

Genomes and Genome Browser Tutorial

- The Genome Browser allows you to
 - Browse the Rice-Japonica, Maize and Arabidopsis genomes.
 - View the location of a particular feature on the rice genome and examine neighboring features.
 - View the gene model of a candidate gene.
 - Identify the genomic sequence to which a particular feature is mapped.
 - Compare the position of features from other species with the location of features in the rice genome.
 - Get sequence information, including base pairs, codons and exons
- This tutorial will show you how to:
 - Search for genes and other features in the Gramene genome browser.
 - Change the size and detail of a region.
 - Select which tracks to view.
 - Export information as text files.

Gramene Species

Rice-japonica

Maize

Arabidopsis

Genome Browser

Genome browser is a dynamic (interactive) graphical display of multiple features identified from rice as well as from maize, sorghum, barley, wheat and other cereals that were mapped on the rice genome.

Examples of these features are sequenced genetic markers, ESTs, cDNAs, CDSs, genes, insertion and repeat elements.

The browser is an option for investigating the organization of rice and other cereal genomes and lets you determine which features to view.

The software application was developed by the Ensembl project (www.ensembl.org) and modified by the Gramene project.



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.

The screenshot shows the GRAMENE Genome Browser website. A large yellow callout box with a black border points to the 'Genomes-Ensembl' link in the 'Quick Search' section. The callout box contains the text: 'Click here to open Genome Browser Home Page'. The website header includes the GRAMENE logo and the title 'A Resource for Comparative Grass Genomics'. The navigation bar lists: Search, Genomes, Species, Download, Resources, About, Help, Feedback. The 'Quick Search' section has a search box and a 'Search' button. Below it, there are links for 'All Available', 'Search', and a list of search modules: Genes, Proteins, Pathways, Ontologies, Literature, Sequences-BLAST, All-GenomeMart. The 'Genomes-Ensembl' link is highlighted. The 'Genomes' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'Species' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'Download' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'Resources' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'About' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'Help' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'Feedback' section lists: Oryza sativa, Oryza rufipogon, Zea mays, Arabidopsis thaliana, Oenothera. The 'Genetic Diversity' section lists: Search for SNPs. The 'Biochemical Pathways' section lists: Search for pathways. The 'Literature' section lists: Search the literature. The 'Submission' section lists: Submit a Rice Gene or Ontology. The 'Gramene Tip' section lists: You can contact Gramene either by e-mailing us at gramene@gramene.org or by sending a question to the curators and developers at Gramene on any page by selecting the Feedback button in the top right hand corner. The 'Note' section lists: 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. The footer includes the USDA logo and the text: 'USDA', 'daz', 'USDA', 'CSH', 'CSH'.

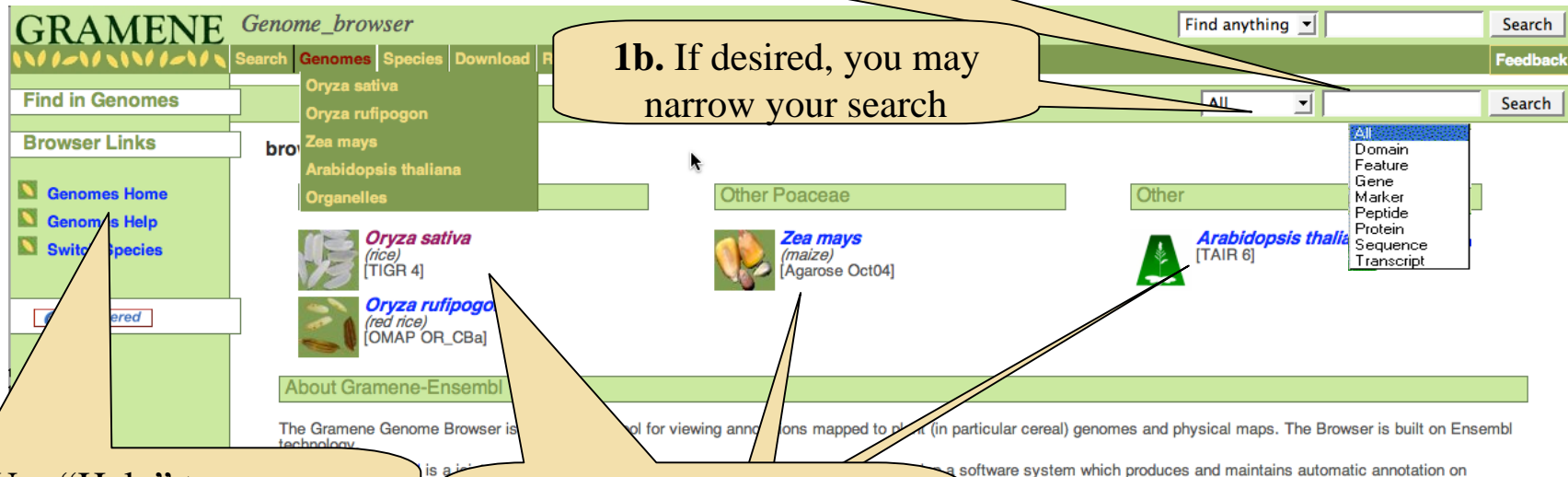
Genomes Home Page

1. Type in the **search term** (a clone/feature's accession number or name) and press "Search."

1b. If desired, you may narrow your search

Use "Help" to access tutorial, FAQ and Help files.

2: Choose **species** from available genomes (*see Slide 7 for Rice*).



Term Search Results

Search for "RM1" in Arabidopsis thaliana	
Oryza_rufipogon Oryza_sativa Zea mays FPC Map Zea mays Sequences	
Chromosome	(0 results)
No match for this search type	
Clone	(0 results)
No match for this search type	
Contig	(0 results)
No match for this search type	
Domain	(0 results)
No match for this search type	
Feature	(0 results)
No match for this search type	
Gene	(10 results)
AT1G28330-TAIR-G drm1 (dormancy-associated protein 1)	AT1G58848-TAIR-G prm1 homolog
AT1G28330-TAIR-G drm1	AT1G59124-TAIR-G prm1 homolog
AT1G58807-TAIR-G prm1 homolog	AT1G59124-TAIR-G identical to cdna rxf10 mrna
AT1G58807-TAIR-G identical to cdna rf45 mrna for prm1 homolog, partial	AT1G59620-TAIR-G cw9 mrna for prm1 homolog
AT1G58848-TAIR-G prm1 homolog	AT5G15380-TAIR-G drm1 (domains rearranged)
Marker	(0 results)
No match for this search type	
Peptide	(0 results)
No match for this search type	
Protein	(18 results)
Q22462 (Q22462 HORVU): Barperm1 perm1	Q69RM1 (Q69RM1 ORYSA): Hypothetical protein P0003B09.6
P27927 (RM16 MAIZE): Mitochondrial 60S ribosomal protein L16 RPL16	Q6ERM1 (Q6ERM1 ORYSA): Hypothetical protein P0003B09.6
P46801 (RM16 ORYSA): Mitochondrial 60S ribosomal protein L16 RPL16	Q6YRM1 (Q6YRM1 ORYSA): Hypothetical protein OSJNBa0091F23.24 OSJNBa0091F23.24 B1203H11.39
Q0DRM1 (Q0DRM1 ORYSA): Os03g0371300 protein	HypotheticalproteinB1203H11.39 HypotheticalproteinOSJNBa0073J19.16 OSJNBa0073J19.16
Q037221300	Q7GBC8 (Q7GBC8 ORYSA): Ubiquitin-related modifier-1 Rurm1

The default search is for Rice, but you may select a different species.

There are no results for these options. When there are results, note that you may be taken to a different module, and will need to refer to that specific tutorial

There is not yet a definitive gene list for Oryza, so you have to wade through multiple potential protein matches and make educated choices.

Browse a Chromosome

The screenshot shows the TIGR Rice Genome Browser interface. On the left, a sidebar contains a 'Find in' search bar and a 'Browser Links' section with links to 'Genomes Home', 'Genomes Help', and a 'Switch' button. Below the 'Switch' button is a list of species: 'Arabidopsis thaliana', 'Oryza rufipogon', 'Oryza sativa' (highlighted with a mouse cursor), 'Zea mays', and 'Organelles'. The main content area is titled 'Browse the Rice genome (Oryza sativa ssp japonica)' and shows 'Current Release TIGR v4'. It includes an 'Assembly' section with text about the TIGR pseudomolecule assembly release 4 of IRGSP finished sequence, and a 'Browse by Chromosome' section with a bar chart of chromosomes 1 through 12. Below this is a 'Lookup a Chromosome Location' section with a dropdown for 'Chr: 1' and a text input for 'from 1 - 20000', followed by a 'Go' button. Further down is a 'Rice Synteny Vs Maize FPC Map' section with a dropdown for 'Rice Chr 1 vs. Maize' and another 'Go' button. At the bottom, an 'Example Features' section lists 'Gene: dl1', 'Transcript: Q6Z0E3', and 'Contig: AP003727'. Several callout boxes provide instructions: 'Click to change species' points to the 'Switch' button; 'Annotation Info' points to the 'Assembly' section; 'Information on the assembly' points to the text in the 'Assembly' section; 'You may enter a chromosome number and location.' points to the 'Lookup a Chromosome Location' section; 'Or you may select a chromosome to browse by clicking on it (see Slide 9).' points to the 'Browse by Chromosome' section; and 'Or choose a Synteny map to view (see Slide 8)' points to the 'Rice Synteny Vs Maize FPC Map' section.

Find in

Browser Links

- Genomes Home
- Genomes Help
- Switch

Arabidopsis thaliana

Oryza rufipogon

Oryza sativa

Zea mays

Organelles

Browse the Rice genome (Oryza sativa ssp japonica)

Current Release TIGR v4

Assembly

This release is based on TIGR pseudomolecule assembly release 4 of IRGSP finished sequence.

Clones which were not used in the assembly have been mapped as features, and are listed [here](#)

Annotation

- Feature data sets mapped to the genome in [detailed](#) form.
- Putative orthologs between rice, Arabidopsis generated using Ensembl's compara pipeline
- Syntenic regions between the maize FPC map and the rice genome assembly were [estimated](#), and loaded into Ensembl.

Browse by Chromosome

Lookup a Chromosome Location

Chr: 1 from 1 - 20000 Go

Rice Synteny Vs Maize FPC Map

Rice Chr 1 vs. Maize Go

Example Features

- Gene: [dl1](#)
- Transcript: [Q6Z0E3](#)
- Contig: [AP003727](#)

Click to change species

Annotation Info

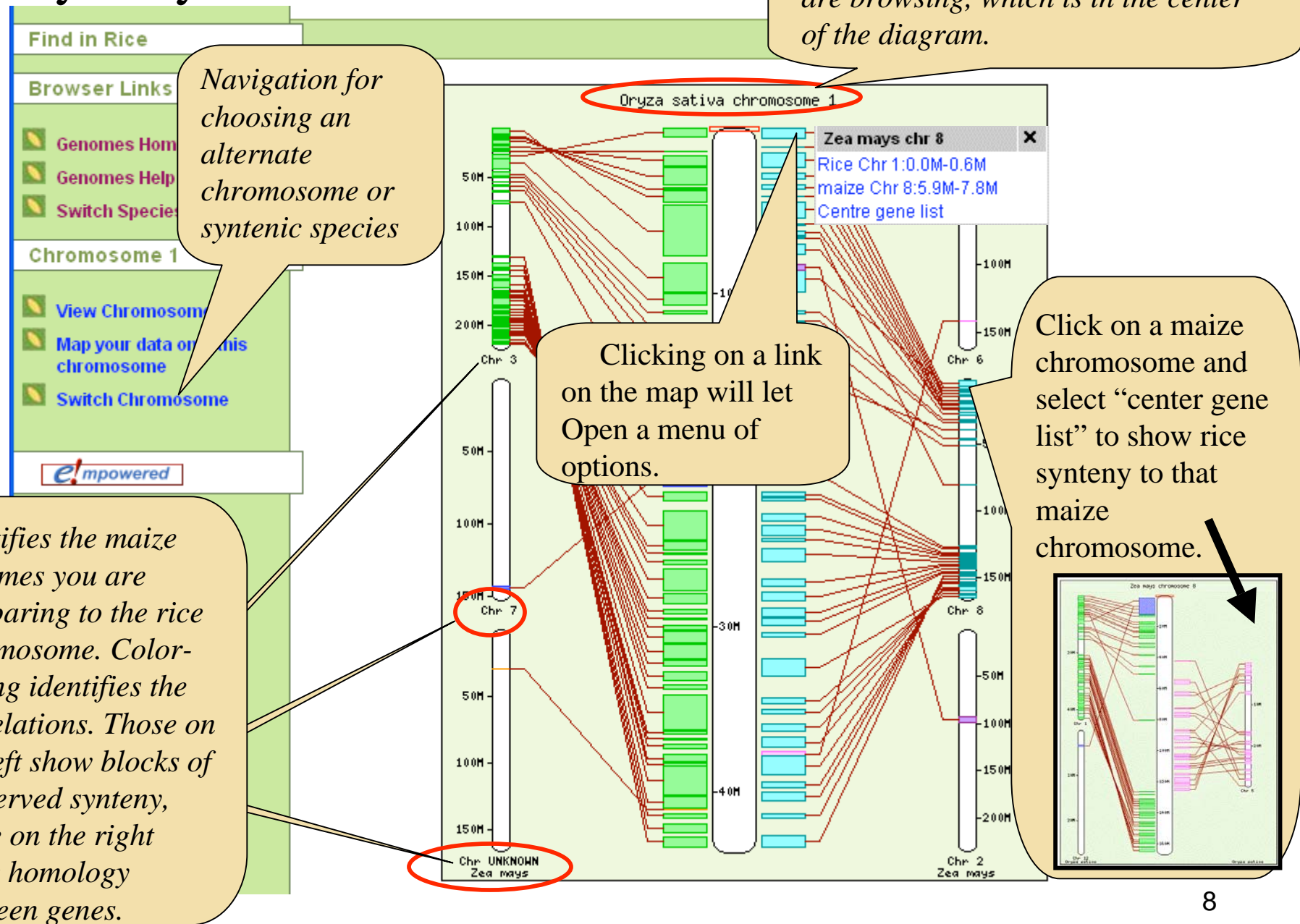
Information on the assembly

You may enter a chromosome number and location.

Or you may select a chromosome to browse by clicking on it (see Slide 9).

Or choose a Synteny map to view (see Slide 8)

Synteny: Rice Chr. 1 vs Maize



Rice

Chromosome 11

Click go to view synteny with current chromosome (as in slide 8).

MapView shows distribution of features at chromosome scales.

Click on image to zoom in (see Slide 12, contig view)

You are here

Choose another chromosome to view.

Access **Karyoview** to design your own map (See Slide 11).

MapView

Find anything Search

Species Download Resources About Help

All Search

TIGR pseudomolecule assembly, release 4, of IRGSP finished
This database does not include the portions of clones not used in the assembly. Clones which were not used in the assembly have been mapped. Other clones are listed [here](#)

Chromosome 11

Barley_ArrayExemplar_Affy22K Count	
Barley_EST Count	
Barley_ESTCluster_PlantGDB Count	
Barley_ESTcluster_TIGR Count	
Chromosome length	
FGENESH Count	
GeneModel Submission Count	1,830
GeneModel TIGR Count	4,297
MaizeCornchip0_ArrayConsensus_Affy8K Count	256
Maize_ArrayConsensus_Affy18K Count	1,768
Maize_ArrayGene_NSF58K Count	4,591
Maize_BACend Count	2,156
Maize_EST Count	52,886
Maize_ESTCluster_PlantGDB Count	6,862
Maize_ESTcluster_MMPconsensus Count	1,249
Maize_ESTcluster_TIGR Count	2,881
Maize_FSTMu Count	571
Maize_HiCotCluster_TIGR Count	3,506
Maize_HiCotMethylFilterCluster_TIGR Count	6,266
Maize_HiCot_Barnetzen Count	6,197
Maize_MAGI Count	3,996

Chromosome information

Use **Anchor view** at bottom of page to select a region by two features. (See next slide)

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Anchor View

Wheat_Marker Count	418
genbank_rna Count	0
genbank_trna Count	7
miRNA_genes Count	6
nonRice_MarkerRFLP Count	108
wgs_06072006 Count	133,165

[Jump to ContigView](#)

Use **Anchor view**, to select a region by two features.

features from this chromosome as anchor points and display the
between them. Both features must be mapped to the current Ensembl
If you select "None" for the second feature, the display will be based
on the first feature.

Please note that if you select widely spaced features there may be a significant
delay while Ensembl builds the DNA display.

Region

From (type): *

To (type):

Context

Bp downstream

Bp upstream

[Go](#)

Fields marked with * are required

Karyo View

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

Display your data

- Input new data
- How to upload your data

Add your data

Karyoview now allows you to display multiple data sets as either two. Your data will be saved in a temporary cache. Once you click of the image options.

Information about valid file formats: e.g. GFF, PSL, BED

Track name (optional)

Paste file content

or upload file

or use file URL

Click here
after entering
data

The basic file format for the data upload is:
Chromosome
Chromosome start coordinate
Chromosome end coordinate
Feature name (optional)
The columns need to be separated from each other by white space. The 'feature label' can also be added as a fourth parameter.

Then Configure results
display and “finish”

Configure karyotype

Chromosome

Number of rows of chromosomes *

Height of the longest chromosome (pixels) *

Padding around chromosomes (pixels) *

Spacing between chromosomes (pixels) *

Spacing between rows (pixels) *

Fields marked with * are required

3/22/07

Viewing Results - Contig View

Accessed from slide #9, Ensembl 'ContigView' is the principal data visualization tool for genome sequence annotation information. It provides a high level view of the contig sequences that form the genome sequence assembly, and of genes and other features that have been placed on it.

Be patient, it may take a few minutes to retrieve all data.



Notice 4 categories, each with [+] or [-] to expand or collapse that section. (All sections have been collapsed here for demonstration purposes.)

Chromosome

The screenshot shows a genome browser interface. At the top, a green bar contains a search box with a dropdown menu set to 'All' and a 'Search' button. Below this, a section titled 'Chromosome 11' shows a horizontal bar representing the chromosome. A red vertical line on the right side of this bar indicates the current view position. To the left of the chromosome bar, a sidebar contains several sections: 'Find in', 'Browser Links' (with links to Genomes Home, Genomes Help, and Switch Species), 'Chromosome 11' (with coordinates 27,812,569 - 27,912,570), 'View of Chromosome 11' (with options like Graphical view, Graphical overview, View Syntenic regions, and View region in CMAP TIGR Assembly), and 'Export data' (with options like Export information about region, Export sequence as FASTA, Export EMBL file, Export Gene info in region, and Export SNP info in region). Callouts provide additional information: one points to the top bar stating 'Entire Chromosome is displayed at the top'; another points to the chromosome bar stating 'Identifies which chromosome you are viewing. Clicking on the chromosome will move view to that area'; a third points to the red vertical line stating 'Area in red outlined box on Chromosome is the area you are viewing and is enlarged to fill the overview below'; and a fourth points to the sidebar stating 'Genomes Menu options'.

Find in

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

Chromosome 11
27,812,569 - 27,912,570

- View of Chromosome 11
- Graphical view
- Graphical overview
- View Syntenic regions
- ...
- View region in CMAP TIGR Assembly

Export data

- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

Chr. 11

Entire Chromosome is displayed at the top

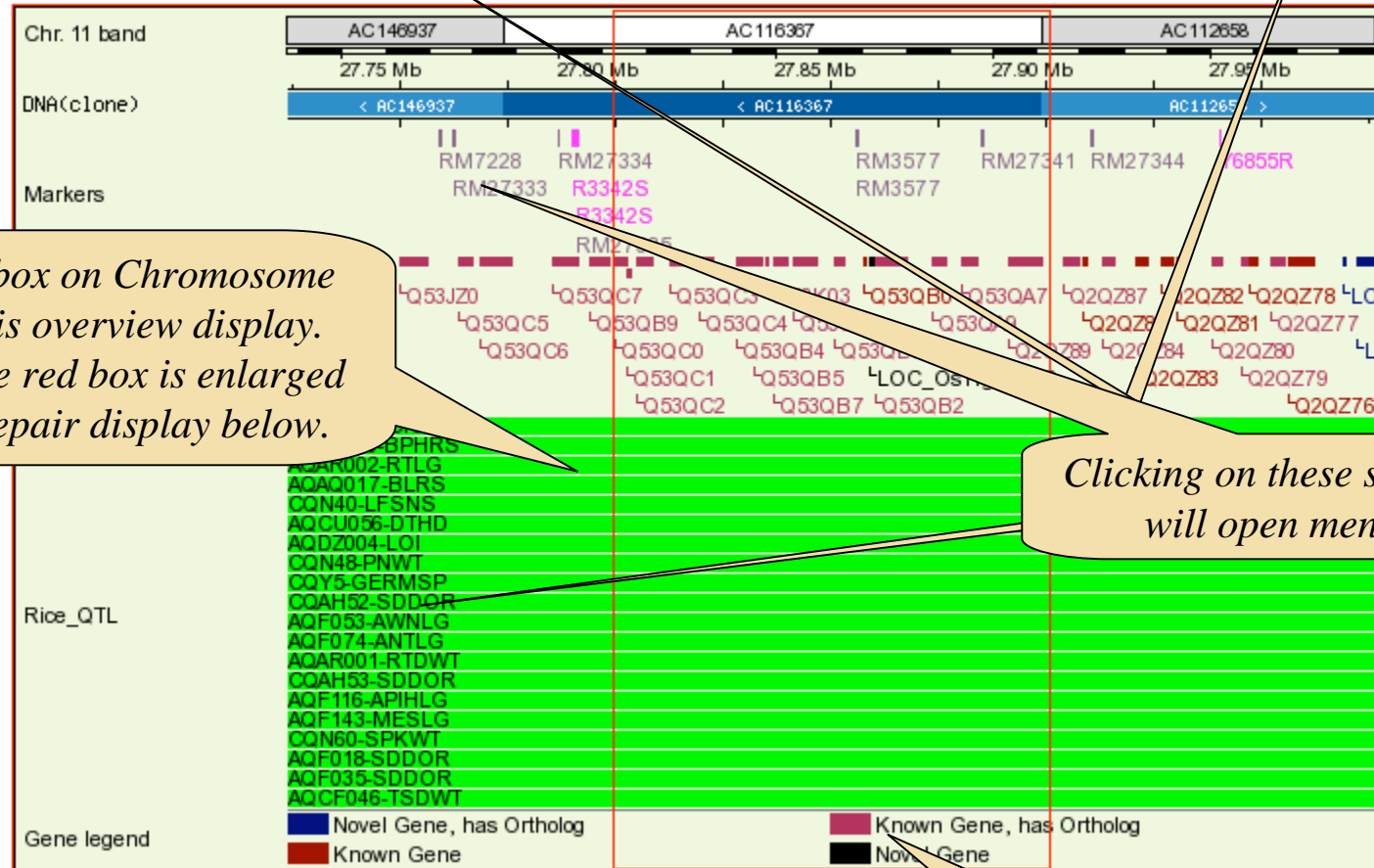
Identifies which chromosome you are viewing. Clicking on the chromosome will move view to that area

Area in red outlined box on Chromosome is the area you are viewing and is enlarged to fill the overview below.

Genomes Menu options

Overview

Overview



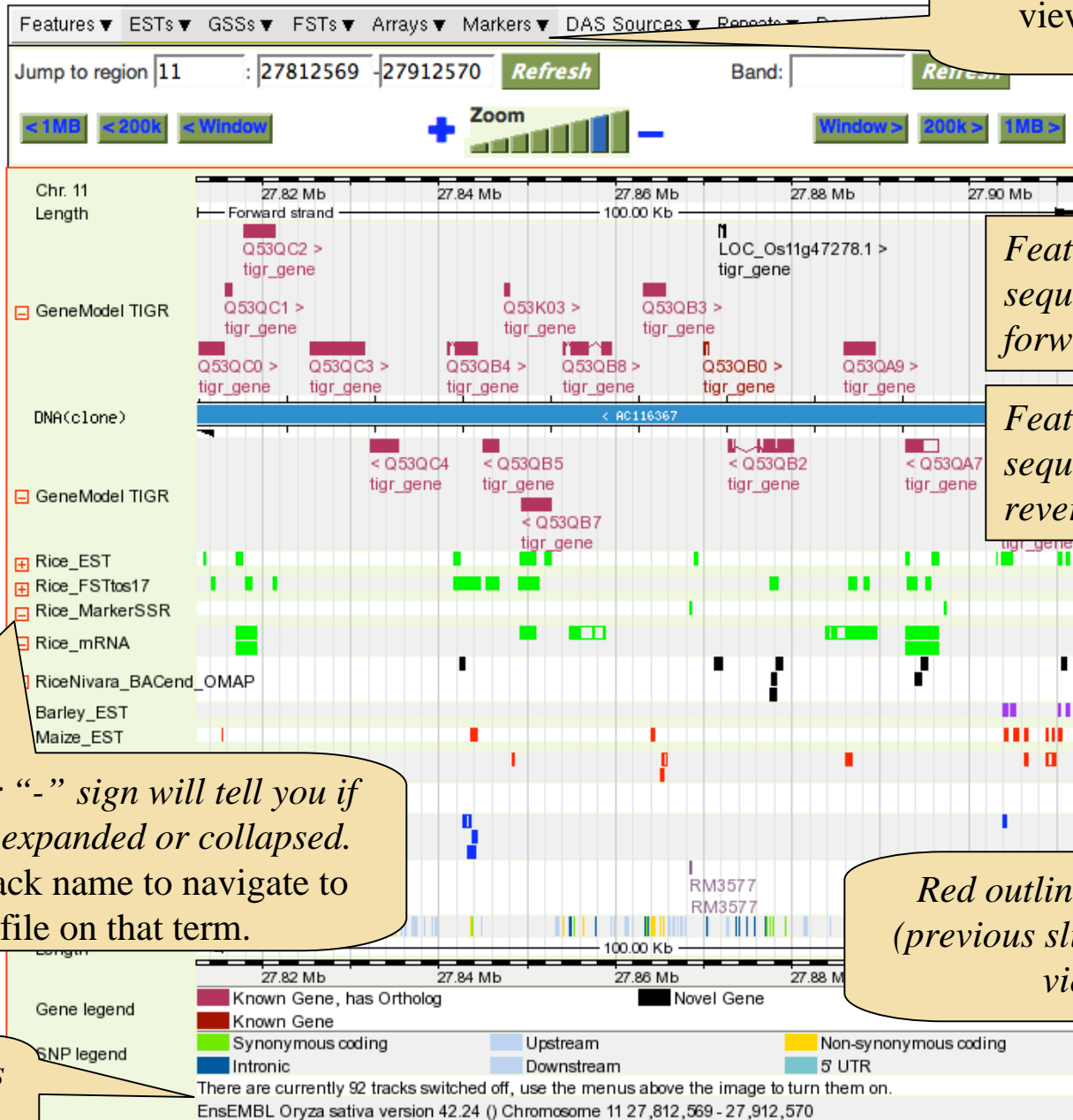
Red outlined box on Chromosome above fills this overview display. The area in the red box is enlarged to fill the basepair display below.

Clicking on these sections will open menus

Color-coded features Key

Detailed View

Select options to Customize view (Slides 16 & 17)



Features above the sequence (clone) are on the forward strand

Features below the sequence (clone) are on the reverse strand

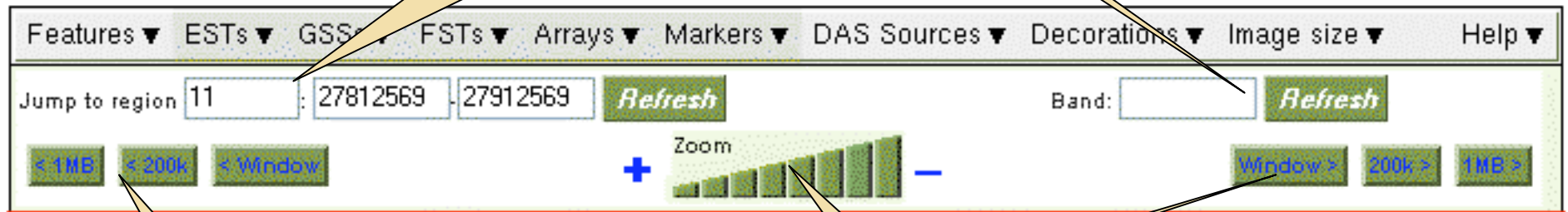
The “+” or “-” sign will tell you if the track is expanded or collapsed. Click on track name to navigate to help file on that term.

Red outlined box on overview (previous slide) fills this detailed view display.

Info on options to view

Detail Navigation

Navigation - Adjust your view by entering coordinates, then refresh



Navigation, use to go to different view.

Zoom in/out to a desired level of resolution

Customize your detailed view display by selecting and deselecting options. Selections will be saved for future visits.

Customizing the Detail View

The screenshot shows a genomic browser interface with several customization menus open. At the top, there are navigation tabs: 'Markers', 'DAS Sources', 'Decorations', 'Image size', and 'Help'. Below these, a 'Jump to region' field shows '10 : 1243467 - 1343468' with a 'Refresh' button. A 'Band:' field and another 'Refresh' button are also present. A 'Zoom' slider is visible. On the left, a 'Features' menu is open, listing various genomic features like SNPs, Markers, GeneModel TIGR, etc. In the center, a 'Markers' menu is open, listing various marker types like Rice_Affy57K, Rice_Affy20K, etc. On the right, a 'Decorations' menu is open, listing various display options like Sequence, Codons, Start/Stop codons, etc. A 'Width' menu is also open, showing options for Width 600px, 700px, 800px, and 900px. A 'Reset options' button is at the bottom. A blue plus sign is in the center of the map area.

Jump to region 10 : 1243467 - 1343468 Refresh Band: Refresh

< 1MB < 200k < Window Zoom Window > 200k > 1MB >

Features

- ☐ SNPs
- ☐ SNPs (OMAP)
- ☐ SNPs (dbSNP)
- ☒ Markers
- ☒ GeneModel TIGR
- ☒ genbank_tma
- ☒ genbank_rna
- ☐ GeneModel Gramene
- ☒ miRNA_genes
- ☐ FGENESH
- ☒ Rice_BAC
- ☐ Rice_QTL
- ☐ Maize_Sorghum_Zea
- ☒ SNPs (OMAP: o_sati)
- ☒ SNPs (OMAP: o_sati)
- ☒ SNPs (OMAP: o_sati)
- ☒ SNPs (OMAP: o_sati)

Markers

- ☐ RiceAita_BACend
- ☐ RiceAustralensis
- ☐ RiceBrachyantha
- ☐ RiceCoarctata_BAC
- ☐ RiceGlaberata_BAC
- ☐ RiceGracilior_BAC
- ☐ RiceMinuta_BAC
- ☒ RiceNivara_BAC
- ☐ RiceOfficialis_BACend_OMAP
- ☐ RicePunctata_BACend_OMAP
- ☐ RiceRidleyI_BACend_OMAP
- ☐ RiceRufipogon_BACend_OMAP
- ☐ Maize_BACend
- ☐ Maize_HiCot_Bonneizen
- ☐ Maize_HiCotCluster_TIGR
- ☒ Maize_HiCotMethylFilterCluster
- ☐ Maize_MethylFilter_CSHL
- ☐ Maize_MethylFilter_Orion
- ☐ Ryegrass_MethylFilter_Orion
- ☐ Ryegrass_MethylFilterCluster_Orion
- ☐ Sorghum_GSS_Klein
- ☐ Sorghum_MethylFilter_Orion
- ☐ Rice_FST-TDNA
- ☒ Rice_FSTos17
- ☐ Rice_FSTtransposon
- ☐ Maize_FSTMu

Decorations

- ☐ Sequence
- ☐ Codons
- ☐ Start/Stop codons
- ☒ Contigs
- ☒ Ruler
- ☒ Scale Bar
- ☐ %GC
- ☒ Show
- ☒ Show
- ☒ Show
- ☐ Half-h
- ☐ Concise labels
- ☐ Rest.Enzymes
- ☒ Rest.Enzymes on zoom

Width

- ☐ Width 600px
- ☒ * Width 700px
- ☐ Width 800px
- ☐ Width 900px

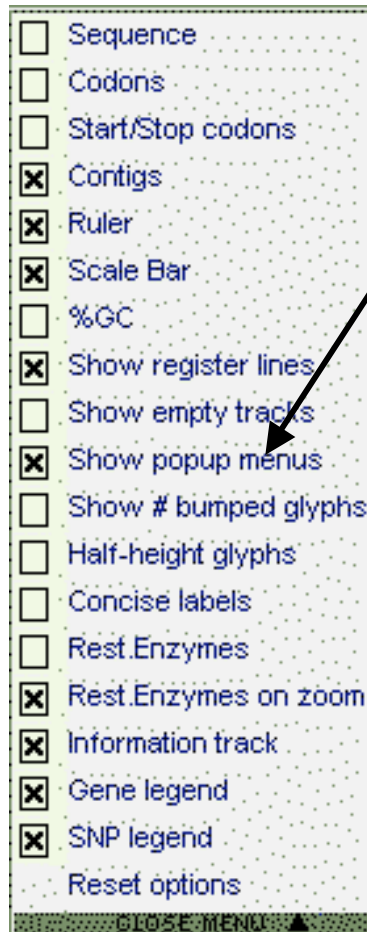
Reset options

Help

Be patient when making changes,, it may take a few minutes to retrieve all data.

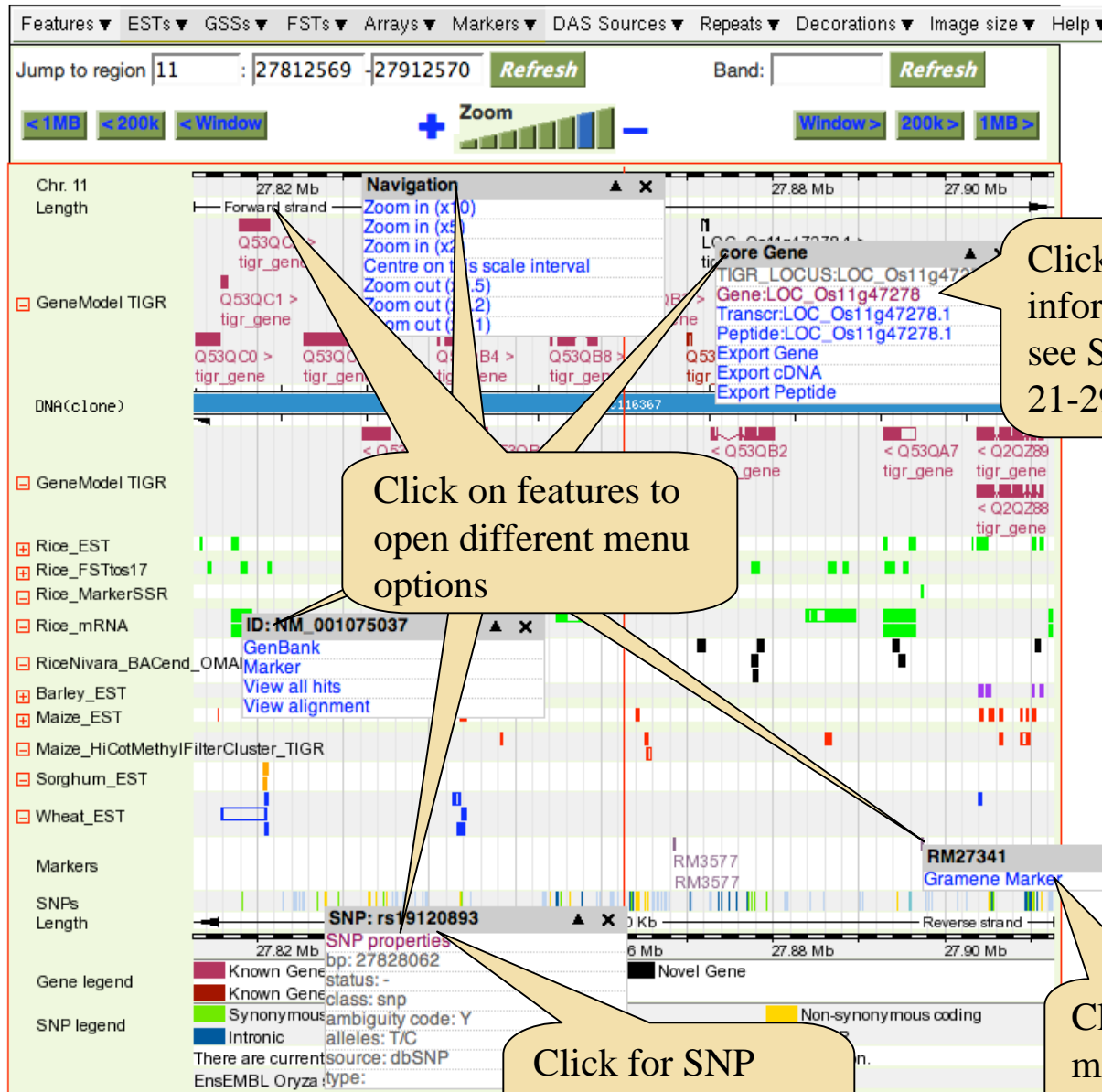
Select options to customize the view. Closing menus will refresh your map

Customization Pop-up menu



- *For this tutorial, the “show popup menus” has been selected from the “decorations” options. Clicking on a feature will open a menu option. You may get different results if you have different selections.*

Detail Menus



Click for information, see Slides 21-29

Click on features to open different menu options

Click for SNP information, See slide 31

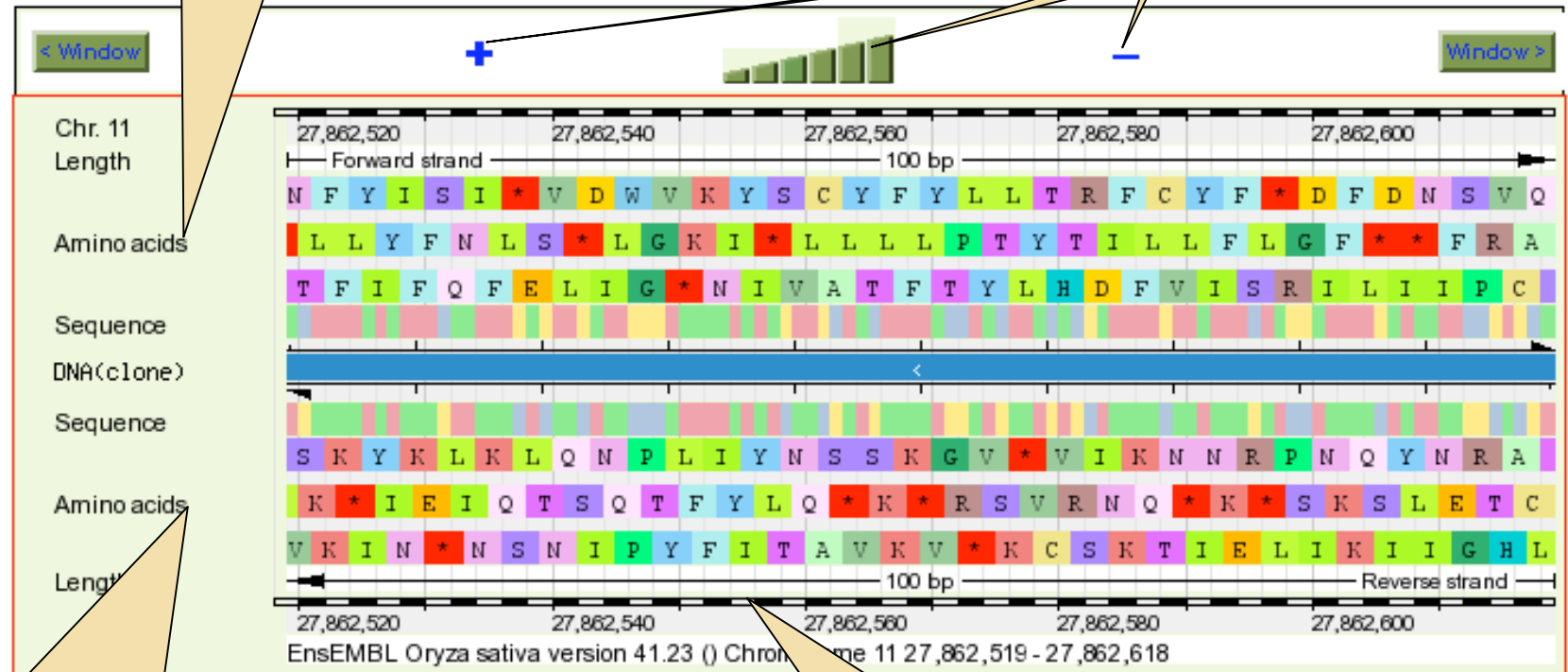
Click for more marker info

Base Pair View

Click for more information on tracks.

☒ Basepair view

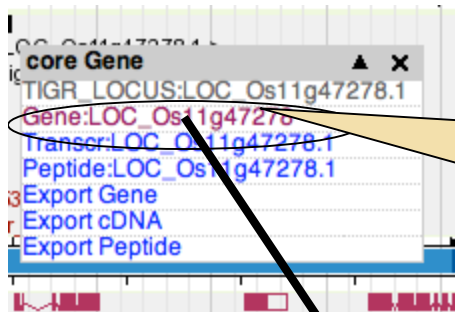
Zoom



Each sequence has three different possible codon (amino acid) sequences, which are displayed here.

Click length ruler to open zoom menu

Gene info



In detail view,
click on a feature
to open a menu
(see slide 19)

Find in All

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

LOC_Os11g47180

- Gene information**
- Genomic sequence
- Genomic sequence alignment
- Gene splice site image
- Gene tree info
- Gene variation info.
- Transcript information
- Exon information
- Protein information
- Export gene data

Chromosome 11
27,817,042 - 27,824,346

Ensembl Gene Report for LOC_Os11g47180

Gene	Q53QC2 (SPTREMBL)
Tigr Gene ID	LOC_Os11g47180
Genomic Location	This gene can be found on Chromosome 11 at location 27,817,912-27,821,316 . The start of this gene is located in Clone AC116367 .
Description	Leucine Rich Repeat family protein, expressed
Prediction Method	Gene annotation by TIGR through a process of automatic and manual curation
Transcripts	<div> LOC_Os11g47180.1 LOC_Os11g47180.1 Q53QC2 [Transcript info] [Exon info] [Peptide info] </div> <div> <p>Features ▼</p> </div>

Describes location
on the Rice
genome. Select to
view detailed info
from the Genome
Browser.

Genomic sequence

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

LOC_Os11g47278

- Gene information
- Genomic sequence
- Genomic sequence alignment
- Gene splice site image
- Gene tree info
- Gene variation info.
- Transcript information
- Exon information
- Protein information
- Export gene data

Chromosome 11
27,871,699 - 27,872,374

- View of Chromosome 11
- Graphical view
- Graphical overview
- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

Gene Sequence information

Gene	LOC_Os11g47278 () To view all Ensembl genes linked to the name click here.
Tigr Gene ID	LOC_Os11g47278
Genomic Location	This gene can be found on Chromosome 11 at location 27,871,699-27,872,374. The start of this gene is located in Clone AC116367.
Markup options	<div> 5' Flanking sequence <input type="text" value="600"/> * </div> <div> 3' Flanking sequence <input type="text" value="600"/> * </div> <div> Exons to display <input type="text" value="Ensembl exons"/> </div> <div> Exons on strand <input type="text" value="Both orientations"/> </div> <div> Show variations <input type="text" value="Do not show Variations"/> </div> <div> Line numbering <input type="text" value="None"/> </div> <div>Update</div> <div>Fields marked with * are required</div>
Marked_up_sequence	<p>THIS STYLE: Location of other exons</p> <p>THIS STYLE: Location of selected exons</p> <pre>>chromosome:TIGR4:11:27871099:27872974:1 ATATTTCAAATCTATATATTTTAAAGATGTCCTTTTATTACCATTTTCATGAAGCGAACT ATTCAAATATGTATTAACGATCAAAGTGTAAACCTATGGATTACATGTTTATAAAATTT AACTCACTCATAGCTAGAGAAAGTAATTAAGAGTGAACAATAAATCAGGAGAACGAACCA GGACTTTATATTATTGTTGATAAGCTCGATTAGCAAGTATTAGTCACGGAAGCACTGAC AGCTCTGATAAATATGTCAAATGTTTCCCGCAAAAAAATGTCAAATGTTTACACCT ACAATCTAACCGTGGGCCGAATTATTGGACCAATTGAGCCAGCCGTAAGGTGTACG TGTCGGCCCAAAACATCAAATCTTATAAAATAAACAGCTAATAAATGCTCAGCATAAAT CAAGGGATATGAGTAAGATAATGTTTGCAATTAATATATGTCAATTTATGGTGGGTATTG TACCCCTATATGAACACCGGCAACAGTGAAGGTCGTAGAAGTAGCTTATCAAAATCATCGG GAGAACAAAAACACTGTAGCCTGATCTTGTGATGGCAATCATTTCCAAGAAAAATAACACA ATGGCCCTCGGCTGCTTGGTGGCTTTTGTGATCTTGGCTGCTCGCTCTCTCATCCTGCAAA GCGGACGTTAGATTAAATTTCTCTCTACAATGTTTGCTACAAATTTAAACATTGCTCC AAATCTTAGATCCATGTCAAATTTAAAGTTTGTATATATGTTAACTACAATTTGTTAAA ATATTTAATTTCTCTAAATATAAATAAATGATTTATTTAAATATTACCAACATAAGC ACAGAAATTTACATTAGAAATACCTAGCTTAAAAAATAAATAGAGTTGTGCCGAA CAAGGCCAATATACAGAGTTTGCCAAACAGATTGAAGATTTTATAAGCGAAGATTTTTC </pre>

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Genomic Sequence alignment

Chromosome 11
27,871,699 - 27,872,374

- View of Chromosome 11
- Graphical view
- Graphical overview
- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

Genomic Location	This gene can be found on Chromosome 11 at location 27,871,699-27,872,374. The start of this gene is located in Clone AC116367 .
Markup options	<div style="margin-bottom: 10px;"> 5' Flanking sequence <input type="text" value="600"/> * </div> <div style="margin-bottom: 10px;"> 3' Flanking sequence <input type="text" value="600"/> * </div> <div style="margin-bottom: 10px;"> Alignment width <input type="text" value="120"/> *Number of bp per line in alignments </div> <div style="margin-bottom: 10px;"> Exons to display <input type="text" value="Ensembl exons"/> </div> <div style="margin-bottom: 10px;"> Exons on strand <input type="text" value="Both orientations"/> </div> <div style="margin-bottom: 10px;"> Show variations <input type="text" value="Do not show Variations"/> </div> <div style="margin-bottom: 10px;"> Line numbering <input type="text" value="None"/> </div> <div style="margin-bottom: 10px;"> Conservation regions <input type="text" value="All conserved regions"/> </div> <div style="margin-bottom: 10px;"> Codons <input type="text" value="Do not show codons"/> </div> <div style="margin-bottom: 10px;"> Title display <input type="text" value="None"/> On mouse over displays exon IDs, length etc </div> <div style="margin-bottom: 10px;"> View in alignment with <input type="text" value="No alignments"/> </div> <div style="text-align: right;"> <input type="button" value="Update"/> </div>
Marked_up_sequence	<p>THIS STYLE: Location of selected exons</p> <p>Oryza_sativa></p> <p>chromosome:TIGR4:11:27871099:27872974:1</p> <pre> ATATTTCAAATCTATATATTTTAAAGATGTCCTTTATTACCATTTTCATGAAGCGAACTATTCAAATATGTATTAACGATCAAAG/ AACTCACTCATAAGTAGAGAAAAGTAATTAAGAGTGAACAATAAAATCAGGAGAACGAACCAGGACTTTATATTATTTGGTTGATAAGC/ AGCTCTGATAAATATGTCAAATGTTTCCCCGCCAAAAAATAAATGTCAAATGTTACACCTACAATCTAACCGTGGGCCGAATTATT/ TGTCGGCCCCAAAACATCAAATCTTATAAAAAAACAGCTAATAAATTGCTCAGCATAAATGCAAGGGATATGAGTAAGATAAATGTT/ TACCCCTATATGAACACCGGCAACAGTGAAGGTCGTAGAAGTAGCTTATCAAATCATCGGGAGAACAAAACACTGTAGCCTGATCT/ ATGGCCCTCGGC TGCTTGGTGGCTTTTGTGATCTTGGCTGTCGCTCTCTCATCC TGC AAAGCGGAC GGT TAGATTTAATTTCCCTCT/ AAATCTTAGATCCATGTCAAATTTAAAGTTTGATATATGTTAACTACAATTGTTTAAAAATTTAATTTCCCTCAAAAATATAAA/ ACAGAATTTCTACATTTAGAAAATACCTAGCTTAAAAAATAAATTAGAGTTGTGCCGAACAAGGCCAATATACAGAGTTGTGCCA/ AAGTTGTGGTAGTTACTACAAATTTGTTTTCTTTAGTACCTACTGTAAGCATGGCATCACTAGAAAATTAATGATTGTAGATGCGC/ GGCATTTTATACAGAGTTTGTGTTTATTTTGTAGAGAGTACAGATGTGTGTTTCTATACGGGCTCCTCCGGGCATGCCAAGTCAGAA/ </pre>

Gene splice site image

Find in

Browser Links

LOC_Os11g47278

Gene information

Genomic sequence

Genomic sequence alignment

Gene splice site image

Gene tree info

Gene variation info.

Transcript information

Exon information

Protein information

Export gene data

Chromosome 11
27,871,699 - 27,872,374

View of Chromosome 11

Graphical view

Graphical overview

Export information about region

Ensembl Gene Splice Report for LOC_Os11g47278

Gene	LOC_Os11g47278 () To view all Ensembl genes linked to the name click here .
Tigr Gene ID	LOC_Os11g47278
Genomic Location	This gene can be found on Chromosome 11 at location 27,871,699-27,872,374. The start of this gene is located in Clone AC116367 .
Description	hypothetical protein

Splice sites for region go gene LOC_Os11g47278

Features Context Image size Export

Length

Forward strand

GeneModel TIGR

DNA(clone)

GeneModel TIGR

GeneModel TIGR

Length

Reverse strand

27,869,000 27,870,000 27,871,000 27,872,000 27,873,000 27,874,000 27,875,000

7.44 Kb

Q53QB0 > tigr_gene

LOC_Os11g47278.1 > tigr_gene

< Q53QB2 tigr_gene

876 bp

3/22/07

24

Gene Tree Image (NEW!)

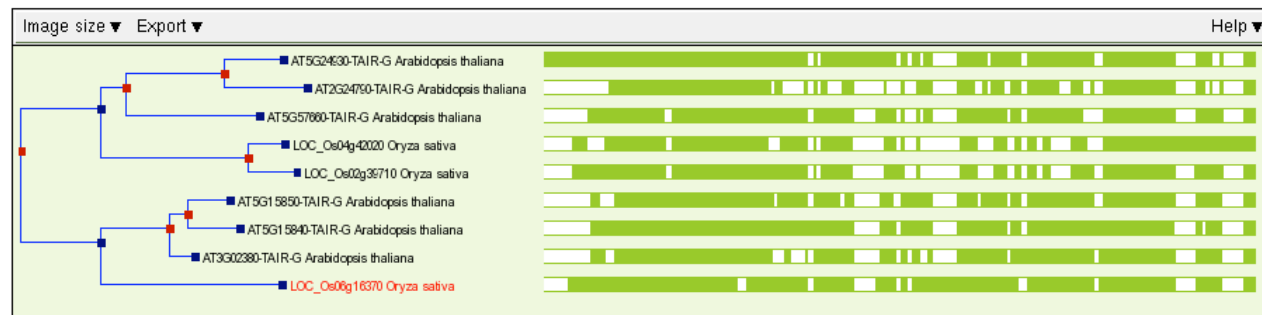
Gene information	
Gene	LOC_Os11g47278 () To view all Ensembl genes linked to the name click here .
Tigr Gene ID	LOC_Os11g47278
Genomic Location	This gene can be found on Chromosome 11 at location 27,871,699-27,872,374 . The start of this gene is located in Clone AC116367 .
Description	hypothetical protein
Gene Tree for gene LOC_Os11g47278	
This gene has no orthologues in Ensembl Compara, so a gene tree cannot be built.	

Our example does not have a gene tree, but below here there is another example of one that does.

LOC_Os11g47278	
	Gene information
	Genomic sequence
	Genomic sequence alignment
	Gene splice site image
	Gene tree info
	Gene variation info.
	Transcript information
	Exon information
	Protein information
	Export gene data
Chromosome 11 27,871,699 - 27,872,374	

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Gene Tree for gene LOC_Os06g16370



Gene Orthologues

Orthologue Prediction

The following gene(s) have been identified as putative orthologues:

Species	Type	Gene identifier
Arabidopsis thaliana	1-to-many	AT3G02380-TAIR-G (COL2) [MultiContigView] [Align] COL2 (CONSTANS-LIKE 2); transcription factor/ zinc ion binding; homologous to the flowering-time gene CONSTANS (CO) encoding zinc-finger proteins
	1-to-many	AT5G15840-TAIR-G (CO) [MultiContigView] [Align] CO (CONSTANS); transcription factor/ zinc ion binding; Encodes a protein showing similarities to zinc finger transcription factors, involved in regulation of flowering under long days.
	1-to-many	AT5G15850-TAIR-G (COL1) [MultiContigView] [Align] COL1 (CONSTANS-LIKE 1); transcription factor/ zinc ion binding; Homologous to the flowering-time gene CONSTANS.

[View alignments of homologies.](#)

Gene variation Info

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

LOC_Os11g47278

- Gene information
- Genomic sequence
- Genomic sequence alignment
- Gene splice site image
- Gene tree info
- Gene variation info.**
- Transcript information
- Exon information
- Protein information
- Export gene data

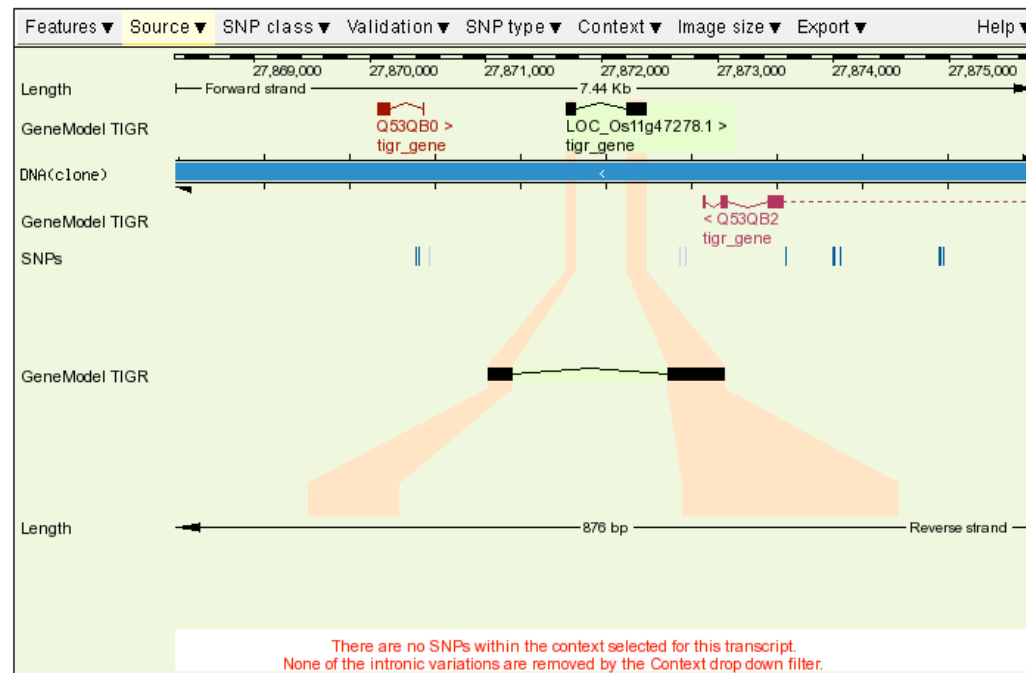
Chromosome 11
27,871,699 - 27,872,374

- View of Chromosome 11
- Graphical view
- Graphical overview
- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

Ensembl Gene Variation Report for LOC_Os11g47278

Gene	LOC_Os11g47278 () To view all Ensembl genes linked to the name click here .
Tigr Gene ID	LOC_Os11g47278
Genomic Location	This gene can be found on Chromosome 11 at location 27,871,699-27,872,374. The start of this gene is located in Clone AC116367 .
Description	hypothetical protein

SNPs and variations in region of gene LOC_Os11g47278



Variations in LOC_Os11g47278.1

Transcript Info

Browser Links


- [Genomes Home](#)
- [Genomes Help](#)
- [Switch Species](#)

LOC_Os11g47278.1

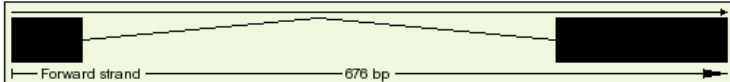
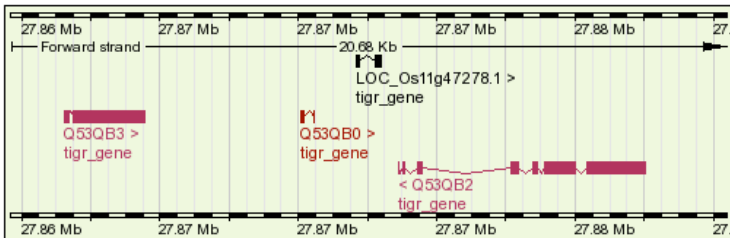
- [Gene information](#)
- [Gene splice site image](#)
- [Genomic sequence](#)
- [Gene variation info.](#)
- [Transcript information](#)
- [Exon information](#)
- [Protein information](#)
- [Export transcript data](#)

Chromosome 11
27,871,699 - 27,872,374

- [View of Chromosome 11](#)
- [Graphical view](#)
- [Graphical overview](#)
- [Export information about region](#)
- [Export sequence as FASTA](#)
- [Export EMBL file](#)
- [Export Gene info in region](#)
- [Export SNP info in region](#)



Ensembl Transcript Report

Transcript	LOC_Os11g47278.1 (TIGR_LOCUS)
Tigr Transcript ID	LOC_Os11g47278.1
Transcript information	Exons: 2 Transcript length: 228 bps Translation length: 75 residues This transcript is a product of gene: LOC_Os11g47278
Genomic Location	This transcript can be found on Chromosome 11 at location 27,871,699 The start of this transcript is located in Clone AC116367 .
Description	hypothetical protein
Similarity Matches	This GeneModel TIGR entry corresponds to the following database identifiers: TIGR_LOCUS: LOC_Os11g47278.1 TIGR_FN: 11981.m08508
GO	The following GO terms have been mapped to this entry via InterProScan
Transcript structure	
Transcript neighbourhood	
Transcript sequence	ATGGCCCTCGGCTGCTTGGTGGCTTTTGTGATCTTGGCTGTCGCTCTCTCATCCTGCAAA GCGGACGAGAGTACAGATGTGTGTTTCTATACGGGCTCCTCGGGCATGCCAAGTGAGAATG TGTGGAGCCTACTGCCTCAAATACTATGGTAATTGGTAGACTGGAAAGCGCCTACTGC AATGAGCAAGTGAATGCTGCTGCCAAGCAAGATCGATTAGTCGTTGA

Show the following features: Exons

Describes location on the Rice genome. Select to view detailed info from the Genome Browser.

Gene Ontology

Exon Info

BROWSER LINKS

- Genomes Home
- Genomes Help
- Switch Species

LOC_Os11g47278.1

- Gene information
- Gene splice site image
- Genomic sequence
- Gene variation info.
- Transcript information
- Exon information**
- Protein information
- Export transcript data

Chromosome 11
27,871,699 - 27,872,374

- View of Chromosome 11
- Graphical view
- Graphical overview
- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

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Ensembl Exon Report

Transcript	LOC_Os11g47278.1 () To view all Ensembl genes linked to the name click here .
Tigr Transcript ID	LOC_Os11g47278.1
Transcript information	Exons: 2 Transcript length: 228 bps Translation length: 75 residues This transcript is a product of gene: LOC_Os11g47278
Genomic Location	This transcript can be found on Chromosome 11 at location 27,871,699-27,872,374. The start of this transcript is located in Clone AC116367 .
Description	hypothetical protein
Rendering options	<div>Flanking sequence at either end of transcript <input type="text" value="50"/></div> <div>Intron base pairs to show at splice sites <input type="text" value="25"/></div> <div>Show full intronic sequence <input type="checkbox"/></div> <div>Show exons only <input type="checkbox"/></div> <div>Go</div>

Exon Information

No.	Exon / Intron	Chr	Strand	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence							cactgtagcctgatcttgatggcaatcattccaagaaaataacaca
1	LOC_Os11g47278.1.exon1	11	1	27,871,699	27,871,765	0	1	67	ATGGCCCTCGGCTGCTTGGTGGCTTTTGTGATCTTGGCTGTCGCTCTCATCTGCAAA GCGGACG
	Intron 1-2	11	1	27,871,766	27,872,213			448	gttagatttaatttcctctctacaa.....acagagtttggtttatgttag
2	LOC_Os11g47278.1.exon2	11	1	27,872,214	27,872,374	1	0	161	AGAGTACAGATGTGTGTTTCTATACGGGTCTCCGGGCATGCCAAGTGAAGATGTGTGGAG CCTACTGCCTCAAATACTATGGTAATTTGGTAGACTGGAAAGGCGCCTACTGCAATGAGC AAGTGAATGCTGCTGCAAAAGCAAGATCGATTAGTCGTTGA
	3' downstream sequence								ataaatcaattaatgtccacctaatcgatcaatctgttgagacggattg.....

Supporting Evidence

The supporting evidence below consists of the sequence matches on which the exon predictions were based and are sorted by alignment score.

Score: 100 >=99 >=97 >=90 >=75 >=50 <=50 NO EVIDENCE

Protein Info

Browser Links

- [Genomes Home](#)
- [Genomes Help](#)
- [Switch Species](#)

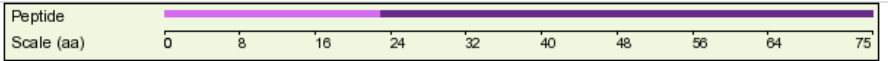
LOC_Os11g47278.1

- [Gene information](#)
- [Genomic sequence alignment](#)
- [Gene splice site image](#)
- [Gene tree info](#)
- [Gene variation info.](#)
- [Genomic sequence](#)
- [Transcript information](#)
- [Exon information](#)
- [Protein information](#)
- [Export protein data](#)

Chromosome 11
27,871,699 - 27,872,374

- [View of Chromosome 11](#)
- [Graphical view](#)
- [Graphical overview](#)
- [Export information about region](#)
- [Export sequence as FASTA](#)

Ensembl Protein Report

Translation	LOC_Os11g47278.1 (TIGR_LOCUS)
Tigr Translation ID	LOC_Os11g47278.1
Translation information	This protein is a translation of transcript LOC_Os11g47278.1 , which is a product of gene LOC_Os11g47278 .
Genomic Location	This translation can be found on Chromosome 11 at location 27,871,699-27,872,374 . The start of this translation is located in Clone AC116367 .
Description	hypothetical protein
GO	The following GO terms have been mapped to this entry via InterProScan :
Protein Features	
Protein Sequence	<p>MALGCLVAFVILAVALLSSCKADESTDVCFYTLRACQVRMCGAYCLKYYGNLVDWKGAYC NEQVKCCCKARSISR</p> <p>Show the following features: <input type="text" value="None"/></p> <p>Number residues: <input type="text" value="No"/></p> <p>Refresh</p>

☐ Domains on LOC_Os11g47278.1

No domains on this peptide

☐ Other features on LOC_Os11g47278.1

No other features on this peptide

☐ Variations on LOC_Os11g47278.1

Export

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

Chromosome 11
27,871,699 - 27,872,374

- View of Chromosome 11
- Graphical view
- Graphical overview
- View Syntenic regions ...
- View region in CMap

Export data

- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

LOC_Os11g47278.1

- Gene information
- Gene splice site image
- Genomic sequence
- Gene variation info.
- Transcript information
- Exon information
- Protein information
- Export transcript data

Select region/feature to Export

Choose one or two features from the same chromosome as anchor points and display the region between them. Both features must be mapped to the current Ensembl golden tiling path. If you select "None" for the second feature, the display will be based around the first feature.

Please note that there is an upper limit of 5Mb that we will export.

Region

Chromosome name/fragment

From (type): *

To (type):

Context

Bp upstream (to the left)

Bp downstream (to the right)

Output format



Output Format

[Continue >>](#)

Fields marked with * are required

The default is to select the feature to export from the page you visited here from.

These links will read differently, depending upon the page you are on (gene, protein, exon, etc.).



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

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SNP Properties

Click for Gene SNP info –(gene variation report) – see slide 25

Go to NCBI

You are here, accessed from Slide 19

Go to Contig view

Use menu to customize

Genomes

Genomes

Switch Spec

dbSNP: rs19120893

Gene SNP info

Gene SNP info

Gene SNP info

Gene SNP info

Gene SNP info

Gene SNP info

rs19120893 - SNP info

Chromosome 11
27,828,062

View of Chromosome 11

Graphical view

Graphical overview

Export information about region

Export sequence as FASTA

Export EMBL file

Export Gene info in region

Export SNP info in region

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SNP	rs19120893 (dbSNP125)
Synonyms	None currently in the database
Alleles	T/C (ambiguity code: Y)
Validation status	Unknown
Molecular type	GENOMIC
Linkage disequilibrium data	No linkage data for this SNP
Run component "tagged_snp"	Function EnsEMBL::Web::Component::SNP::tagged_snp fails to execute due to the following error: EnsEMBL::Web::Component::SNP::tagged_snp called at modules/EnsEMBL/Web/Document/Panel.pm line 554.
Sequence region	ATCCGTGAAGTCATCCATCCGGAGTGGTTGGCGAATCCGGYGGTCGTTCCCAAGGCGAAC GGCAAGCTTCGGATGTGCATC (SNP highlighted)

☐ Genotype frequencies per population
This SNP has not been genotyped in a population.

☐ Allele frequencies per population
This SNP has no allele frequencies per population.

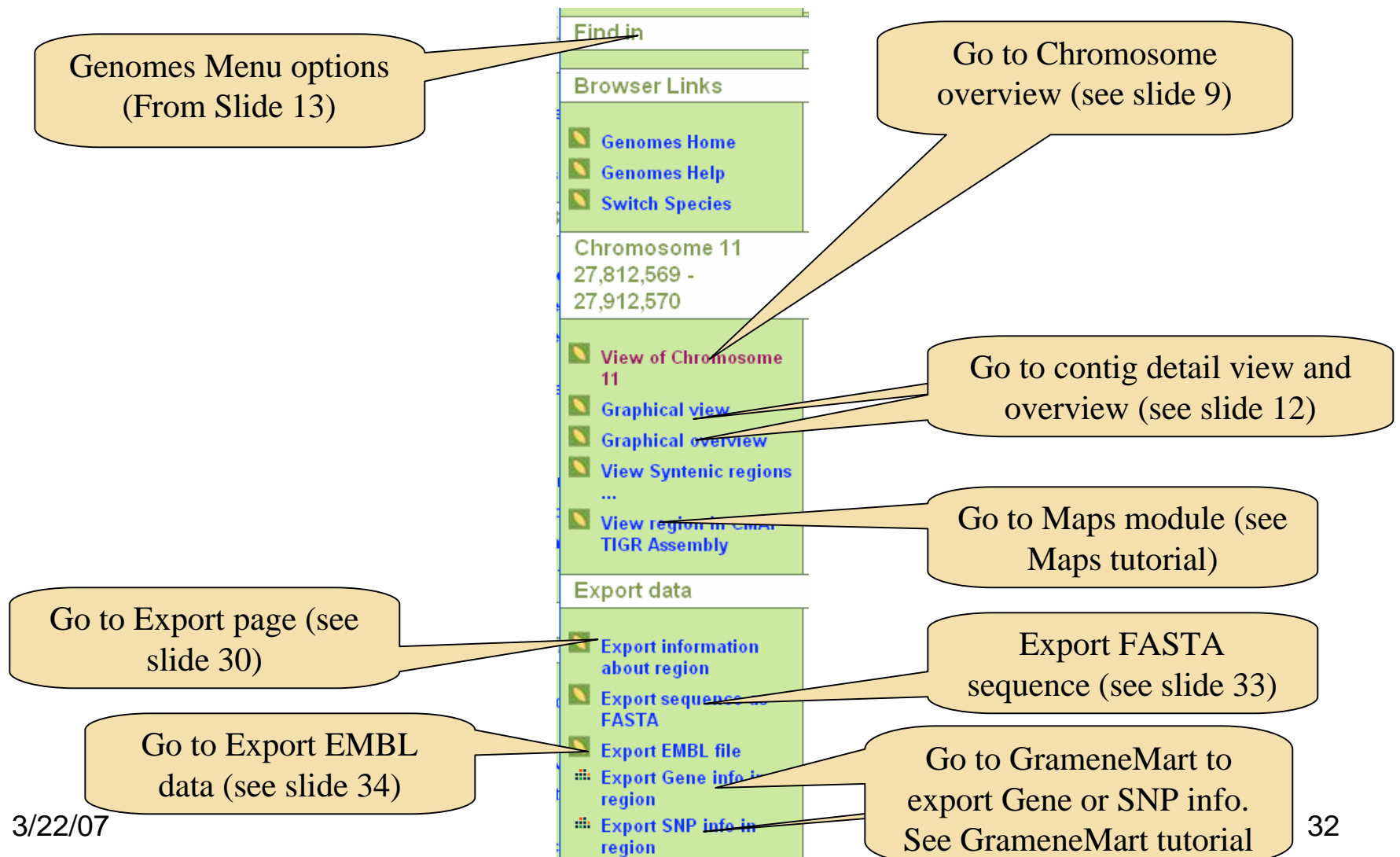
☐ SNP rs19120893 is located in the following transcripts

Genomic location (strand)	Location	Transcript: start-end	GeneSNPView link	Translation: start-end	Peptide allele	Type
11: 25857316-25857316 (1)	SNP maps several times: Choose this location	LOC_Os11g43670.1: 2606-2606	View in gene context	LOC_Os11g43670.1: 869-869	V/A	NON_SYNONYMOUS_CODING
1: 465759-465759 (1)	SNP maps several times: Choose this location	LOC_Os11g43680.1: n/a	View in gene context	LOC_Os11g43680.1: n/a		DOWNSTREAM
		LOC_Os01g01850.1: 2606-2606	View in gene context	LOC_Os01g01850.1: 869-869	V/A	NON_SYNONYMOUS_CODING
		LOC_Os01g01860.1: n/a	View in gene context	LOC_Os01g01860.1: n/a		DOWNSTREAM
11: 27828062-27828062 (1)	Current location	LOC_Os11g47190.1: 2606-2606	View in gene context	LOC_Os11g47190.1: 869-869	V/A	NON_SYNONYMOUS_CODING
		LOC_Os11g47200.1: n/a	View in gene context	LOC_Os11g47200.1: n/a		DOWNSTREAM

☐ SNP Context - chromosome 11 27828062

Features	Source	SNP class	SNP type	Decorations	Export	Image size	Help
genbank_rrna				No genbank_rrna in this region			
siRNA_genes				No siRNA_genes in this region			
genbank_trna				No genbank_trna in this region			

Genomes Menu



Export FASTA

Find in

Browser Links

- Genomes Home
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- Switch Species

Chromosome 11
27,812,569 - 27,912,569

- View of Chromosome 11
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- Graphical overview
- View Syntenic regions ...
- View region in CMAP TIGR Assembly

Export data

- Export information about region
- Export sequence as FASTA**
- Export EMBL file
- Export Gene info in region
- Export SNP info in region

Configuring FASTA File output for FASTA format text file

You are exporting Chromosome 11 27,812,569 - 27,912,569.

FASTA format options

Output format

☒ HTML ☐ Text

☐ Compressed text (.gz)

Continue >>

Select options and follow instructions

e!mpowered

Export EMBL

Browser Links

- Genomes Home
- Genomes Help
- Switch Species

Chromosome 11
27,812,569 - 27,912,570

View of Chromosome 11

- Graphical view
- Graphical overview
- View Syntenic regions ...
- View region in CMap

Export data

- Export information about region
- Export sequence as FASTA
- Export EMBL file**
- Export Gene info in region
- Export SNP info in region

Configuring Flat File output for EMBL

You are exporting Chromosome 11 27,812,569 - 27,912,570.

Flat file format options

Features to export

- ☐ Similarity features
- ☐ Repeat features
- ☐ Prediction features (genscan)
- ☐ Contig Information
- ☐ Variation features
- ☐ Marker features
- ☐ Gene Information
- ☐ EST Gene Information

Output format

- ☒ HTML
- ☐ Text
- ☐ Compressed text (.gz)

[Continue >>](#)

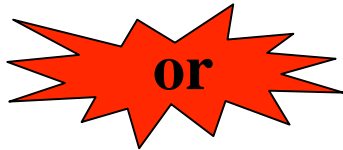
USDA

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Email Gramene at gramene@gramene.org