Genome sequencing projects statistics

Organism	Complete	Draft assembly	In progress	total
Prokaryotes	597	397	492	1486
Archaea	47	3	30	80
Bacteria	550	394	462	1406
Eukaryotes	23	131	184	338
Animals	4	54	89	147
Mammals	2	22	25	49
Birds		1	2	3
Fishes		3	6	9
Insects	1	19	20	40
Flatworms		1	3	4
Roundworms	1	3	13	17
Amphibians			2	2
Reptiles			2	2
Other animals		6	19	25
Plants	3	3	34	40
Land plants	2	2	27	31
Green Algae	1	1	7	9
Fungi	10	53	30	93
Ascomycetes	8	46	21	75
Basidiomycetes	1	5	5	11
Other fungi	1	2	4	7
Protists	6	19	27	52
Apicomplexans	1	10	6	17
Kinetoplasts	1	2	6	9
Other protists	4	7	14	25
total:	**620**	**528**	**676**	**1824**

Revised: Nov 07, 2007

Summary pages

Entrez Gene	4683		
HGED Symbol Report	NBS1		
KEGG gene	4683		
euGenes	HUgn0004683		
CGAP	25812		
SOURCE	4683		

Genomic resources

Genomic sequences	AB013139.1	AF069291.1	
GDB	9598211		
GenAtlas	NBS1		
UCSC Genome Browser	chr8:91014739-91066075		
Vista Genome Browser	Align sequence to [17 other genomes]		
AceView	NBS1		
dbSNP	rs14448	rs769414	rs769416
	rs769420	rs1063054	rs2735383
	rs3026268	rs3087624	rs3780123
	rs3358	rs16786	More...

Transcripts

RefSeq	NM_002485		
cDNA sequences	AF051334	AF058696	AK001017
	BC005293	BC040519	BX640816
TIGR	THC16941		

Protein sequences

TrEMBL	O60934		
GenPept	AAC39732	AAC39752	

Protein structure and domains

InterPro domains	IPR001357	IPR000253	IPR008984
Pfam	PF00533	PF00498	
ProDom	IPR001357	IPR000253	IPR008984
PROSITE	PS50006		

Protein function and disease links

OMIM	602667	251260

Networks and pathways

PubGene	NBS1

Literature Links

PubMed	24 PubMed articles

UCSC Genome Bioinformatics

Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Proteome - FAQ - Help

Genome Browser

ENCODE

Blat

Table Browser

Gene Sorter

In Silico PCR

VisiGene

Proteome Browser

About the UCSC Genome Bioinformatics Site

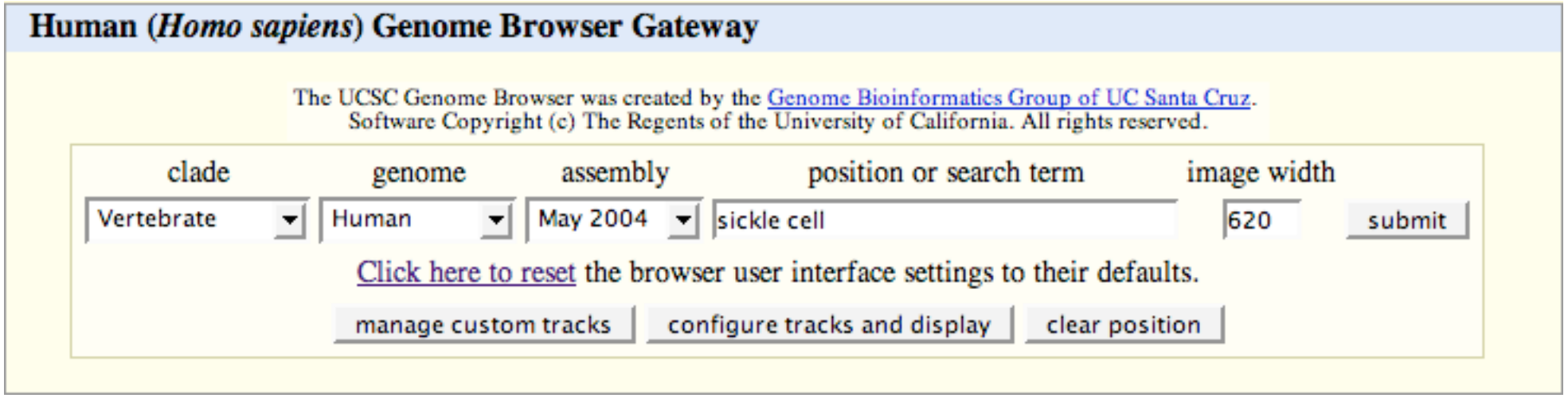
This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides a portal to the ENCODE project.

We encourage you to explore these sequences with our tools. The Genome Browser zooms and scrolls over chromosomes, showing the work of annotators worldwide. The Gene Sorter shows expression, homology and other information on groups of genes that can be related in many ways. Blat quickly maps your sequence to the genome. The Table Browser provides convenient access to the underlying database. VisiGene lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns.

News

News Archives ▶

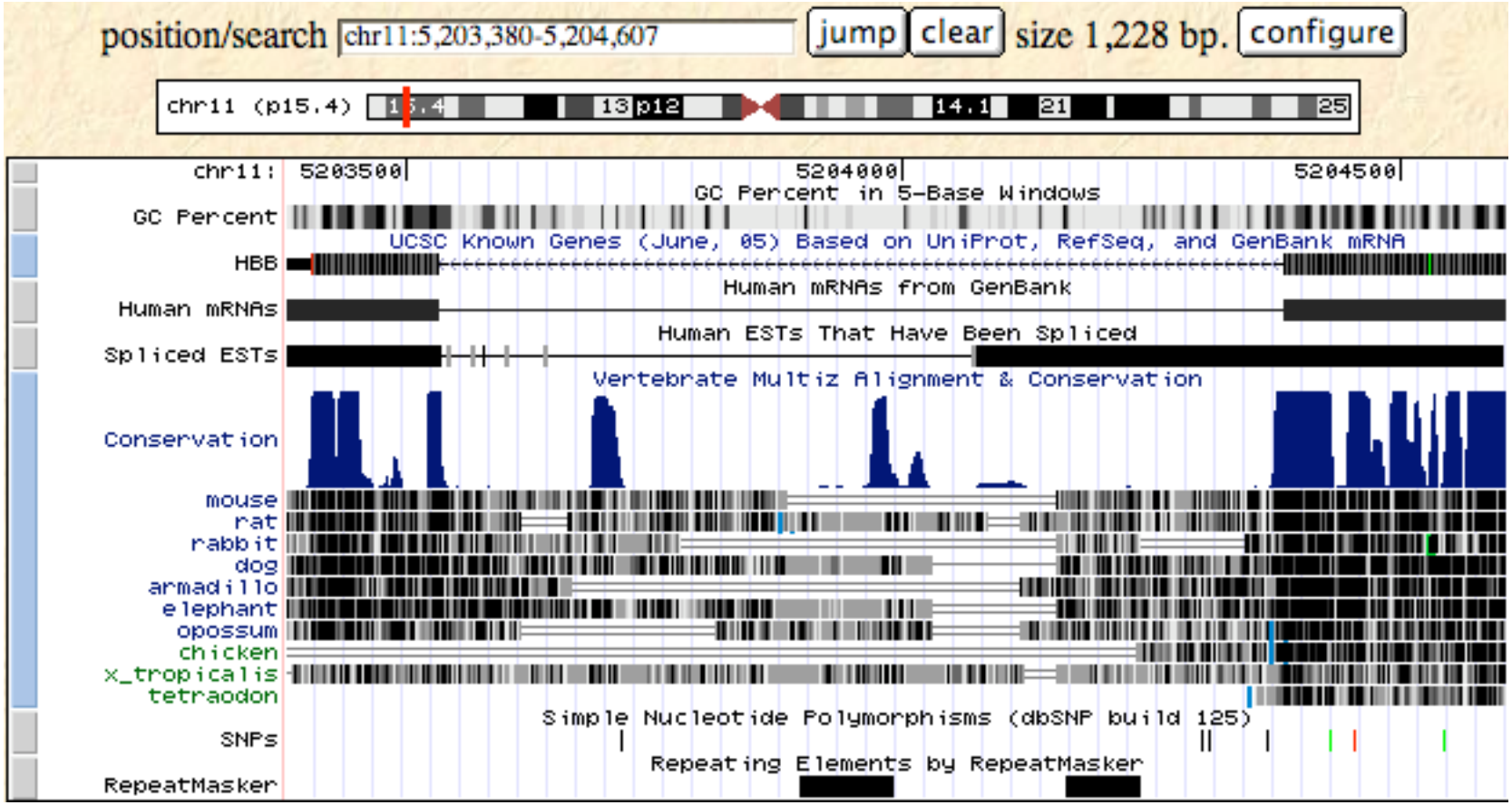
To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the genome-announce mailing list.


Human (Homo sapiens) Genome Browser Gateway
The UCSC Genome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
Software Copyright (c) The Regents of the University of California. All rights reserved.
clade
genome
assembly
position or search term
image width
Vertebrate
Human
May 2004
sickle cell
620
submit
Click here to reset the browser user interface settings to their defaults.
manage custom tracks
configure tracks and display
clear position

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, or a cytological band, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the User's Guide for more information.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p arm telomere
chr3:1000000+2000	Displays a region of chr3 that spans 2000 bases, starting with position 1000000
D16S3046	Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side as well.
RH18061;RH80175	Displays region between STS markers RH18061;RH80175. Includes 100,000 bases on each side as well. This syntax may also be used for other range queries, such as between cytobands and uniquely-determined ESTs, mRNAs, refSeqs, etc.
AA205474	Displays region of EST with GenBank accession AA205474 in BRCA1 cancer gene on chr 17
AC008101	Displays region of clone with GenBank accession AC008101
AF083811	Displays region of mRNA with GenBank accession number AF083811
PRNP	Displays region of genome with HUGO Gene Nomenclature Committee identifier PRNP
NM_017414	Displays the region of genome with RefSeq identifier NM_017414
NP_059110	Displays the region of genome with protein accession number NP_059110
pseudogene mRNA	Lists transcribed pseudogenes, but not cDNAs
homeobox caudal	Lists mRNAs for caudal homeobox genes
zinc finger	Lists many zinc finger mRNAs
kruppel zinc finger	Lists only kruppel-like zinc fingers
huntington	Lists candidate genes associated with Huntington's disease
zahler	Lists mRNAs deposited by scientist named Zahler
Evans,J.E.	Lists mRNAs deposited by co-author J.E. Evans


position/search
chr11:5,203,380-5,204,607
jump
clear
size 1,228 bp.
configure
chr11 (p15.4)
13
p12
14.1
21
25
chr11:
5203500
5204000
5204500
GC Percent in 5-Base Windows
GC Percent
UCSC Known Genes (June, 05) Based on UniProt, RefSeq, and GenBank mRNA
HBB
Human mRNAs from GenBank
Human mRNAs
Human ESTs That Have Been Spliced
Spliced ESTs
Vertebrate Multiz Alignment & Conservation
Conservation
mouse
rat
rabbit
dog
armadillo
elephant
opossum
chicken
x_tropicalis
tetraodon
Simple Nucleotide Polymorphisms (dbSNP build 125)
SNPs
Repeating Elements by RepeatMasker
RepeatMasker

default tracks | hide all | manage custom tracks | configure | refresh

Use drop down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.

Custom Tracks

Base Position: full
newSnp: dense

Mapping and Sequencing Tracks

Chromosome Band: hide	STS Markers: hide	FISH Clones: hide	Recomb Rate: hide	Map Contigs: hide
Assembly: hide	Gap: hide	Coverage: hide	BAC End Pairs: hide	Fosmid End Pairs: hide
GC Percent: hide	WSSD Duplication: hide	Short Match: hide	Restr Enzymes: hide	Blat Sequence: hide

Phenotype and Disease Associations

RGD QTL: hide
Locus Variants: hide

Genes and Gene Prediction Tracks

Known Genes: pack	CCDS: hide	RefSeq Genes: pack	Other RefSeq: hide	MGC Genes: hide
Vega Pseudogenes: hide	Ensembl Genes: full	AceView Genes: hide	ECgene Genes: hide	
SGP Genes: hide	Geneid Genes: hide	Genscan Genes: hide	Exoniphy: hide	

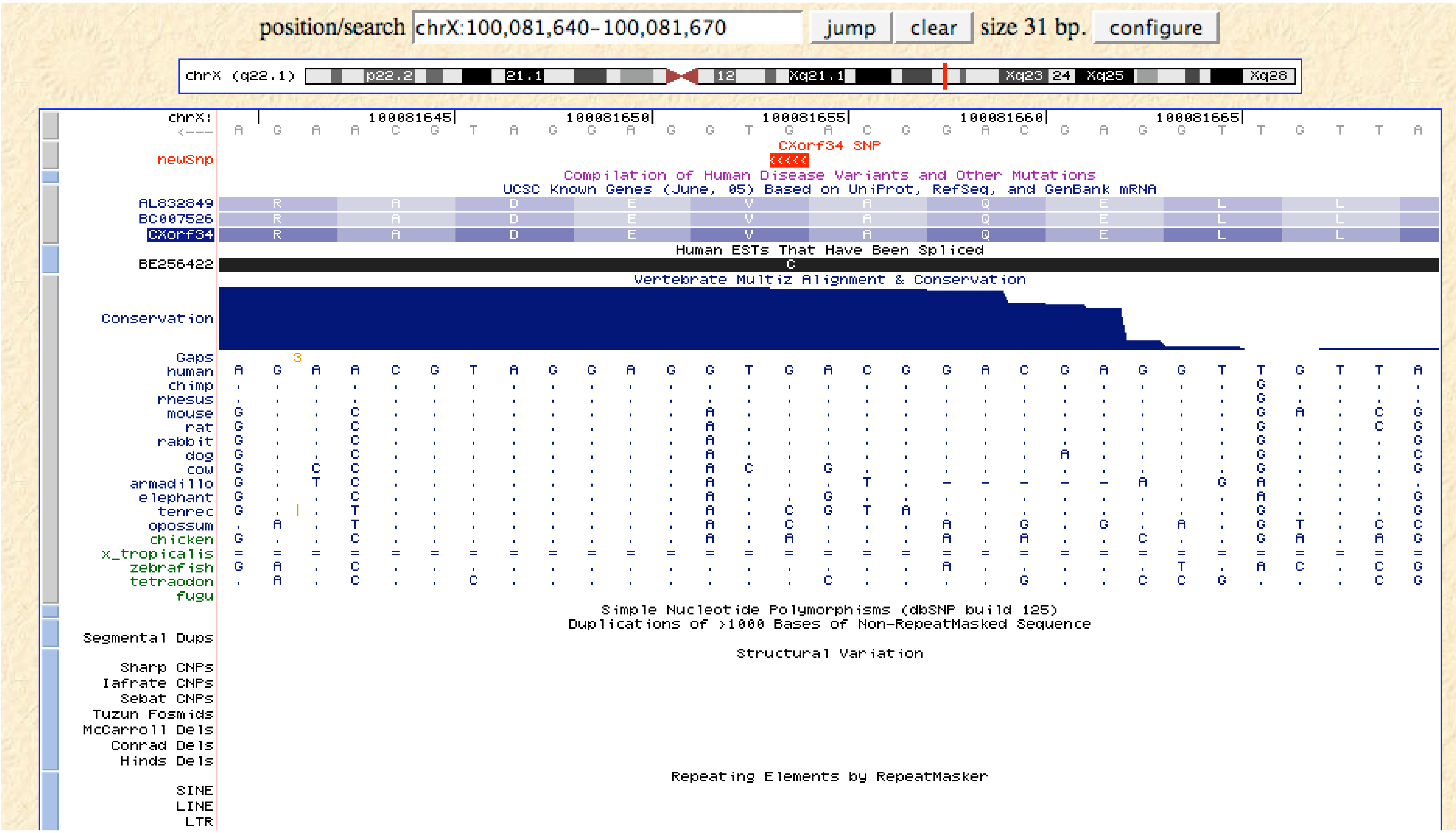
Known Genes options: hide, dense, squish, pack, full

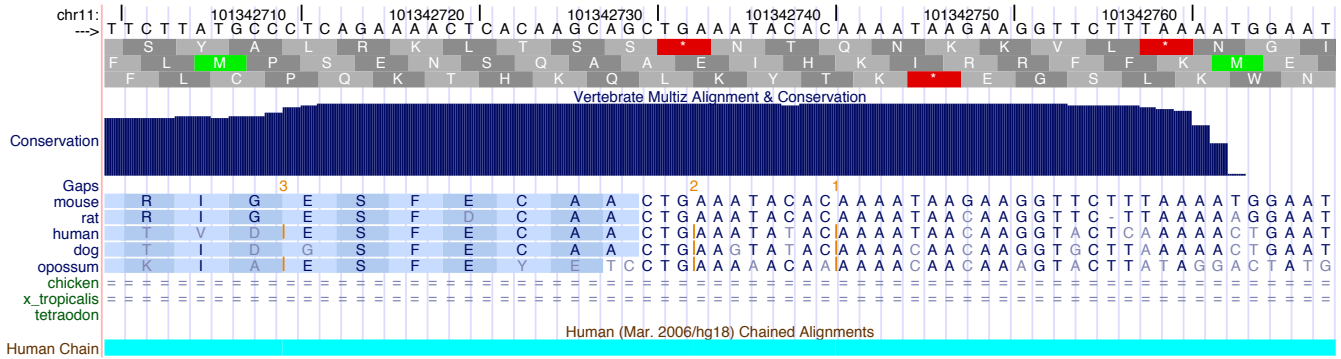
Display mode: full Submit

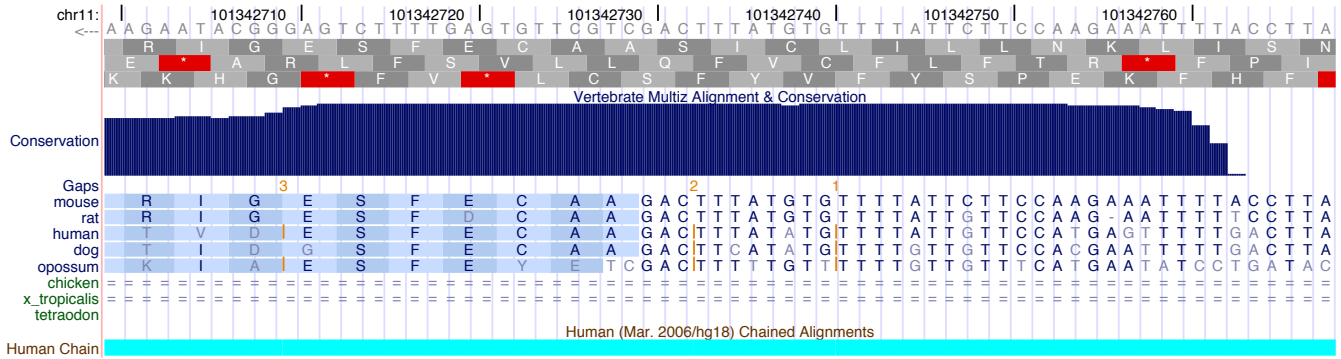
Filter: red green blue exclude include **Combination Logic:** and or

accession:	author:	library:	tissue:
BE256422			
cell:	**keyword:**	**gene:**	**product:**
description:			

Color track by bases: different mRNA bases


position/search
chrX:100,081,640-100,081,670
jump
clear
size 31 bp.
configure
chrX (q22.1)
p22.2
21.1
12
Xq21.1
Xq23
24
Xq25
Xq28
chrX:
100081645
100081650
100081655
100081660
100081665
CXorf34 SNP
newSnp
Compilation of Human Disease Variants and Other Mutations
UCSC Known Genes (June, 05) Based on UniProt, RefSeq, and GenBank mRNA
AL832849
BC007526
CXorf34
Human ESTs That Have Been Spliced
BE256422
Vertebrate Multiz Alignment & Conservation
Conservation
Gaps
human
chimp
rhesus
mouse
rat
rabbit
dog
cow
armadillo
elephant
tenrec
opossum
chicken
x_tropicalis
zebrafish
tetraodon
fugu
Simple Nucleotide Polymorphisms (dbSNP build 125)
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Structural Variation
Sharp CNPs
Iafrate CNPs
Sebat CNPs
Tuzun Fosmids
McCarroll Dels
Conrad Dels
Hinds Dels
Repeating Elements by RepeatMasker
SINE
LINE
LTR


chr11:
101342710
101342720
101342730
101342740
101342750
101342760
--> T T C T T A T G C C C T C A G A A A A C T C A C A A G C A G C T G A A A T A C A C A A A A T A A G A A G G T T C T T T A A A A T G G A A T
S Y A L R K L T S S * N T Q N K K V L * N G I
F L M P S E N S Q A A E I H K I R R F F K M E
F L C P Q K T H K Q L K Y T K * E G S L K W N
Vertebrate Multiz Alignment & Conservation
Conservation
Gaps
mouse
rat
human
dog
opossum
chicken
x_tropicalis
tetraodon
Human (Mar. 2006/hg18) Chained Alignments
Human Chain


chr11:
101342710
101342720
101342730
101342740
101342750
101342760
Vertebrate Multiz Alignment & Conservation
Conservation
Gaps
mouse
rat
human
dog
opossum
chicken
x_tropicalis
tetraodon
Human (Mar. 2006/hg18) Chained Alignments
Human Chain

Human Gene HBB Description and Page Index

Description: beta globin
Alternate Gene Symbols: AF117710, AF181989, AF349114, AY136510, AY509193, BC007075, CR536530, M25113, V00497
CCDS: CCDS7753.1
Representative Refseq: NM_000518 **Protein:** P68871 (aka HBB_HUMAN)
RefSeq Summary: The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, Hb A. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon -- gamma-G -- gamma-A -- delta -- beta--3'. Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Entrez Gene record to access additional publications.
Position: chr11:5203272-5204877
Strand: -
Genomic Size: 1606
Exon Count: 3

Page Index	Quick Links	UniProt Comments	Sequence	Microarray	RNA Structure
Protein Structure	Other Species	GO Annotations	mRNA Descriptions	Pathways	Methods

Quick Links to Tools and Databases

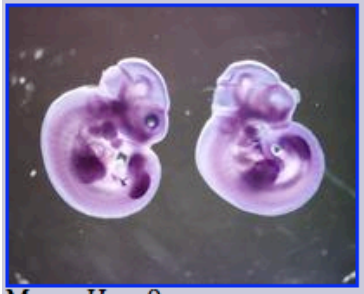
Gene Sorter	Genome Browser	Proteome Browser	Table Schema	VisiGene	Allen Brain Atlas
CGAP	Ensembl	Entrez Gene	ExonPrimer	GeneCards	GeneLynx
H-INV	HGNC	HPRD	Jackson Labs	OMIM	PubMed
Stanford SOURCE	UniProt	Gepis Tissue			

Comments and Description Text from UniProt (Swiss-Prot/TrEMBL)

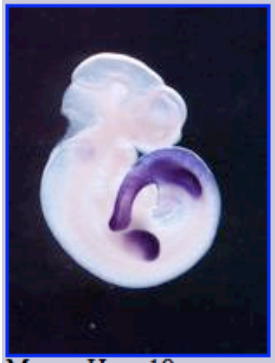
ID: HBB_HUMAN
DESCRIPTION: Hemoglobin beta subunit (Hemoglobin beta chain) (Beta-globin).
FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.
SUBUNIT: Heterotetramer of two alpha chains and two beta chains in adult hemoglobin A (HbA).
TISSUE SPECIFICITY: Red blood cells.

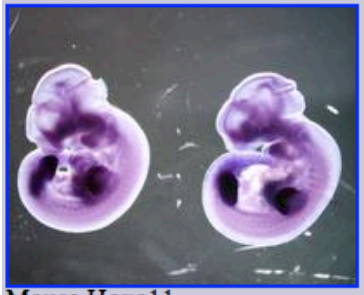
UCSC VisiGene | hoxa* | search | Zoom: out | in | full | fit | Help

171 images match


Mouse Hoxa9


Mouse Hoxa10


Mouse Hoxa10


Mouse Hoxa11

source: Mahoney Lab **source:** MGI **Reference:** Mouse Brain Organization Revealed Through Direct Genome-Scale TF Expression Analysis.
Year: 2004 **Contributors:** Gray P.A.,Fu H.,Luo P.,Zhao Q.,Yu J.,Ferrari A.,Tenzen T.,Yuk D.I.,Tsung E.F.,Cai Z.,Alberta J.A.,Cheng L.P.,Liu Y.,Stenman J.M.,Valerius M.T.,Billings N.,Kim H.A.,Greenberg M.E.,McMahon A.P.,Rowitch D.H.,Stiles C.D.,Ma Q.,
Gene: Hoxa9 **Probe:** RNA from primers **GenBank:** AB005458
Organism: Mus musculus **Sex:** n/a **Strain:** C57BL **Genotype:** wild type
Stage: 10.5 day old embryo (Theiler 17) **Body Part:** whole
Expression: central nervous system(0.17) **Section Type:** whole mount
Acknowledgements: Thanks to Paul Gray for transferring the images.

Home

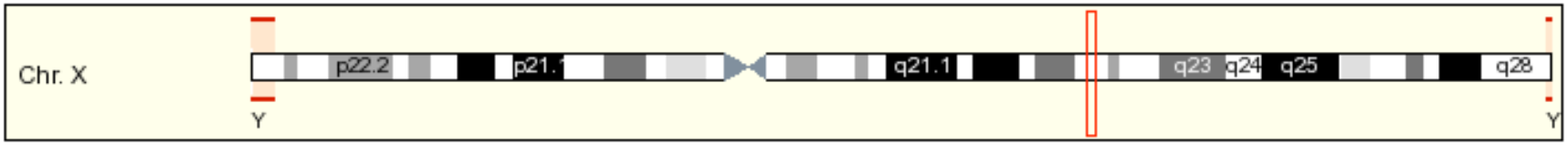
UCSC Human Gene Sorter

genome Human assembly May 2004 search CXorf34 Go!

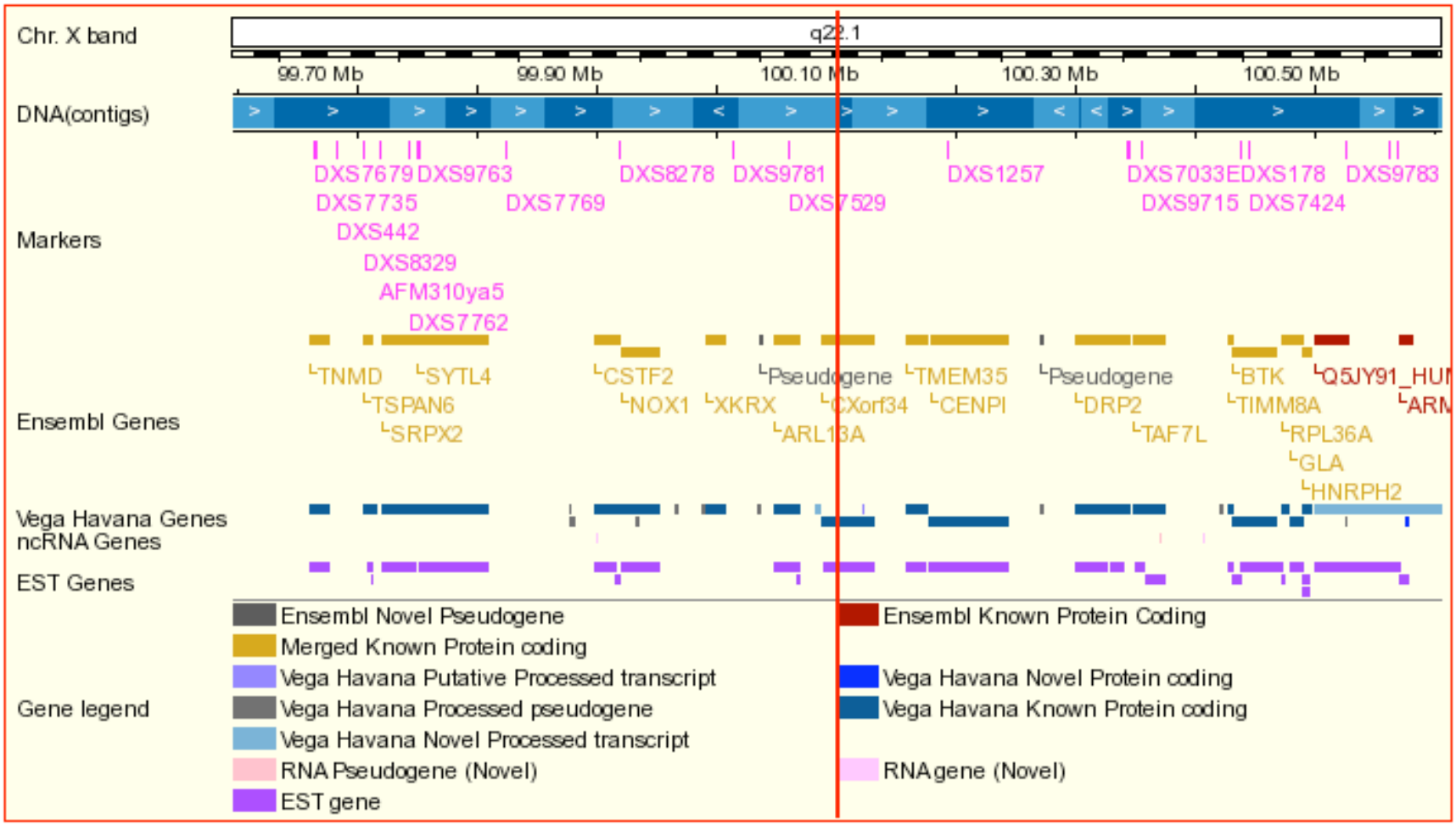
sort by Protein Homology - BLASTP configure filter (now off) display 50 output sequence text

#	Name		BLASTP E-Value	Genome Position	Description
1	CXorf34		0	chrX 100,091,954	hypothetical protein LOC79979
2	CR592601		1e-75	chr22 18,476,857	HpaII tiny fragments locus 9c protein.

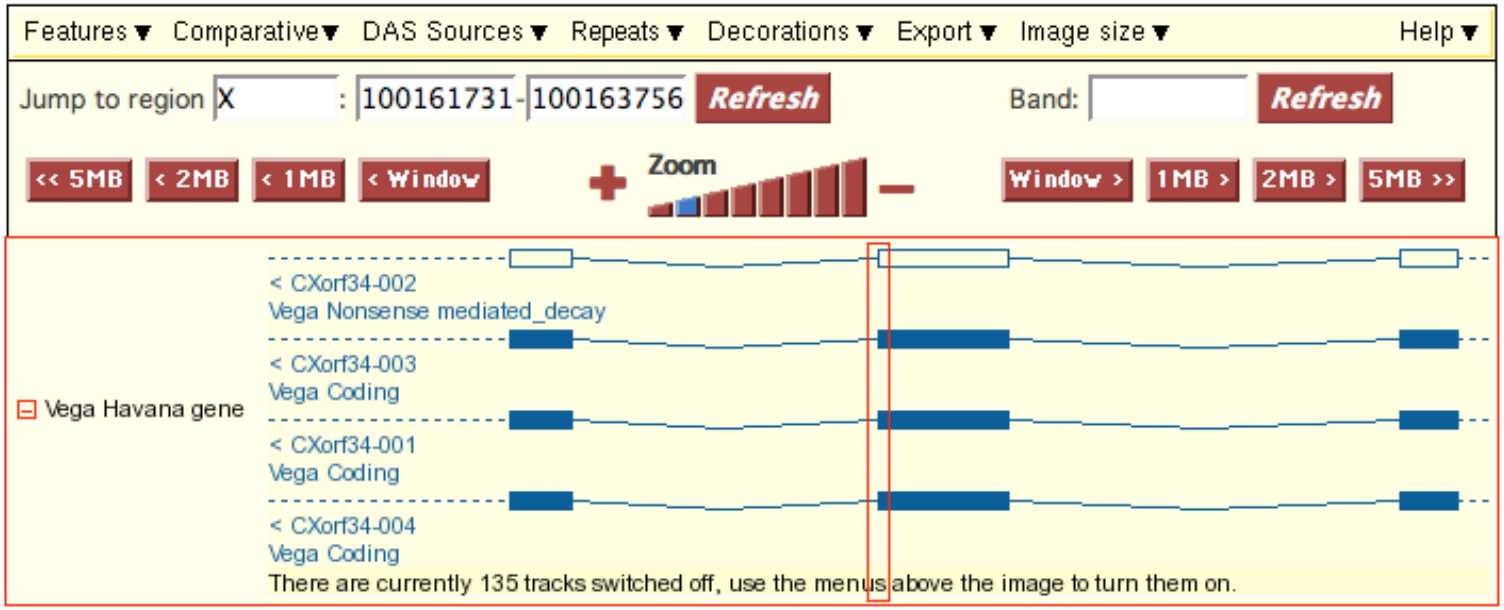
Chromosome X



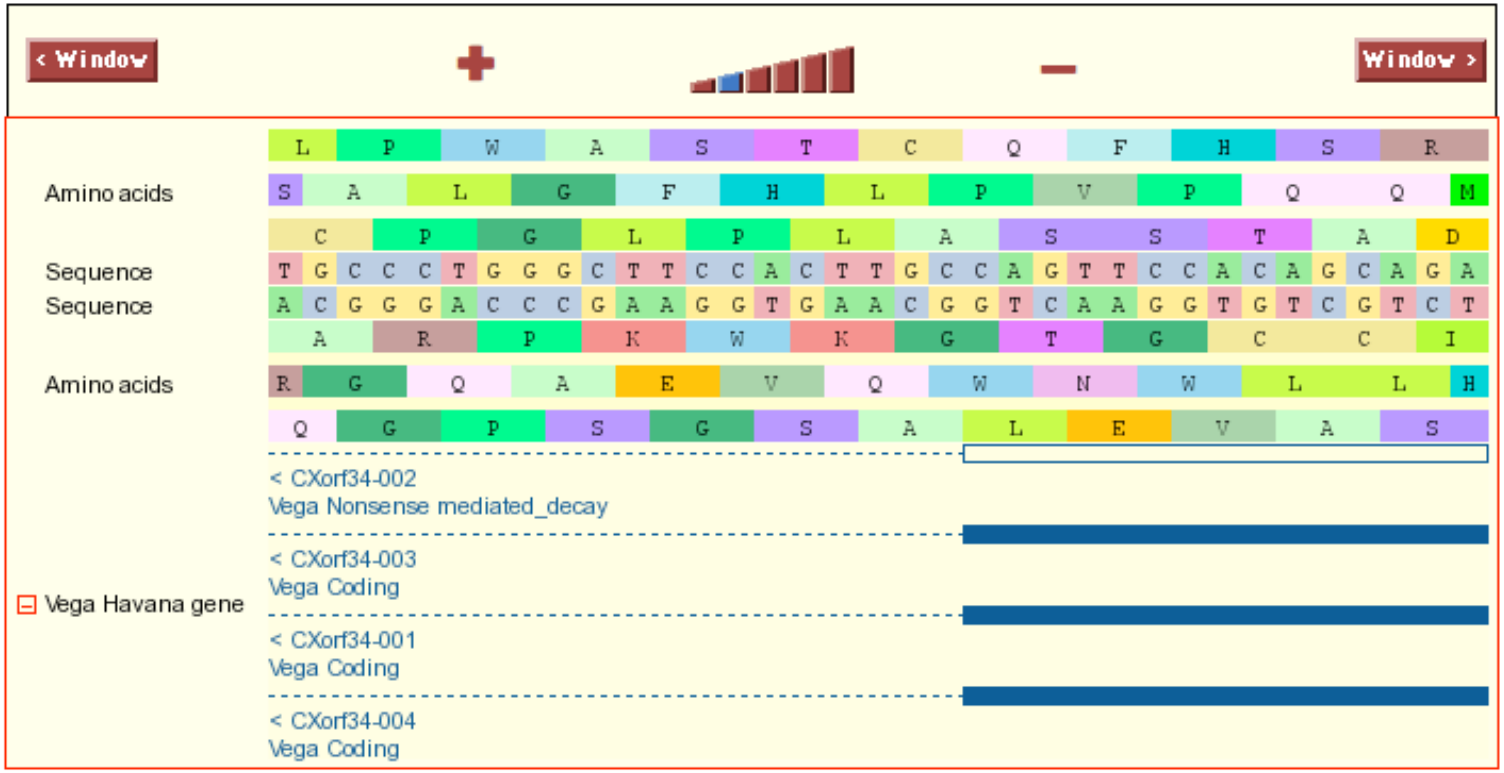
Overview

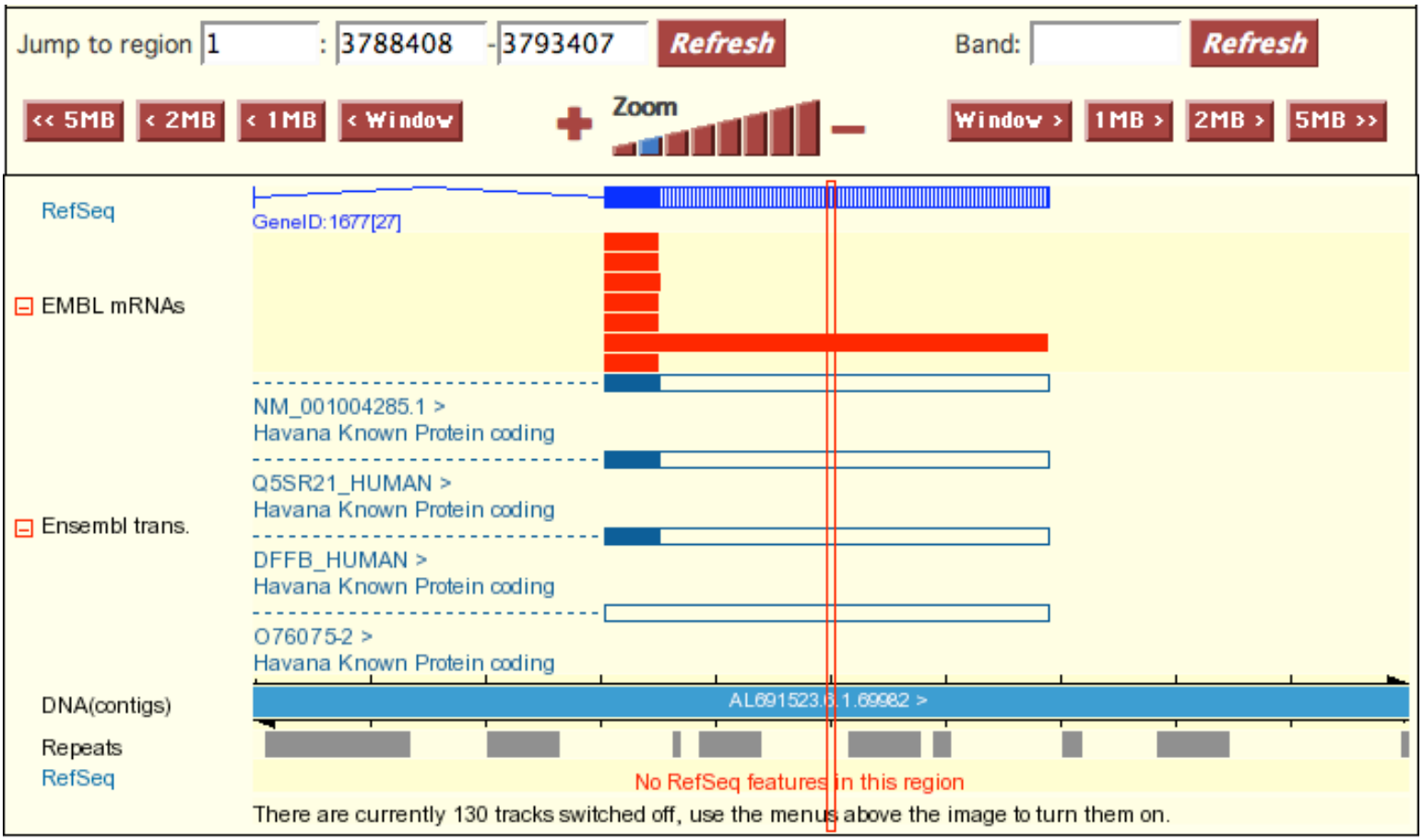


Detailed view

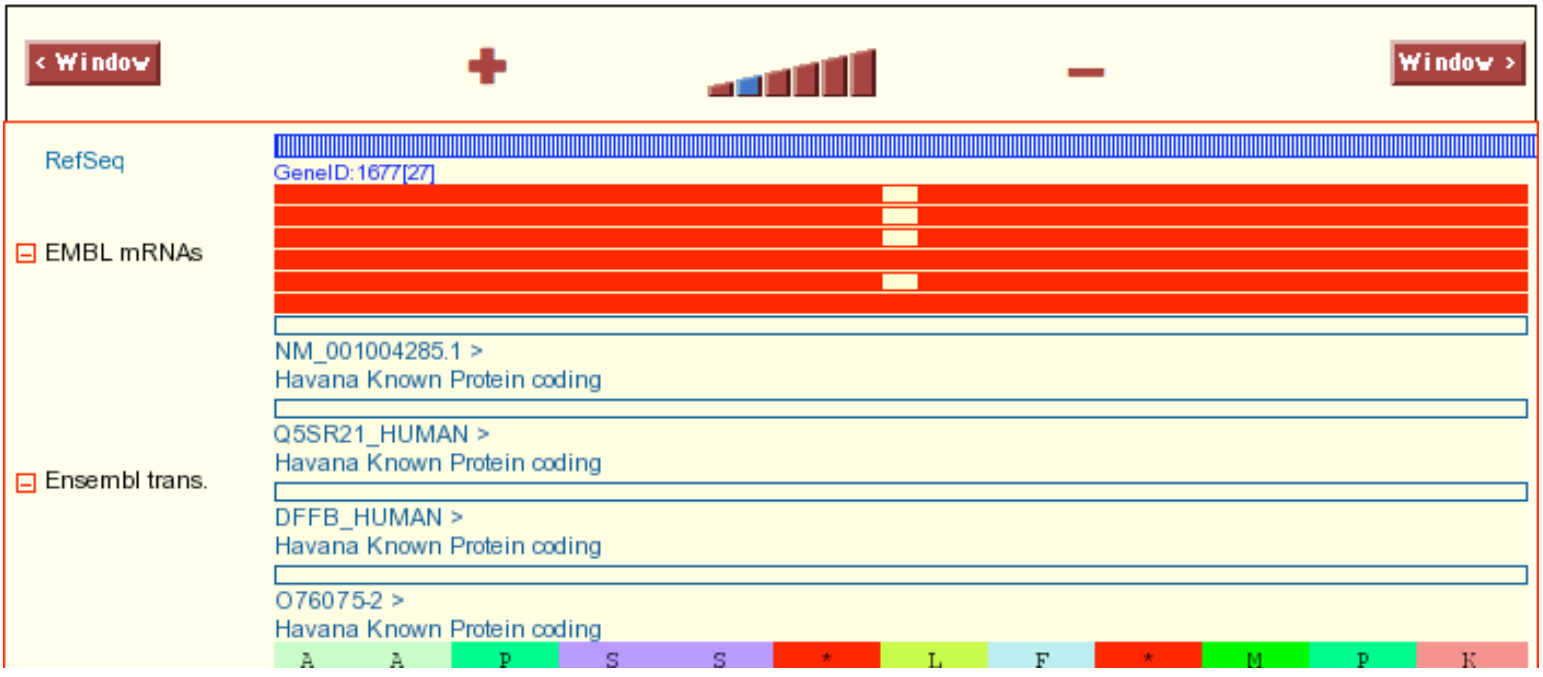


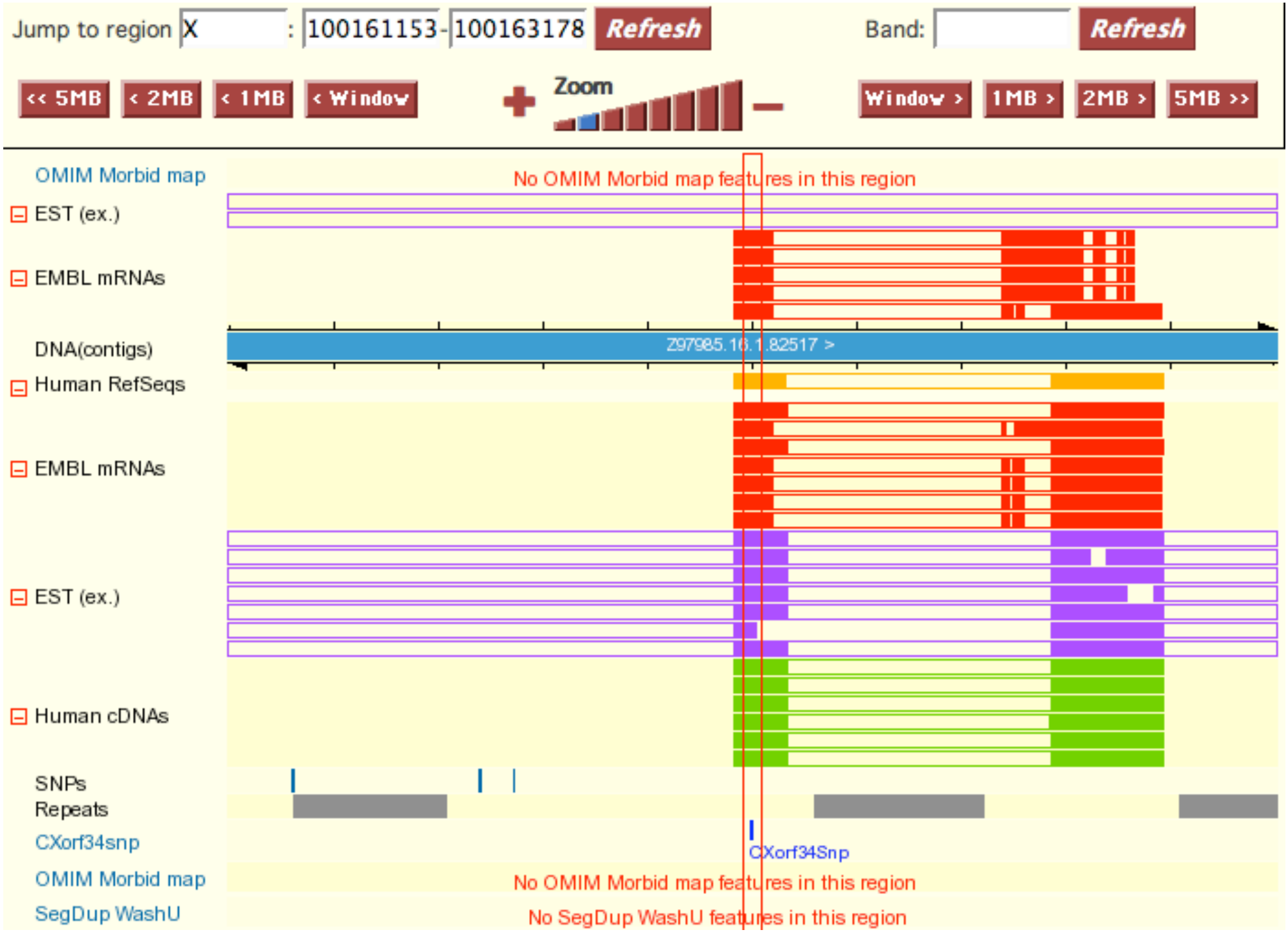
Basepair view

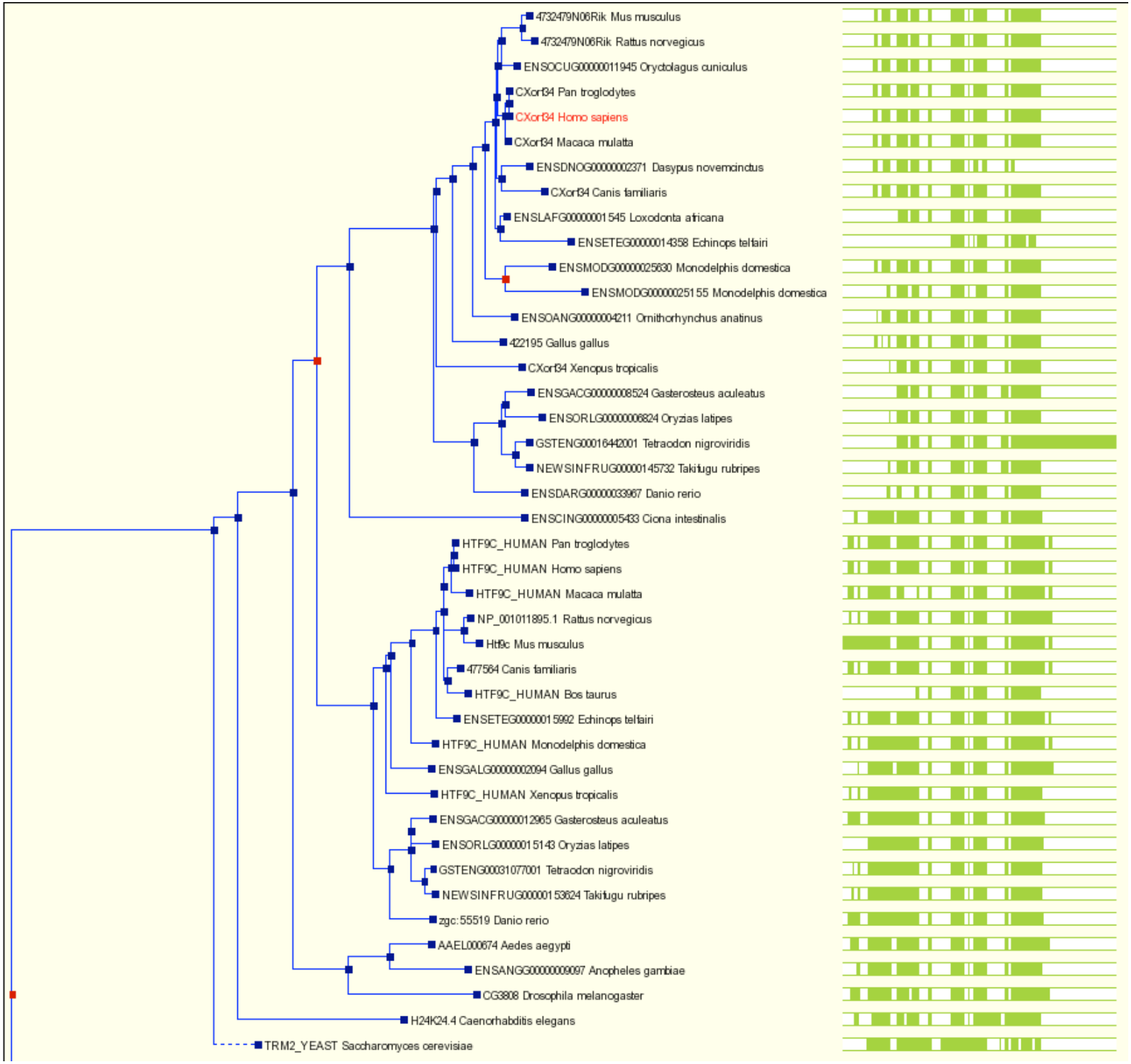


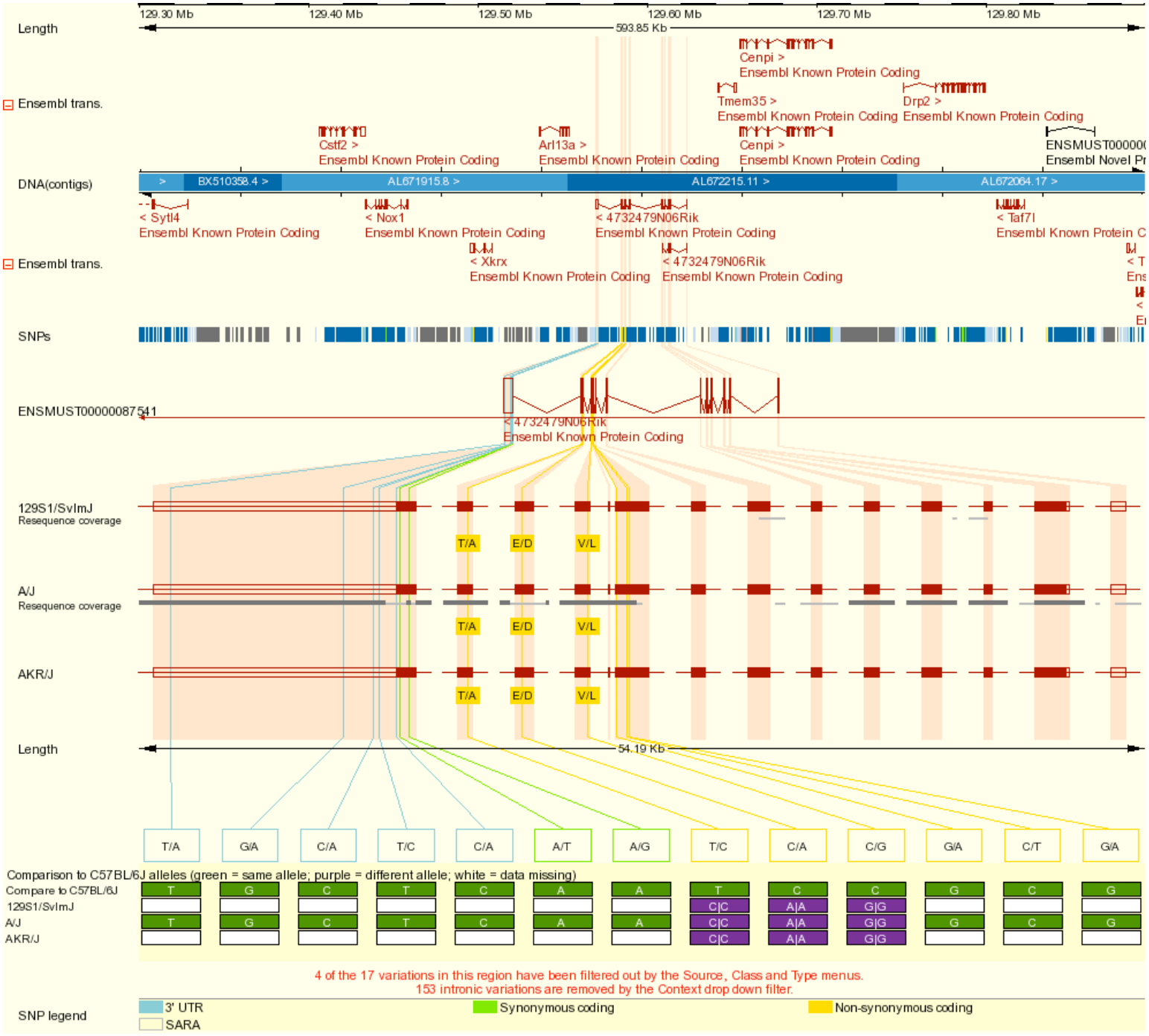


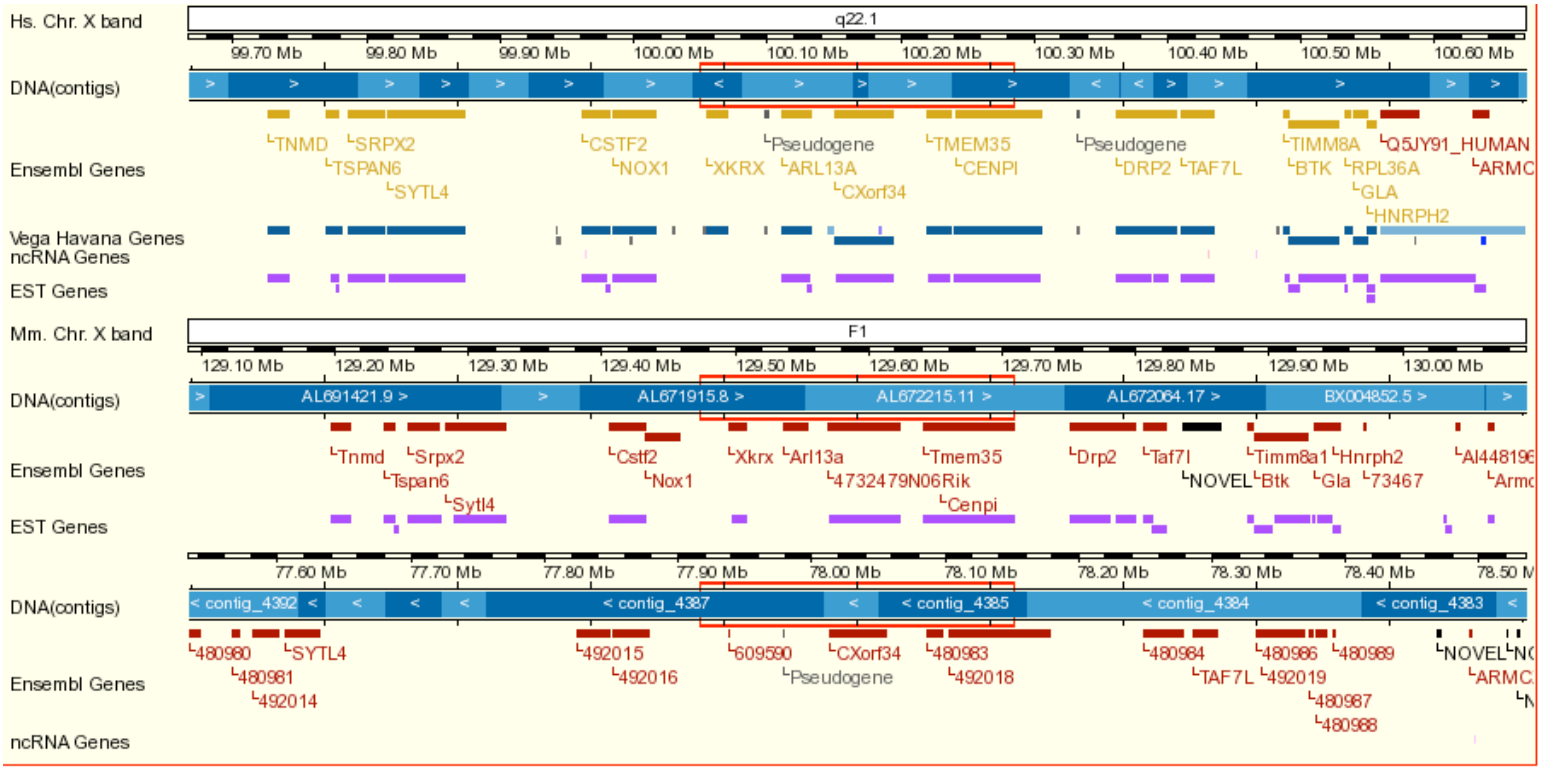
Basepair view



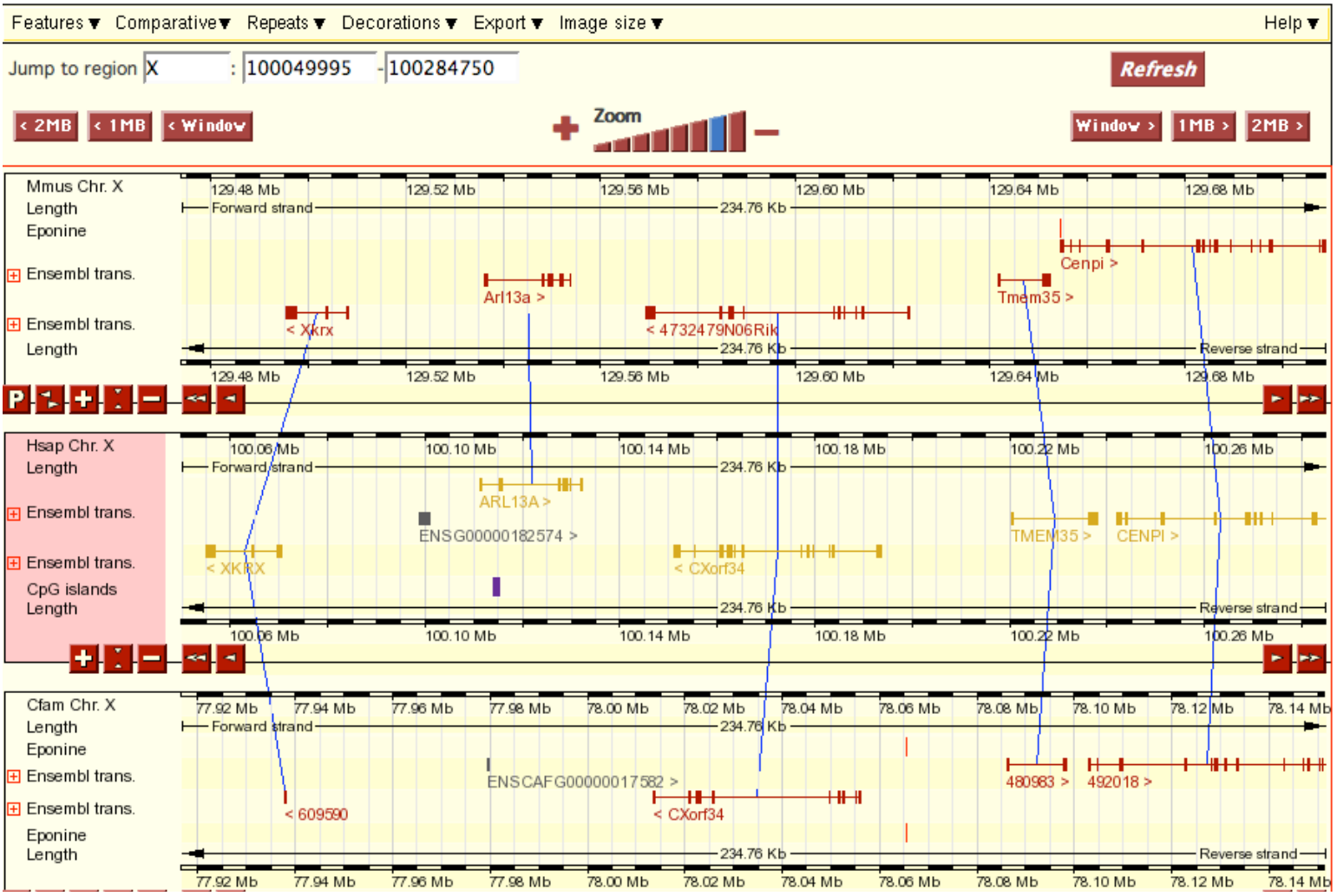

Jump to region X : 100161153-100163178 Refresh
Band: Refresh
<< 5MB
< 2MB
< 1MB
< Window
Zoom
Window >
1MB >
2MB >
5MB >>
OMIM Morbid map
No OMIM Morbid map features in this region
EST (ex.)
EMBL mRNAs
DNA(contigs)
Z97985.16.1.82517 >
Human RefSeqs
EMBL mRNAs
EST (ex.)
Human cDNAs
SNPs
Repeats
CXorf34snp
CXorf34Snp
OMIM Morbid map
No OMIM Morbid map features in this region
SegDup WashU
No SegDup WashU features in this region


4732479N06Rik Mus musculus
4732479N06Rik Rattus norvegicus
ENSOCUG00000011945 Oryctolagus cuniculus
CXorf34 Pan troglodytes
CXorf34 Homo sapiens
CXorf34 Macaca mulatta
ENSDNOG00000002371 Dasypus novemcinctus
CXorf34 Canis familiaris
ENSLAFG00000001545 Loxodonta africana
ENSETEG00000014358 Echinops telfairi
ENSMODG00000025630 Monodelphis domestica
ENSMODG00000025155 Monodelphis domestica
ENSOANG00000004211 Ornithorhynchus anatinus
422195 Gallus gallus
CXorf34 Xenopus tropicalis
ENSGACG00000008524 Gasterosteus aculeatus
ENSORLG00000006824 Oryzias latipes
GSTENG00016442001 Tetraodon nigroviridis
NEWSINFRUG00000145732 Takifugu rubripes
ENSDARG00000033967 Danio rerio
ENSCING00000005433 Ciona intestinalis
HTF9C_HUMAN Pan troglodytes
HTF9C_HUMAN Homo sapiens
HTF9C_HUMAN Macaca mulatta
NP_001011895.1 Rattus norvegicus
Htf9c Mus musculus
477564 Canis familiaris
HTF9C_HUMAN Bos taurus
ENSETEG00000015992 Echinops telfairi
HTF9C_HUMAN Monodelphis domestica
ENSGALG00000002094 Gallus gallus
HTF9C_HUMAN Xenopus tropicalis
ENSGACG00000012965 Gasterosteus aculeatus
ENSORLG00000015143 Oryzias latipes
GSTENG00031077001 Tetraodon nigroviridis
NEWSINFRUG00000153624 Takifugu rubripes
zgc:55519 Danio rerio
AAEL000674 Aedes aegypti
ENSANGG00000009097 Anopheles gambiae
CG3808 Drosophila melanogaster
H24K24.4 Caenorhabditis elegans
TRM2_YEAST Saccharomyces cerevisiae


129.30 Mb
129.40 Mb
129.50 Mb
129.60 Mb
129.70 Mb
129.80 Mb
Length
593.85 Kb
Ensembl trans.
Cenpi >
Ensembl Known Protein Coding
Tmem35 >
Ensembl Known Protein Coding
Drp2 >
Ensembl Known Protein Coding
Cstf2 >
Ensembl Known Protein Coding
Arl13a >
Ensembl Known Protein Coding
Cenpi >
Ensembl Known Protein Coding
ENSMUST000000
Ensembl Novel Pr
DNA(contigs)
BX510358.4 >
AL671915.8 >
AL672215.11 >
AL672064.17 >
< Sytl4
Ensembl Known Protein Coding
< Nox1
Ensembl Known Protein Coding
< 4732479N06Rik
Ensembl Known Protein Coding
< Taf7l
Ensembl Known Protein C
Ensembl trans.
< Xkrx
Ensembl Known Protein Coding
< 4732479N06Rik
Ensembl Known Protein Coding
SNPs
ENSMUST00000087541
< 4732479N06Rik
Ensembl Known Protein Coding
129S1/SvImJ
Resequence coverage
T/A
E/D
V/L
A/J
Resequence coverage
T/A
E/D
V/L
AKR/J
T/A
E/D
V/L
Length
54.19 Kb
T/A
G/A
C/A
T/C
C/A
A/T
A/G
T/C
C/A
C/G
G/A
C/T
G/A
Comparison to C57BL/6J alleles (green = same allele; purple = different allele; white = data missing)
Compare to C57BL/6J
T G C T C A A T C C G C G
129S1/SvImJ
C|C A|A G|G
A/J
T G C T C A A C|C A|A G|G G C G
AKR/J
C|C A|A G|G
4 of the 17 variations in this region have been filtered out by the Source, Class and Type menus.
153 intronic variations are removed by the Context drop down filter.
SNP legend
3' UTR
Synonymous coding
Non-synonymous coding
SARA


Hs. Chr. X band
q22.1
99.70 Mb
99.80 Mb
99.90 Mb
100.00 Mb
100.10 Mb
100.20 Mb
100.30 Mb
100.40 Mb
100.50 Mb
100.60 Mb
DNA(contigs)
Ensembl Genes
TNMD
SRPX2
TSPAN6
SYTL4
CSTF2
NOX1
XKRX
ARL13A
CXorf34
Pseudogene
TMEM35
CENPI
Pseudogene
DRP2
TAF7L
TIMM8A
Q5JY91_HUMAN
BTK
RPL36A
ARMC
GLA
HNRPH2
Vega Havana Genes
ncRNA Genes
EST Genes
Mm. Chr. X band
F1
129.10 Mb
129.20 Mb
129.30 Mb
129.40 Mb
129.50 Mb
129.60 Mb
129.70 Mb
129.80 Mb
129.90 Mb
130.00 Mb
DNA(contigs)
AL691421.9 >
AL671915.8 >
AL672215.11 >
AL672064.17 >
BX004852.5 >
Ensembl Genes
Tnmd
Srpx2
Tspan6
Sytl4
Cstf2
Nox1
Xkrx
Arl13a
Tmem35
4732479N06Rik
Cenpi
Drp2
Taf7l
NOVEL
Timm8a1
Btk
Hnrph2
Gla
73467
EST Genes
77.60 Mb
77.70 Mb
77.80 Mb
77.90 Mb
78.00 Mb
78.10 Mb
78.20 Mb
78.30 Mb
78.40 Mb
DNA(contigs)
< contig_4392
< contig_4387
< contig_4385
< contig_4384
< contig_4383
Ensembl Genes
480980
SYTL4
480981
492014
492015
492016
609590
CXorf34
Pseudogene
480983
492018
480984
TAF7L
480986
492019
480989
480987
480988
NOVEL
ARMC
ncRNA Genes

ailed View


Features
Comparative
Repeats
Decorations
Export
Image size
Help
Jump to region X : 100049995 - 100284750
Refresh
< 2MB
< 1MB
< Window
Zoom
Window >
1MB >
2MB >
Mmus Chr. X
Length
Forward strand
234.76 Kb
Eponine
Ensembl trans.
Ensembl trans.
Length
Reverse strand
129.48 Mb
129.52 Mb
129.56 Mb
129.60 Mb
129.64 Mb
129.68 Mb
Cenpi >
Arl13a >
Tmem35 >
< Xkrx
< 4732479N06Rik
Hsap Chr. X
Length
Ensembl trans.
Ensembl trans.
CpG islands
Length
100.06 Mb
100.10 Mb
100.14 Mb
100.18 Mb
100.22 Mb
100.26 Mb
ARL13A >
ENSG00000182574 >
TMEM35 >
CENPI >
< XKRX
< CXorf34
Cfam Chr. X
Length
Eponine
Ensembl trans.
Ensembl trans.
Eponine
Length
77.92 Mb
77.94 Mb
77.96 Mb
77.98 Mb
78.00 Mb
78.02 Mb
78.04 Mb
78.06 Mb
78.08 Mb
78.10 Mb
78.12 Mb
78.14 Mb
ENSCAFG00000017582 >
480983 >
492018 >
< 609590
< CXorf34

Ensembl

Ensembl release 42 - Dec 2006

HOME · BLAST · BIOMART · SITEMAP

Your Ensembl

- Login or Register
- About User Accounts

Help & Documentation

- Table of Contents
- Helpdesk
- What's New
- About Ensembl
- Downloading data
- Displaying your own data
- Ensembl software

Select a species

- Mammals

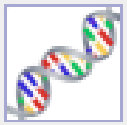
Search Ensembl

Search: All species for

Go

e.g. mouse chromosome 2 or X:10000..20000 or human gene BRCA2

Ensembl tools



Start a sequence search →
Search Ensembl for nucleotide and peptide sequences with BLAST and SSAHA.

Mine Ensembl with BioMart →
Cross-reference Ensembl datasets with BioMart, a powerful data-mining tool.

Ensembl 42 | Pre! species

Popular genomes

Homo sapiens
NCBI 36 | Vega

Mus musculus
NCBI m36 | Vega

Danio rerio

Enter the Query Sequence

Either Paste sequences (max 30 sequences) in FASTA or plain text:

GTCCTTGGGATTGAATTGTTGGAGCAGGCACTGGAGGATGCAAGATGGACTGCAGCCTT

Or Upload a file containing one or more FASTA sequences

Browse...

Or Enter a sequence ID or accession (EMBL, UniProt, RefSeq)

Retrieve

Or Enter an existing ticket ID:

Retrieve

- (•) dna queries
- ( ) peptide queries

Select the databases to search against

Select species:
Use 'ctrl' key to select multiple species

- Gallus_gallus
- Gasterosteus_aculeatus
- Homo_sapiens

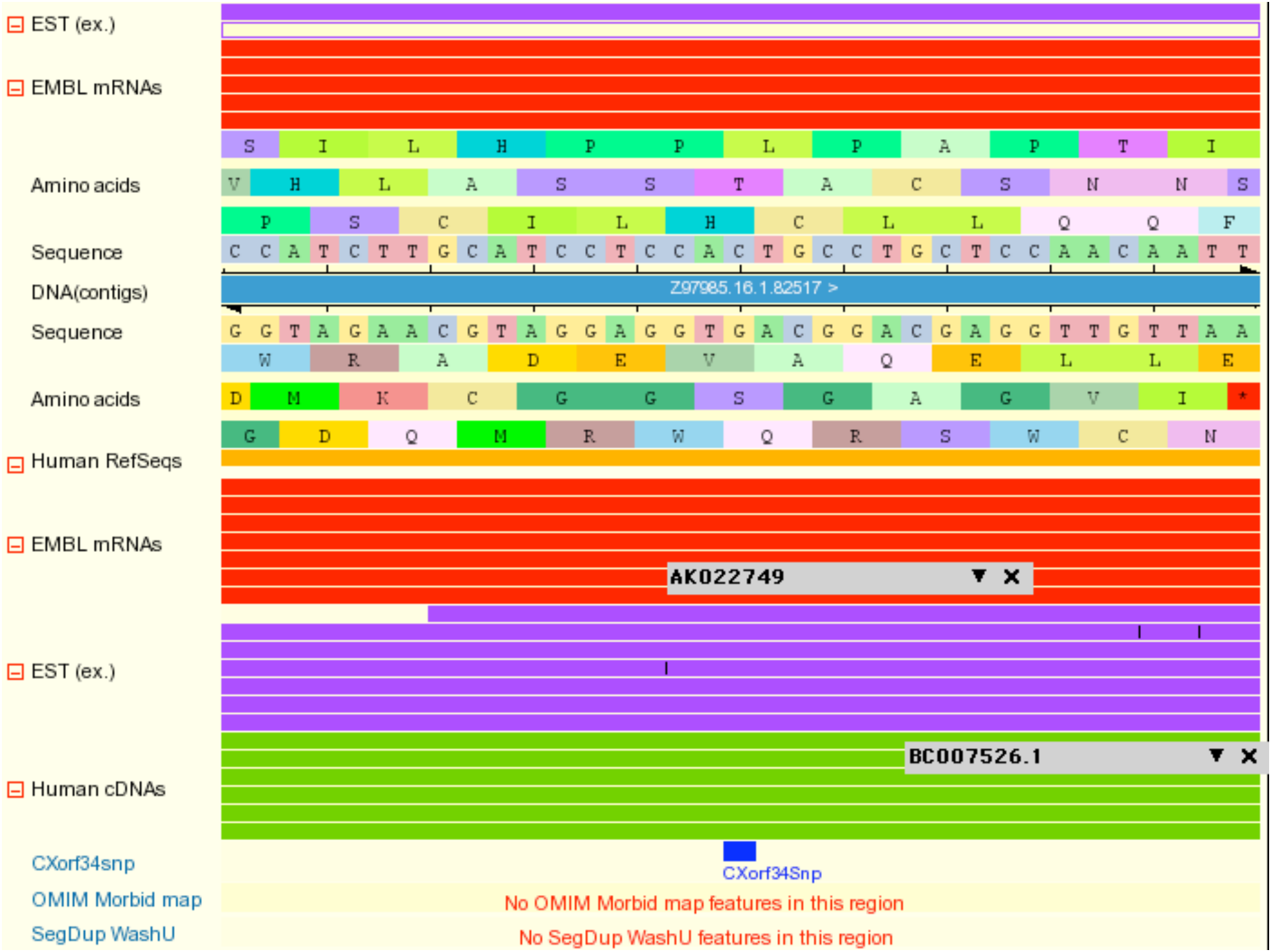
- (•) dna database — Genomic sequence
- ( ) peptide database — Known Consensus CDS Peptides (CCDS peptides)

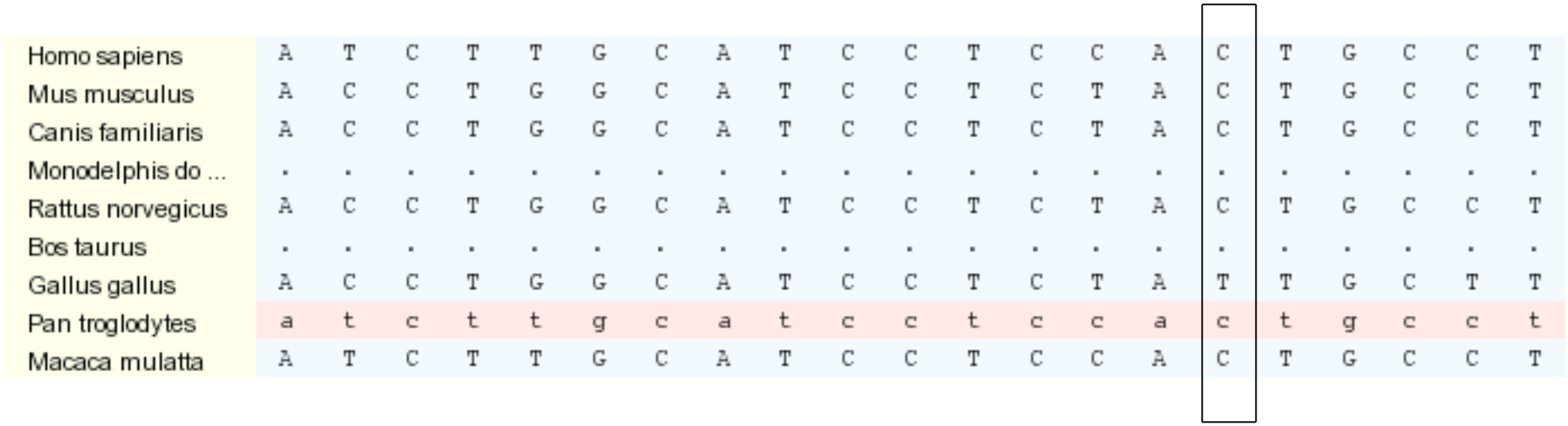
Select the Search Tool

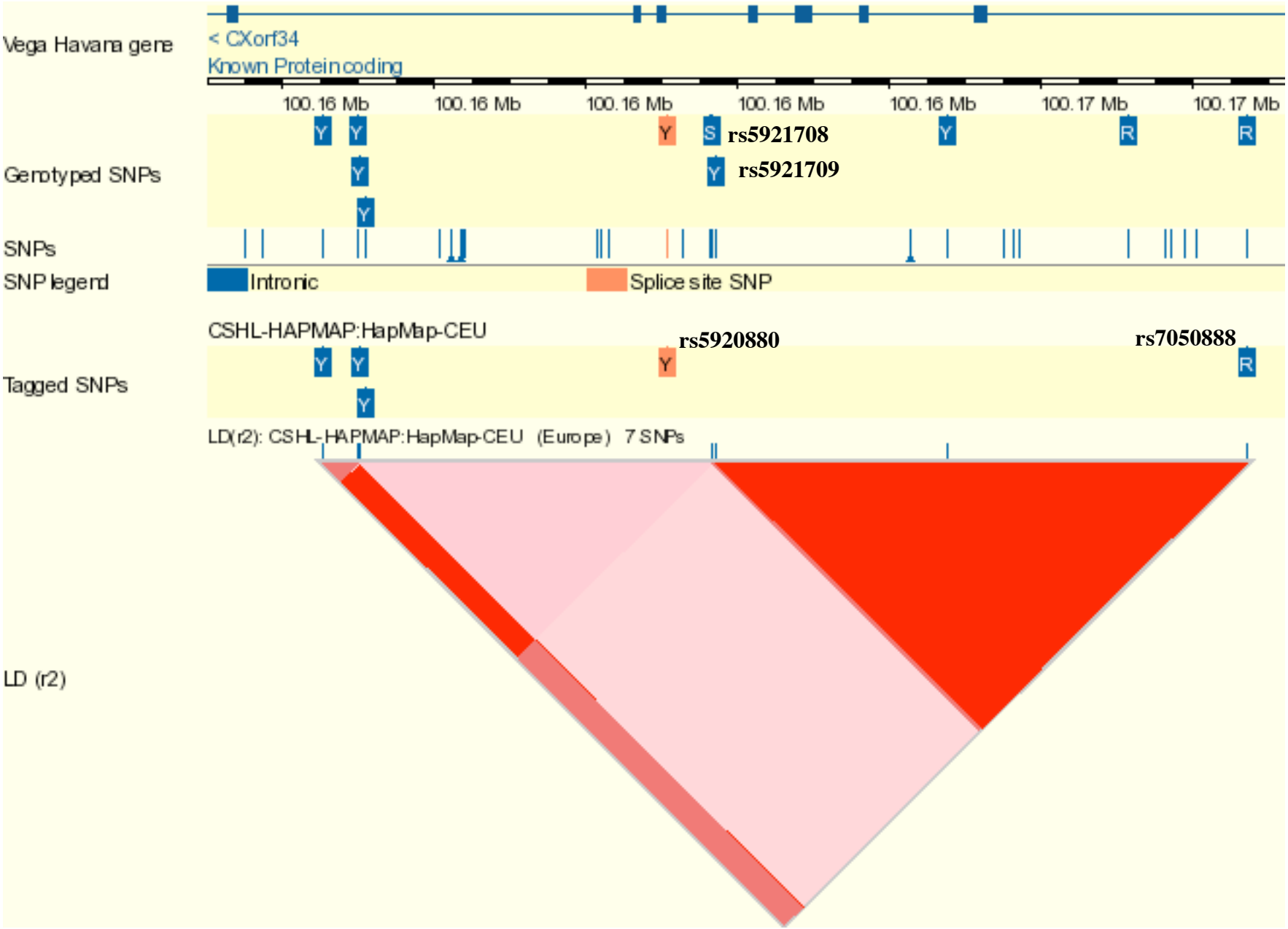
- BLASTN
- SSAHA2
- TBLASTX

configure▶ RUN▶

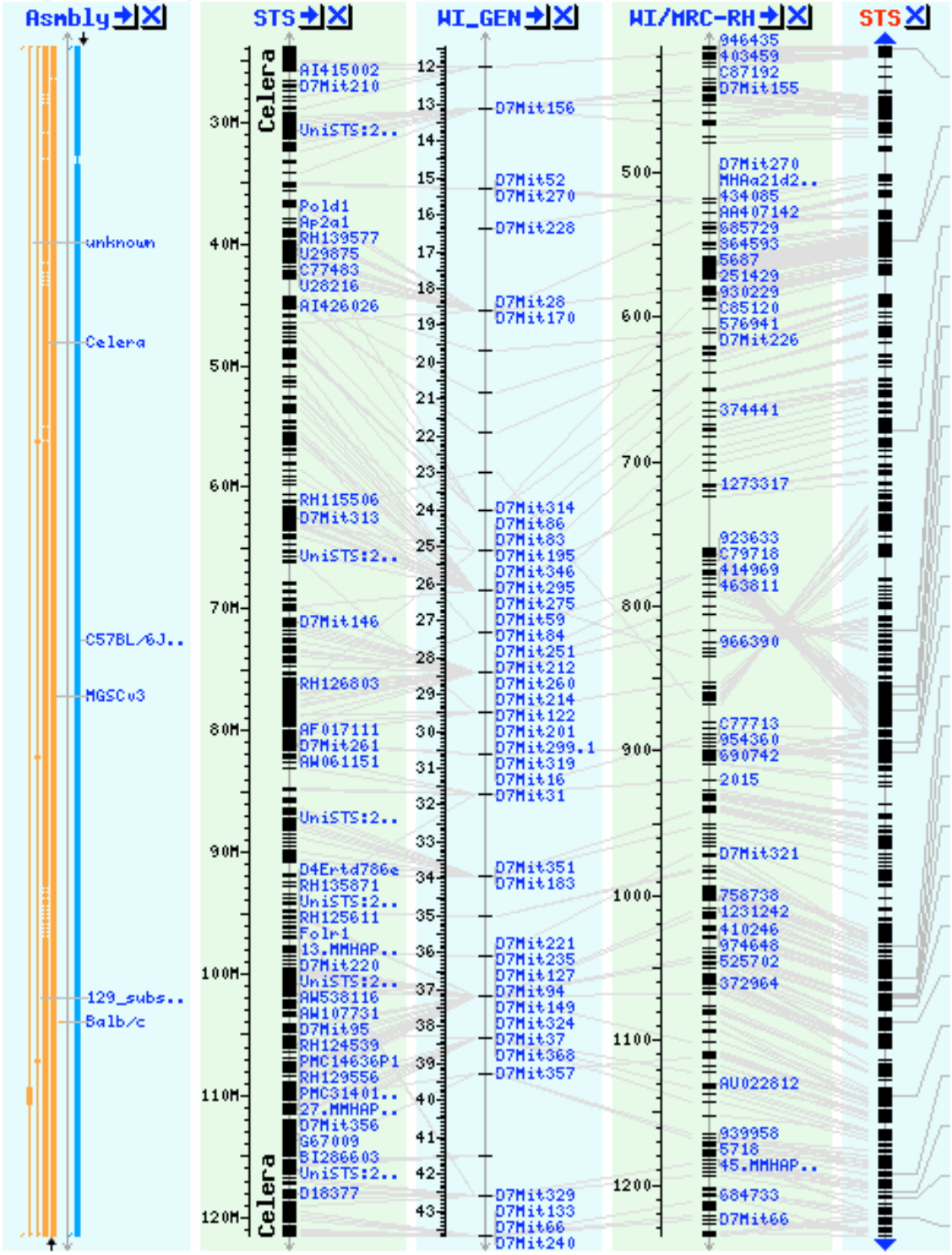
Search sensitivity: Near-exact matches


EST (ex.)
EMBL mRNAs
S I L H P P L P A P T I
Amino acids
V H L A S S T A C S N N S
P S C I L H C L L Q Q F
Sequence
C C A T C T T G C A T C C T C C A C T G C C T G C T C C A A C A A T T
DNA(contigs)
Z97985.16.1.82517 >
Sequence
G G T A G A A C G T A G G A G G T G A C G G A C G A G G T T G T T A A
W R A D E V A Q E L L E
Amino acids
D M K C G G S G A G V I *
G D Q M R W Q R S W C N
Human RefSeqs
EMBL mRNAs
AK022749
EST (ex.)
BC007526.1
Human cDNAs
CXorf34snp
CXorf34Snp
OMIM Morbid map
No OMIM Morbid map features in this region
SegDup WashU
No SegDup WashU features in this region


Homo sapiens A T C T T G C A T C C T C C A C T G C C T
Mus musculus A C C T G G C A T C C T C T A C T G C C T
Canis familiaris A C C T G G C A T C C T C T A C T G C C T
Monodelphis do ... .
Rattus norvegicus A C C T G G C A T C C T C T A C T G C C T
Bos taurus . . . .
Gallus gallus A C C T G G C A T C C T C T A T T G C T T
Pan troglodytes a t c t t g c a t c c t c c a c t g c c t
Macaca mulatta A T C T T G C A T C C T C C A C T G C C T

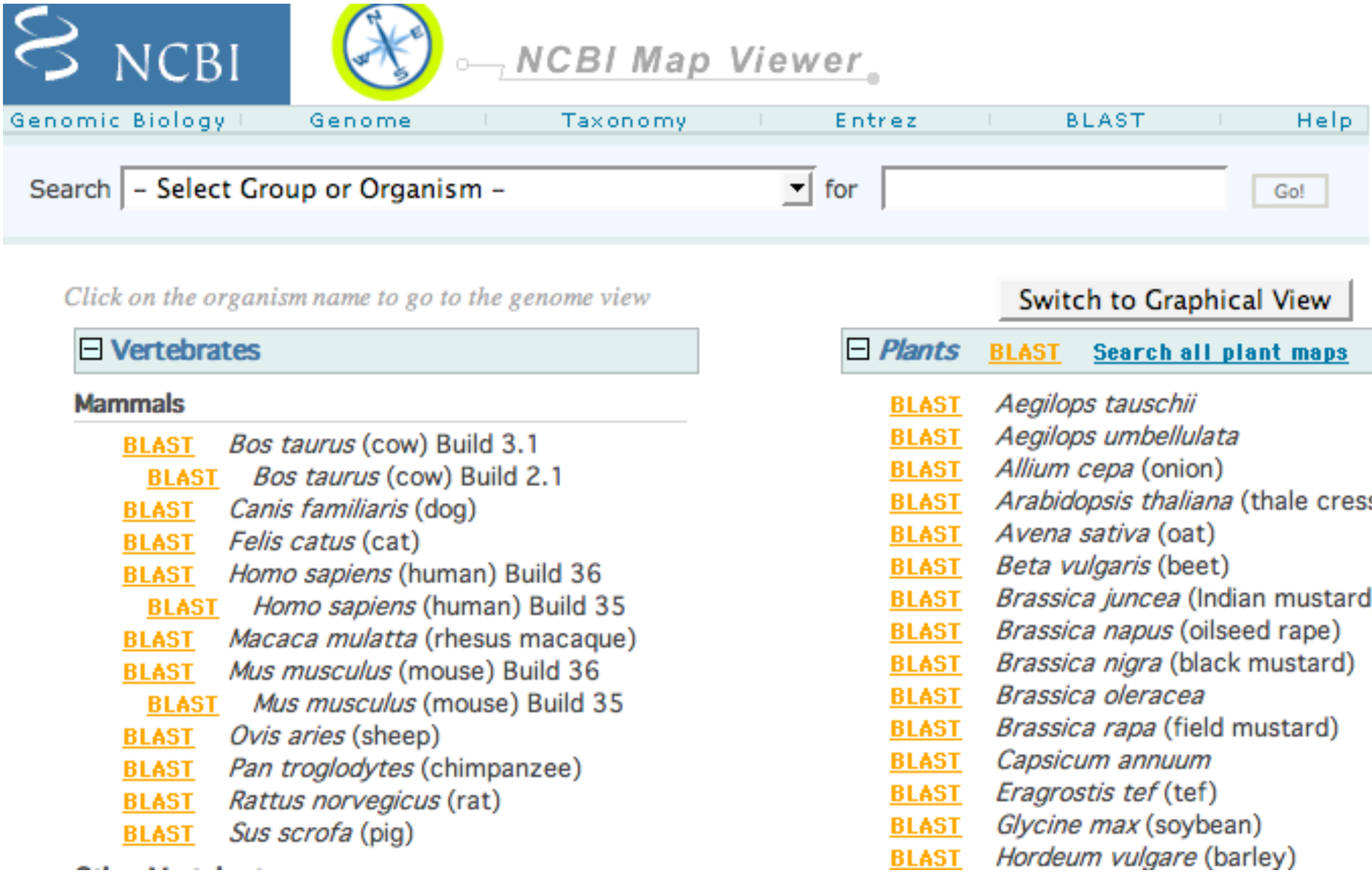

Vega Havana gene
< CXorf34
Known Protein coding
100.16 Mb
100.16 Mb
100.16 Mb
100.16 Mb
100.16 Mb
100.17 Mb
100.17 Mb
Genotyped SNPs
rs5921708
rs5921709
SNPs
SNP legend
Intronic
Splice site SNP
CSHL-HAPMAP:HapMap-CEU
rs5920880
rs7050888
Tagged SNPs
LD(r2): CSHL-HAPMAP:HapMap-CEU (Europe) 7 SNPs
LD (r2)

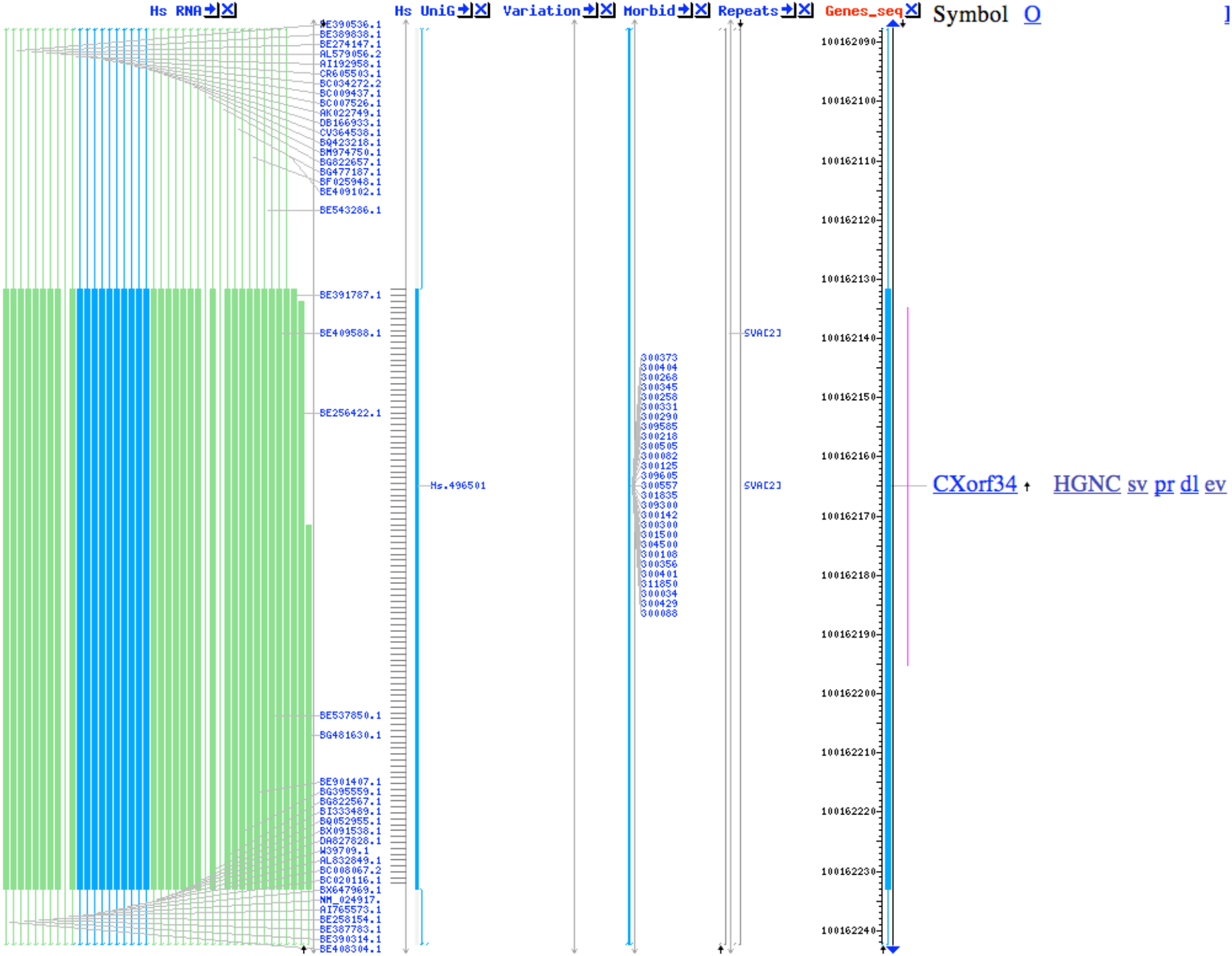
Region Displayed: **30M-120M bp**

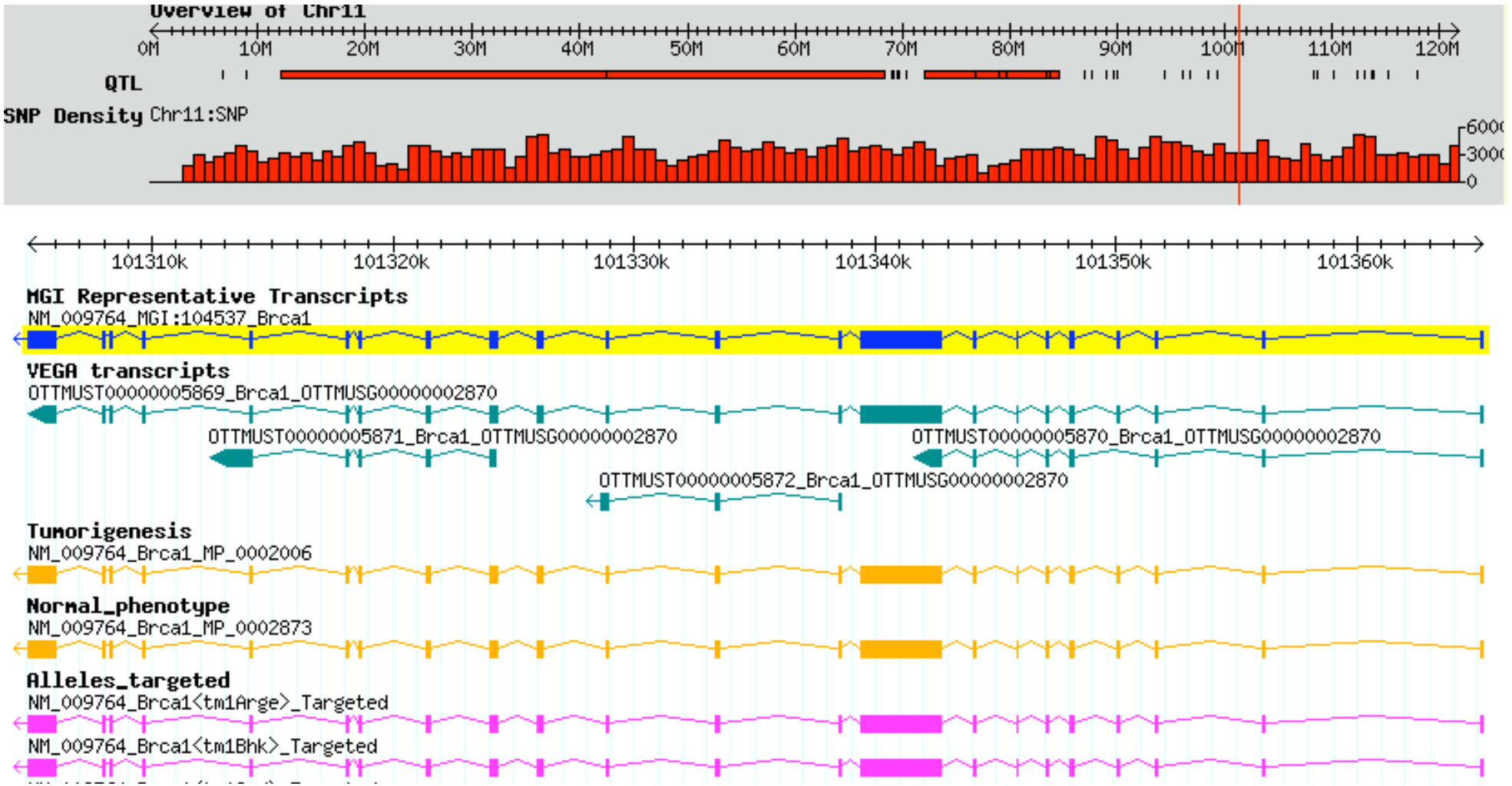


Marker

- UniSTS:235646
- AI426861
- RH125092
- D7Mit296
- D10Mit98
- 31.MMHAP61FRC10.seq
- D7Mit214
- PMC21264P1
- D7Mit90
- RH136415
- UniSTS:235704
- 18.MMHAP10FRF9.seq
- U85020
- D4Ertd786e
- Folr2
- RH140986
- BE200246
- AI894158
- UniSTS:259551
- D7Mill9
- UniSTS:144491
- D7Mit40
- 46.MMHAP57FLH4.seq
- UniSTS:235760


NCBI
NCBI Map Viewer
Genomic Biology
Genome
Taxonomy
Entrez
BLAST
Help
Search
– Select Group or Organism –
for
Go!
Click on the organism name to go to the genome view
Switch to Graphical View
Vertebrates
Mammals
BLAST Bos taurus (cow) Build 3.1
BLAST Bos taurus (cow) Build 2.1
BLAST Canis familiaris (dog)
BLAST Felis catus (cat)
BLAST Homo sapiens (human) Build 36
BLAST Homo sapiens (human) Build 35
BLAST Macaca mulatta (rhesus macaque)
BLAST Mus musculus (mouse) Build 36
BLAST Mus musculus (mouse) Build 35
BLAST Ovis aries (sheep)
BLAST Pan troglodytes (chimpanzee)
BLAST Rattus norvegicus (rat)
BLAST Sus scrofa (pig)
Plants
BLAST
Search all plant maps
BLAST Aegilops tauschii
BLAST Aegilops umbellulata
BLAST Allium cepa (onion)
BLAST Arabidopsis thaliana (thale cress)
BLAST Avena sativa (oat)
BLAST Beta vulgaris (beet)
BLAST Brassica juncea (Indian mustard)
BLAST Brassica napus (oilseed rape)
BLAST Brassica nigra (black mustard)
BLAST Brassica oleracea
BLAST Brassica rapa (field mustard)
BLAST Capsicum annuum
BLAST Eragrostis tef (tef)
BLAST Glycine max (soybean)
BLAST Hordeum vulgare (barley)


Region Displayed: 100,162,088-100,162,242 bp
Download/View Sequence
Hs RNA
Hs UniG
Variation
Morbid
Repeats
Genes_seq
Symbol
BE390536.1
BE389838.1
BE274147.1
AL579056.2
AI192958.1
CR605503.1
BC034272.2
BC009437.1
BC007526.1
AK022749.1
DB166933.1
CV364538.1
BQ423218.1
BM974750.1
BG822657.1
BG477187.1
BF025948.1
BE409102.1
BE543286.1
BE391787.1
BE409588.1
BE256422.1
Hs.496501
BE537850.1
BG481630.1
BE901407.1
BG395559.1
BG822567.1
BI333489.1
BQ052955.1
BX091538.1
DA827828.1
W39709.1
AL832849.1
BC008067.2
BC020116.1
BX647969.1
NM_024917.
AI765573.1
BE258154.1
BE387783.1
BE390314.1
BE408304.1
300373
300404
300268
300345
300258
300331
300290
309585
300218
300505
300082
300125
309605
300557
301835
309300
300142
300300
301500
304500
300108
300356
300401
311850
300034
300429
300088
SVAC2J
SVAC2J
100162090
100162100
100162110
100162120
100162130
100162140
100162150
100162160
100162170
100162180
100162190
100162200
100162210
100162220
100162230
100162240
CXorf34
HGNC sv pr dl ev


Overview of Chr11
0M
10M
20M
30M
40M
50M
60M
70M
80M
90M
100M
110M
120M
QTL
SNP Density
Chr11:SNP
101310k
101320k
101330k
101340k
101350k
101360k
MGI Representative Transcripts
NM_009764_MGI:104537_Brca1
VEGA transcripts
OTTMUST00000005869_Brca1_OTTMUSG00000002870
OTTMUST00000005871_Brca1_OTTMUSG00000002870
OTTMUST00000005870_Brca1_OTTMUSG00000002870
OTTMUST00000005872_Brca1_OTTMUSG00000002870
Tumorigenesis
NM_009764_Brca1_MP_0002006
Normal_phenotype
NM_009764_Brca1_MP_0002873
Alleles_targeted
NM_009764_Brca1<tm1Arge>_Targeted
NM_009764_Brca1<tm1Bhk>_Targeted

Phenotypic Allele Detail

Your Input Welcome

Allele

Symbol: **Brca1^{tm1Arge}**
Name: targeted mutation 1, Argiris Efstratiadis
ID: MGI:1930613

Synonyms

Brca1^{ex2}

Allele details

Allele Type: Targeted (knock-out)
Strain of Origin: 129S/SvEv-Gpi1^{c}
ES Cell Line: CCE/EK.CCE
ES Cell Line Strain: 129S/SvEv-Gpi1^{c}
Mutation: Disruption caused by insertion of vector
Replacement of exon 2, encoding part of the RING finger motif, and part of the flanking introns with a neomycin cassette. (*J:40594*)
Gene Expression in Brca1^{tm1Arge} mutants (3 assay results)
International Mouse Strain Resource: (Search for IMSR strains with Brca1 mutations)
References and Additional Notes: (See Below)

Gene information

Symbol: Brca1
Name: breast cancer 1
Chromosome: 11
Genetic Position: 60.5 cM, cytoband D
Genome Coordinates: Chr11:101304854-101368045 bp, - strand (From VEGA annotation of NCBI Build 36)
Human Ortholog: BRCA1

Phenotypes

Phenotypic details for all genotypes that include at least one Brca1^{tm1Arge} allele

Phenotype	Genotype	
	Allelic Composition	Genetic Background
Go To	Brca1^{tm1Arge}/Brca1^{tm1Arge}	involves: 129S/SvEv * C57BL/6
Go To	Brca1^{tm1Arge}/Brca1^{+}	involves: 129S/SvEv * C57BL/6
Go To	Brca1^{tm1Arge}/Brca1^{tm1Arge} Trp53^{tm1Tyj}/Trp53^{tm1Tyj}	involves: 129S/SvEv * 129S2/SvPas * C57BL/6
Go To	Brca1^{tm1Arge}/Brca1^{tm1Arge} Brca2^{tm1Arge}/Brca2^{tm1Arge}	involves: 129S/SvEv * C57BL/6
Go To	Bard1^{tm1Thl}/Bard1^{tm1Thl} Brca1^{tm1Arge}/Brca1^{tm1Arge}	involves: 129S/SvEv * 129S1/Sv

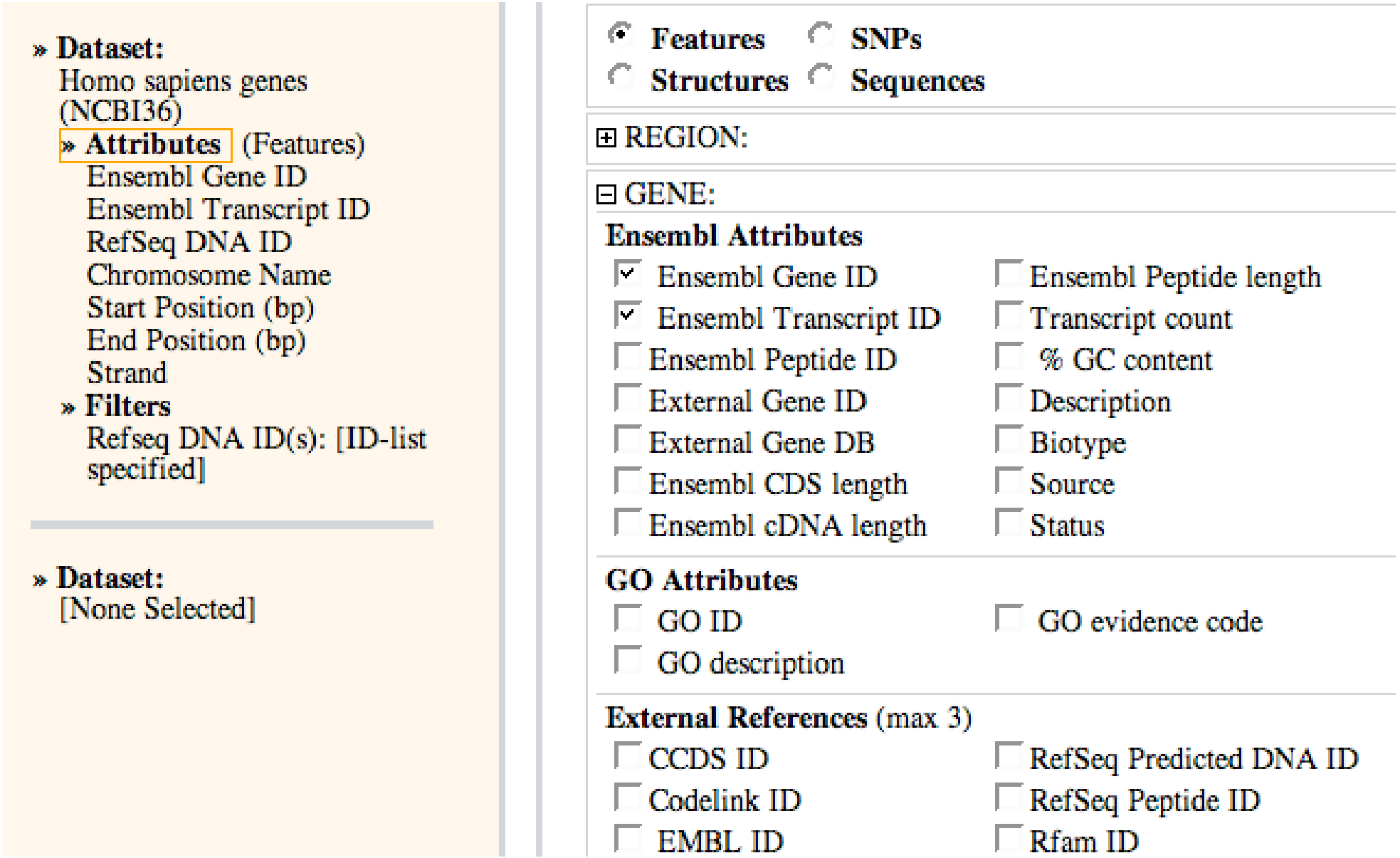
Allelic Composition	Genetic Background
Brca1^{tm1Arge}/Brca1^{tm1Arge}	involves: 129S/SvEv * C57BL/6

lethality/embryonic-perinatal

- embryonic lethality before turning of embryo (*J:40594*)
  - E5.5 -E8.5

embryogenesis

- absent mesoderm (*J:40594*)
- abnormal embryonic tissue morphology (*J:40594*)
  - many empty decidua found; some decidua contained only giant cells and extraembryonic membranes, and others also contained some embryonic remnants
  - abnormal egg cylinder morphology (*J:40594*)
    - at e5.5, embryonic tissue, when present, appears as small and short egg cylinders compared to controls; no clear division between embryonic and extraembryonic tissue is apparent
    - at e6.5, embryos, when present, are half the size of controls and were two-layered cylinders
    - at e6.5, mutants lack amniotic folds and the primary giant cells are prominent and large
    - at e7.5, embryos are small egg cylinders without amniotic folds and embryonic mesoderm is not visible; some extraembryonic tissue development appears normal
    - at E8.5, remaining embryos are variable in shape and achieved developmental stage; some consist of only extraembryonic tissue, some have rudimentary embryonic epithelium with no mesoderm, while others appear to have developed further to the heart beat stage, although the embryo is severely reduced in size
    - at E9.5, remaining embryos are variable in shape and achieved developmental stage
- absent amniotic folds (*J:40594*)
- embryonic growth retardation (*J:40594*)


» Dataset:
Homo sapiens genes (NCBI36)
» Attributes (Features)
Ensembl Gene ID
Ensembl Transcript ID
RefSeq DNA ID
Chromosome Name
Start Position (bp)
End Position (bp)
Strand
» Filters
Refseq DNA ID(s): [ID-list specified]
» Dataset:
[None Selected]
Features
SNPs
Structures
Sequences
REGION:
GENE:
Ensembl Attributes
Ensembl Gene ID
Ensembl Transcript ID
Ensembl Peptide ID
External Gene ID
External Gene DB
Ensembl CDS length
Ensembl cDNA length
Ensembl Peptide length
Transcript count
% GC content
Description
Biotype
Source
Status
GO Attributes
GO ID
GO description
GO evidence code
External References (max 3)
CCDS ID
Codelink ID
EMBL ID
RefSeq Predicted DNA ID
RefSeq Peptide ID
Rfam ID

Ensembl Gene ID	Ensembl Transcript ID	RefSeq DNA ID	Chromosome Name	Start Position (bp)	End Position (bp)	Strand
ENSG00000113525	ENST00000231454	NM_000879	5	131905035	131907113	-1
ENSG00000100296	ENST00000358079	NM_001002879	22	28231868	28279703	-1
ENSG00000172531	ENST00000312989	NM_001008709	11	66922228	66925978	-1
ENSG00000204075	ENST00000372866	NM_001008739	6	42966199	42966504	-1
ENSG00000146955	ENST00000275874	NM_001008749	7	139753916	139772419	1
ENSG00000163806	ENST00000296122	NM_001008779	2	28828118	28926981	1
ENSG00000171649	ENST00000307468	NM_001010879	19	62787320	62795570	1
ENSG00000105146	ENST00000302804	NM_001015879	19	62434240	62438727	1
ENSG00000127241	ENST00000337774	NM_001879	3	188418632	188492446	-1
ENSG00000003402	ENST00000309955	NM_003879	2	201689135	201737246	1

Human Ens. Gene ID	Mouse Ens Gene ID	Mouse chromosome
ENSG00000205070	ENSMUSG00000069038	Y
ENSG00000102144	ENSMUSG00000066632	12
ENSG00000174028	ENSMUSG00000029672	6
ENSG00000123130	ENSMUSG00000047565	15

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. See Using the Table Browser for a description of the controls in this form. For more complex queries, you may want to use our public MySQL server. Refer to the Credits page for the list of contributors and usage restrictions associated with these data.

clade: Vertebrate **genome:** Human **assembly:** Mar. 2006

group: Variation and Repeats **track:** SNPs

table: snp126 describe table schema

region: genome position chrX:151073054-151383976 lookup

identifiers (names/accessions): paste list upload list

filter: create

intersection: create

correlation: create

output format: all fields from selected table

output file: (leave blank to keep output in browser)

file type returned: plain text gzip compressed

get output summary/statistics

Schema for SNPs - Simple Nucleotide Polymorphisms (dbSNP build 126)

Database: hg18 **Primary Table:** snp126 **Row Count:** 12,351,941
Description: Polymorphism data from dbSnp database or genotyping arrays

field	example	SQL type	description
bin	585	smallint(5) unsigned	Indexing field to speed chromosome range queries.
chrom	chr10_random	varchar(15)	Reference sequence chromosome or scaffold
chromStart	490	int(10) unsigned	Start position in chrom
chromEnd	491	int(10) unsigned	End position in chrom
name	rs28694205	varchar(15)	Reference SNP identifier or Affy SNP name
score	0	smallint(5) unsigned	Not used
strand	+	enum('?','+','-')	Which DNA strand contains the observed alleles
refNCBI	A	blob	Reference genomic from dbSNP
refUCSC	A	blob	Reference genomic from nib lookup
observed	A/T	varchar(255)	The sequences of the observed alleles from rs-fasta files
molType	genomic	enum('unknown','genomic','cDNA')	Sample type from exemplar ss
class	single	enum('unknown','single','in-del','het','microsatellite','named','no var','mixed','mnp','insertion','deletion')	The class of variant (simple, insertion, deletion, range, etc.)
valid	unknown	set('unknown','by-cluster','by-frequency','by-submitter','by-2hit-2allele','by-hapmap')	The validation status of the SNP
avHet	0	float	The average heterozygosity from all observations
avHetSE	0	float	The Standard Error for the average heterozygosity
func	intron	set('unknown','locus','coding','coding-synon','coding-nonsynon','untranslated','intron','splice-site','cds-reference')	The functional category of the SNP (coding-synon, coding-nonsynon, intron, etc.)
locType	exact	enum('unknown','range','exact','between','rangeInsertion','rangeSubstitution','rangeDeletion')	How the variant affects the reference sequence
weight	1	int(10) unsigned	The quality of the alignment

Filter on Fields from hg18.snp126

bin	is ignored			
chrom	does match	*		AND
chromStart	is ignored			AND
chromEnd	is ignored			AND
name	does match	*		AND
score	is ignored			AND
strand	does match	*		AND
refNCBI	does match	*		AND
refUCSC	does match	*		AND
observed	does match	*		AND
molType	does match	*		AND
class	does match	*		AND
valid	does include	*		AND
avHet	is ignored			AND
avHetSE	is ignored			AND
func	does include	*		AND
locType	does match	*		AND
weight	is ignored			AND

AND Free-form query:

submit cancel

Lift Genome Annotations

This tool converts genome coordinates and genome annotation files between assemblies. The input data can be pasted into the text box, or uploaded from a file.

Original Genome:	Original Assembly:	New Genome:	New Assembly:
Human	May 2004	Human	Mar. 2006

Minimum ratio of bases that must remap:	0.95
Minimum chain size in target:	0
Minimum hit size in query:	0
Allow multiple output regions:	
Min ratio of alignment blocks/exons that must map:	1
If thickStart/thickEnd is not mapped, use the closest mapped base:	

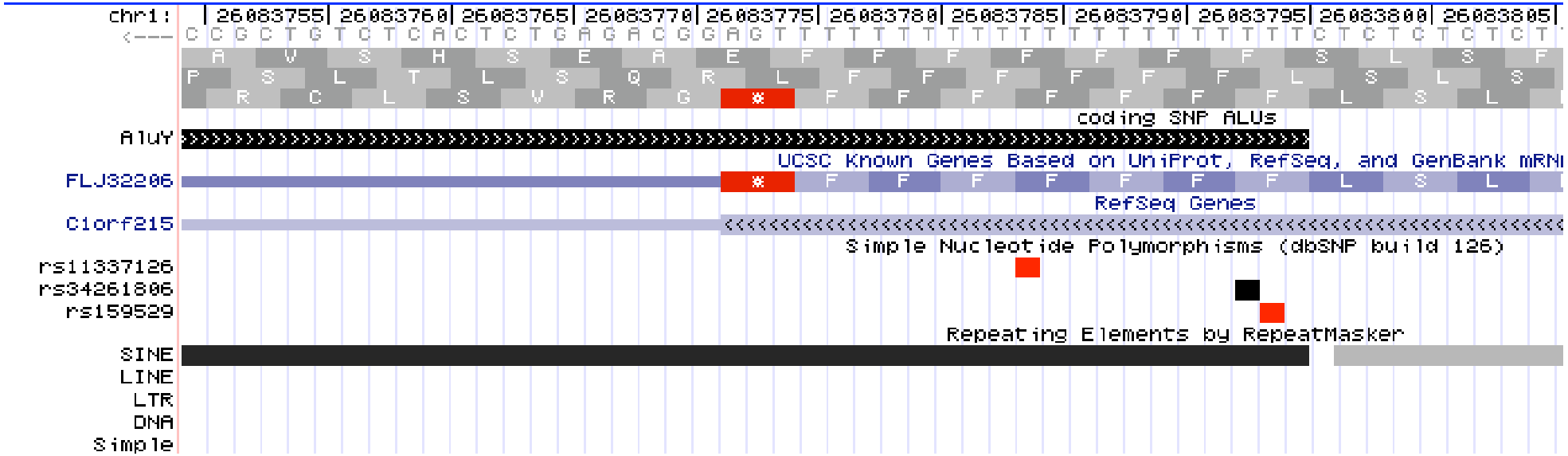
For descriptions of the supported data formats, see the bottom of this page.

Data Format: BED

Paste in data:

```
chr1    164495305       164495447       X93828  0       +
chr1    65011673        65011804        CV354059        0       +
chr1    179175367       179175462       AA906903        0       -
chr1    6289274 6312880 BF920027        0       -
```

Submit


chr1:
26083755
26083760
26083765
26083770
26083775
26083780
26083785
26083790
26083795
26083800
26083805
coding SNP ALUs
AluY
UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA
FLJ32206
RefSeq Genes
C1orf215
Simple Nucleotide Polymorphisms (dbSNP build 126)
rs11337126
rs34261806
rs159529
Repeating Elements by RepeatMasker
SINE
LINE
LTR
DNA
Simple

Tools

Get Data
Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
Join, Subtract and Group

- Join two Queries side by side on a specified field
- Compare two Queries to find common or distinct rows
- Subtract Whole Query from another query
- Group data by a column and perform aggregate operation on other columns.

Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
Evolution: HyPhy
EMBOSS

Visit Galaxy Talk and Posters at the Genome Informatics Meeting in Cold Spring Harbor (November 1 - 5, 2007)

Download Galaxy brochure here.

Unsequenced Genomes of the World | November 2007

Spectacled Flying Fox (Pteropus conspiculatus) | Queensland, Australia

Galaxy is for Biologists
Use this site to access popular sources of data like the UCSC Table Browser. Run analyses right on the spot using a variety of integrated tools. Your results are always available and can be easily shared with others. Just watch how.

Galaxy is for Developers
Galaxy is an easy-to-use, open-source, scalable framework for tool and data integration. Stop wasting time writing interfaces and get your tools used by biologists! Galaxy includes everything you need to get started, so download and start integrating!

History (options)

refresh | collapse all

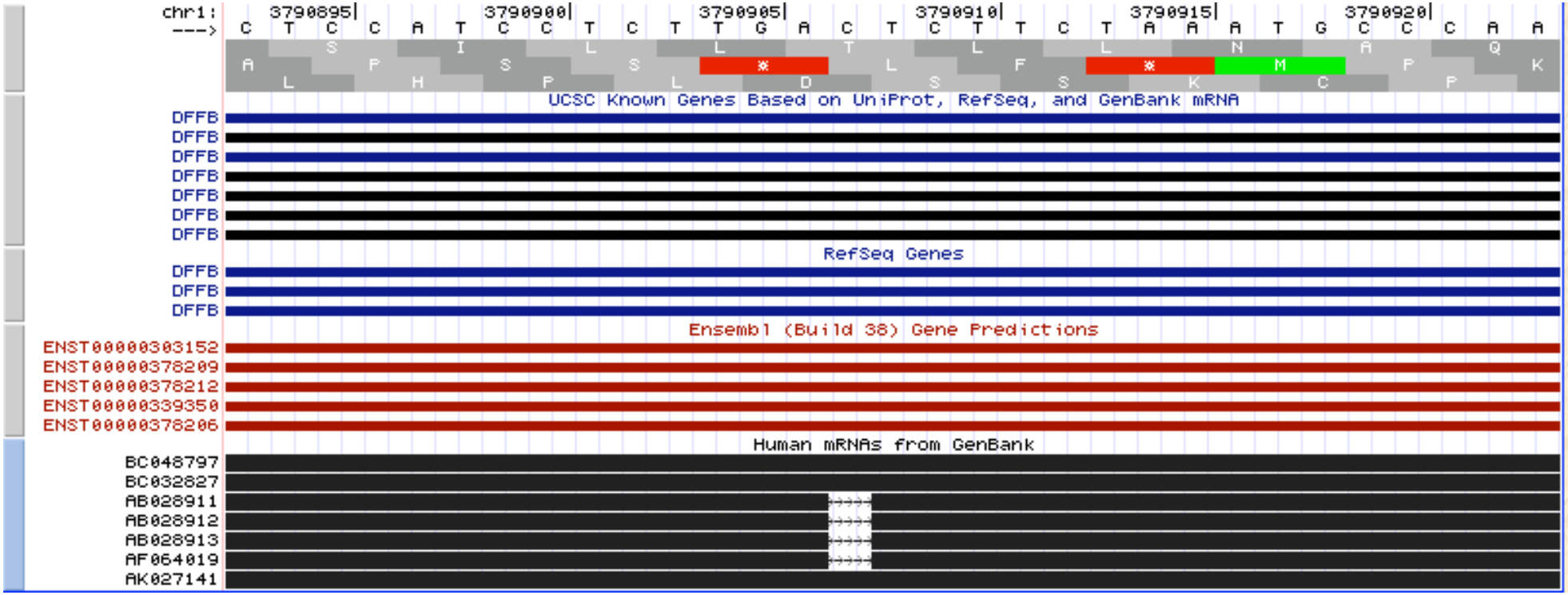
3: shortExons
2,444 regions, format: bed, database: hg18
Info: Filtering with c7 < 10,
save | display at UCSC main

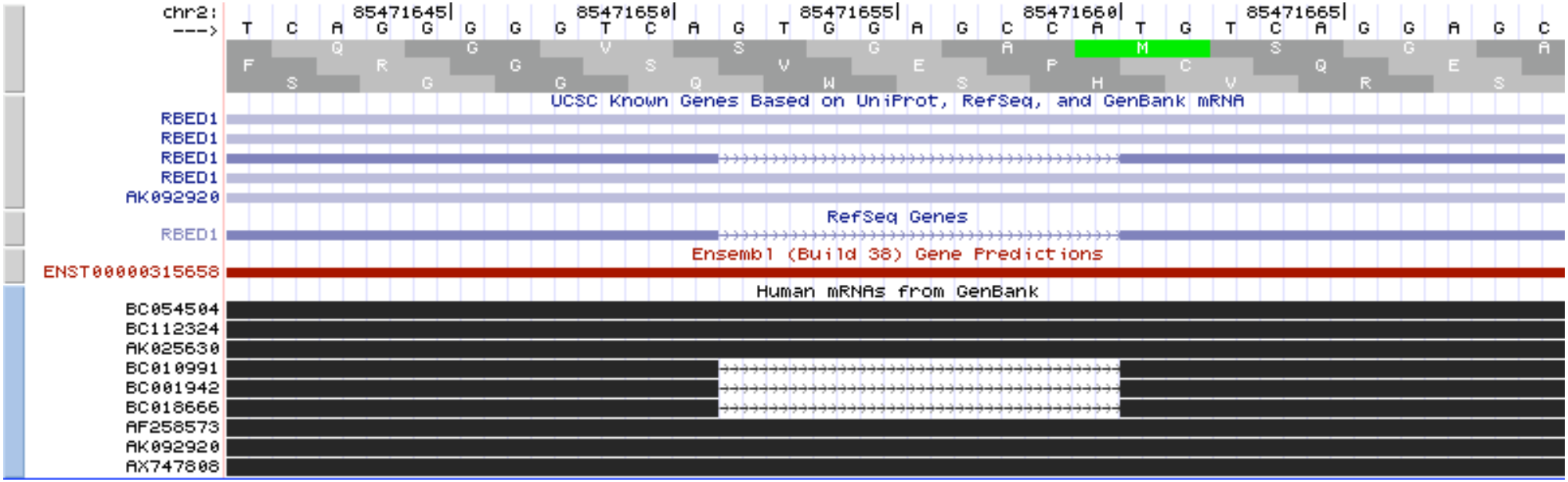
1	2	3	
chr1	7440	7444	ENST00000326632_
chr1	853117	853124	ENST00000338633_
chr1	855852	855859	ENST00000338633_
chr1	886796	886799	ENST00000338591_
chr1	1209148	1209150	ENST00000379101_
chr1	1212414	1212419	ENST00000379101_

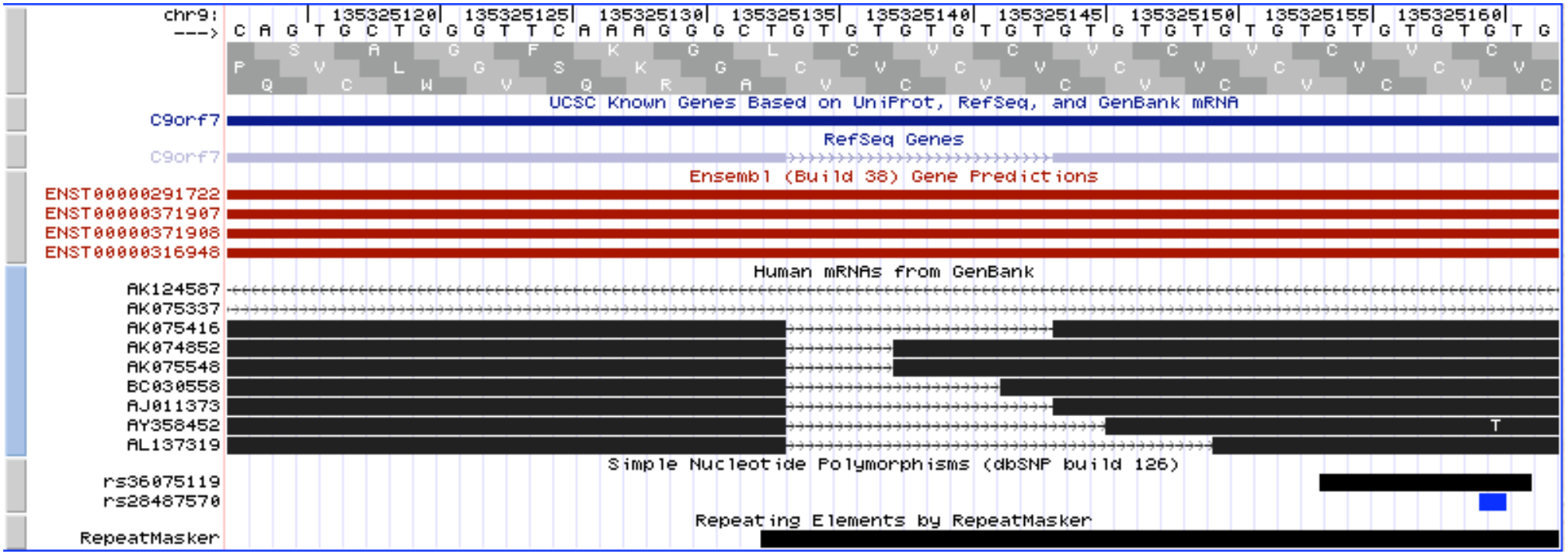
2: ensExonWithLength
490,526 regions, format: bed, database: hg18
Info: Creating column 7 with expression c3-c2
save | display at UCSC main

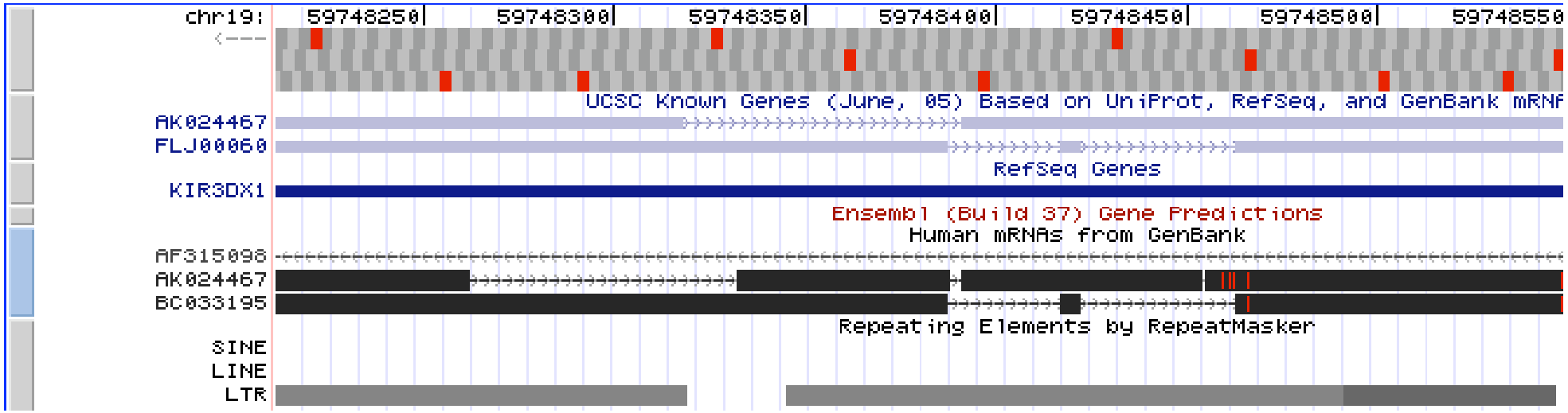
1	2	3	4
chr1	4273	4391	ENST00000326632_exon_0
chr1	4870	4901	ENST00000326632_exon_1
chr1	5658	5764	ENST00000326632_exon_2
chr1	5766	5810	ENST00000326632_exon_3
chr1	6469	6608	ENST00000326632_exon_4
chr1	6610	6628	ENST00000326632_exon_5


First query
Intervals to intersect with (Second Query)
Overlapping intervals
Overlapping pieces of intervals


chr1:
3790895
3790900
3790905
3790910
3790915
3790920
C T C C A T C C T C T T G A C T C T T C T A A A T G C C C A A
S I L L T L L N A Q
A P S S * L F * M P K
L H P L D S S K C P
UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA
DFFB
DFFB
DFFB
DFFB
DFFB
DFFB
DFFB
RefSeq Genes
DFFB
DFFB
DFFB
Ensembl (Build 38) Gene Predictions
ENST00000303152
ENST00000378209
ENST00000378212
ENST00000339350
ENST00000378206
Human mRNAs from GenBank
BC048797
BC032827
AB028911
AB028912
AB028913
AF064019
AK027141


chr2:
85471645
85471650
85471655
85471660
85471665
T C A G G G G G T C A G T G G A G C C A T G T C A G G A G C
F Q R G G V S V G E A P M C S Q G E A
S G G Q W S H V R S
UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA
RBED1
RBED1
RBED1
RBED1
AK092920
RefSeq Genes
RBED1
Ensembl (Build 38) Gene Predictions
ENST00000315658
Human mRNAs from GenBank
BC054504
BC112324
AK025630
BC010991
BC001942
BC018666
AF258573
AK092920
AX747808


chr9:
135325120
135325125
135325130
135325135
135325140
135325145
135325150
135325155
135325160
UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA
C9orf7
RefSeq Genes
C9orf7
Ensembl (Build 38) Gene Predictions
ENST00000291722
ENST00000371907
ENST00000371908
ENST00000316948
Human mRNAs from GenBank
AK124587
AK075337
AK075416
AK074852
AK075548
BC030558
AJ011373
AY358452
AL137319
Simple Nucleotide Polymorphisms (dbSNP build 126)
rs36075119
rs28487570
Repeating Elements by RepeatMasker
RepeatMasker


chr19:
59748250
59748300
59748350
59748400
59748450
59748500
59748550
UCSC Known Genes (June, 05) Based on UniProt, RefSeq, and GenBank mRNA
AK024467
FLJ00060
RefSeq Genes
KIR3DX1
Ensembl (Build 37) Gene Predictions
Human mRNAs from GenBank
AF315098
AK024467
BC033195
Repeating Elements by RepeatMasker
SINE
LINE
LTR

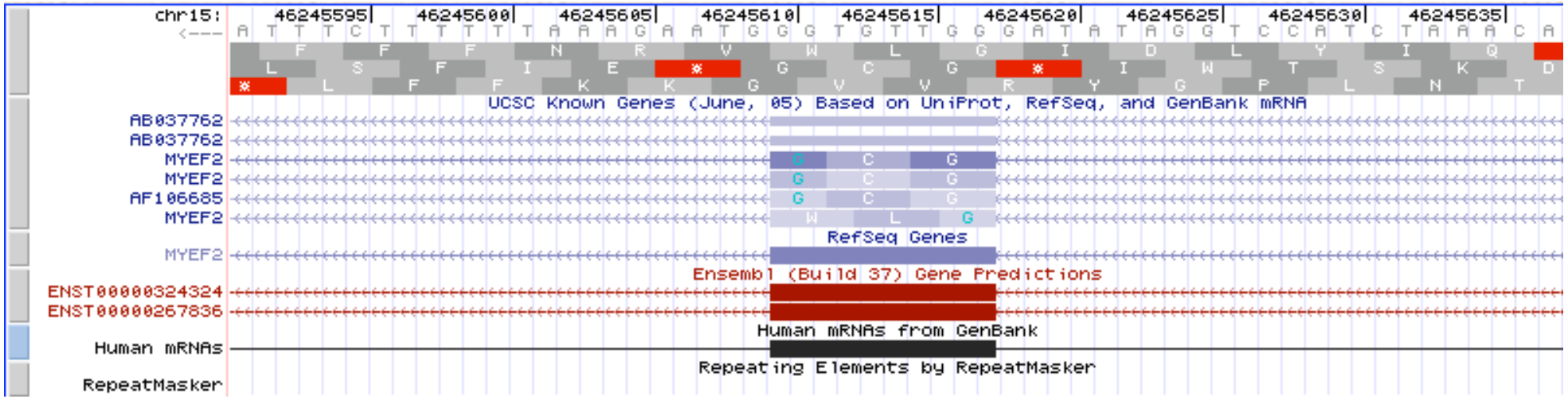

chr15:
46245595
46245600
46245605
46245610
46245615
46245620
46245625
46245630
46245635
UCSC Known Genes (June, 05) Based on UniProt, RefSeq, and GenBank mRNA
AB037762
AB037762
MYEF2
MYEF2
AF106685
MYEF2
RefSeq Genes
MYEF2
Ensembl (Build 37) Gene Predictions
ENST00000324324
ENST00000267836
Human mRNAs from GenBank
Human mRNAs
Repeating Elements by RepeatMasker
RepeatMasker

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. See Using the Table Browser for a description of the controls in this form. For more complex queries, you may want to use our public MySQL server. Refer to the Credits page for the list of contributors and usage restrictions associated with these data.

clade: Vertebrate **genome:** Human **assembly:** Mar. 2006

group: All Tables **database:** proteome

table: proteome.spDisease describe table schema

identif list upload list

filter:

outpu d table

outpu (leave blank to keep output in browser)

file typ zip compressed

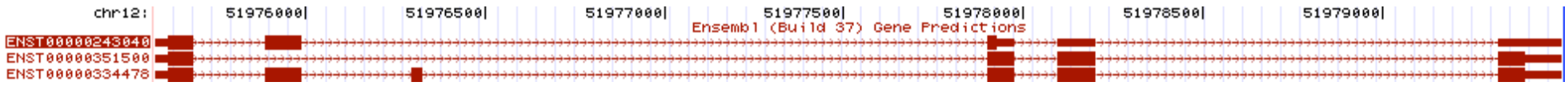
get o

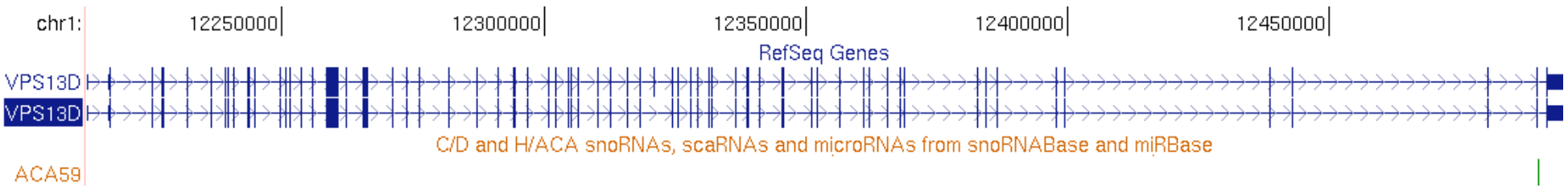
To rese custom tracks), click here.

- proteome.pepMolWtDist
- proteome.pepMwAa
- proteome.pepPi
- proteome.pepPiDist
- proteome.pepResDist
- proteome.pfamDesc
- proteome.pfamXref
- proteome.sfAssign
- proteome.sfDes
- proteome.spDisease
- proteome.spOldNew
- proteome.spOrganism
- proteome.spReactomeEvent
- proteome.spReactomeId
- proteome.spSecondaryID
- proteome.spVariant
- proteome.spXref2
- proteome.spXref3
- proteome.swInterPro
- proteome.tableDescriptions

Using

This s descriptions of the Table Browser controls. For more inform he Table Browser User's Guide.


chr12:
51976000|
51976500|
51977000|
51977500|
51978000|
51978500|
51979000|
Ensembl (Build 37) Gene Predictions
ENST00000243040
ENST00000351500
ENST00000334478


chr1:
12250000
12300000
12350000
12400000
12450000
RefSeq Genes
VPS13D
VPS13D
C/D and H/ACA snoRNAs, scaRNAs and microRNAs from snoRNABase and miRBase
ACA59

Summary

Bio::Seq - Sequence object, with features

Package variables

No package variables defined.

Included modules

Bio::Annotation::Collection
Bio::PrimarySeq

Inherit

Bio::AnnotatableI Bio::DescribableI Bio::FeatureHolderI Bio::IdentifiableI Bio::F

Synopsis

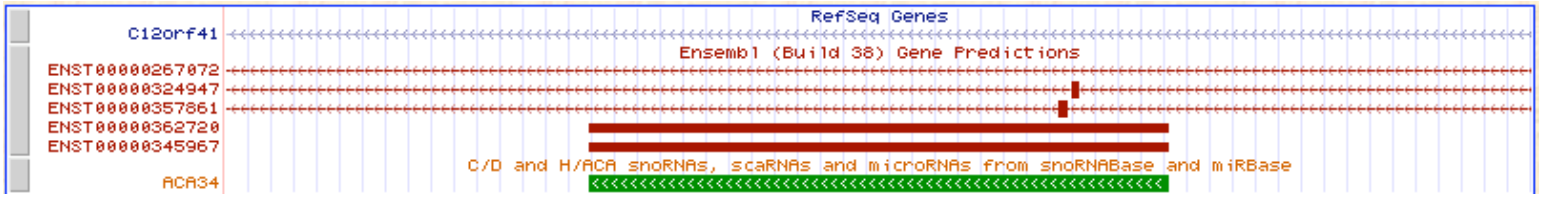
```
    # This is the main sequence object in Bioperl

    # gets a sequence from a file
    $seqio  = Bio::SeqIO->new( '-format' => 'embl' , -f
    $seqobj = $seqio->next_seq();

    # SeqIO can both read and write sequences; see Bio:
    # for more information and examples

    # get from database
    $db = Bio::DB::GenBank->new();
    $seqobj = $db->get_Seq_by_acc('X78121');

    # make from strings in script
    $seqobj = Bio::Seq->new( -display_id => 'my_id',
                             -seq => $sequence_as_strin
```

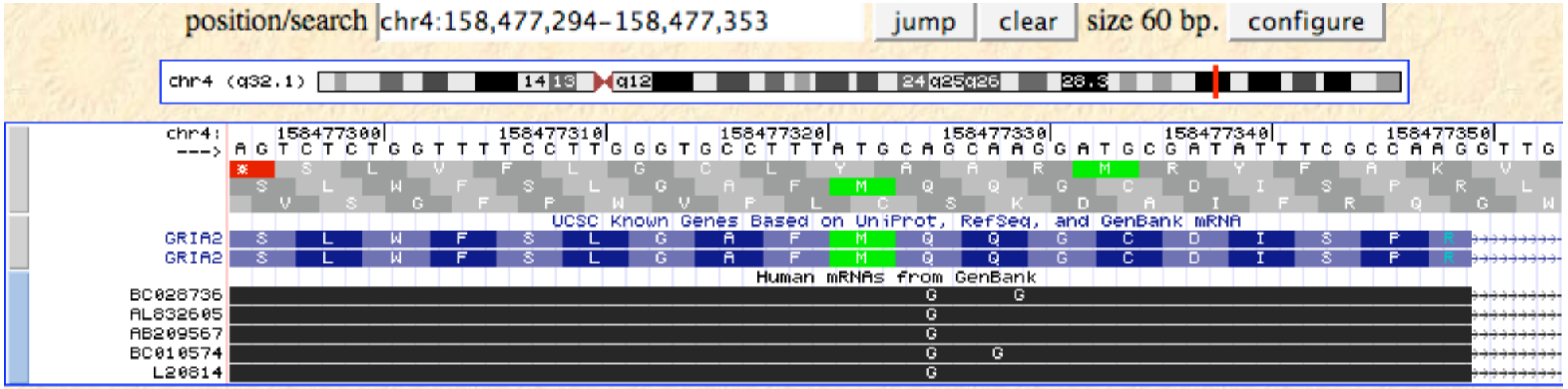
OR select a class from the list:

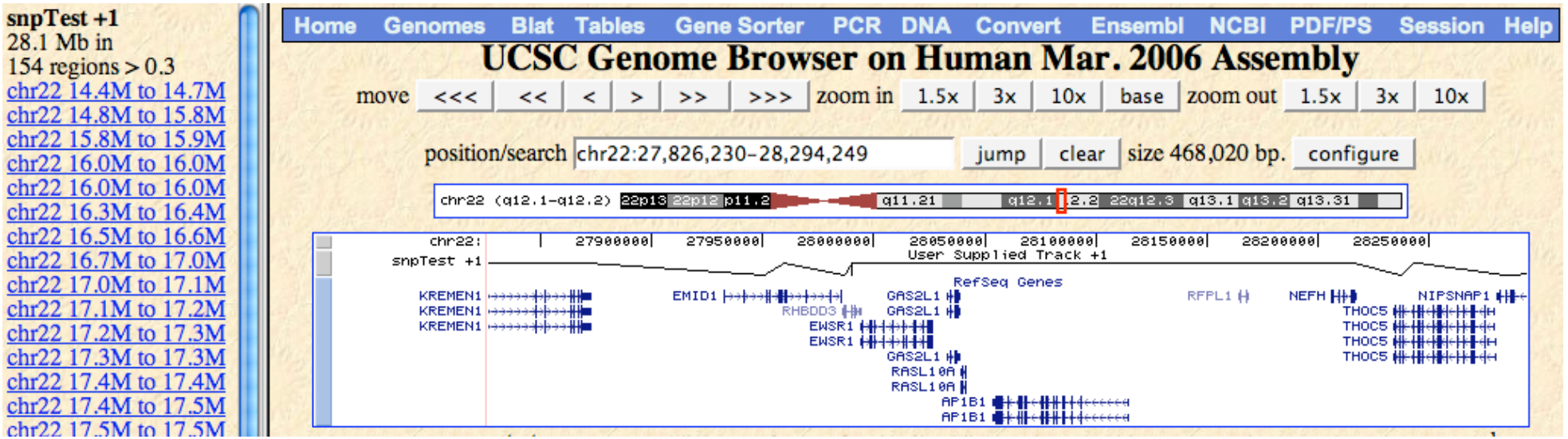
Bio::DB::GFF::Aggregator::ucsc_genscan	UCSC genscan aggregator
Bio::Tools::Genscan	Results of one Genscan run

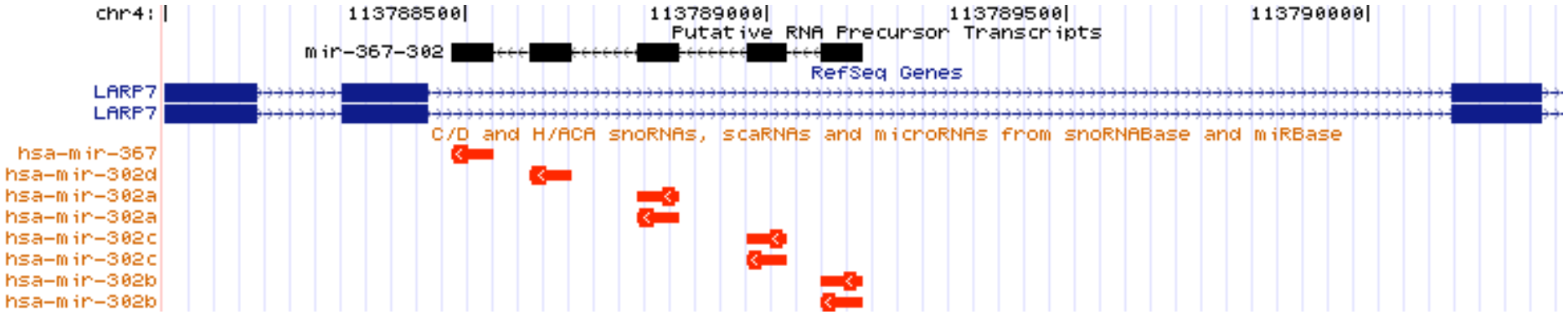
sort by method

methods for **Bio::Tools::Genscan**			
next_feature	Bio::Tools::Genscan	A Bio::Tools::Prediction::Gene object.	while($gene = $genscan->next_feature())
next_prediction	Bio::Tools::Genscan	A Bio::Tools::Prediction::Gene object.	while($gene = $genscan->next_prediction
noclose	Bio::Root::IO	value of noclose (a scalar)	$obj->noclose($newval)
otherwise	Bio::Root::Root	not documented	not documented
parse	Bio::Tools::AnalysisResult	not documented	not documented
qualify	Bio::Tools::Genscan	not documented	not documented
qualify_to_ref	Bio::Tools::Genscan	not documented	not documented
rmtree	Bio::Root::IO	number of files successfully deleted	Bio::Root::IO->rmtree($dirname);
stack_trace	Bio::Root::RootI	array containing a reference of arrays	@stack_array_ref= $self->stack_trace
stack_trace_dump	Bio::Root::RootI	not documented	not documented


RefSeq Genes
C12orf41
Ensembl (Build 38) Gene Predictions
ENST00000267072
ENST00000324947
ENST00000357861
ENST00000362720
ENST00000345967
C/D and H/ACA snoRNAs, scaRNAs and microRNAs from snoRNABase and miRBase
ACA34


position/search
chr4:158,477,294-158,477,353
jump
clear
size 60 bp.
configure
chr4 (q32.1)
14
13
q12
24
q25
q26
28.3
chr4:
158477300
158477310
158477320
158477330
158477340
158477350
UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA
GRIA2
GRIA2
Human mRNAs from GenBank
BC028736
AL832605
AB209567
BC010574
L20814


snpTest +1
28.1 Mb in
154 regions > 0.3
chr22 14.4M to 14.7M
chr22 14.8M to 15.8M
chr22 15.8M to 15.9M
chr22 16.0M to 16.0M
chr22 16.0M to 16.0M
chr22 16.3M to 16.4M
chr22 16.5M to 16.6M
chr22 16.7M to 17.0M
chr22 17.0M to 17.1M
chr22 17.1M to 17.2M
chr22 17.2M to 17.3M
chr22 17.3M to 17.3M
chr22 17.4M to 17.4M
chr22 17.4M to 17.5M
chr22 17.5M to 17.5M
Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl NCBI PDF/PS Session Help
UCSC Genome Browser on Human Mar. 2006 Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position/search chr22:27,826,230-28,294,249 jump clear size 468,020 bp. configure
chr22 (q12.1-q12.2) 22p13 22p12 p11.2 q11.21 q12.1 12.2 22q12.3 q13.1 q13.2 q13.31
chr22: 27900000 27950000 28000000 28050000 28100000 28150000 28200000 28250000
snpTest +1
User Supplied Track +1
RefSeq Genes
KREMEN1
KREMEN1
KREMEN1
EMID1
RHBDD3
EWSR1
EWSR1
GAS2L1
GAS2L1
GAS2L1
RASL10A
RASL10A
AP1B1
AP1B1
RFPL1
NEFH
NIPSNAP1
THOC5
THOC5
THOC5
THOC5

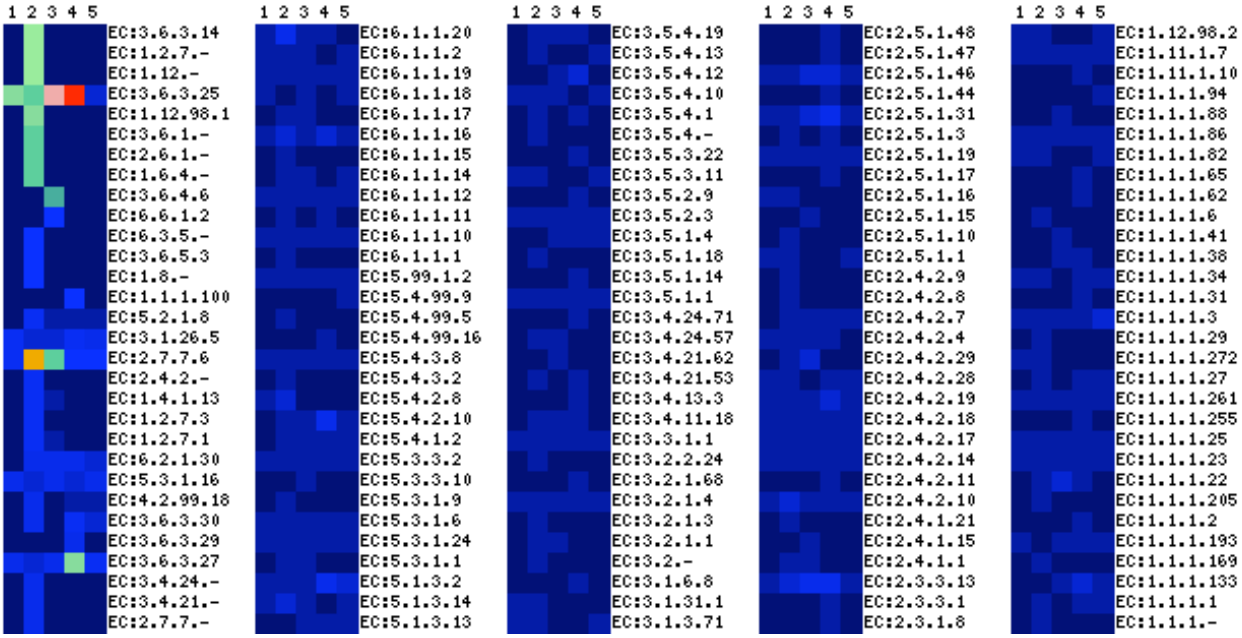

chr4:
113788500
113789000
113789500
113790000
Putative RNA Precursor Transcripts
mir-367-302
RefSeq Genes
LARP7
LARP7
C/D and H/ACA snoRNAs, scaRNAs and microRNAs from snoRNABase and miRBase
hsa-mir-367
hsa-mir-302d
hsa-mir-302a
hsa-mir-302a
hsa-mir-302c
hsa-mir-302c
hsa-mir-302b
hsa-mir-302b

Abundance Profile

434 clusters retrieved.

Mouse over labels to see additional information.
Clicking on the column number will sort rows for that column in descending gene count order.
Clicking on row cluster ID will add the cluster to the appropriate analysis cart (if cart is supported).
Mouse over heat map to see gene counts. Clicking on gene count will take you to the gene list.

1 - Methanocaldococcus jannaschii DSM 2661
2 - Methanococcus maripaludis S2
3 - Methanosaeta thermophila PT
4 - Methanosarcina acetivorans C2A
5 - Methanothermobacter thermautotrophicus Delta H

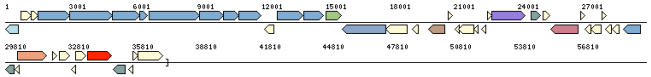


Chromosome Viewer

Loaded.

AMO community : amo_AY714822 (37318bp gc=0.44)
(coordinates **1-37318**)

hint: *Mouse over a gene to to see details.*



Get Nucleotide Sequence For Range

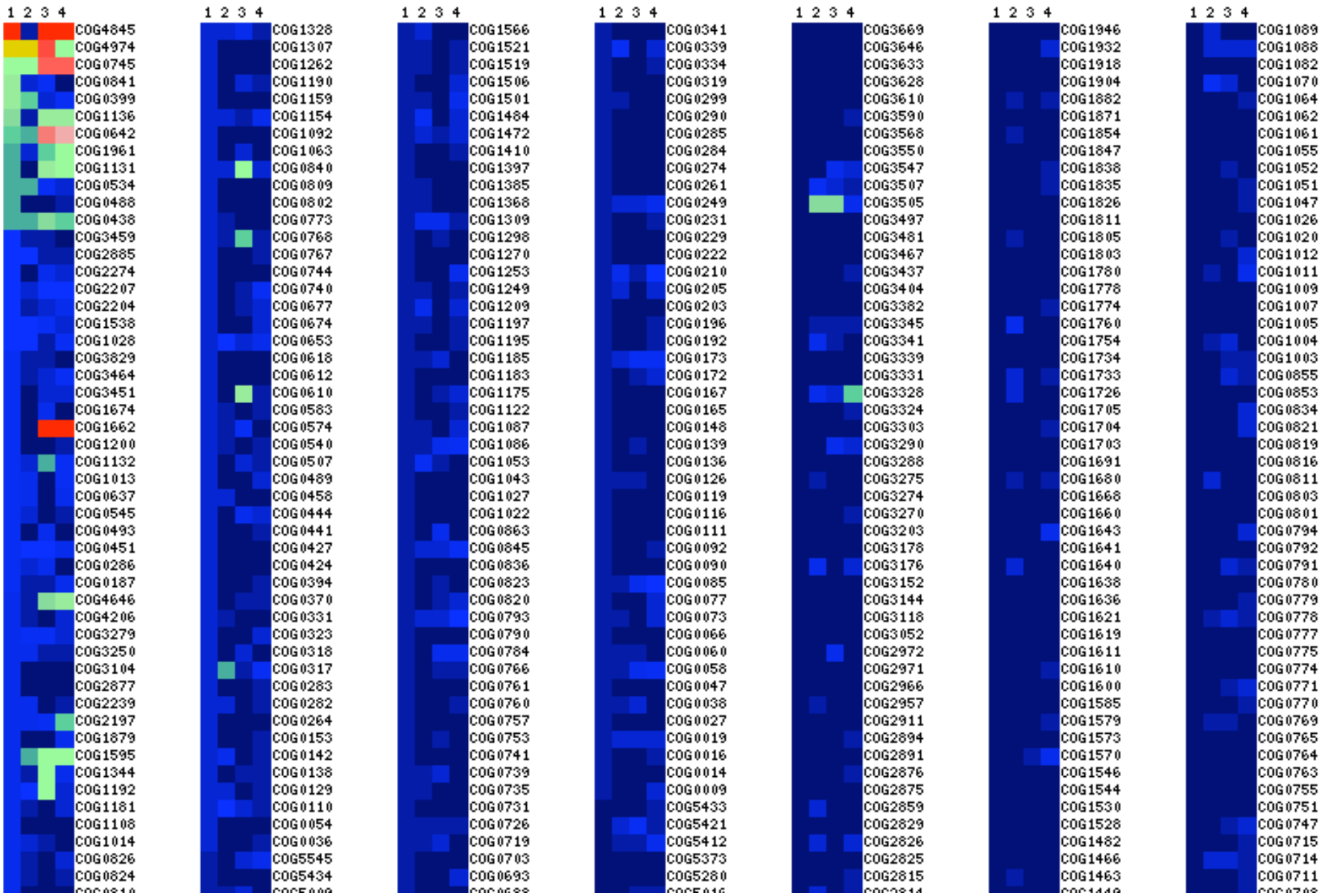
(RNA's are shown in black.)
||||||| CRISPR array.

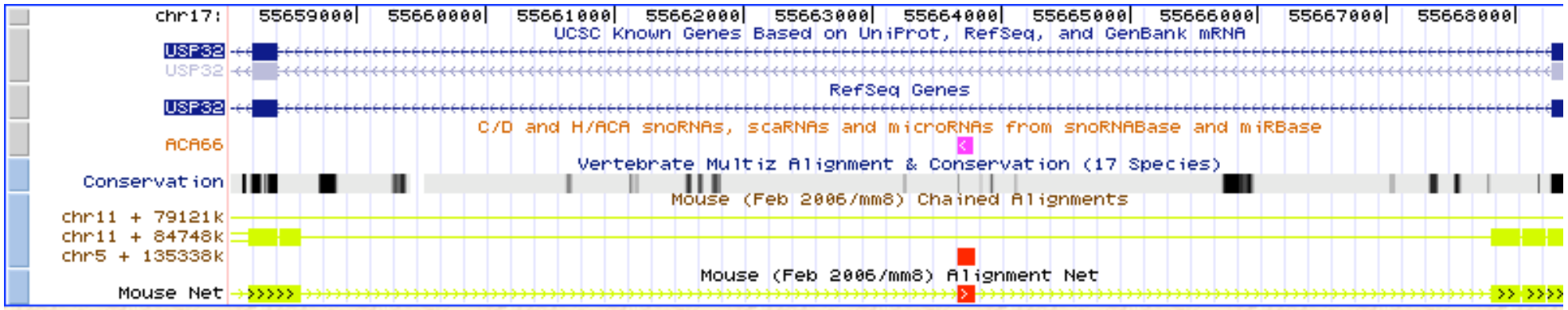
COG Coloring Selection

Color code of function category for top COG hit is shown below.
You may select a subset to view specific categories.

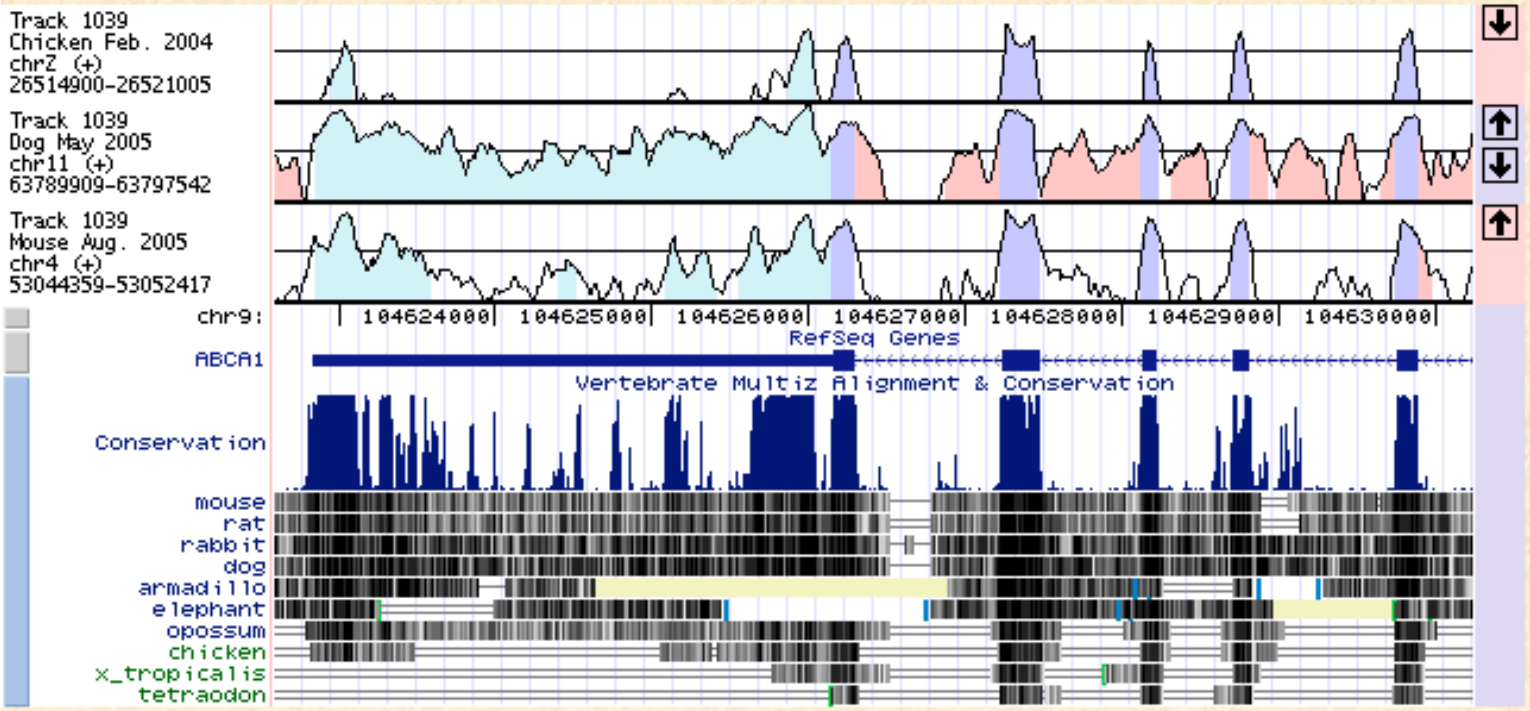
Show Color	COG Code	COG Function Definition
☑	[A]	RNA processing and modification
☑	[B]	Chromatin structure and dynamics
☑	[C]	Energy production and conversion
☑	[D]	Cell cycle control, cell division, chromosome partitioning
☑	[E]	Amino acid transport and metabolism
☑	[F]	Nucleotide transport and metabolism

1 - Mouse Gut Community lean1
2 - Mouse Gut Community lean2
3 - Mouse Gut Community ob1
4 - Mouse Gut Community ob2




chr17:
55659000
55660000
55661000
55662000
55663000
55664000
55665000
55666000
55667000
55668000
UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA
USP32
USP32
RefSeq Genes
USP32
C/D and H/ACA snoRNAs, scaRNAs and microRNAs from snoRNABase and miRBase
ACA66
Vertebrate Multiz Alignment & Conservation (17 Species)
Conservation
Mouse (Feb 2006/mm8) Chained Alignments
chr11 + 79121k
chr11 + 84748k
chr5 + 135338k
Mouse (Feb 2006/mm8) Alignment Net
Mouse Net

position/search chr9:104,622,591-104,630,241 jump clear size 7,651 bp. configure



move start < 2.0 >

Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.

move end < 2.0 >

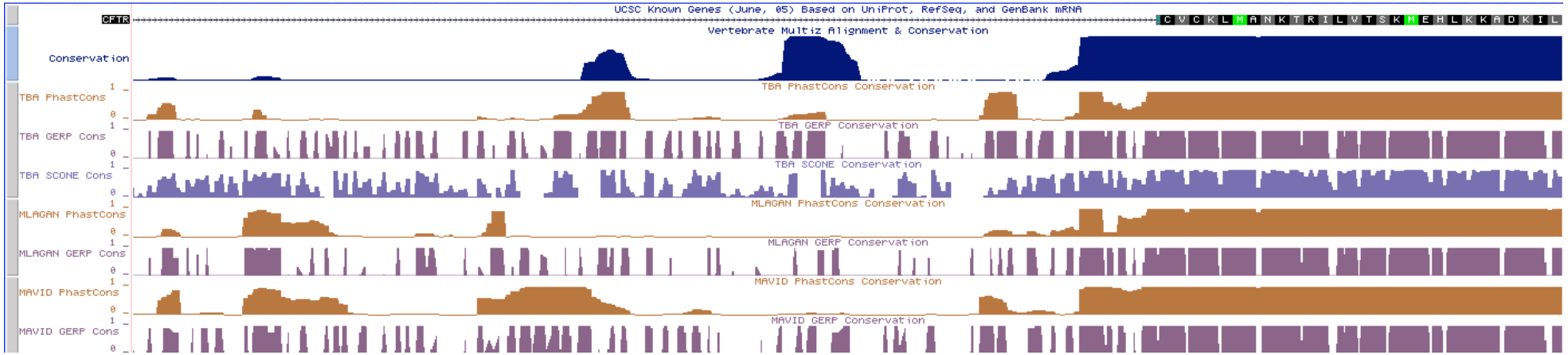
default tracks | hide all | add custom tracks | configure | refresh

Use drop down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.

VISTA Tracks

All tracks: sliding window: 100 genes: RefSeq genes

	Chicken (track 1039)	Rat (track 1039)	Dog (track 1039)	Mouse (track 1039)
mode	dense	hide	dense	dense
contigs				
conservation	70	70	70	70


UCSC Known Genes (June, 05) Based on UniProt, RefSeq, and GenBank mRNA
CFTR
C V C K L M A N K T R I L V T S K M E H L K K A D K I L
Vertebrate Multiz Alignment & Conservation
Conservation
TBA PhastCons Conservation
TBA PhastCons
TBA GERP Conservation
TBA GERP Cons
TBA SCONE Conservation
TBA SCONE Cons
MLAGAN PhastCons Conservation
MLAGAN PhastCons
MLAGAN GERP Conservation
MLAGAN GERP Cons
MAVID PhastCons Conservation
MAVID PhastCons
MAVID GERP Conservation
MAVID GERP Cons
1
0