

Welcome to the Gramene 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.

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 Help



The hand icon indicates a link that allows you to go to the same page in your web browser.



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

Action Options are noted in this type of font.

Notes or comments use this style font.

Gramene Home Page

GRAMENE *A Resource for Comparative Grass Genomics* v20 (Dec 2005)

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

Quick Search

Did you know...?

- Gramene now has [tutorials](#) for every module.

Gramene Tips:

You can view Gramene's archive of all its [News](#) items.

[All Tips](#)

Genomes-Ensembl

Maps-CMap

Markers

QTL

Genes

Proteins

Ontologies

Literature

Sequences-BLAST

All-GrameneMart

Quick Start

Click here to open Genome Browser Home Page

[Browse by Gene Ontology using GO](#)

al maps for [Rice](#), [Maize](#), [wheat](#), [Barley](#), [Oats](#), [Sorghum](#), and other grasses, or use the Comparative Map Viewer (CMap) to compare maps of different types and species.

MOLECULAR MARKERS: Use the Simple Sequence Repeat Identification Tool (SSRIT); or search by [marker type](#) or species, including [Rice](#), [Maize](#), [Sorghum](#) and [Others](#).

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

Featured News

- Breaking news on genomic research
- [Rice News Worldwide](#) from IRRI
- [Gramene News Archive](#)

Visit us at

- [Plant and Animal Genome XIV Conference](#), January 14-18, 2006, San Diego, CA, USA
- [Rice Technical Working Group Meeting](#), Feb. 26-Mar. 1, 2006, The Woodlands, Texas, USA



Genomes Home Page

GRAMENE Genome Browser

Search Genomes

Search Feedback

Find: All [v] RbcS **Lookup**

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

1b. If desired, you may narrow your search

Or

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

Version of TIGR being used

Click for BLAST tool. See BLAST tutorial.

Click to enter **Gramene Mart**. See Gramene Mart Tutorial

Click to read release notes for the current version of Genome Browser

Species in Gramene

Species	Release Date	Version
Rice-japonica	Dec 2004	TIGR v3
Maize	Oct 2004	AGI
Arabidopsis	May 2004	TIGR v5

Links

- Batch data/sequence retrieval
- Sequence similarity searches
- Release note
- [GrameneMart](#)
- [BlastView](#)
- [Release Notes](#)

SPECIES

USDA NCBI CSH



Term Search Results

Search for "RbcS" in *Oryza_sativa*

[Retry in](#) [Arabidopsis_thaliana](#) [Zea mays FPC Map](#) [Zea mays Sequenced](#)

Chromosome

No match for this search type

Clone

No match for this search type

Contig

No match for this search type

Domain

No match for this search type

Feature

No match for this search type

Gene

No match for this search type

Marker

No match for this search type

Peptide

No match for this search type

Protein

P05347 (RBS1_ORYSA): Ribulose biphosphate carboxylase small chain, chloroplast precursor RBCS

RuBisCO small subunit .

P05348 (RBS_MAIZE): Ribulose biphosphate carboxylase small chain, chloroplast precursor RBCS

RuBisCO small subunit .

P18566 (RBS2_ORYSA): Ribulose biphosphate carboxylase small chain A, chloroplast precursor

RBCS-A RuBisCO small subunit A .

P18567 (RBS3_ORYSA): Ribulose biphosphate carboxylase small chain C, chloroplast precursor

RBCS-C RuBisCO small subunit C .

Q36688 (Q36688_ORYSA): Ribulose 1,5-bisphosphate carboxylase rbcS .

Q38793 (RBS_AEGTA): Ribulose biphosphate carboxylase small chain, chloroplast precursor RBCS

RuBisCO small subunit .

Q41373 (RBS_SACHY): Ribulose biphosphate carboxylase small chain, chloroplast precursor RBCS

RuBisCO small subunit .

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

(0 results)

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

(0 results)

(0 results)

(0 results)

(6 results)

Q9SDY7 (Q9SDY7_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SDY8 (Q9SDY8_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SDY9 (Q9SDY9_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNW4 (Q9SNW4_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ6 (Q9SNZ6_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ7 (Q9SNZ7_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ8 (Q9SNZ8_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ9 (Q9SNZ9_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ10 (Q9SNZ10_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ11 (Q9SNZ11_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ12 (Q9SNZ12_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ13 (Q9SNZ13_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ14 (Q9SNZ14_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ15 (Q9SNZ15_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ16 (Q9SNZ16_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

Q9SNZ17 (Q9SNZ17_9POAL): Ribulose-1,5-bisphosphate carboxylase small subunit rbcS .

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

You may enter a **chromosome number and location**.

Oryza sativa (japonica) Genome Browser v18

Current Release TIGR v3

- ▶ TIGR pseudomolecule assembly release 3 of IRGSP finished sequence.
- ▶ Clones which were not used in the assembly have been mapped as features, and are listed [here](#)
- ▶ Feature data sets mapped to the genome can be viewed in [summary](#) and [detailed](#) form.
- ▶ Putative orthologs between [rice](#), [Arabidopsis](#) and [maize](#) gene models were generated using Ensembl's compara pipeline.
- ▶ Syntenic regions between the [maize FPC map](#) and the rice genome assembly were [estimated](#), and loaded into Ensembl.

Example entry points

- ▶ Gene: [LOC_Os01g14200](#)
- ▶ Transcript: [LOC_Os08g23430.1](#)
- ▶ Chromosome: [12](#)
- ▶ Contig: [AP003727](#)

Lookup

▶ Chr: from -

Browse a Chromosome

Rice Synteny Vs Maize FPC Map

Rice-japonica **Arabidopsis**

Rice Chr 1 vs. Maize

- Rice Chr 1 vs. Maize
- Rice Chr 2 vs. Maize
- Rice Chr 3 vs. Maize
- Rice Chr 4 vs. Maize
- Rice Chr 5 vs. Maize
- Rice Chr 6 vs. Maize
- Rice Chr 7 vs. Maize
- Rice Chr 8 vs. Maize
- Rice Chr 9 vs. Maize
- Rice Chr 10 vs. Maize
- Rice Chr 11 vs. Maize
- Rice Chr 12 vs. Maize

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

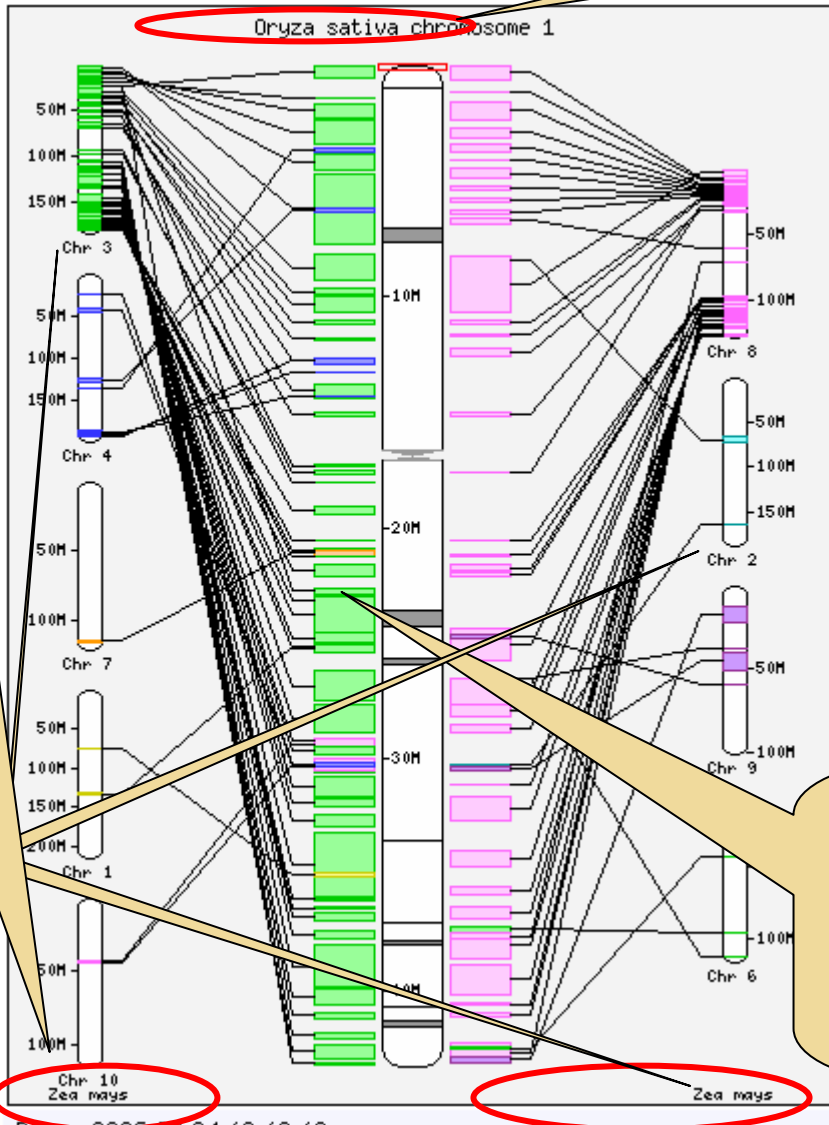
Or choose a **Synteny map** to view (see *Slide 8*)

Synteny: Rice Chr. 1 vs Maize



Identifies the rice chromosome you are browsing, which is in the **center** of the diagram.

Identifies the maize genomes you are comparing to the rice chromosome. Color-coding identifies the correlations. Those on the left show blocks of conserved synteny, those on the right show homology between genes.



Change Chromosome

Jump to Chromosome:
[Jump to mapview for chromosome statistics.](#)

Synteny

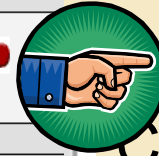
View Rice Chr 1 vs

Navigation for choosing an alternate chromosome or syntenic species

Clicking on a link on the map will let you view either the rice or the maize chromosome at that location (see Slide 11), or to display the Maize Chromosome centrally (example slide 26).

Rice

Chromosome 11



Click on a band to go to **contig view** or jump to a contig view (see slide 11)

MapView shows distribution of features at chromosome scales.

Choose another chromosome to view.

Chromosome information

Click to select a region based on two features (**Anchor view**). (see slide 10).

Click to choose viewing specific features (see slide 10).

Select a species and click go to view synteny with current chromosome (see slide 8).

Change Chromosome

Chromosome: 11

Chromosome

Length: 17 bps

GeneModel_Submission:	
Rice_GeneModel_FGENESH:	
Rice_GeneModel_TIGR:	
Rice_ArrayConsensus_Affy57K:	
Rice_ArrayOligo_NSf20K:	
Rice_BAC:	
Rice_CDS:	
Rice_EST:	
Rice_ESTcluster_PlantGDB:	5978
Rice_ESTcluster_TIGR:	375
Rice_FST-TDNA:	1095
Rice_FSTos17:	187
Rice_FSTtransposon:	4718
Rice_MPSStag_Meyers:	
Rice_MarkerRFLP:	
Rice_MarkerSSR:	
Rice_SAGEtag_MGOS:	
RiceAlta_BACend_OMAP:	
RiceAustraliensis_BACend_OMAP:	
RiceBrachyantha_BACend_OMAP:	
RiceCoarctata_BACend_OMAP:	
RiceGlaberrima_BACend_OMAP:	
RiceIndica_EST_BGI:	8009
RiceIndica_ESTcluster_BGI:	2371

Jump to Contig View

Click anywhere on the chromosome ideogram or one of the feature distribution plots to jump to a contig view of features at that point.

Jump to clone: AP003727

[Display contig-level view between any two features.](#)

Synteny

View Rice Chr 1 vs maize ☒

Map your data

[Map your own data on the karyotype using KaryoView.](#)

Anchor and Karyo Views

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

Use **Karyoview** to design your own map.

AnchorView

Anchorview allows you to choose 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 then the display will be based around 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

Chromosome: 1

From:

- ☐ Band AP000570
- ☐ Region
- ☐ Marker
- ☐ Gene
- ☐ Basepair

To:

- ☐ Band AP000570
- ☐ Region
- ☐ Marker
- ☐ Gene
- ☐ Basepair
- ☒ None

Context

Basepairs downstream : 0

Basepairs upstream : 0

[View in configview](#)

Use the form below to enter a region on a customisable karyotype image. Hit the "Display Karyotype" button to view the results.

You can change the configuration or data after displaying the karyotype.

If you have any comments or feedback about KaryoView, we'd like to hear from you.

Upload Data Set

Accepted [file formats](#)

Paste file:

Type or paste into the box to the right a list of features you want to display on a karyotype, with each feature on a separate line. Feature data must be separated by spaces or tabs, and must contain, in order:

- **chromosome**
- **start base** (in chromosome coordinates)
- **end base** (in chromosome coordinates)
- **feature name or ID**

e.g. 3 12000000 15000000 my_feature

Upload file:

File URL:

[Browse...](#)

[Go](#)

Configure Display Options

Display data points in the following style: Outline wide box

Display data points in the following colour: red

Show menus on mouseover: on

Number of rows of chromosomes: 1

Height of the longest chromosome (pixels): 300

Padding around chromosome (pixels): 4

Spacing between chromosomes (pixels): 6

Spacing between rows (pixels): 50

Choose features (following directions at left).

Upload data

Configure results display

Viewing Results - Contig View

This is an **outline** of information in 'contig view'. These sections may display data when you come here.

Clones which were not used in the assembly have been masked. Features. Other clones are listed [here](#).

+ Chromosome #

+ Overview

+ Detailed view

Jump to region: 1 bp 2227259 to 2277257

◀◀ 2 Mb ◀ 1 Mb Window Zoom ▶ 1 Mb ▶▶ 2 Mb Refresh

Features ▼ ESTs ▼ GSSs ▼ FSTs ▼ Markers ▼ Arrays ▼ Decorations ▼ Export ▼ Jump to ▼ Window Help ▼

+ Basepair view

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

Customizing and Navigation bar
for detailed view (see slide 13 on
customizing your view)

Chromosome

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

TIGR pseudomolecule assembly, phase 3, of IRGSP finished sequence. 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 as features. Other clones are listed [here](#).

[-] Chromosome 11

Chr. 11

Entire Chromosome is displayed above

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



Overview

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

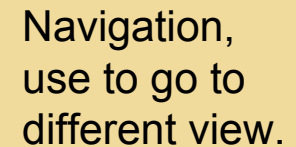
Region of rice/maize synteny.

Clicking on this section will magnify and center to the section you clicked on.

Color-coded features
are identified in left-
hand column as
indicated

Boxes represent annotated TIGR genes

Zoom in/out to a desired level of resolution



Changes
display size.

Customization Pop-up menu



- For this tutorial, the “popup on click” and “show popup menus” have 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.
- If you deselect the “popup on click,” hovering over a feature will reveal the popup menu.
- If neither option is selected, clicking on a feature will take you to an appropriate page with more information on that particular feature.

Customize view to
choose options
(previous 2 slides)

Jump to region: 11 bp 28148704 to 28168928

Refresh

2 Mb 1 Mb Window

Features ESTs GSSs FSTs Markers Arrays Decorations Export Jump to Width Help

Length 28.15 Mb 28.15 Mb 28.15 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.17 Mb 28.17 Mb

Rice_GeneModel_FGENESH

GeneModel TIGR

DNA(clone)

GeneModel TIGR

Rice_GeneModel_FGENESH

Rice_EST

Rice_MarkerRFLP

Rice_MarkerSSR

Rice_MarkerBACend_OMAP

Barley_EST

Maize_EST

Maize_HiCotH

Cluster_TIGR

Sorghum_EST

Sugarcane_EST

Wheat_EST

SNPs

Length

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

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

Click on a feature to open menu options (see slides 18-24)

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.

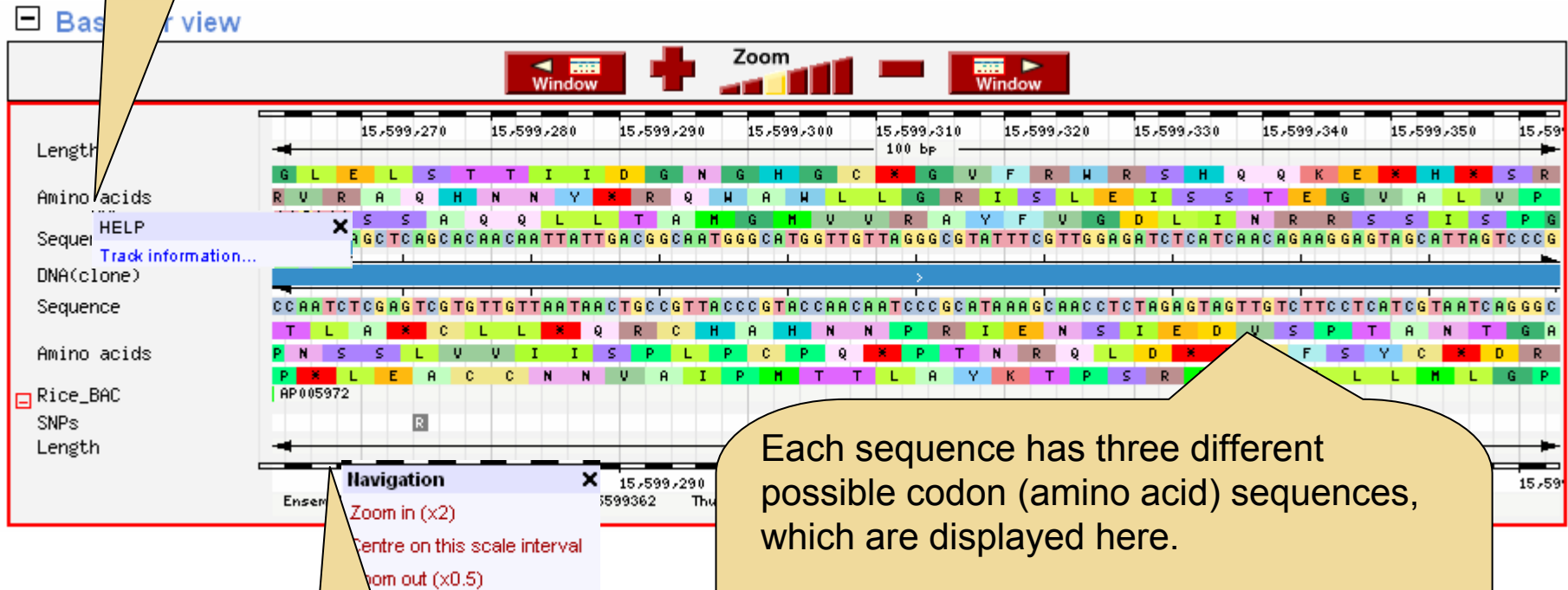
Red outlined box on overview above fills this detailed view display. The area in the red box is enlarged to fill the basepair display below. (You may wish to center in on a coding region.)

Click on a feature
to open menu
options (see slides
18-24)

Red outlined box on overview above fills this detailed view display. The area in the red box is enlarged to fill the basepair display below. (You may wish to center in on a coding region.)

Click for more information on tracks.

Base Pair View



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

For example TTGTCTTCTCA can be viewed in any of the following three ways:

TTG TCT TCC TCA
 ...TT GTC TTC CTC A..
 ...T TGT CTT CCT CA...

Click length ruler to open zoom menu

In detail view, click on a feature to open this menu

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

Note : slides 18 through 23 are interconnected, and many of the links on one leads to another.

LOC_Os11g47740 (TIGR LOCUS ID)	LOC_Os11g47740
View gene in genomic location: 28154450 - 28155503 bp (28.2 Mb) on chr11 This gene is located in sequence: AC134045	
hypothetical protein	
This gene was annotated by TIGR through a process of automatic and manual curation.	
view genomic sequence for this gene with exons highlighted	
Export Data	Export gene data in EMBL, GenBank or FASTA
SNP information	View information about variations on this gene.
1: LOC_Os11g47740.1 (LOC_Os11g47740.1) [Transcript information] [Exon information] [Protein information]	
Transcript Structure	
Transcript/Translation Summary	Stable ID: LOC_Os11g47740.1 Exons: 2 Transcript length: 355 bp Translation length: 118 aa [Transcript information] [Exon information] [Protein information] This Tigr_gene entry corresponds to the following database identifiers: GRAMENE OLD: GRMT00000130317 TIGR FN: 11687.m04487 TIGR LOCUS: LOC_Os11g47740.1 TIGR MODEL: 5273.m00189
Similarity Matches	
Transcript Structure	
Protein Features	

(see slide 19).

(see slide 20).

Detailed information on the transcript and its structure (see slides 21, 22 and 23.)

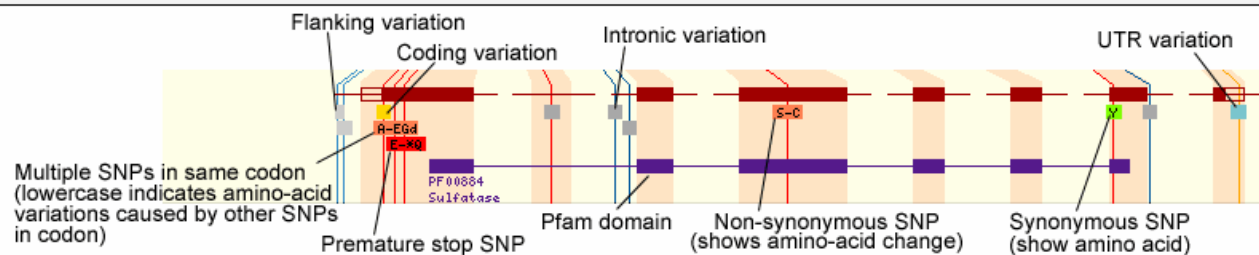
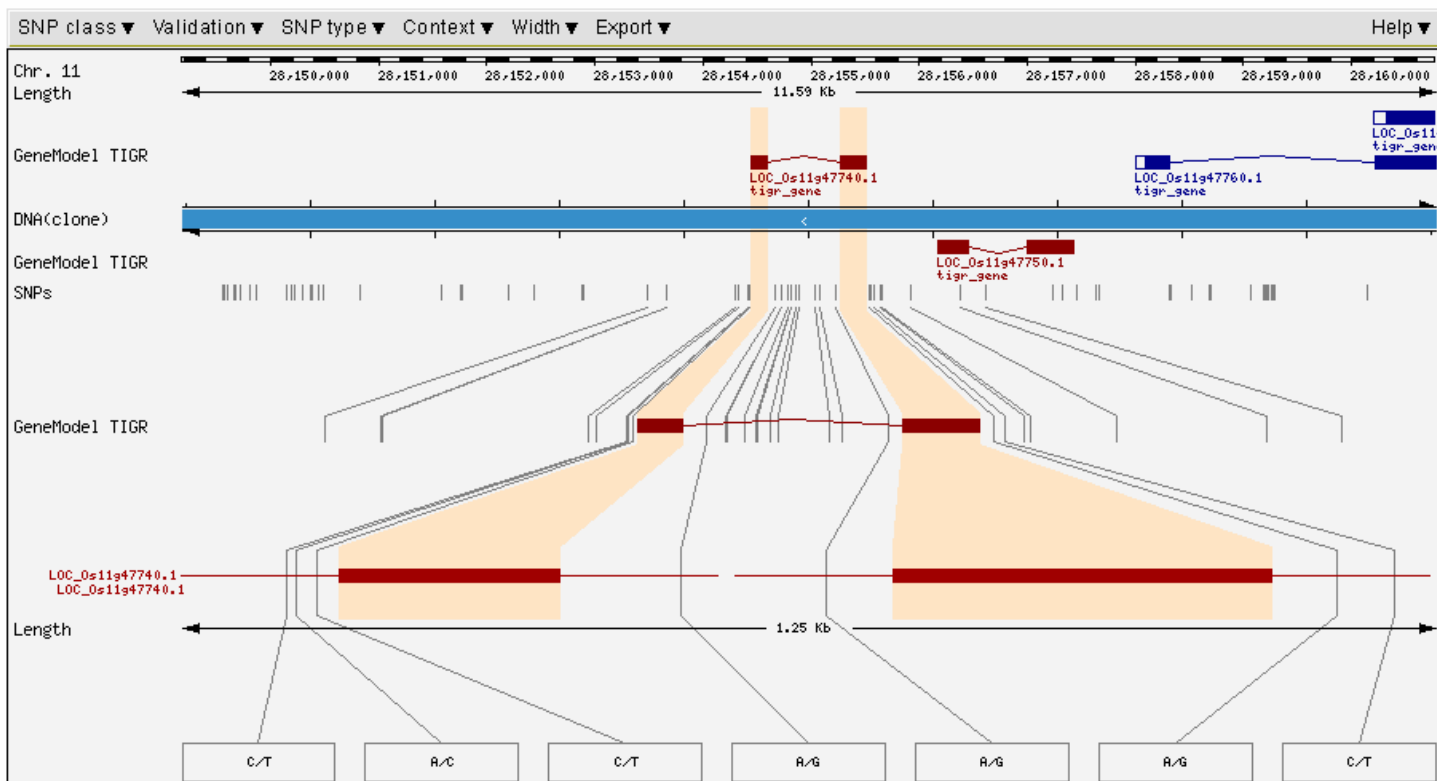
Select to view Ensembl Protein Report (see slide 22).

Gene	LOC_Os11g47740 (TIGR_LOCUS ID)
Ensembl Gene ID	LOC_Os11g47740
Genomic Location	View gene in genomic location: 28154450 - 28155503 bp (28.2 Mb) on chromosome 11 This gene is located in sequence: AC134045
Markup Options	5' Flanking sequence 600 3' Flanking sequence 600 Exon markup Ensembl exons Both orientations SNP markup All SNPs Line numbering No numbers update
Gene Sequence	THIS STYLE: Location of other exons THIS STYLE: Location of selected exons THIS STYLE: Location of SNPs >chromosome:TIGR3:11:28153850:28155103:1 ATATATGCGTTCTTTCTTACTTAAAAAGTAAAAAATATATAAAAAAGTAGTCTTCTAGTA GTACTTAGCCGAAACCCCTTTTCTCGTACAAAGTTTGGTTGTTTGGATGGAATCCAAAAA TATACCCCTACCAATATTTTGTAGCGGTTTTTGTAAAGCCAAATATTGGCATTGCAA TGCTCTAACTTGGCACATTCTAGATTATAAATCAGGGTTTTGGTTTCTTATTGATATCAAA TCAAAACACCATTTTATCCTATCAAAATAAATAGTAGTGCTAAAAGTCTAGCTAGGATAATGA ACCAAAACAAAGTCCGTTAAGTAGGGTAATGAACCTTACTACATGGGCCCGCGGCTTTGGGAC ATCCACAGGGCTGACAGGCATGCAGATGCTGATAAAGGAATGGAATGGAATAAAGTCCATTT TGCTCCCTCATCTCTTGCCTTGCCTGAATAAATCCCTCAACTGGAAAACGGGATATA ACGCCCTCCTTCTCTCTGAAAACAGAGCAAAATCACCTCCCTCAGTGGTTTGGCTGGCGG TTTCGTCGACGTGGCGTCGTTGACCTGTTGACGAGCTGACTCTGTGTGGTGGGACCCAC ATGTCAAGTGCBAACCTCTCCTTTCTTCTCTCCTCCTCTCTCTCTCCTCCTCTCTCTCT CCCGTGGCCTCTCTCTCCACCTTGGCCAGAGCARTGGCGGACGCGGTGGCAGCAGCGCTC GGAGCARTCGGTCCGCGCTCTACCAAAAGTAGCGAGAGCACGCAGGACGTGGAGAAAGGGAG AGAGAGATTGAGAGAGTCTCTCTCGTCACCGCCGTGCCACGCGCGAAGAGAAAGAAAGGAA ACCGAGGATAAAGGGAGAGAGAGAGTCTCTCCGTCACTGCCGCTGCCGCCGTCTAGAGA TCCCTTCGCGAGCTGTGTCCCGCCACACGCGCGTCCACACCGGTCGCCGTCCCGTGCTC CTTCCGTCTCCCGGGCGGAGAAAGAAAGGAAAGACCGGGGAGAGAGGGGGCAGAGAGAGCC ATCCGTCAACGGCAGCTGCGCCGCCCTTGGAGCGTTGCCGATGCTACTTCTGGCTTCTTCTCT GCCGATGCTACTGAGGATGAAGAAAGCCCTCTGTCTAGGTAAATCTTTTTCTTCTTTCTCT CACTCACTCATCAGCTGCTAGCTTTGCTAGCTAGGAGTAGCTAGCTGCTTGCTGCTCTTG CTGTGAGAGGAGGAGAAAGAAAGTCTGAGGCTGTTGGCTGTCTGTGTGCTATGGCTGCTAT TCAGAGCCCCGACGGTGATGTATCGACAGCGTGCCGCTGCACCTGCACCCGGCGTTTGA CCACCCGAAGCTCATTCAATTTTGTTCAAATTTGCAGTGATCGTTTCTATCTCCAGCGAC GTTTCTTGATCTGTGTTTGTGATTGTGTGCGCGTGACAGTTTGGCCGGAGCCAGAGGAGAG GCCCAAGGTGGGTGGCGCGCGCGCGCGCARTGGGAGGCGCGCGCGAGAGGAGGTCTGTT CCCGATGGCGTGGAGGAGCAGCAGGTTGTGCCCGAGGGGAGCGGTGCGCGTGGCGC GACGAGCAGAGCGCGAGCTGTGAGGTCCAGCTCCTCTCCCTGTTTGGGGATGAGCAGAGCC TCGTGCCCGGCTGCCGCTGGTGTCTGCCGCTGAGGAAGAAAGATGGGATGGGGGGGCTAC TGACAGTGGGGCCCATAAGCTGACTCAGCAAGTCAATGGAGGGGCCACCGTCACTGTAAG TGCCAGCTAGGACAAAACCGCTCCGAAACCATCGAGGGAGGATGATTGCTGTGGTTTTT ACGAAAGATGAGAGGCATTATACCCGTTTTCCGGTTGAGGGATGTTATTATCCAAAGTAC ATGAGATGAGGAGGTAAAAAGGACTTATTCGAAATGGAATAGCTAAAAGGAAAAAGTAC ACCGAAAGTCCCTCAACTTGTCTCGAGTTACAAAATCATCCCCAAACGCAGAAACCGGGT ATAACGATCCCAAACTTACAAAACCATTACAAATAGGTCCCTTAGTGTTTGTGATCCG GTTTTGTCTATGTGGCAGCTGAGCCAGCGTGGGACTTATGTGGACCTACCTGTCACTA TGCCACGTGAGCAGGTACCTGTTTCCCTCCTCTCCCTTGTCTCTCTCTCACACACAC TCTTCTCTGGAAGGCCGGCGGGCGGTGGGAGGAGGTCGCCGGCGAGGAGGTCCGA CGGCCGGCGCGGATCGCGCGCGCGCGCGCAGGCG base 447: C/T base 473: C/T base 567: C/T base 573: A/C base 586: C/T base 815: A/G base 873: A/G base 878: C/T base 929: C/T base 964: C/T base 968: A/G base 1007: A/G base 1033: G/T base 1193: C/T base 1231: A/G base 1375: A/G base 1696: A/G base 1732: C/T base 1792: C/T base 1812: A/G base 2077: A/T

Sequence Markup

SNP Information

Gene	LOC_Os11g47740 (TIGR LOCUS ID)
Ensembl Gene ID	LOC_Os11g47740
Genomic Location	View gene in genomic location: 28154450 - 28155503 bp (28.2 Mb) on chromosome 11 This gene is located in sequence: AC134045
Description	hypothetical protein
Gene information	View information about this gene.



LOC_Os11g47740.1 (Peptide LOC_Os11g47740.1)

ID	class	alleles	ambiguity	status	chr	pos	SNP type	AA change	AA co-ordinate
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Transcript Information

Transcript	LOC_Os11g47740.1 (TIGR LOCUS ID)
Tigr_gene Transcript ID	LOC_Os11g47740.1 Tigr_gene
Tigr_gene Transcript	Exons: 2 Transcript length: 375bp Translation length: 124 residues This transcript is a product of gene: LOC_Os11g47740 [Exon information] [Protein information]
Genomic Location	View transcript in genomic location: 28154450 - 28155503 bp (28.2 Mb) on chromosome 11 This transcript is located in sequence: AC134045
Description	hypothetical protein
Prediction Method	This gene was annotated by TIGR through a process of automatic and manual curation.
Similarity Matches	This Tigr_gene entry corresponds to the following database identifiers: GRAMENE OLD: GRMT00000130317 TIGR FN: 11687.m04487 TIGR LOCUS: LOC_Os11g47740.1 TIGR MODEL:
Export Data	Export transcript

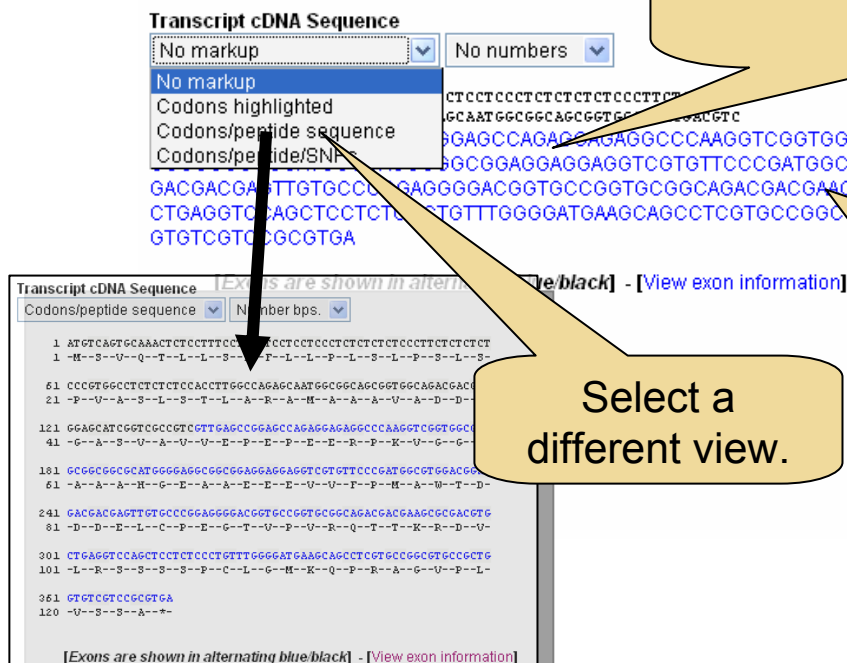
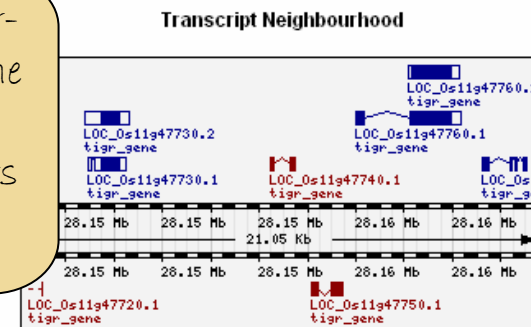
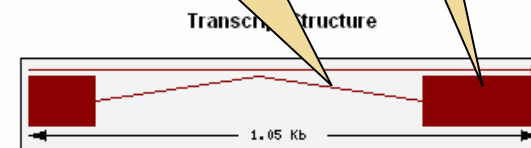
Exon -
coding
sequence

Intron -
non-coding
sequence

Deduced protein sequence
with the corresponding gene
sequence

Legend with color-coded details of the Transcript.
Alternating colors are alternate exons.

Select a different view.





Exon Information

Tigr_gene Exon Report

Transcript	LOC_Os11g47740.1 (TIGR_LOCUS ID)
Tigr_gene Transcript ID	LOC_Os11g47740.1 Tigr_gene
Tigr_gene Transcript	This transcript is a product of Ensembl gene LOC_Os11g47740 [Transcript Information] [Peptide Information]
Genomic Location	View transcript in genomic location: 28154450 - 28155503 bp (28.2 Mb) on chromosome 11 This transcript is located in sequence: AC134045
Description	hypothetical protein

Exon sequences
in Black

Exon Information

No.	Exon / Intron	Chr	Strand	Start	End	Length	Sequence
1	5' upstream sequence 11687.e18555	11	1	28154450	28154587	138 bp	cgtggcgtcgttgacctgttgacgagctgactctgtgtggtgggaccac ATGTCAGTGCAAACCTCTCCTTTCTTCTCCTCCTCCCTCTCTCTCTCCTTCTCTCTCT CCCGTGGCCTCTCTCTCCACCTTGGCCAGAGCAATGGCGGCAGCGGTGGCAGACGACGTC GGAGCATCGGTGCGCCGTC
2	Intron 1-2 11687.e18556	11	1	28154588	28155266	679 bp	gtaccaaagtagcgagagcacgcag.....tgtttgtattgtgtgcgcgtgcag
		11	1	28155267	28155503	237 bp	GTTGAGCCGGAGCCAGAGGAGAGGCCCAAGGTCGGTGGCGCGCGCGCGCGCATGGGGAG GCGGCGGAGGAGGAGGTCGTGTTCCCGATGGCGTGGACGGACGACGACGAGTTGTGCCCCG GAGGGGACGGTGCCGGTGCGGCAGACGACGAAGCGCGACGTGCTGAGGTCCAGCTCCTCT CCCTGTTTGGGGATGAAGCAGCCTCGTGCCGGCGTGCCGCTGGTGTCTGTCGCGCTGA ggaagaagatgggatgggggggctactgacaggtggggccataagctga.....
	3' downstream sequence						

KEY: -Up/downstream region
-Intron sequence
-UTR region

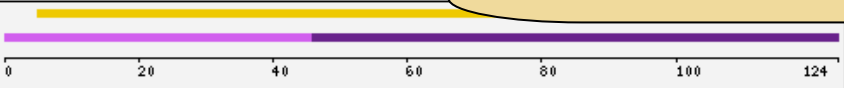
Display bases either side of intron.

View full intron sequence ☐

Display bases of 5' 3' flanking sequence. View only exon sequence ☐

Redraw

Protein Information

Peptide	LOC_Os11g47740.1 (TIGR LOCUS ID)
Tigr_gene Translation ID	LOC_Os11g47740.1
Tigr_gene Translation	This peptide is a product of gene LOC_Os11g47740 [Transcript Information] [Exon Information]
Description	hypothetical protein
Prediction Method	This gene was annotated by TIGR through a process of automatic and manual curation.
Protein Features	Low complexity Peptide Scale (aa) 
Export Data	Export peptide data in EMBL, GenBank or FASTA

Links provide detailed information on the corresponding Gene, Transcript and Exons

Allows you to export data in various formats.

Peptide Sequence

No markup ☐

No numbers ☐

MSVQTLSSFFLLPLSLPLSLSPVASLSTLARAAMAAVADVDGASVAVVEPEPL
AAARGEAASKEEVVFFMAWTDDDELCPFGQTVFVRQTTKRDVLRSSSPCLGK
VSSA

Peptide Stats

Isoelectric point = 4.2697
Charge = -6.5
Molecular weight = 12829.60
Number of residues = 124
Ave. residue weight = 103.465

Domain type	Start	End
Seg	5	73

Export View

Click the Export menu.

Jump to region: 9 bp 21373303 to 21423301

◀◀ 2 Mb ◀ 1 Mb Window Zoom ▶ 1 Mb ▶▶ 2 Mb Refresh

Features ▼ ESTs ▼ GSSs ▼ FSTs ▼ Markers ▼ Arrays ▼ Decorations ▼ Export ▼ Jump to ▼ Width ▼

- ☐ Include PDF links
- ☐ Include SVG links
- ☐ Include POSTSCRIPT links
- FASTA
- Flat file
- CLOSE MENU ▲

Select the image format options.

Choose FASTA for sequence, Flat File for annotations & other features.

Adjust Export Options

The screenshot shows a web-based interface for exporting genomic data. At the top, there are tabs for 'Flat File', 'FASTA', 'Feature List', and 'Pip'. The 'FASTA' tab is currently selected and highlighted with a red circle. Below the tabs, the interface is divided into several sections: 'Feature', 'Region', 'Select data to export', 'Select sequence type', and 'Select output format'. The 'Feature' section has a dropdown menu set to 'Transcript' and an 'ID' field. The 'Region' section has a 'Chromosome' dropdown set to '12' and 'Bases from' fields set to '2227259' to '2277257'. The 'Select data to export' section has a 'Show context of' field. The 'Select sequence type' section has radio buttons for 'Genomic', 'cDNA', 'Coding', 'Peptide', '5' UTR', and '3' UTR'. The 'Select output format' section has radio buttons for 'Text', 'HTML', and 'Zip'. At the bottom, there is an 'Export as' section with radio buttons for 'EMBL' and 'GenBank'. Below this is a list of features to export, all of which are checked: 'Similarity features', 'Repeat features', 'Prediction features (genscan)', 'Contig Information', 'Variation features', 'Marker Features', and 'Gene Information'. At the very bottom, there are 'Export' and 'Reset' buttons. Several yellow callout boxes provide instructions: 'Choose file format.' points to the 'FASTA' tab; 'Select features to include in export.' points to the checked list of features; 'Choose "Text" for download, "HTML" for web-display, "Zip" for compression.' points to the 'Text' radio button; and '13e: Click Export when ready.' points to the 'Export' button.

FASTA

Select data to export

Feature

☐ Gene ID:

Show context of: basepairs either side of feature

Region

Chromosome: 12 or fragment

☐ Bands from: to

☒ Bases from: 2227259 to 2277257

Select sequence type

☒ Genomic ☐ cDNA ☐ Coding ☐ Peptide ☐ 5' UTR ☐ 3' UTR

Select output format

☒ Text ☐ HTML ☐ Zip

Export Reset

Choose file format.

Export as ☒ EMBL ☐ GenBank

Export the following features:

- ☒ Similarity features
- ☒ Repeat features
- ☒ Prediction features (genscan)
- ☒ Contig Information
- ☒ Variation features
- ☒ Marker Features
- ☒ Gene Information

Select features to include in export.

Choose "Text" for download, "HTML" for web-display, "Zip" for compression.

13e: Click **Export** when ready.

Select output format

☐ Text ☒ HTML ☐ Zip

Export Reset

Flat File FASTA **Feature List** Pip

Select data to export

Feature

☐ Gene ID:

Show context of: basepairs either side of feature

Region

Chromosome: or fragment

☐ Bands from: to

☒ Bases from: to

Select export options

Export as ☒ GFF format ☐ Tab separated values ☐ Comma separated values

Export the following features:

☐ Similarity features

☐ Repeat features

☐ Prediction features (genscan)

☐ Variation features

☐ Gene Information

☐ Add gene type

Select output format

☒ Text ☐ HTML ☐ Zip

Flat File FASTA Feature List **Pip**

This exports a sequence and annotation file for use in comparative sequence analysis tools like [PipMaker](#), [Vista](#) or [zPicture](#).

Select data to export

Feature

☐ Gene ID:

Show context of: basepairs either side of feature

Region

Chromosome: or fragment

☐ Bands from: to

☒ Bases from: to

Select export options

Export for ☒ PipMaker/zPicture ☐ Vista

Select output format

☒ Archive (tar.gz) ☐ Individual files

Exported File

```
>1 dna:chromosome chromosome:TIGR3:1:2227259:2277257:1
TCAAAAAACAACCTTTAACCCTATTTTCTATTGTAATATATATAAAAAATATTAATAAAATA
TATATGATTTTATTGAAATACCTTTTAAAGATATGCATATAATCTCCGTAATTCTAGAAAT
TATTCAGAGTTAAAGAGATTTTAAAGTTTACATTGATCTTGTTCAAAAATAAATAATTATT
ATCAACCCGGAGGGAGTAATAGCTATCAACTCTCAATACTCTCTATATATGTCGTATTAT
TCAGCTCACTAACTATATGGATCTCAAAGTCCATTCAAGCTGCGAT
ATATTGTAGCTTGTACACTTCAGCCTATGATGTTTCCCTGAGAAA
GCTCCCAATTTTGTGCGCACCGATCCTATCCATGCAGTTTCCTTGT
AGATATGACATACATATACATACATATATATATATATATATATGTATGTATGGCTTTTTT
TTTTCTTTTAGATGCAAGCAACTTCTAATATACTGACGTGCAATTAATCTTTTTCGCGCA
TTCGAAAAAACAGGTGCATGCATGATATTGTTACAGTATCATGTAGGATTGGGAGGCAT
AAAAAATGTGGAGTATGTGTCCACAACGAAAGCTTTTCGACACTGGAGATTCCACCGGAC
AGCATCGGTTTGAAGGTGCGATCGATAAATTGGTTTCAGCAAGCTTCGGTACGAGGATGAT
TTCGACTGATGGAAGAGAGGATACTGATCTATACTGAGGGGTTGGAAGAAGTATAGCAG
AGGTCTTTTGCTGCTTGTTCGATCACGTGACAAGAACAGAAGAGGGATCAATCAACAGCG
AACTTGTCTATTTTCAGTTGTCAACAATTGCGACGACAATTAATGCATTTTCCTCTACTTT
AAGCCCTTTTTTTTTCTTTTCCGTGAGATCTTTTTTTCCTAATGACATAACAACCTTTTAG
CTATAAATCTGGACACATAGTTGTCTAATTTTATAGCTAAAAATCTTATGTTTGGGAC
GGAGGTAGTAGCAGATATAGTACATATATACCA
GAAAGAAGGAATAAATATATAATTTTATAATAA
AATGGTGGGTGTTATCACATTGCTAATCCCATA
GAAGATATTGTGCATAACATAAAGACGCCAATA
TACATGCAGTTACTGCAAAAGATACATGCATGT
AAGATATCTTCAGACTTCAATGATCATGCATCT
AACATTGGTCGATCGACTAGATCGAGCTCGATCG
ACAAATGCAATGATATATGATGCAAACTTTCACTATG
```

FASTA

The data you export
will look something
like this...

```
FT /db_xref="cmap:AB156208.1"
FT /note="map_weight=1"
FT misc_feature 1..49741
FT /note="contig AP002483 13041..62781(1) "
FT misc_feature 49742..49999
FT /note="contig AP003311 8248..8505(1) "
XX
SQ Sequence 49999 BP; 14199 A; 10653 C; 10255 G; 14892 T; 0 other;
TCAAAAAACA AACTTTAACCCTATTTTCTATTGTAATATA TATAAAAAATA TTAATAAAATA 60
TATATGATTTTATGTCATATA ATCTCCGTAA TTCTAGAAAT 120
TATTCAGAGTACATTGATCT TGTTCAAAAA AATAATTATT 180
ATCAACCCGGTCTCAATACT CTCTATATAT GTCGTATTAT 240
TCAGCTCACT AACTAGTTCA GTACTGTCAT ATGGATCTCA AAGTCCATT CAGCTGCGAT 300
ATATTGTAGC TTGTAGTTTA CATCCCTACA CACTTCAGCC TATGATGTTT CCCTGAGAAA 360
GCTCCCAATT TTGTAGTTTC ACAAATGCGC GCACCGATCC TATCCATGCA GTTTCCTTGT 420
AGATATGACA TACATATACA TACATATATA TATATATATA TATGTATGTA TGGCTTTTTT 480
TTTTCTTTTA GATGCAAGCA ACTTCTAATA TACTGACGTG CAATTAATCT TTTTCGCGCA 540
TTCGAAAAAA ACAGGTGCAT GCATGATATT GTTACAGTAT CATGTAGGAT TGGGAGGCAT 600
AAAAAATGTG GAGTATGTGT CCACAACGAA AGCTTTTCGA CACTGGAGAT TCCACCGGAC 660
AGCATCGGTT TGAAGGTGCG ATCGATAACT TGGTTCAGCA AGCTTCGGTA CGAGGATGAT 720
TTCGACTGAT GGAAGAGAGG ATACTGATCT ATACTGAGGG GTTGGAAAAG AGTATAGCAG 780
AGGTCTTTGC TGCTTGTTC GATCACGTGA CAAGAACAGA AGAGGGATCA ATCAACAGCG 840
```

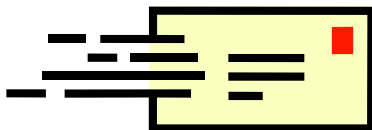
Flat File

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or



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