

# Gramene Workshop

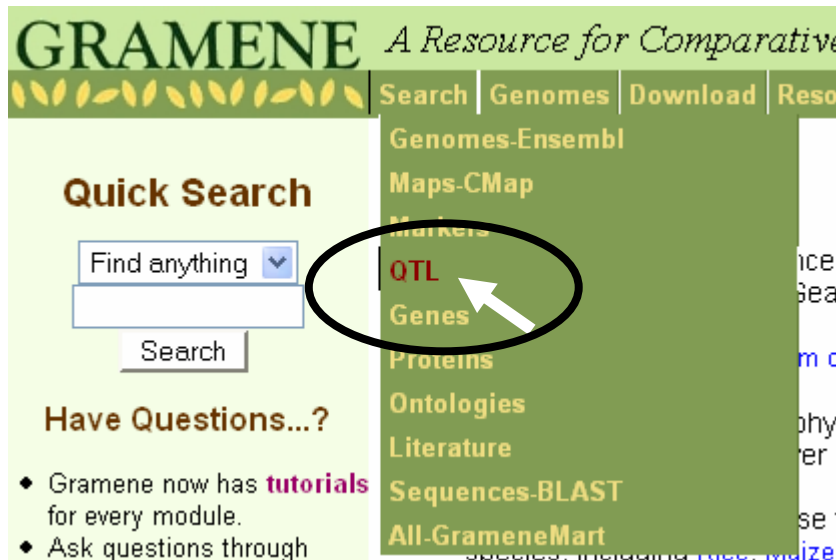
2/25/06

## Hands-On Exercise: Grain Yield after Milling

Begin on the web at [www.gramene.org](http://www.gramene.org)

### ➔ 1) Conduct a trait search for milling yield.

(At Gramene, the QTL database is searchable by trait. On the Gramene home page point your mouse to 'Search' on the menu. Click on 'QTL' in the dropdown box. Type "milling yield" in the quick search box and click submit).



You will find out that there are no results for this trait.

A screenshot of the 'QTL Search' results page. The page has a header 'QTL Search' and a sub-header 'Search by Trait Category:'. Below this are several links: 'Abiotic stress', 'Anatomy', 'Biochemical', 'Biotic stress', 'Development', 'Quality', 'Sterility or fertility', 'Vigor', and 'Yield'. A section labeled 'OR' contains three input fields: 'Search for \*:' with the text 'milling yield', 'Search in:' with a dropdown menu showing '-All Fields-', and 'Species:' with a dropdown menu showing '-All Species-'. To the right of these fields are 'Submit' and 'Reset' buttons. Below the input fields is a line of text: '\* eg, development, vegetative\*, VGTM, QTL\*, CQA11. Or view help.' At the bottom of the page, the text 'Sorry, no QTL entries have been found.' is displayed in a large, bold, brown font and is circled with a black oval.

The QTL search for "milling yield" came up empty, therefore you have two options: Search the whole database for information on it (#2), or go to "Ontologies" to find a better term (#3).

### ➔ 2) Search all of Gramene for "milling yield".

(Use the box at the top of the page for a search of the whole database. Type “milling yield” in the ‘find anything’ search box at the top right, and click ‘search’.)

Results have turned up in the literature and other publications. Since “milling yield” is in the title of the first literature database result, it looks like a good match.

→ a. **Select that article on milling yield and get data on published results.** (Click on ‘More info’)

### Search the Gramene Database

Results: [Literature](#) | [Newsletter & Docs](#)

Search for (object name, identifier, or keyword):

Database:  ☒ Include Rice Genetics Newsletter & Gramene Documentation

[Gramene Mart](#)  
[Blast search](#)

#### Literature Search Result

Items 1-2 of 2      Page 1 of 1      Select page:

- [Mei-H, Luo-L, Guo-L, Wang-Y, Yu-X, Ying-C, Li-Z](#)  
Molecular mapping of QTLs for rice **milling yield** trait. [\(More info\)](#)  
Acta-Genetica-Sinica, 2002, vol.29, pp791-797
- [Martinez-Bustos-F, Delgado-L-L, Victorio-M-G, Morales-S-E](#)  
Characterization of yellow rice and development of instant flours by hydrothermal process [\(More info\)](#)  
Archivos latinoamericanos de nutricion, 1997, vol.47, pp50-56

Items 1-2 of 2      Page 1 of 1      Select page:

#### Rice Genetics Newsletter & Documentation Search Result

69 matches in Rice Genetic Newsletter & Documentation

Score	Document
1000	<a href="#">Registration of Rice Varieties1</a> <a href="#">Registration of 'Arkrose' rice</a> <a href="#">Registration of 'Bluebonnet' rice</a> <a href="#">Registration of 'Bluebonnet 50' rice</a> <a href="#">Registration of 'Blue Rose' rice</a> <a href="#">Registration of 'Calrose' rice</a> <a href="#">Registration of 'Century Patna 231' rice</a> <a href="#">Registration of 'Colusa' rice</a> <a href="#">Registration of 'Fortuna' rice</a> <a href="#">Registration of 'Improved Bluebonnet' rice</a>

You should look to see what ‘associations’ there are in the database with this article. There are 3 QTL associated with this article.

→ b. **Select the QTL for more information on them** (click on ‘QTLs (3)’ ).

Search result	
Reference ID	7776
Title	Molecular mapping of QTLs for rice milling yield traits.
Source	Acta-Genetica-Sinica , 2002, 29, pp.791-797
Authors	<a href="#">Mei-H, Luo-L, Guo-L, Wang-Y, Yu-X, Ying-C, Li-Z</a>
Abstract	QTLs of three milling yield traits, including brown rice (BR, %), milled rice (MR, %) and head milled rice (HR, %) ,were mapped using a set of 212 Lemont/Teging RI population, an RFLP linkage map with 182 markers and a mixed model approach (QTLMapper V1.0). The population showed continuous distributions with transgressive segregation on both sides for all traits while HR had a wider variation than BR and MR. One and four main effect QTLs were detected for MR and HR. Two QTLs for HR (QHR6 and QHR7) had large additive effects. Twelve five and sixteen pairs of digenic epistatic loci were associated with BR, MR and HR respectively. Epistasis was more important than main effect QTLs according to the mapping result. A complex relationship was observed for epistatic pairs mapped in same trait or among different traits by sharing intervals.
Cross-reference	Not available
Associated Data	<a href="#">QTLs (3)</a>

**Please note:**  
To request reprints, please contact the authors or the source/journal website. Due to copyright issues Gramene does not distribute reprints.

This will bring up a table that lists those three QTL, and following those links will provide more

information.

- c. Select the first QTL to get more information. (Click on 'AQL001'.)

Reference ID	7776		
Title	Molecular mapping of QTLs for rice milling yield traits.		
Associated QTL	Accession	Published Symbol	
	AQL001	QMr12	
	AQL002	QMr2	
	AQL004	QMr6	

You will be able to select the link to learn the trait name (milled rice ratio) and to view this QTL on a map. Note that there are synonyms. The trait is called “Milled Rice Ratio”.

### QTL Detail "AQL001"

QTL Accession ID	AQL001
Species	Rice (GR_tax:013681)
Published Symbol	QMr12
Trait Symbol	MR
Trait Name	milled rice ratio
Trait Ontology Accession	TO:0000144
Trait Synonyms	milled rice milled rice percentage
Trait Category	Quality
Linkage Group	12
Map Position	Rice-TAMU Lem/Teq RI QTL 1995-12 (15.00-15.00 cM) [ <a href="#">View On Map</a> ]
Comments	Trait was related with grain quality.
DBXRefs	Gramene Literature 7776

The second option to your lack of QTL search for “milling yield” is to determine if you need another ‘keyword’. Perhaps others used different vocabulary (ontologies) to describe the trait. You should ...

- 3) Conduct a search for “milling yield” in the ontologies database in order to look for other terms to consider.

*On the Gramene navigation bar point your mouse to ‘Search’ on the menu, then click on ‘Ontologies’ in the dropdown box. Type “milling yield” in the quick search box and select ‘Trait Ontology’ to narrow your search. Click ‘Search’.)*

- a. Try a different term. Conduct a search for “milling ” in the ontologies database.  
→ b. Try a different term. Conduct a search for “mill ” in the ontologies database.

Searches for “milling yield” and “milling” come up negative, but shortening our search term to simply “mill” gives us 14 results. (milled, millimeters, millet, etc), but only one – milled rice, synonym milled rice ratio – seems to be a match for milling yield.

Type ID or keyword to search

select ontology (optional)

mill

☐ Gene (GO)
☐ Plant structure (PO)
☐ Growth stage (GRO)
☒ Trait (TO)
☐ Environment (EO)
☐ Taxonomy (GR\_tax)

Search

Clear

[e.g. [flower](#) or [TO:0000303](#)]

Summary for mill

Items 1 to 14 of 14

#	Term Accession	Aspect	Term Name	Synonym	Definition
1	<a href="#">TO:0000024</a>	Trait	ligule length	LgL, LIGLG.	The actual measurement of ligules measured in <b>millimeters</b> from the base of the collar to the tip.
2	<a href="#">TO:0000132</a>	Trait	basal internode diameter	BAINDIA, DBI.	Actual measurements in <b>millimeters</b> from the outer diameter of the culms at the basal portion of the main culm. Sample size = 3
3	<a href="#">TO:0000134</a>	Trait	alkali digestion	AlkD, ALKDIG.	Is an indirect measure of gelatinization temperature. Observed by placing six <b>milled-rice</b> kernels in 10ml 1.7% KOH in a shallow container and arrange them so that they do not touch. Let them stand for 23hrs at 30degC temperature and score for spreading. Measure for Alkali digestion is inversely proportional to the gelatinization temperature, e.g. if alkali digestion is low, the gelatinization temperature is high.
4	<a href="#">TO:0000144</a>	Trait	<b>milled rice</b>	<b>milled rice ratio, MR.</b>	No Definition Available
5	<a href="#">TO:0000149</a>	Trait	seed width	kernel plumpness, kernel width, percentatge of plump kernels, plump grain, plump seed, SDWD.	Determined by the actual measurement of width in <b>millimeters</b> as the distance across the seed (with hull).
6	<a href="#">TO:0000222</a>	Trait	head rice	head <b>milled</b> rice, head rice ratio, HEADR.	No Definition Available
7	<a href="#">TO:0000266</a>	Trait	chalky endosperm	chalkiness of endosperm, Clk.	Defines a representative <b>milled</b> sample for the degree (extent) of chalkiness that will best describe the sample with respect to (a) white belly, (b) white center, (c) white back

→ c. Select the Trait Accession for ‘milled rice ratio.’ (Click on “TO:0000144”)

Ontologies show relationships between terms, and this reflects that milled rice (ratio) is an example of seed quality, which is an example of a quality trait. There are 8 QTL that are associated with this trait, which we will come back to in a minute.

First, however, you should know that sometimes it can be helpful to explore related terms so that we can consider other terms to search for.

→ d. Select the parent term of milled rice. (Click on “seed quality (TO:0000162).”)

Summary for TO Term: <i>milled rice</i> (TO:0000144)	
Term Name	milled rice
Synonym	milled rice ratio, MR.
Aspect	Trait
Derivation	<ul style="list-style-type: none"> <li>• <a href="#">trait ontology (TO:0000387)</a> #10679 <ul style="list-style-type: none"> <li>◦ [i] <a href="#">quality trait (TO:0000597)</a> #963 <ul style="list-style-type: none"> <li>▪ [i] <a href="#">seed quality (TO:0000162)</a> #907 <ul style="list-style-type: none"> <li>▪ [i] <b>milled rice</b> (TO:0000144) #8</li> </ul> </li> </ul> </li> </ul> </li> </ul>
Parent Term (1)	<ul style="list-style-type: none"> <li>• [i] <a href="#">seed quality (TO:0000162)</a></li> </ul>
Total Number of Annotations:	8 objects, 8 associations
QTL:	<b>8 oryza sativa QTL</b>

More terms are revealed that are also associated with seed quality. Many of these will also affect milling yield, so in further research you may wish to explore some of these other options.

- ➡ 4) For now, go back to “milled rice (TO:0000144)” and select the link to the 8 associated QTL.  
(Use the Browser “back” button, or simply click on ‘milled rice’) click on ‘8 oryza sativa QTL.’)

- [trait ontology \(TO:0000387\)](#) #10679 +
  - [i] [quality trait \(TO:0000597\)](#) #963 +
    - [i] [seed quality \(TO:0000162\)](#) #907
      - [milled rice \(TO:0000144\)](#) #8
      - [i] [head rice \(TO:0000222\)](#) #17
      - [i] [seed viability \(TO:0000345\)](#) #130 +
      - [i] [brown rice ratio \(TO:0000375\)](#) #4
      - [i] [cracked grain percentage \(TO:0000381\)](#) #14
      - [i] [grain color \(TO:0000385\)](#) #0
      - [i] [grain size \(TO:0000397\)](#) #0
      - [i] [grain thickness \(TO:0000399\)](#) #0
      - [i] [grain width \(TO:0000402\)](#) #19
      - [i] [seed shattering \(TO:0000473\)](#) #21
      - [i] [seed shape \(TO:0000484\)](#) #212 +
      - [i] [seed color \(TO:0000486\)](#) #40 +
      - [i] [seed composition based quality trait \(TO:0000488\)](#) #220 +
      - [i] [endosperm quality \(TO:0000587\)](#) #58 +
      - [i] [seed density \(TO:0000612\)](#) #79
      - [i] [groat percentage \(TO:0000613\)](#) #36
      - [i] [crushed grain percentage \(TO:0000618\)](#) #2
      - [i] [seed fertility \(TO:0000639\)](#) #1
      - [i] [cooking or brewing quality \(TO:0000667\)](#) #135 +
      - [i] [bran percentage \(TO:0000672\)](#) #6
      - [i] [starch yield \(TO:0000697\)](#) #14

You will receive a table with information about these 8 QTL.

- ➡ 5) Learn how these QTL were identified. (Click on ‘IAGP’ in the “Evidence” column.)

Term <i>milled rice</i> ( TO:0000144 ) Associations						
Items 1 to 8 of 8						
Term Name	Object Type	Object Accession ID	Object Symbol	Object Name	Object Synonyms	Object Species
milled rice	QTL	AQFU013	MR	milled rice ratio	mr5	Oryza sativa
milled rice	QTL	AQEE012	MR	milled rice ratio		Oryza sativa
milled rice	QTL	AQFU049	MR	milled rice ratio		Oryza sativa
milled rice	QTL	CQR3	MR	milled rice ratio		Oryza sativa
milled rice	QTL	AQL001	MR	milled rice ratio	QMr12	Oryza sativa
milled rice	QTL	AQFU014	MR	milled rice ratio	mr7	Oryza sativa
milled rice	QTL	CQR2	MR	milled rice ratio		Oryza sativa
milled rice	QTL	AQFU048	MR	milled rice ratio		Oryza sativa
						Evidence
						IAGP
						IAGP
						IAGP
						IAGP
						IAGP
						IAGP
						IAGP

The evidence for these QTL being associated with milled rice ratio is strong, based on experiments showing an association between the QTL and the phenotype (*see below*) (as opposed to another form of evidence, such as a non-traceable author statement.)

### IAGP *\*inferred by association of genotype from phenotype*

- Polymorphism or segregation of genetic markers eg. isozymes, RFLPs (Random Fragment Length Polymorphism), RAPDs (Random amplified polymorphic DNA), AFLPs (Amplified Fragment Length Polymorphism), SNPs (Single Nucleotide Polymorphisms), Microsatellite markers or SSR (Simple Sequence Repeats), TD (Transposon Display).
- Polymorphism or segregation of physical markers eg. FISH, centromeric, heterochromatic regions, chromosomal banding patterns.
- Detection of polymorphisms in segregating plant material derived from Bi-parental crosses eg. F2 lines, F3 families, Back cross populations, viz., BC1, BC2 etc. ; Doubled Haploid lines (DH), Recombinant Inbred Lines (RIL).
- Detection of polymorphisms in genetic stocks, e.g., Near Isogenic Lines (NIL), Introgression Lines (IL), Radiation Hybrids (RH), Cytogenetic Stocks (CG), i.e., trisomics, aneuploids, etc.

➡ 6) **For this exercise, select AQFU049.** (In most cases you may wish to review all 8 of these QTL to learn what data is known about them.)

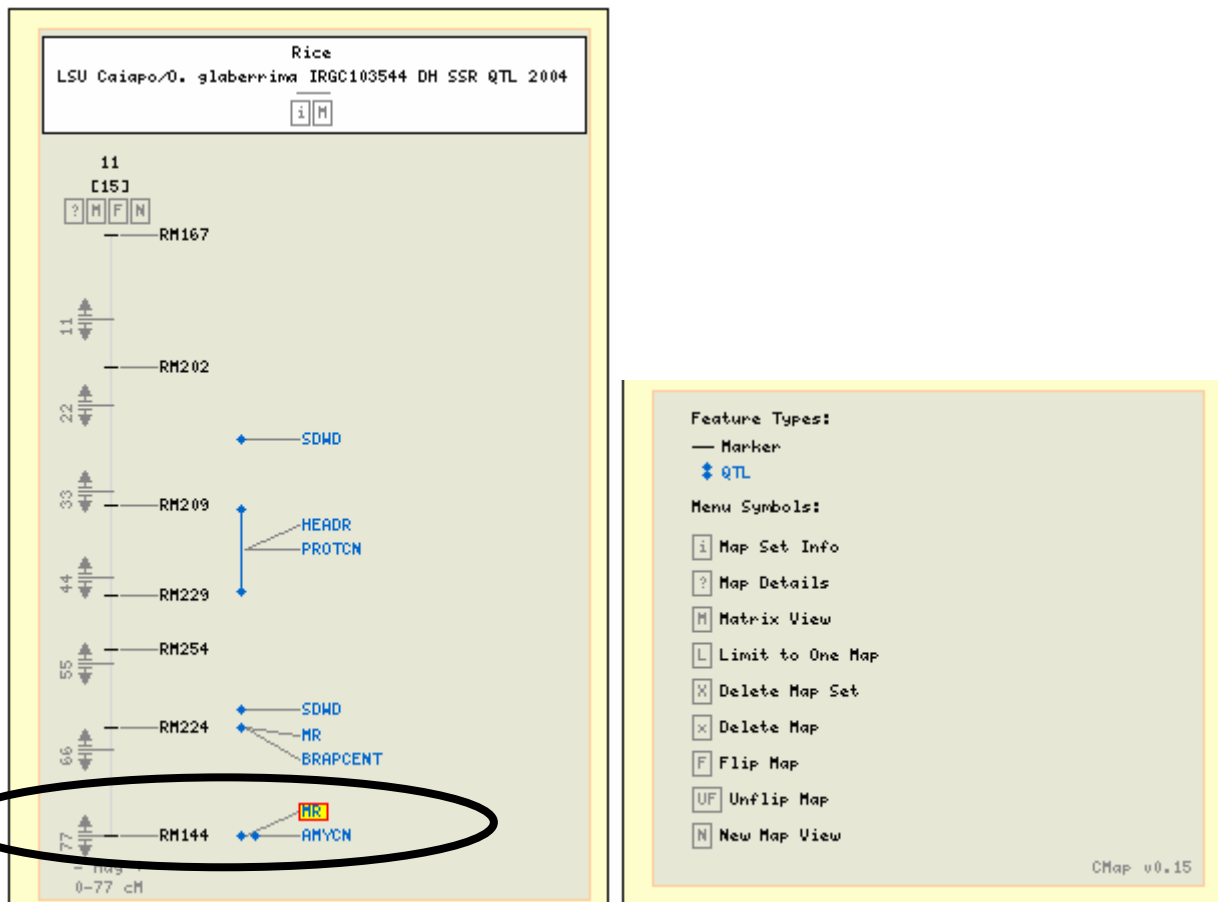
Once again you can see that this is a rice QTL for milled rice ratio. You can also learn that it is on chromosome 11. If you would like more reference information for this QTL you should select the literature reference link, since it is different than the previous article we reviewed.

a. **View the map for “AQFU049”** (Click on “View on Map”)

#### QTL Detail "AQFU049"

QTL Accession ID	AQFU049
Species	Rice (GR_tax:013681)
Published Symbol	NA
Trait Symbol	MR
Trait Name	milled rice ratio
Trait Ontology Accession:	TO:0000144
Trait Synonym(s)	milled rice milled rice percentage
Trait Category	Quality
Linkage Group	11
Map Position	Rice-LSU Caiapo/IRGC103544 QTL 2004-11 (77.00-77.00 cM) <a href="#">View On Map</a>
Comments	This locus was found to have significant interaction with another locus, AQFU048.
DBXRefs	<a href="#">Gramene Literature 8212</a>

Notice that the QTL is highlighted as “MR”, and is located near Marker RM144. You may also find it interesting to learn that it is also co-located with the QTL AMYCN, which is a QTL for amylose content.



Clicking on any of the features on the map will link you to the detail page for that feature.

## ➡ 7) View “RM144” marker detail information. (Click on ‘RM144’)

We can see that this marker has been mapped to several different maps and map types. However, you are still in the maps module (*look at the module heading to know which module you are in*) and you want to get to the markers module.

- ➡ a. Go to the markers module detail page. (*Select the first “View Oryza sativa SSR marker “RM144” in Marker DB” to view the marker in the markers module.*)

## Feature "RM144"

Feature Name: RM144

Aliases: N/A

Accession ID: alg2004a-97

Feature Type: Marker

[\[ View Feature Type Info \]](#)

Map: Rice-LSU Caiapo/O. glaberrima IRGC103544 DH SSR QTL 2004-11

[\[ View Map Details \]](#)

Start: 77.00 cM

Stop: 77.00 cM

Cross-references: [\[ View Marker Details \]](#)

[\[ View Oryza sativa SSR marker "RM144" in Marker DB \]](#)

[\[ View Oryza sativa SSR marker "RM144" in Marker DB \]](#)

[\[ View "RM144" in Genome Browser \]](#)

Correspondences						
Feature	Map	Map Type	Aliases	Evidence Type	Actions	
RM144	Rice-Class I SSR (93-11) 2005-11	Sequence	AUT27367, RM27367	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Class I SSR (IRGSP) 2005-11	Sequence	AUT27367, RM27367	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Class I SSR (TIGR) 2005-11	Sequence	AUT27367, RM27367	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-I-Map (FPC) [OBSOLETE]-ctg248	Physical	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Cornell SSR 2001-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Cornell SSR 2001-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-IRMI 2003-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-IRMI 2003-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>

You are now in the Markers Database. (look at the module heading)

## Markers Search

Marker Name:  Marker Type:  Species:

E.g., "AG020731,AG020732", "rm\*", Oat RFLP markers like "CDO\*", or view [help](#).



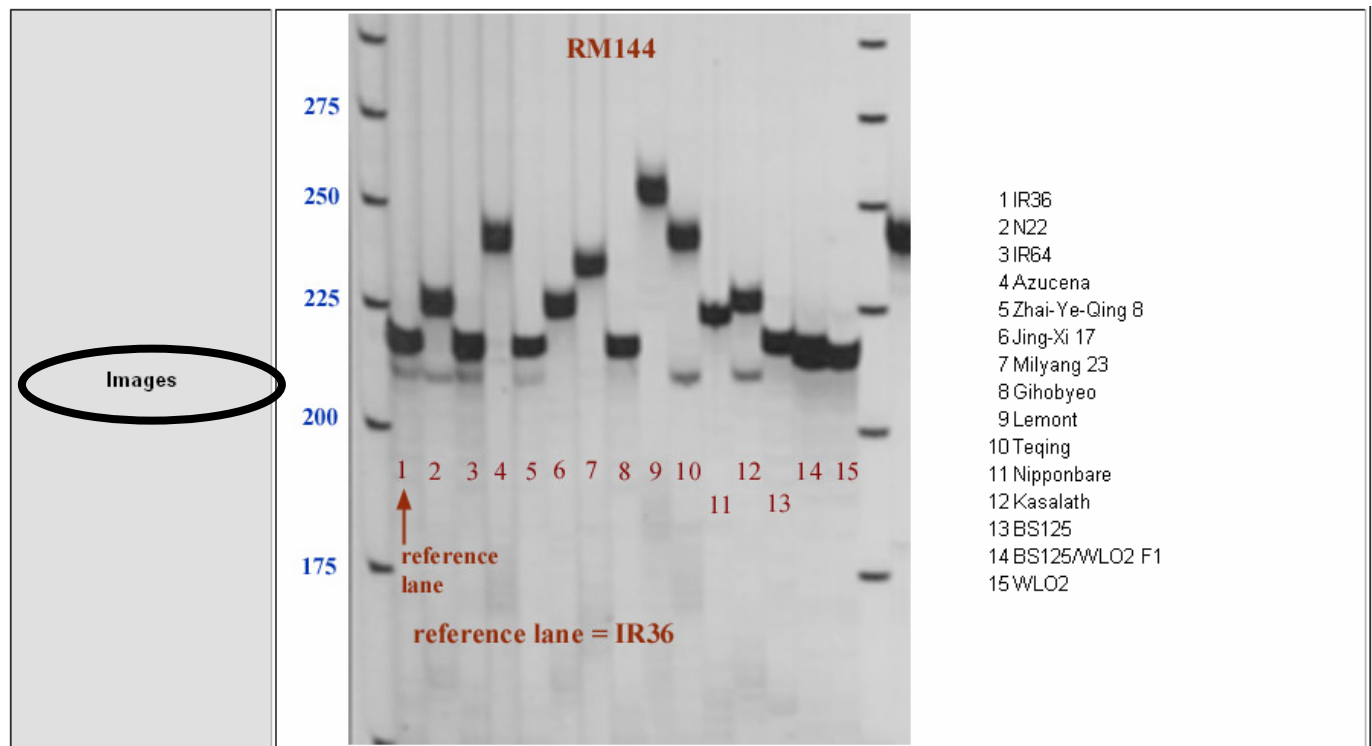
### 8) Notice the following:

- a. **Forward and Reverse Primers** – these are the primary defining characteristics of the SSR markers that make it unique. You need to know this if you want to synthesize the primer for yourself.
- b. **Anneal Temperature** – need to know this to program the PCR
- c. **Expected PCR Product size** – approximate size of the band that you should expect to see
- d. **Genome Positions** – click to see marker displayed in the genome browser.
- e. **Images** – May or may not be available. The images gives a better idea of the range of band sizes on representative germplasm. If you don't see a band in the expected size you may need to adjust your PCR conditions.



[View Rice SSR marker "RM144"](#)

Marker ID	6083									
Marker Name	RM144									
Synonyms (1)	X67711 (GENBANK_ACCESSION)									
Type	SSR									
Species	Oryza sativa (Rice)									
Germplasm	Nipponbare									
Library	UNKNOWN									
Description										
Mappings (12)	Species	Map Type	Map Set	Map	Name	Start	Stop	CMap Links		
	Oryza sativa (Rice)	Genetic	IRMI 2003	11	RM144	117.3		<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	M202/IR50 UCD QTL 2003	11	RM144	91.5	91.5	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	Cornell IR64/Azu DH QTL 2001	11	RM144	123.2	123.2	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	IRRI RD23/Olong F2 QTL 2003	11	RM144	175	175	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	TKU Integrated QTL 2002	11	RM144	131.5	131.5	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	CNZU IR1552/Azu RI QTL 2003	11	RM144	17.6	17.6	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	Genetic	Cornell SSR 2001	11	RM144	123.2		<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	CNZU IR1552/Azu RI QTL 2004	11	RM144	17.6	17.6	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	QTL	NDSU EM93/SS18 BC QTL 2004	11	RM144	160.3	160.3	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	Physical	I-Map (FPC) [OBSOLETE]	ctg248	RM144	3	43	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
	Oryza sativa (Rice)	Sequence	GR TIGR Assm IRGSP Seq 2005	Chr. 11	RM144	28,158,704	28,158,928	<a href="#">View on Map</a>	<a href="#">Feature Details</a>	
Oryza sativa (Rice)	Sequence	GR TIGR Assm IRGSP Seq 2005	Chr. 11	RM144	28,158,704	28,158,928	No CMap Feature Accession			
Correspondences	No correspondences.									
Clone										
Repeat Motif	(ATT)11									
Forward Primer	TGCCCTGGCGCAAATTTGATCC									
Reverse Primer	GCTAGAGGAGATCAGATGGTAGTGCATG									
Anneal Temperature	55									
Expected PCR Product Size	237									
Remarks										
Sequence Source										
Genome Positions	RM144 (89706) RM144 (89703)									
Database Cross-references	Gramene Literature	Temnykh-S Park-W-D Ayres-N-M Cartinhour-S Hauck-N Lipovich-L Cho-Y-G Ishii-T McCouch-S-R, <i>Mapping and genome organization of microsatellite sequences in rice (Oryza sativa L.)</i> , <i>Theoretical and applied genetics</i> , 100, 2000, pp. 697-712								



➡ 9) **Return to the Cmap view in #6 (click the browser's 'Back' button two times.)**

➡ 10) **Compare this map to a genetic map to see what other features may be in the same region.**  
*(Genetic maps will give a general order to surrounding features, but do not offer the exact sequence and distance. Underneath the map select 'Show Reference Menu.' We will put the comparison map on the right, so under the appropriate heading select the 'Select Map Set' menu to open a list of maps with comparisons. Click on "Genetic: Rice – Cornell SSR 2001 [14]. If there were more than one chromosome with correlations you would need to select the ones you wanted to compare. In this case, the only comparisons (14 of them) are on chromosome 11. Click on 'Redraw Map.)*

Save Link\*

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

☐ Hide Reference Menu

Ref. Species: Rice (Oryza sativa)

Ref. Set: QTL : Rice - LSU Caiapo/IRGC103544 QTL 2004

☐ Hide Comparison Menu

Ref Map Start:

Ref Map End:

Current Map Sets: Rice-LSU Caiapo/IRGC103544 QTL 2004 (Ref.)

Min. No. Correspondences for Left Slot:

Min. No. Correspondences for right Slot:

Min. No. Correspondences for the menu:

Comparative Maps (Left):

Comparative Maps (Right):

Select Map Set

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

☐ Show Options Menu

☐ Show Additional Options Menu

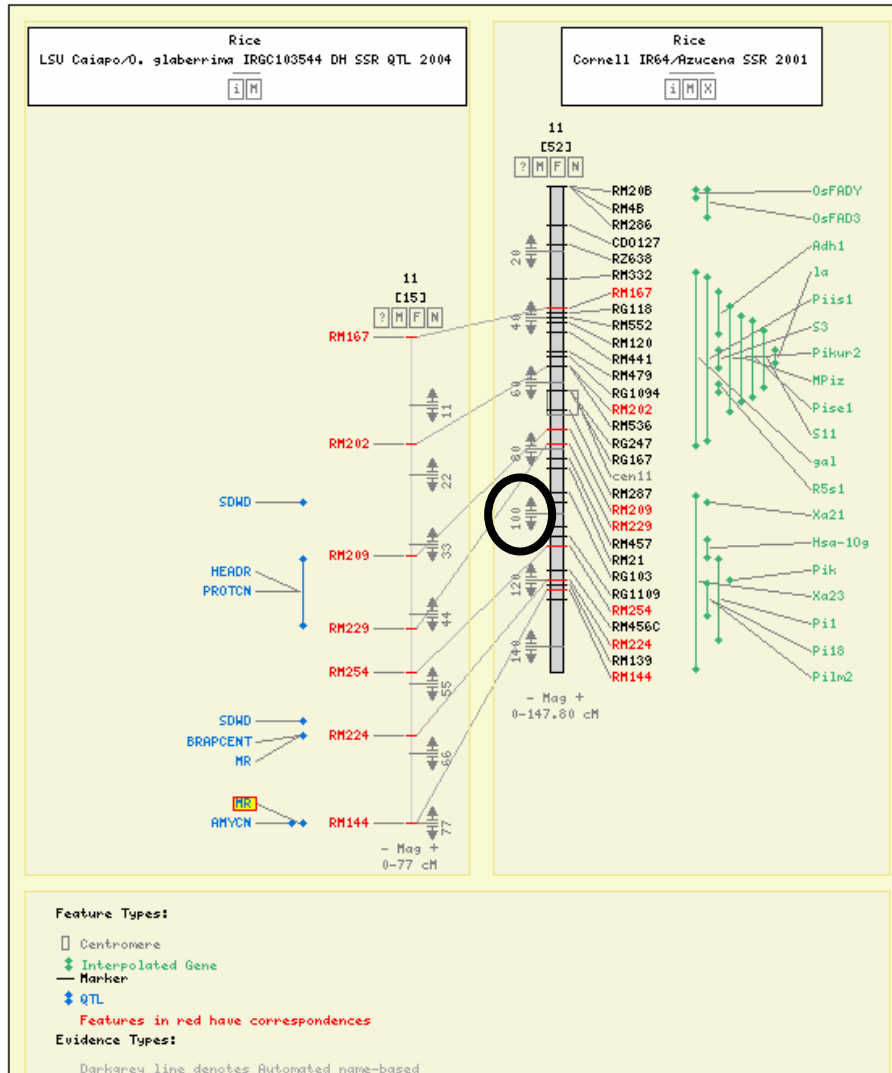
Select Map Set

- Sequence : Rice - Class I SSR (93-11) 2005 [3]
- Sequence : Rice - Class I SSR (IRGSP) 2005 [3]
- Sequence : Rice - Class I SSR (TIGR) 2005 [3]
- Physical : Rice - AGI FPC 2002 [OBSOLETE] [1]
- Physical : Rice - IMap (FPC) [OBSOLETE] [4]
- Genetic : Rice - IGCN 1998 [12]
- Genetic : Rice - Cornell RFLP 2001 [6]
- Genetic : Rice - IRMI 2003 [2]
- Genetic : Rice - Cornell SSR 2001 [14]**
- Genetic : Rice - KRGRP 1998 [1]
- Maize Bin : Maize - Bins [2]

You will see that the marker that is associated with your QTL is also located near several other markers and some interpolated genes. Once again, following those links will provide more information that may or may not be useful or interesting to you.

## ➡ 11) Use the CMAP tools to alter the view.

- Crop the maps to magnify the view** (Click on the arrows for cropping.)
- Use “options” and “additional options” menus.** (Located below the map image. Click on ‘Show Options Menu’ and ‘Show Additional Options Menu’)



☐ Hide Options Menu

Highlight Features: "AQFU049"

Feature Types:

Feature	Ignore	Display if Correspondence	Always Display
Centromere	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Interpolated Gene	<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"/>
Default	<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"/>

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"/>	<input type="text" value="0"/>
Insilico	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="text" value="0"/>
Name-based	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="text" value="0"/>
	<input type="button" value="Check All"/>	<input type="button" value="Check All"/>			

Aggregate Correspondences: ☒ No ☐ 1 Line ☐ 2 Lines ☐ Cluster

Number of Clusters (if clustering): ☒ 2 ☐ 3 ☐ 4

Total Magnification:

☐ Hide Additional Options Menu

Image Size: ☐ Tiny ☒ Small ☐ Medium ☐ Large

Font Size: ☒ Small ☐ Medium ☐ Large

Image Type: ☒ PNG ☐ JPEG ☐ GIF ☐ SVG \*

Show Labels: ☐ None ☐ Landmarks ☒ All

Collapse Overlapping Features: ☐ No ☒ Yes

Draw Maps Using Same Scale: ☐ No ☒ Yes

Correspondence lines drawn to: ☒ Feature ☐ Map

Stack the Reference Maps: ☒ No ☐ Yes

Clean View (no navigation buttons): ☒ No ☐ yes

Clickable Image ☒ Default ☐ Omit Features ☐ Omit All Buttons

View Intra-Slot Correspondences: ☒ No ☐ yes

Aggregate evidence types separately: ☒ No ☐ yes

Menu Order of Comparative Maps: ☒ Predefined Order ☐ Number of Correspondences

Ignore Image Map ☒ No ☐ Yes

Sanity Check: ☒ No ☐ Yes

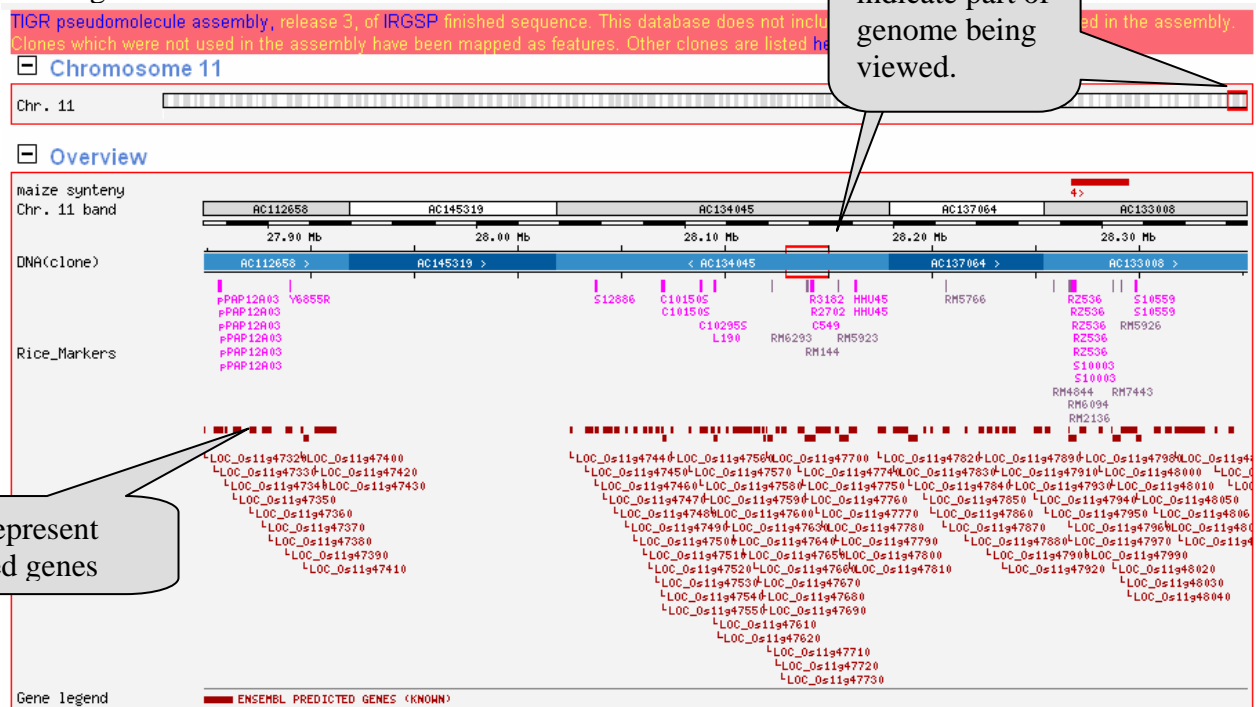
- ➡ 12) **View RM144 in the Rice Genome Browser** (Once again, click on the ‘RM144’ on the map to open the detail page. Under ‘Cross-References’ select ‘[View “RM144” in Genome Browser]’. This will open a page with where you need to click on the location. Select “**Location 28158704 - 28158928 bps**”.

### Chromosome Map Marker RM144

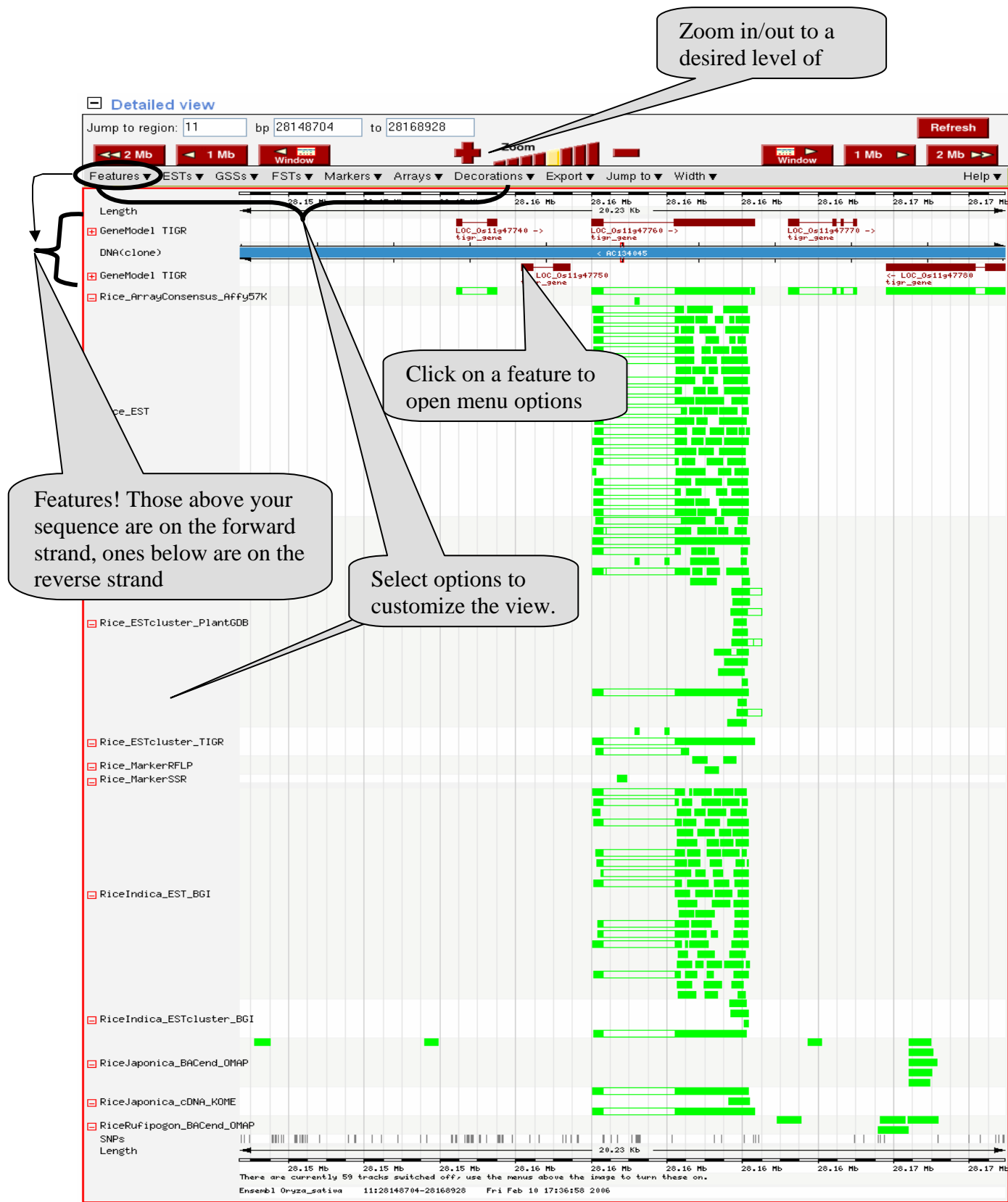
Marker Location	Location <b>28158704 - 28158928 bps</b> on chromosome 11 [Export Data]
Marker Type	SSR (Simple Sequence Repeat)
Marker Synonyms	Cmap : RM144 RM144
Marker Primers	Marker RM144 primers are not in the database

(You May use “Export the data” to get this information in text format, but selecting the location bps (base pairs) will show you the same information in a diagram, which can aid in understanding the data.) It may take a few moments for the results to load in your browser, but the first thing you will notice is that this marker is located at one end of chromosome 11.

The “overview” diagram identifies other features mapped to this area, including synteny with other species. This view is magnified from the chromosome view, so along the track there is a box indicating the selected area on the chromosome view.

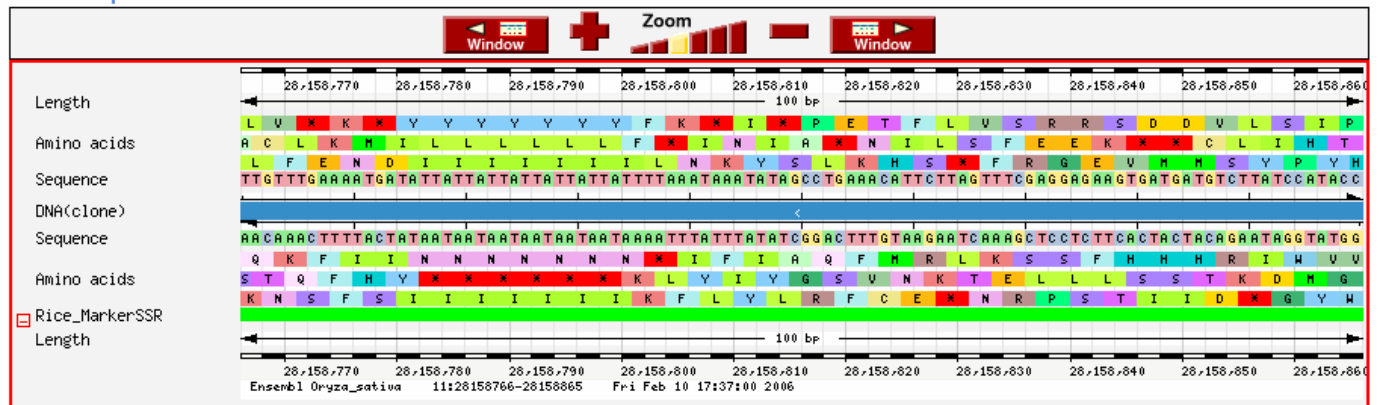


The detailed view is once again magnified from the overview, and zooms in to cover only the area in the selected section of the chromosome. It can be customized to provide information of interest to you by changing the magnification, genomic area, features and decorations through the menus at the top of the display box.



Finally, at the bottom of this page you will find the Basepair View. This diagram shows the sequence and the possible codon sequences for this section.

## Basepair view



In this exercise you have simply begun to learn what Gramene can do. For more complete details on all the features available from each module, review the module tutorials available on the web.

Use the feedback button at the top of every page to submit private questions to the Gramene team. The appropriate person will get back to you. For public discussion, join the Gramene listserve.

Thank you!

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Or use the Feedback button at the top of every page on the Gramene website

[www.gramene.org](http://www.gramene.org)