	6	0.14/M	729	16.72/M	2024	46.43/M	62	1.42/M
Chr. 2 (spider)	1044	29.06/M	23632	0.66/K	1.00	35924366.00	73	2.											1397	38.89/M	227	6.32/M	80	2.23/M	573	15.95/M	1732	48.21/M	75	2.09/M
Chr. 3 (spider)	1116	30.71/M	32415	0.89/K	1.00	36345483.00	107	2.											1986	54.64/M	385	10.59/M	28	0.77/M	759	20.88/M	1792	49.30/M	116	3.19/M
Chr. 4 (spider)	564	16.00/M	13988	0.40/K	1.00	35244021.00	34	0.											910	25.82/M	157	4.45/M	27	0.77/M	417	11.83/M	1163	33.00/M	61	1.73/M
Chr. 5 (spider)	699	23.40/M	21179	0.71/K	1.00	29874019.00	46	1.											1149	38.46/M	321	10.75/M	334	11.18/M	473	15.83/M	1239	41.47/M	92	3.08/M
Chr. 6 (spider)	848	27.14/M	18071	0.58/K	1.00	31242608.00	60	1.											879	28.13/M	337	10.79/M	55	1.76/M	431	13.80/M	1212	38.79/M	31	0.99/M
Chr. 7 (spider)	561	18.90/M	15050	0.51/K	1.00	29678581.00	35	1.											886	29.85/M	167	5.63/M	71	2.39/M	424	14.29/M	1034	34.84/M	26	0.88/M
Chr. 8 (spider)	640	22.61/M	13792	0.49/K	1.00	28307495.00	25	0.											696	24.59/M	112	3.96/M	56	1.98/M	351	12.40/M	1168	41.26/M	43	1.52/M
Chr. 9 (spider)	604	26.25/M	13116	0.57/K	1.00	23011004.00	45	1.											598	25.99/M	160	6.95/M	42	1.83/M	267	11.60/M	886	38.50/M	42	1.83/M
Chr. 10 (spider)	511	22.34/M	13274	0.58/K	1.00	22876596.00	15	0.											495	21.64/M	104	4.55/M	72	3.15/M	255	11.15/M	855	37.37/M	46	2.01/M
Chr. 11 (spider)	563	19.78/M	9608	0.34/K	1.00	28459272.00	19	0.											514	18.06/M	161	5.66/M	22	0.77/M	284	9.98/M	991	34.82/M	41	1.44/M
Chr. 12 (spider)	498	18.11/M	10918	0.40/K	1.00	27496040.00	28	1.											665	24.19/M	95	3.46/M	26	0.95/M	308	11.20/M	997	36.26/M	45	1.64/M
Chr. chloroplast (spider)	9	66.92/M	66	0.49/K	1.00	134481.00	0	0											0	0	0	0	0	0	0	0	0	0	0	0
Chr. mitochondrion (spider)	0	0/unit	0	0/unit	1.00	457225.00	0	0											0	0	0	0	0	0	0	0	0	0	0	0

Feature Search

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



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.

3. Choose a feature type (optional)

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

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 14)*

Items 1 - 5 of 61. Page 1 of 3 | Next

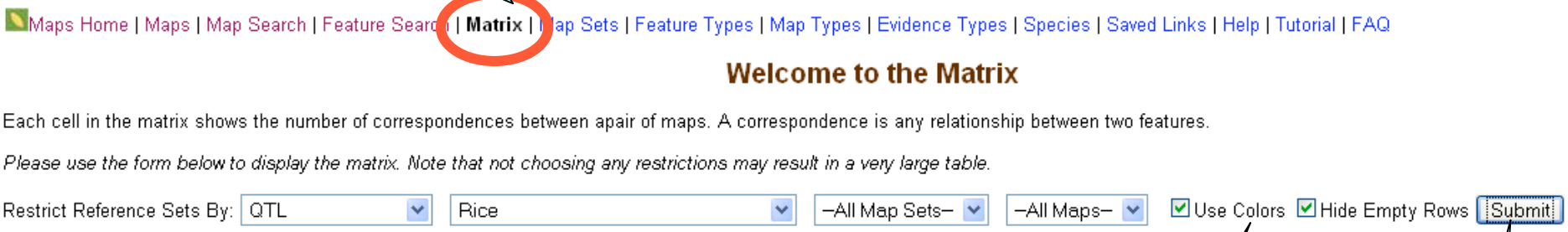
Feature Name	Feature Type	Species	Map Set	Map Name	Position	Aliases		
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	0.00-7.80 cM	AQES032, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cM	AQEU025, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cM	AQEU026, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cM	AQES050, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	33.90-40.00 cM	AQES017, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	19.50-62.00 cM	AQES018, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	62.00-71.90 cM	AQEU027, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	4	79.80-126.10 cM	AQES051, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	24.30-34.40 cM	AQEU029, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	24.30-34.40 cM	AQEU028, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	24.30-34.40 cM	AQEU030, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	9.10-24.30 cM	AQES069, TO:0000327	[View on Map]	[Feature Details]
BIOMYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	6	9.10-24.30 cM	AQES019, TO:0000327	[View on Map]	[Feature Details]
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	0.00-7.80 cM	AQES030, TO:0000388	[View on Map]	[Feature Details]
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	0.00-7.80 cM	AQES047, TO:0000388	[View on Map]	[Feature Details]
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	28.50-29.20 cM	AQEU012, TO:0000388	[View on Map]	[Feature Details]
FRGYLD	QTL	Pearl Millet	IGER H77/BRLT QTL 2002	2	33.90-40.00 cM	AQES013, TO:0000388	[View on Map]	[Feature Details]
			IGER H77/BRLT QTL 2002	3	21.30-22.90 cM	AQES066, TO:0000	[View on Map]	[Feature Details]
			IGER H77/BRLT QTL 2002	4	0.00-19.50 cM	AQES067, TO:0	[View on Map]	[Feature Details]
			IGER H77/BRLT QTL 2002	4	0.00-19.50 cM	AQES014, TO	[View on Map]	[Feature Details]
			IGER H77/BRLT QTL 2002	4				

Select to view the "Map Set Info" *(see slide 40)*

Select to view this feature highlighted on a map *(as in slide 15)*

Correspondence Matrix

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



Options

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

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

	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		May 2006	May 2006	Oct 2004	FPC Oct 2004	OA_AB May 2006	
AGEBC KDM105/ RI QTL 2000	301(29)	291(29)	14 (12)	19(14)	19(14)	208(26)	-	-	-	68	68	64	3	-	
Aberdeen Bala/Az TL 2002	390(23)	428(26)	9(5)	9(5)	9(5)	173(22)	-								
Brazil BG90-2/RS 6 QTL 2002	132(11)	132(11)	28 (10)	32(11)	32(11)	-	-								
CAU IRAT109/YUEFU QTL 2004	366(26)	354(26)	30 (14)	31(15)	31(15)	204(19									
CIRAD IR64/Azu DH QTL 2003	651(34)	790(42)	-	-		302(25)	76	87	76(10)	325	328	256	103	108	
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 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)	-	-	-	-	-	-	-	-	

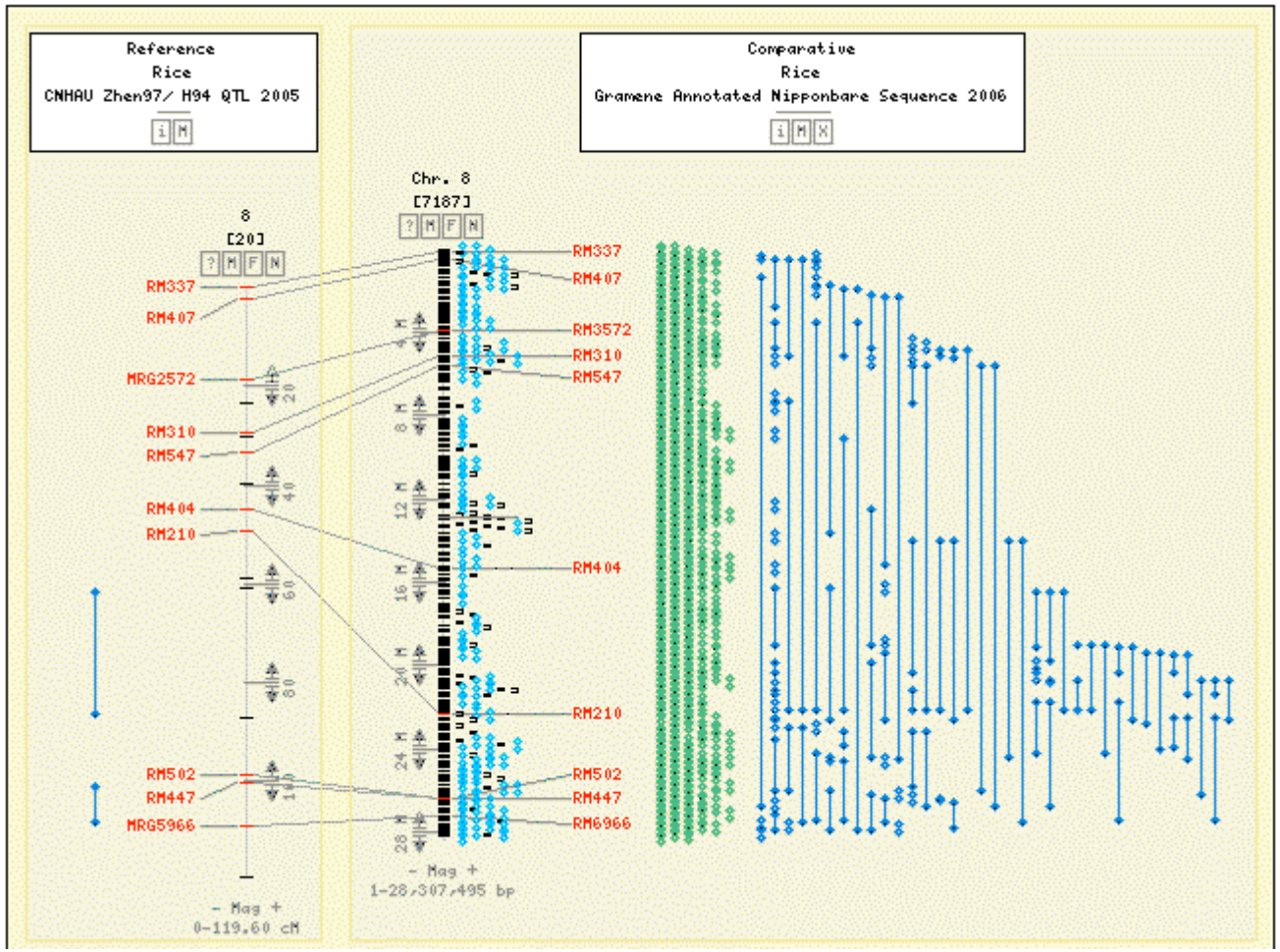
Two-MapSet Matrix

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		
		12	-	-	-	-	-	-	-	-	-	-	-	20(1)	12		
										Chr. 8	Chr. 9	Chr. 10	Chr. 11	Chr. 12			
										re Sequence 2006							

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

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

There are207 map sets.

Map Set Info

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

Restrict by Species: --All Species--

Restrict by Map Type: --All Map Types--

Submit

Items 1 to 25 of 207. Page 1 of 9 | Next

Map Set Name:	**BGI 93-11 Sequence 2005**				[Show Only This Set]
Abbreviated Name:					[Download Map Set Data]
Accession ID:	bgi2005				[View Map Set In Matrix]
Species:	Oryza sativa (indica cultivar-group) (Oryza sativa (indica cultivar-group))				[View Species Info]
Map Type:	Sequence				[View Map Type Info]
Map Units:					
Published On:	N/A				
Maps:	Chr. 1	[Map Viewer]	[Map Details]	[Matrix Viewer]	[Download Map Data]
	Chr. 2	[Map Viewer]	[Map Details]	[Matrix View	[Download Map Data]
	Chr. 3	[Map Viewer]	[Map Details]	[Matrix Vi	[Download Map Data]
	Chr. 4	[Map Viewer]	[Map Details		[Download Map Data]
	Chr. 5	[Map Viewer]	[Map Detai		[Download Map Data]
	Chr. 6	[Map Viewer]	[Map Detai		[Download Map Data]

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 | FAQs

There are 25 feature types

Select a single feature

Feature Type Info

Display: --All Feature Types-- Submit

Items 1 to 25 of 25.

Feature Type:	**AFLP**
Accession ID:	aflp
Color:	mediumseagreen
Shape:	line
Description:	Amplified Fragment Length Polymorphism
	[Search for All Features of This Type]
Feature Type:	**Br**
Accession ID:	
Color:	
Shape:	
Description:	Interval between chromost
	[Search fo
Feature Type:	
Accession ID:	
Color:	
Shape:	
Description:	

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.

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).

Map Type

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

Map Type Info

Display: --All Map Types-- Submit

Items 1 to 7 of 7.

Map Type:	**Bin**
Accession ID:	bin
Map Units:	bins
Is Relational Only:	No
Appearance:	lightgrey box
Description:	Bins are arbitrarily-defined segments delimited by two fixed core markers. A bin includes all loci from the leftmost or top core marker to the next core marker.

[Show All Map Sets Of This Map Type]

Map Type:	**Deletion**
Accession ID:	deletion
Map Units:	arm fraction
Is Relational Only:	No
Appearance:	lightgrey box
Description:	The deletion-based cytogenetic map of an organism is a type of low-resolution physical map. It collection) of mutant lines containing sub-chromosomal deletions and a reference wild-type li 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**

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 | FAQs

Evidence Type Info

Display: --All Evidence Types-- Submit

Items 1 to 18 of 18.

	Marker Identity
	ID
	1
	lightblue
	e marker (i.e., probe, primer, sequence, etc) was used to map the corresponding features.
	Wheat EST Breakpoint Interval
	wheat-est-bi
	3
	lightblue
	Maize bin marker
	bin_marker
Rank:	2
Line Color:	lightblue
Description:	Marker assigned to a maize bin by MaizeGDB.
Evidence Type:	**RFLP Sequence**
Accession ID:	rflp_sequence
Rank:	2
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 | FAQs

Species Info

Display: --All Species--

Gramene currently has maps for 28 species.

List of mapsets may be filtered by individual species.

Items 1 to 25 of 28. Page 1 of 2 | Next

African rice [Show Only This Species]

Oryza glaberrima

Accession ID:

Map Sets (4): [Show Map Sets

Physical Maps

Curated FPC Chr OG_BB Feb 2006
Curated FPC OG_BB Feb 2006
FPC Chr OG_BB Jun 2007
FPC OG_BB Jun 2007

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

Common Name: **Barley** [Show Only This Species]
Full Name: Hordeum vulgare
Accession ID: barley
Map Sets (13): [Show Map Sets From This Species]

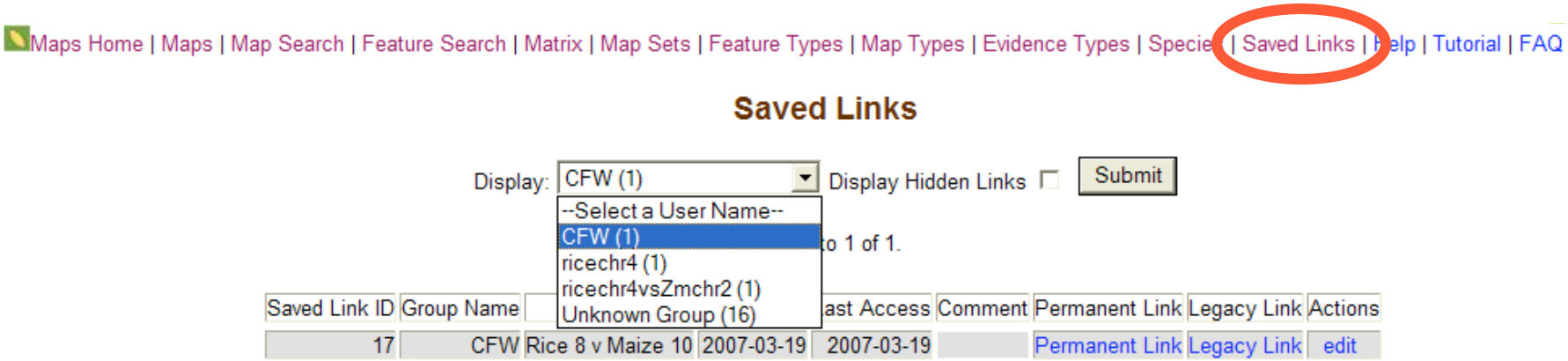
Genetic Maps

Barley consensus 2003	[View Map Set Info]	[View Map Set In Matrix]
NABGMP SxM 1993	[View Map Set Info]	[View Map Set In Matrix]
Barley consensus 1996	[View Map Set Info]	[View Map Set In Matrix]

Gramene has over 100 mapsets for rice.

Follow links for map information

Saved Links



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 | FAQs

Gramene Maps and CMap Database Help Document

A. Maps Concepts
B. Searching/Browsing
C. Comparing and Customizing Maps
D. Other Help

Maps Help Menu

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.

Maps Concepts

A. Maps and Map Sets

In Maps, a map is a linear array of interconnected features. This map, or a single contig for physical maps. Related maps are grouped into map sets, such as the set of linkage groups produced by a genetic mapping study. For more information about the map sets contained in the database, visit the Map Set Info page.

B. Reference and Comparative Maps

In Maps, you can use the CMap tool to compare maps. (For more information on CMap see http://www.gmod.org/cmap.) To set up a comparison, first select a reference map set, then a reference map. This serves as the basis for any comparisons that will be made. Once the reference map image has been rendered, select one or two comparative maps. These comparative maps may be added to both the left and the right of the reference map. Additional maps may be added for as long as valid comparisons are available.

C. Features and Feature Types

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

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: Get Adobe Reader | Office PowerPoint viewer

Download software for viewing tutorials.

Link to any of the Gramene tutorials.

Maps Home | Maps | Map Search | Feature Search | Matrix | Map Sets | Feature Types | Map Types | Evidence Types | Species | Imported Links | Help | Tutorial | FAQ

FAQ

GRAMENE *Help*

Documents

Search | Genomes | Species | Download | Resources | About | Help | Feedback

Search FAQ

Use Feedback to ask a question

Maps and CMap

- Why did you change the name of this module from "CMap" to "Maps"?
- Is there a tutorial or help section on how to use the Maps module and the comparative map viewer?
- What are some examples of scientific queries that can be answered using the comparative map viewer?

  In Maps, you can determine the location of a particular trait or marker and to which grass species they have been mapped. The comparative map ... user to draw comparisons between different maps. These maps can be of different type (e.g., genetic and physical) and from different species (e.g., rice and maize). Users can view where genes, markers, and QTL are located in one grass species compared to where they ... examine the colinearity of a particular region in one species with another, or infer which linkage group in one spe... species. Users can also determine which maps are the best to compare to each other using the maps Matrix (http://ww... mber of correspondences between maps.

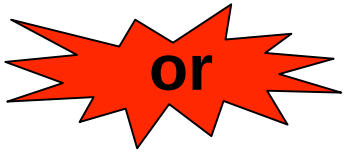
Click on a question or FAQ section to open and close the information..

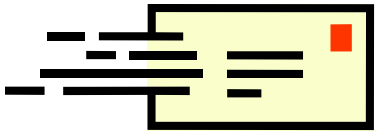
- Does Maps run on a database?
- Is CMap available for local installation?
- Where does Gramene get its map information from?

  Gramene maps come from a number of sources including published data, other genome databases and direct contributions. In addition, Gramene generates its own rice sequence map. This is based on the TIGR assembly for the rice genome and integrates markers, ESTs, proteins and other information from rice and other crops.
- What is the difference between a map set and a map?
- What are the type of maps that Gramene has?
- Can I view a list of all the maps that Gramene has?
- Which species does Gramene have maps for?
- How do I see a list of various maps from a given species?
- What does the label [obsolete] imply when located next to a map set name?
- What is the Matrix and how can it be useful?
- What is the difference between a feature and a marker?
- Some features in the Map are classified as Interpolated Genes. How is this done?
- What map sets do you use to curate and display interpolated genes?

Contact Gramene

Use the feedback button, located at the top of every page, to provide feedback or to ask questions about Gramene.





Email Gramene at gramene@gramene.org