

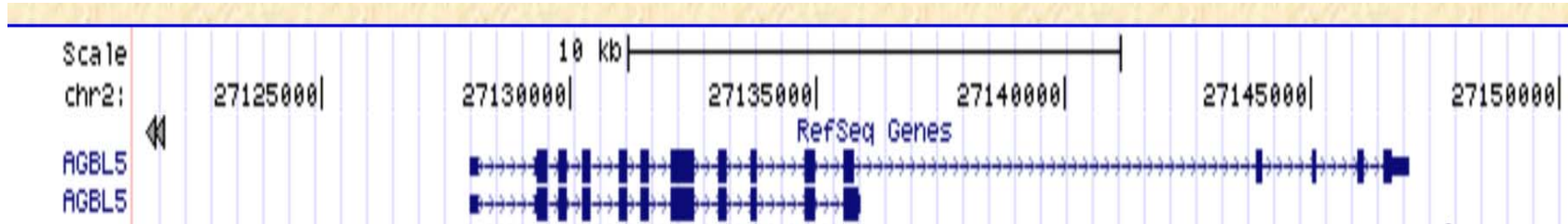


# UCSC Genome Browser

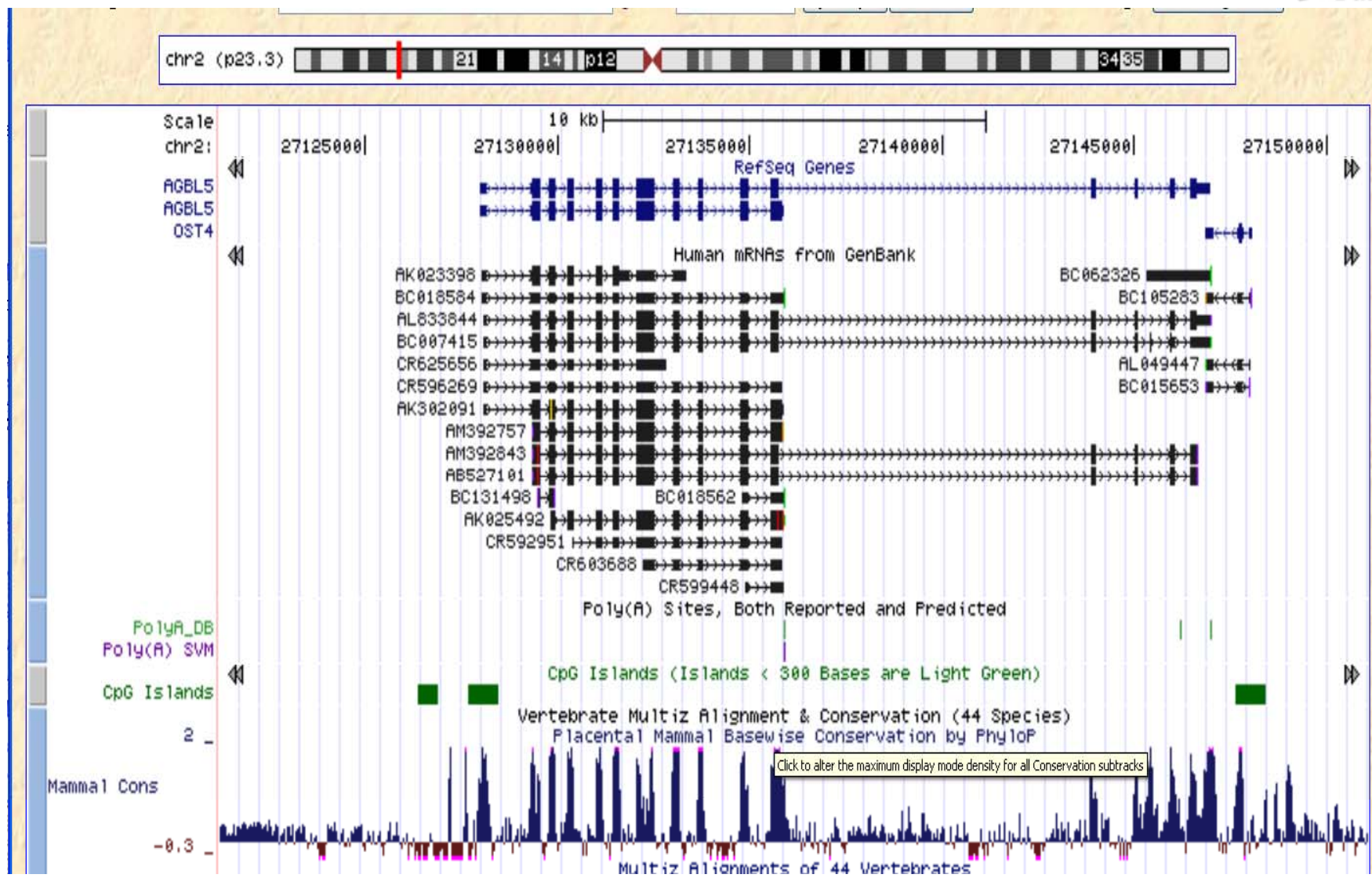
Bingbing Yuan

May 20, 2010

# How many isoforms AGBL5 has?



# Comprehensive View



# Genome Browser



- Ensembl Browser: <http://www.ensembl.org/index.html>
  - BLAST/BLAT: low similarity
  - Genetic Variation
- UCSC Browser: <http://genome.ucsc.edu/>
  - Easy to use
  - lots of tracks
- GBrowse: <http://gmod.org/wiki/Gbrowse>
  - private data
  - long setup & maintenance time
- IGV: <http://www.broadinstitute.org/igv/>
  - easy navigation
  - good for large data analysis



Ensembl genome browser 56: H.sapiens - Variation Image - Gene: TCF12 (ENSG00000140262)

Location: 15:57,212,896-57,216,915 Gene: TCF12 Transcript: TCF12-001 Variation: rs35615435

### Gene: TCF12 (ENSG00000140262)

Transcription factor 12 (Transcription factor HTF-4)(E-box-binding protein)(DNA-binding protein HTF4) [Source: UniProtKB/Swiss-Prot Q99081](#)

**Location** [Chromosome 15: 57,210,823-57,582,051](#) forward strand.

**Transcripts** There are 5 transcripts in this gene: [hide transcripts](#)

Name	Transcript ID	Protein ID	Description
TCF12-001	<a href="#">ENST00000267811</a>	<a href="#">ENSP00000267811</a>	protein_coding
TCF12-002	<a href="#">ENST00000333725</a>	<a href="#">ENSP00000331057</a>	protein_coding
TCF12-201	<a href="#">ENST00000343827</a>	<a href="#">ENSP00000342459</a>	protein_coding
TCF12-202	<a href="#">ENST00000438423</a>	<a href="#">ENSP00000388940</a>	protein_coding
TCF12-203	<a href="#">ENST00000452095</a>	<a href="#">ENSP00000396881</a>	protein_coding

#### Transcript and Gene level displays

In Ensembl a gene is made up of one or more transcripts. We provide displays at two levels:

- Transcript views which provide information specific to an individual transcript such as the cDNA and CDS sequences and protein domain annotation.
- Gene views which provide displays for data associated at the gene level such as orthologues and paralogues, regulatory regions and splice variants.

This view is a gene level view. To access the transcript level displays select a Transcript ID in the table above and then navigate to the information you want using the left hand side of the page. To return to viewing gene level information click on the Gene tab in the menu bar at the top of the page.

[Variation Table](#) **Variation Image** [help](#) [External Data](#)

ENST00000267811  
TCF12-001

PROSITE profiles  
PS50324 PS50888 HLH\_basic PF00010 HLH\_basic

Pfam domain



## 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.

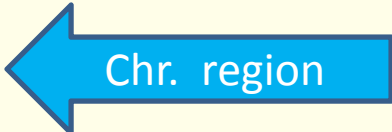


clade	genome	assembly	position or search term	gene	image width	
Mammal	Human	Mar. 2006 (NCBI36/hg18)	chr21:36,432,011-36,436,125		800	submit

[Click here to reset](#) the browser user interface settings to their defaults.

[manage custom tracks](#) [configure tracks and display](#) [clear position](#)

### 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	
RH18061;RH80175 15q11;15q13	Displays region between STS markers RH18061 and RH80175 or chromosome bands 15q11 to 15q13. This syntax may also be used for other range queries, such as between uniquely-determined ESTs, mRNAs, refSeqs, etc.	
D16S3046	Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side as well.	
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	

UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr22:17,012,759-17,040,162 gene  jump clear size 27,405 bp. configure

chr22 (q11.21) 22q13.2 22q13.1 22q13.2 22q13.3 22q13.31

Scale 10 kb

Chromosome coordinates list

USP10

Human mRNAs

Spliced ESTs

RepeatMasker

Conservation

Rhesus

Mouse

Dog

Elephant

Opossum

Platypus

Chicken

Z. tropica

SNPs (158)

Affy SNP 6.0

Affy SNP 6.0 SV

Illumina Infinium

Illumina Infinium

Illumina Infinium

RepeatMasker

move start Click on a feature for details. Click or drag in the base position track to zoom in. move end

< 2.0 >

Click gray/blue bars on left for track options and descriptions.

default tracks hide all manage custom tracks configure reverse refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. expand all

Tracks with lots of items will automatically be displayed in more compact modes.

Custom Tracks refresh

Mapping and Sequencing Tracks refresh

Phenotype and Disease Associations refresh

Genes and Gene Prediction Tracks refresh

UCSC Genes	Old UCSC Genes	Alt Events	Gencode Genes	CCDS	RefSeq Genes
pack	hide	hide	hide	hide	pack
Other RefSeq	MGC Genes	ORFome Clones	TransMap...	Vega Genes	Ensembl Genes
hide	hide	hide	hide	hide	hide
AceView Genes	STB Genes	N-SCAN	CONTRAST	SGP Genes	Gened Genes
hide	hide	hide	hide	hide	hide
GenScan Genes	Exonichy	Augustus	RNA Genes	ACEScan	EvoFold
hide	hide	hide	hide	hide	hide
sno/mRNA	Pos Sel Genes				
hide	hide				

mRNA and EST Tracks refresh

Expression refresh

Regulation refresh

Comparative Genomics refresh

Variation and Repeats refresh

Pilot ENCODE Regions and Genes refresh

Pilot ENCODE Transcription refresh

Pilot ENCODE Chromatin Immunoprecipitation refresh

Pilot ENCODE Chromatin Structure refresh

Pilot ENCODE Comparative Genomics and Variation refresh

refresh



## Genome Viewer

## Tracks (group of data)





# UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

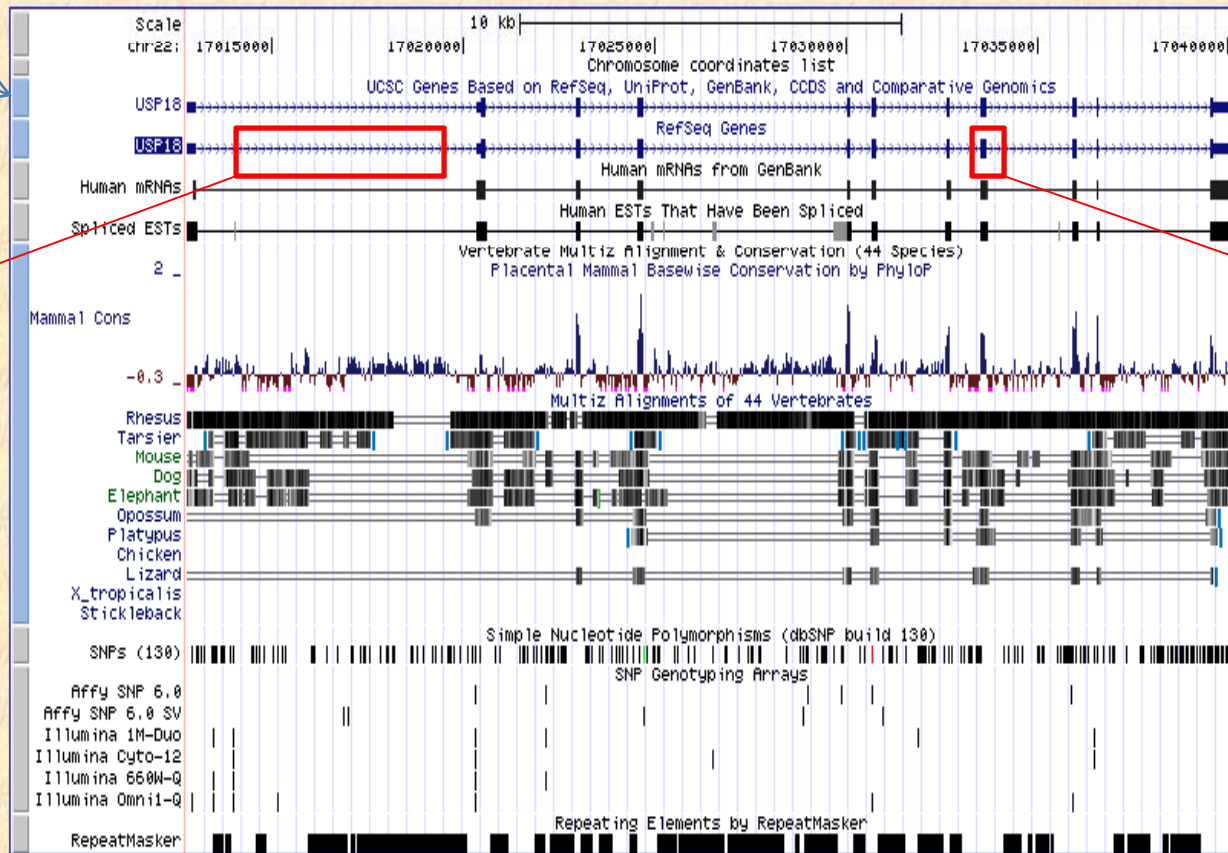
Navigate

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr22:17,012,758-17,040,162 gene jump clear size 27,405 bp. configure

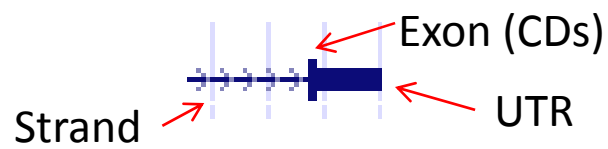
chr22 (q11.21) 22p13 22p12 p11.2 11.21 q12.1 12.2 22q12.3 q13.1 q13.2 22q13.31

Track Setting



intron

exon







Navigate

Drag-and-zoom

UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr22:17,012,759-17,040,162 gene [ ] jump clear size 27,405 bp. configure

chr22 (q11.21) 22q13.2 22q13.1 22q13.2 22q13.3 22q13.31

Scale 10 kb

Chromosome coordinates list

USP10 RefSeq Genes

Human mRNAs Human ESTs That Have Been Spliced

Spliced EST 2

Vertebrate Multiz Alignment & Conservation (44 Species)

Fluorocental Human Subsequence Conservation (by Phylo)

Human Cons

Rhesus Tarsier Mouse Dog Elephant Opossum Platypus Chicken Zebra

X\_tropicalis

SNPs (15k)

Affy SNP 6.0 Affy SNP 6.0 SV Illumina Infinium Illumina CpG-12 Illumina Infinium Illumina Omni-1

SNP Genotyping Arrays

RepeatMasker

move start Click on a feature for details. Click or drag in the base position track to zoom in. move end

Click gray/blue bars on left for track options and descriptions.

< 2.0 >

default tracks hide all manage custom tracks configure reverse refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. expand all

Tracks with lots of items will automatically be displayed in more compact mode.

Custom Tracks refresh

Mapping and Sequencing Tracks refresh

Phenotype and Disease Associations refresh

Genes and Gene Prediction Tracks refresh

UCSC Genes	Old UCSC Genes	Alt Events	Gencode Genes	CCDS	RefSeq Genes
pack	hide	hide	hide	hide	pack
Other RefSeq	MGC Genes	ORFome Clones	TransMap...	Vega Genes	Ensembl Genes
hide	hide	hide	hide	hide	hide
AceView Genes	STB Genes	N-SCAN	CONTRAST	SGP Genes	Gened Genes
hide	hide	hide	hide	hide	hide
GenScan Genes	Exonichy	Augustus	RNA Genes	ACEScan	EvoFold
hide	hide	hide	hide	hide	hide
sno/mRNA	Pos Sel Genes				
hide	hide				

mRNA and EST Tracks refresh

Expression refresh

Regulation refresh

Comparative Genomics refresh

Variation and Repeats refresh

Pilot ENCODE Regions and Genes refresh

Pilot ENCODE Transcription refresh

Pilot ENCODE Chromatin Immunoprecipitation refresh

Pilot ENCODE Chromatin Structure refresh

Pilot ENCODE Comparative Genomics and Variation refresh

refresh

Genome Viewer

Configure

Tracks (group of data)



## Configure Image

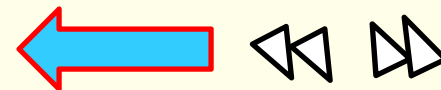
submit

image width:  pixels

label area width:  characters

text size:

<input checked="" type="checkbox"/>	Display chromosome ideogram above main graphic
<input checked="" type="checkbox"/>	Show light blue vertical guidelines
<input checked="" type="checkbox"/>	Display labels to the left of items in tracks
<input checked="" type="checkbox"/>	Display description above each track
<input checked="" type="checkbox"/>	Show track controls under main graphic
<input checked="" type="checkbox"/>	Next/previous item navigation
<input checked="" type="checkbox"/>	Next/previous exon navigation
<input checked="" type="checkbox"/>	Enable track re-ordering
<input checked="" type="checkbox"/>	Enable advanced javascript features





move start  move end

Click on a feature for details. Click or drag in the base position track to zoom in.  
Click gray/blue bars on left for track options and descriptions.

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

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

**Custom Tracks** refresh

coords  
full

**+** Mapping and Sequencing Tracks refresh

**+** Phenotype and Disease Associations refresh

**-** Genes and Gene Prediction Tracks refresh

<a href="#">UCSC Genes</a> pack	<a href="#">Old UCSC Genes</a> hide	<a href="#">Alt Events</a> hide	<input checked="" type="checkbox"/> <a href="#">Gencode Genes</a> hide	<a href="#">CCDS</a> hide	<a href="#">RefSeq Genes</a> pack
<a href="#">Other RefSeq</a> hide	<a href="#">MGC Genes</a> hide	<a href="#">ORFeome Clones</a> hide	<a href="#">TransMap...</a> hide	<a href="#">Vega Genes</a> hide	<a href="#">Ensembl Genes</a> hide
<a href="#">AceView Genes</a> hide	<a href="#">SIB Genes</a> hide	<a href="#">N-SCAN</a> hide	<a href="#">CONTRAST</a> hide	<a href="#">SGP Genes</a> hide	<a href="#">Ensembl Genes</a> hide
<a href="#">Genscan Genes</a> hide	<a href="#">Exoniphy</a> hide	<a href="#">Augustus</a> hide	<a href="#">RNA Genes</a> hide	<a href="#">ACEScan</a> hide	<a href="#">Ensembl Genes</a> hide
<a href="#">sno/mRNA</a> hide	<a href="#">Pos Sel Genes</a> hide				<a href="#">Ensembl Genes</a> hide

**+** mRNA and EST Tracks refresh

**+** Expression refresh

**+** Regulation refresh

**+** Comparative Genomics refresh

**+** Variation and Repeats refresh

**+** Pilot ENCODE Regions and Genes refresh

**+** Pilot ENCODE Transcription refresh

**+** Pilot ENCODE Chromatin Immunoprecipitation refresh

**+** Pilot ENCODE Chromatin Structure refresh

**+** Pilot ENCODE Comparative Genomics and Variation refresh

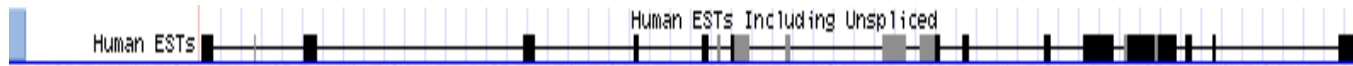
refresh

Track Mode

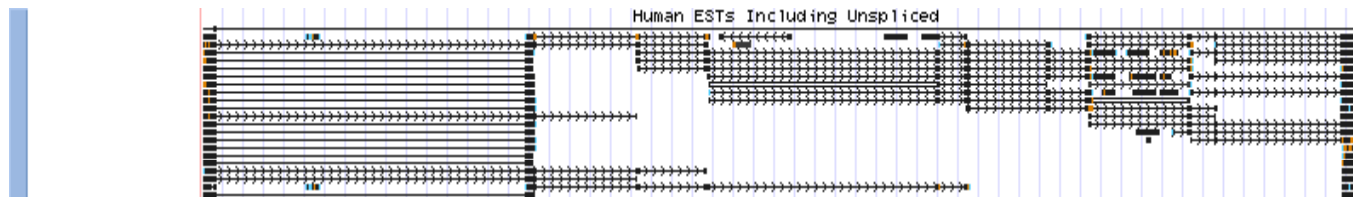
## mode of an individual annotation track:

**Hide:** the track is not displayed at all.

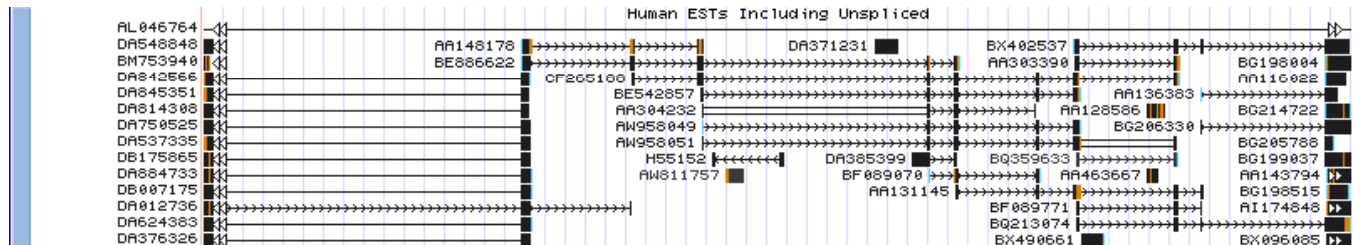
**Dense:** the track is displayed with all features collapsed into a single line.



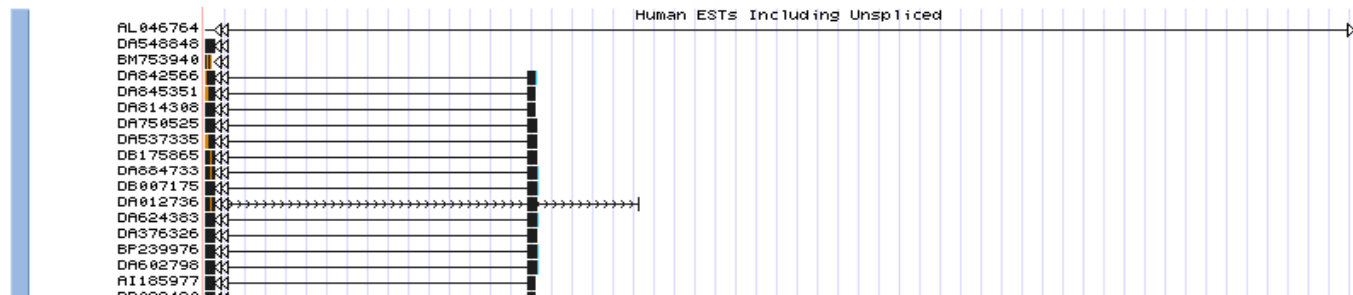
**Squish:** the track is displayed with each annotation feature shown separately, but at 50% the height of full mode. Features are unlabeled.



**Pack:** the track is displayed with each annotation feature shown separately and labeled



**Full:** the track is displayed with each annotation feature on a separate line.





Track Setting

+ Neandertal Assembly and Analysis						refresh
- Variation and Repeats						refresh
<input checked="" type="checkbox"/> <a href="#">Common Cell CNV</a>	<input checked="" type="checkbox"/> <a href="#">GIS DNA PET</a>	<a href="#">SNPs (130)</a>	<a href="#">SNPs (129)</a>	<a href="#">SNPs (128)</a>	<a href="#">SNPs (126)</a>	
hide ▾	hide ▾	dense ▾	hide ▾	hide ▾	hide ▾	
<a href="#">SNP Arrays</a>	<a href="#">HGDP Allele Freq</a>	<a href="#">HGDP Smoothd FST</a>	<a href="#">HGDP Hetzygsty</a>	<a href="#">HGDP iHS</a>	<a href="#">HGDP XP-EHH</a>	
dense ▾	hide ▾	[No data-chrX]	[No data-chrX]	hide ▾	[No data-chrX]	
<a href="#">HapMap SNPs</a>	<a href="#">HapMap LD Phased</a>	<a href="#">Tajima's D SNPs</a>	<a href="#">Tajima's D</a>	<a href="#">HGSV Discordant</a>	<a href="#">Segmental Dups</a>	
hide ▾	[No data-chrX]	hide ▾	hide ▾	hide ▾	hide ▾	
<a href="#">Structural Var</a>	<a href="#">Exapted Repeats</a>	<a href="#">RepeatMasker</a>	<a href="#">RepMask 3.2.7</a>	<a href="#">Interrupted Rpts</a>	<a href="#">Intr Rpts 3.2.7</a>	
hide ▾	hide ▾	dense ▾	hide ▾	hide ▾	hide ▾	
<a href="#">Simple Repeats</a>	<a href="#">Microsatellite</a>	<a href="#">Self Chain</a>	<a href="#">Genome Variants</a>			
hide ▾	hide ▾	hide ▾	hide ▾			
+ Pilot ENCODE Regions and Genes						refresh
+ Pilot ENCODE Transcription						refresh





# Simple Nucleotide Polymorphisms (dbSNP build 130)

Display mode:

Include Chimp state and observed human alleles in name:   
(If enabled, chimp allele is displayed first, then '>', then human alleles).

On details page, show function and coding differences relative to:

- UCSC Genes     Old UCSC Genes     Gencode Manual     Gencode Auto  
 Gencode PolyA     CCDS     RefSeq Genes     Other RefSeq

- Vega  
 SIB G  
 Gene  
 Augu

Minimum  
Maximum

SNP Feature for Color Specification:

The selected feature above has the following values below. For each value, a selection of colors is available. If a SNP has more than one of these properties, resulting in more than one color, then the stronger color will override the weaker color. In order from strongest to weakest, the colors are red, green, blue, gray, black.

Unknown     Locus     Coding - Synonymous     Coding - Non-Synonymous   
Untranslated     Intron     Splice Site

[View table schema](#)

Data last updated: 2009-08-18

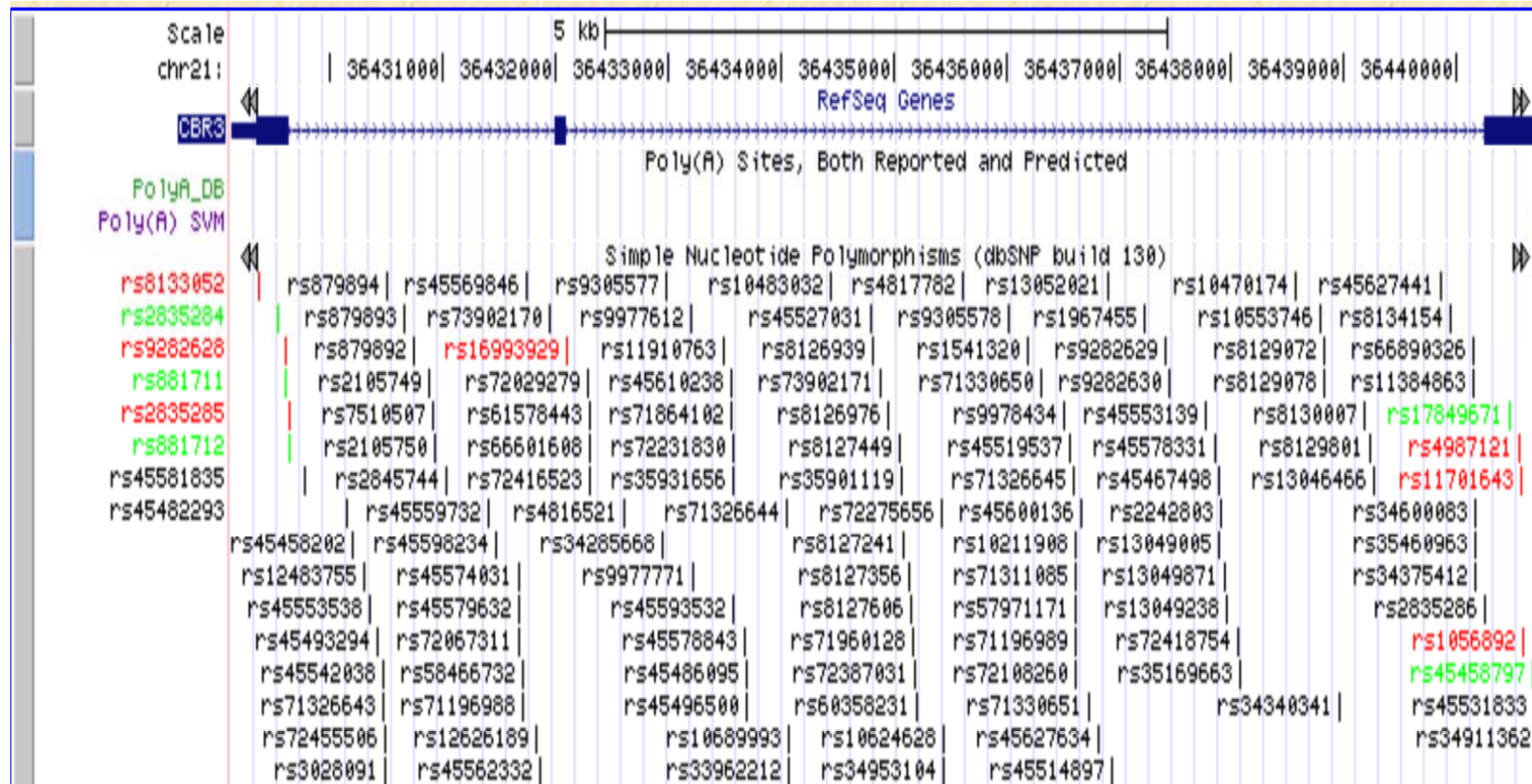
## Description

This track contains information about single nucleotide polymorphisms and small insertions and deletions (indels) — collectively Simple Nucleotide Polymorphisms — from [dbSNP](http://dbSNP) build 130, available from [ftp.ncbi.nih.gov/snp](http://ftp.ncbi.nih.gov/snp).

## Interpreting and Configuring the Graphical Display

Variants are shown as single tick marks at most zoom levels. When viewing the track at or near base-level resolution, the displayed width of the SNP corresponds to the width of the variant in the reference sequence. Insertions are indicated by a single tick mark displayed between two nucleotides, single nucleotide polymorphisms are displayed as the width of a single base, and multiple nucleotide variants are represented by a block that spans two or more bases.





## Simple Nucleotide Polymorphisms (dbSNP build 130)

### dbSNP build 130 rs4987121

dbSNP: [rs4987121](#)

Position: [chr21:36440549-36440549](#)

Band: [21q22.12](#)

GenView  
Sun  
Str  
Obs  
Ref  
Chi  
Ora  
Mac

Chimp allele:	A	Chimp strand:	+	Chimp position:	<a href="#">chr</a>
Orangutan allele:	A	Orangutan strand:	+	Orangutan position:	<a href="#">chr</a>
Macaque allele:	A	Macaque strand:	-	Macaque position:	<a href="#">chr</a>

**Class:** single

**Validation:** by-cluster,by-frequency,by-hapmap

**Function:** missense

**Molecule Type:** genomic

**Average Heterozygosity:** 0.015 +/- 0.084

**Weight:** 1

[Clas](#)

[Val](#)

[Fun](#)

[Mo](#)

[Ave](#)

[We](#)

#### Coding annotations by dbSNP:

NM\_001236: missense M (ATG) --> L (TTG)

#### UCSC's predicted function relative to selected gene tracks:

UCSC Genes AB004851 (uc002yvf.1) intron

UCSC Genes CBR3 (uc002yve.1) missense M (ATG) --> L (TTG)

UCSC Genes BC047014 (uc002yvd.1) intron

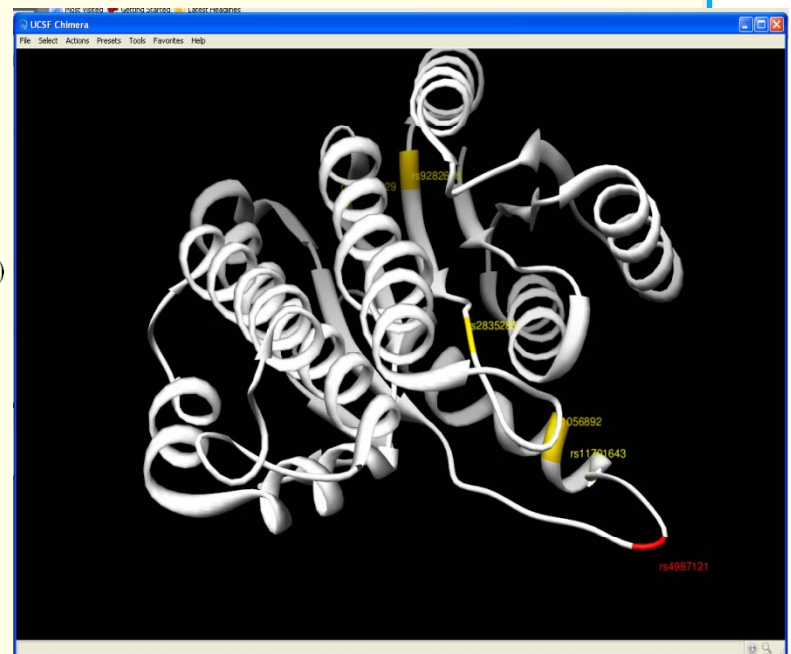
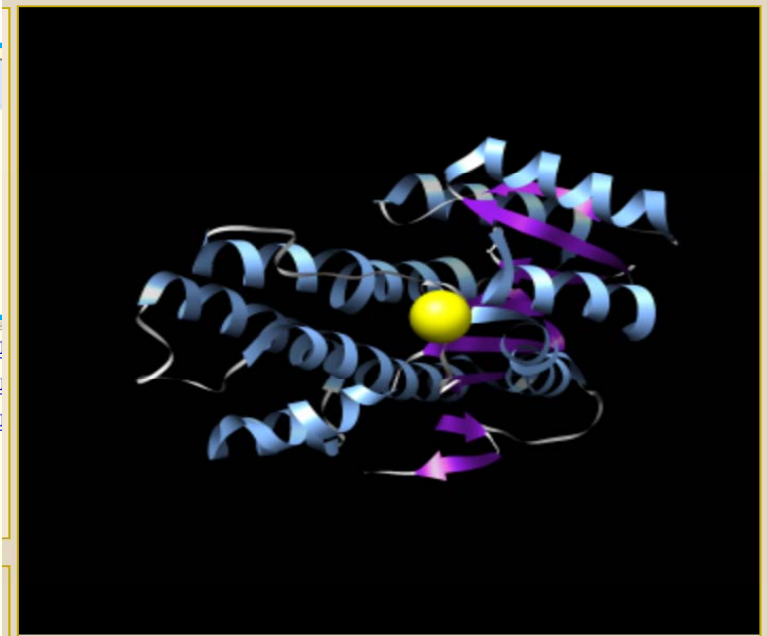
UCSC Genes CR594732 (uc002yvc.1) intron

#### [HapMap SNP](#)

#### Mappings to PDB protein structures

[2hrb](#) [X-Ray](#) [LS-SNP](#) [Chimera](#)

[Chimera help](#)



move start  move end

Click on a feature for details. Click or drag in the base position track to zoom in.  
Click gray/blue bars on left for track options and descriptions.

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

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

**Custom Tracks** refresh

coords  
full

**+** Mapping and Sequencing Tracks refresh

**+** Phenotype and Disease Associations refresh

**-** Genes and Gene Prediction Tracks refresh

<a href="#">UCSC Genes</a> pack	<a href="#">Old UCSC Genes</a> hide	<a href="#">Alt Events</a> hide	<input checked="" type="checkbox"/> <a href="#">Gencode Genes</a> hide	<a href="#">CCDS</a> hide	<a href="#">RefSeq Genes</a> pack
<a href="#">Other RefSeq</a> hide	<a href="#">MGC Genes</a> hide	<a href="#">ORFeome Clones</a> hide	<a href="#">TransMap...</a> hide	<a href="#">Vega Genes</a> hide	<a href="#">Ensembl Genes</a> hide
<a href="#">AceView Genes</a> hide	<a href="#">SIB Genes</a> hide	<a href="#">N-SCAN</a> hide	<a href="#">CONTRAST</a> hide	<a href="#">SGP Genes</a> hide	<a href="#">Ensembl Genes</a> hide
<a href="#">Genscan Genes</a> hide	<a href="#">Exoniphy</a> hide	<a href="#">Augustus</a> hide	<a href="#">RNA Genes</a> hide	<a href="#">ACEScan</a> hide	<a href="#">Ensembl Genes</a> hide
<a href="#">sno/mRNA</a> hide	<a href="#">Pos Sel Genes</a> hide				<a href="#">Ensembl Genes</a> hide

**+** mRNA and EST Tracks refresh

**+** Expression refresh

**+** Regulation refresh

**+** Comparative Genomics refresh

**+** Variation and Repeats refresh

**+** Pilot ENCODE Regions and Genes refresh

**+** Pilot ENCODE Transcription refresh

**+** Pilot ENCODE Chromatin Immunoprecipitation refresh

**+** Pilot ENCODE Chromatin Structure refresh

**+** Pilot ENCODE Comparative Genomics and Variation refresh

refresh

Direct to add track site





## Manage Custom Tracks

genome: Human assembly: Mar. 2006 (NCBI36/hg18) [hg18]

Name	Description	Type	Doc	Items	Pos	delete
<a href="#">User Track</a>	User Supplied Track	bed		352191	<a href="#">chr16:</a>	<input type="checkbox"/>

add custom tracks

go to genome browser

go to table browser

## Managing Custom Tracks

This section provides a brief overview and details about managing custom tracks.

- **Name** - a hyperlink
- **Description** - the variable name and description is included

## Add Custom Tracks

clade  genome  assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [BED](#), [bigBed](#), [BEDGRAPH](#), [GFF](#), [GTF](#), [WIG](#), [bigWig](#), [MAF](#), [BAM](#) or [PSL](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). URLs for data in the bigBed and bigWig formats must be embedded in a track line in the box below. Publicly available custom tracks are listed [here](#). Examples are [here](#).

Paste URLs or data:

Or upload:

Optional track documentation:

Or upload:

Click [here](#) for an HTML document template that may be used for Genome Browser track descriptions.





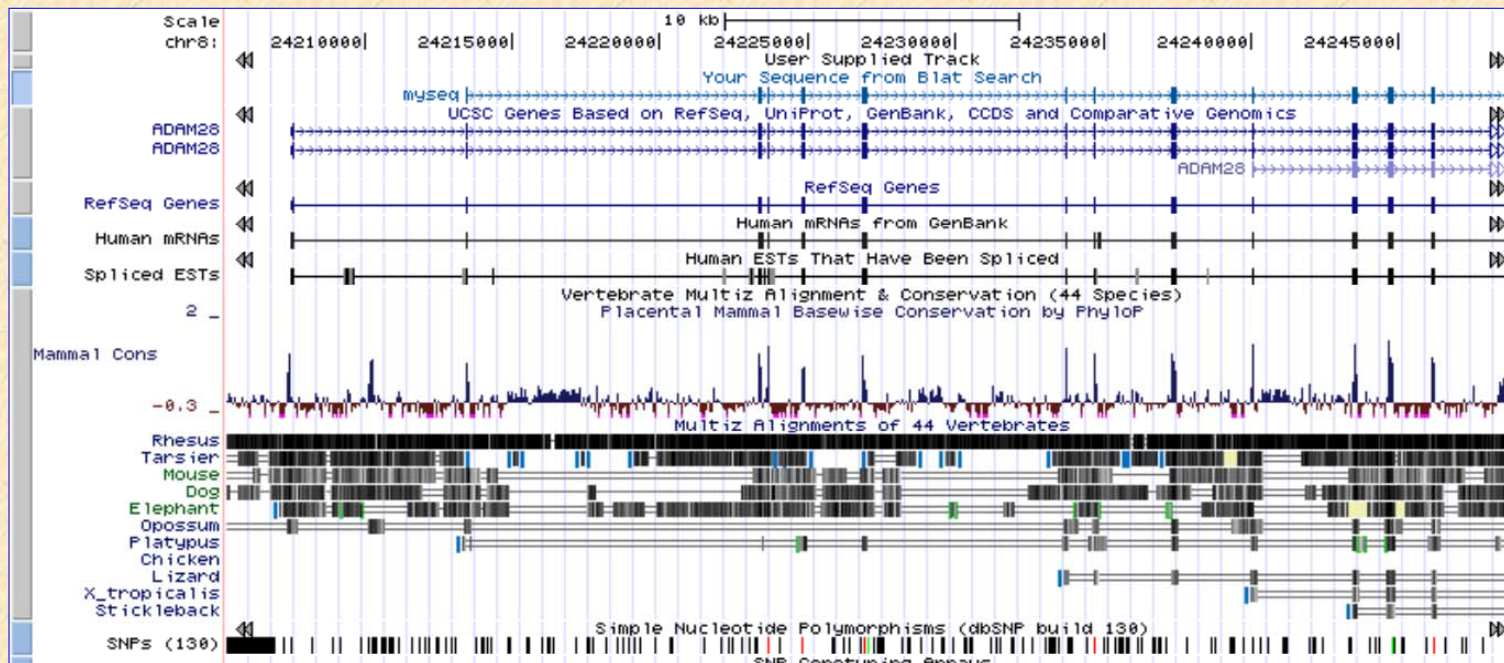
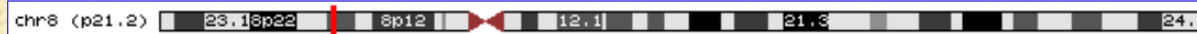
Extract DNA sequence

Home Genomes Blat Tables Gene Sorter PCR **DNA** Convert Ensembl NCBI PDF/PS Session Help

### UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr8:24,205,345-24,248,958| gene | jump clear size 43,614 bp. configure





### Get DNA in Window

#### Get DNA for

Position

Note: if you would prefer to get DNA for features of a particular track or table, try the [Table Browser](#) using the output format sequence.

#### Sequence Retrieval Region Options:

Add  extra bases upstream (5') and  extra downstream (3')

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

#### Sequence Formatting Options:

- All upper case.
- All lower case.
- Mask repeats:  to lower case  to N
- Reverse complement (get '-' strand sequence)

Note: The "Mask repeats" option applies only

### Extended DNA Case/Color

## Extended DNA Case/Color Options

Use this page to highlight features in genomic DNA text. DNA covered by a particular track can be highlighted by case, underline, bold, italic, or color. See below for details about color, and for examples. Tracks in "hide" display mode are not shown in the grid below.

**Note:** repeat masking style from previous page will **not** apply to this page. Use the case/color options for the RepeatMasker track below.

Position  Reverse complement

Letters per line  Default case:  Upper  Lower

Track Name	Toggle Case	Under-line	Bold	Italic	Red	Green	Blue
Blat Sequence	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>
Chromosome Band (Ideogram)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>
RefSeq Genes	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="text" value="255"/>	<input type="text" value="0"/>	<input type="text" value="0"/>
Human mRNAs	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>
Spliced ESTs	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>
SNPs (130)	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>
RepeatMasker	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text" value="0"/>	<input type="text" value="0"/>	<input type="text" value="0"/>

### Extended DNA Output

```
>chr13:32888617-32973809
AGAACCAACGAATTCGGAGATGAAGTCAGGTCTTCCAGTTCAGCCTGCGAGGAAGACAGGTGATCCGAATCCTAAGAATGCAAAAAGATGGGCCGGGTGTG
GTGGCTCATGCCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCACCTGAGGTCGGGAGGTTGAGACCAGACTGACCAACACACGGAGAAACCC
CGTCTCTACTTAAAAATGCAAAGTTAGCCGTGCGTGGTGGCCCATGCCTGTATTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAACCCTTGATCCCTGG
AGGCGGAAGTTGCGGTGAGCGGAGATTGCGCCATTGCACACCAGCCCGGGCCACAAGAGCGAAACTCCGCTCAAAAAAAAAAAGCAAAAGATACTACCAA
GCCCTGCGGAGCAAGGTACCTCACACTTCATGAGCGAGTTAAGATGGGTTTACAAATTTTTCAAGCAAGGAAACGGGCTCGGAGGTCTTGAACACCTGCT
ACCCAATAGCAGAACAGCTACTGAACTAAAATCCTCTGATTTCAAATAACAGCCCCGCCACTACCACTAAGTGAAGTCATCCACAACCACACCCGAC
CACTCTAAGCTTTTGTAAAGATCGGCTCGCTTTGGGGAACAGGTCTTGAGAGAACATCCCTTTAAGGTGAGAACAAAGGTATTTTCATAGGTCCCAGGTGG
TGTCCCAGGGCGCCACCCAAACATGAGCTGGAGCAAAAAGAAAGGATGGGGGACTTGGAGTAGGCATAGGGGCGGCCCTCCAAGCAGGGTGGCCTG
GGACTCTTAAGGTCAGCGAGAAAGAGAACACACTCCAGTCCCGCTTTATTCGGTCAGATACTGACGGTTGGGATGCCTGACAAGGAATTTCTTTTCG
CCACACTGAGAAATACCCGACGCGGCCACCCAGGCCTGACTTCCGGTGGTGGTGTGCTGCGTGTGCGGTGACGGCGTCACGTGGCCAGCGCGGGCTT
GTGGCGGAGCTTCTGAACTAGGCGGCAGAGGCGGAGCCGCTGTGGCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTTTTGGGGCGGTGGGTGGCCG
CCGGGAGAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTTGTGAGCTTACTCCGGCCAAAAAAGAACTGCACCTCTGGAGCGGGTGTAGTGGTGGT
GGTAGTGGGTTGGGACGAGCGCGTCTTCCGAGTCCCAGTCCAGCGTGGCGGGGAGCGCCTCACGCCCCGGTTCGCTGCCGCGCTTCTTGCCTTTT@0
```





Home Genomes Blat Tables Gene Sorter Session FAQ Help

### UCSC In-Silico PCR

Genome:  Assembly:  Target:  Forward Primer:  Reverse Primer:

Max Product Size:  Min Perfect Match:  Min Good Match:  Flip Reverse Primer:



### UCSC In-Silico PCR

**Genome browser**

```
>chr22:34304505+34304954 450bp TAACAGATTGATGATGCATGAAATGGG CCCATGAGTGGCTCCTAAAGCAGCTGC
TtACAGATTGATGATGCATGAAATGGGgggtggccaggggtggggggtga
gactgcagagaaaggcagggtggttcataacaagctttgtgcgtcccaa
tatgacagctgaagttttccagggctgatggtgagccagtgagggtgaa
tacacagaacatcctagagaaaccctcattccttaaagattaaaaataaa
gacttgctgtctgtaagggattggattatcctatttgagaaattctgtta
tccagaatggcttaccaccacaatgctgaaaagtgtgtaccgtaatctcaa
agcaagctcctcctcagacagagaaacaccagccgtcacaggaagcaaag
aaattggcttcacttttaagggtgaatccagaaccagatgtcagagctcc
aagcactttgctctcagctccacGCAGCTGCTTTAGGAGCCACTCATGaG
```

### Primer Melting Temperatures

**Forward:** 66.7 C taacagattgatgatgcatgaaatggg  
**Reverse:** 73.8 C cccatgagtggctcctaaagcagctgc

The temperature calculations are done assuming 50 mM salt and 50 nM annealing oligo concentration. The code to calculate the melting temp comes from [Primer3](#).

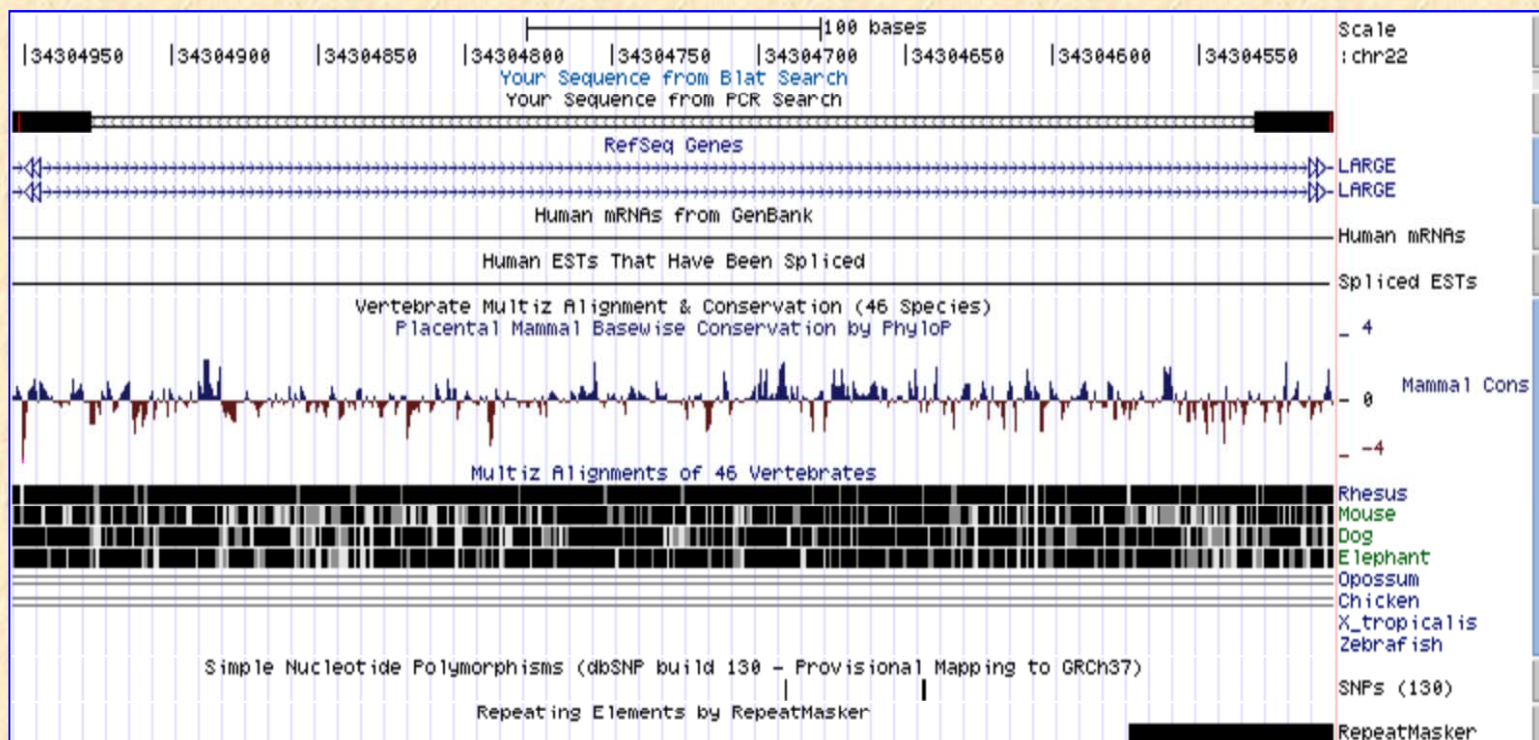
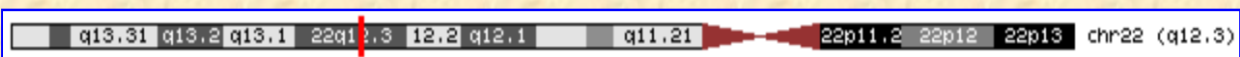


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## UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr22:34,304,505-34,304,954| gene  jump clear size 450 bp. configure



# Encyclopedia of DNA Elements (ENCODE) Consortium

Founded by National Human Genome Research Institute ([NHGRI](#))



- Expression refresh					
<a href="#">Affy Exon...</a> hide	<a href="#">Affy GNF1H</a> hide	<input checked="" type="checkbox"/> <a href="#">Affy RNA Loc</a> hide	<a href="#">Affy U133</a> hide	<a href="#">Affy U133Plus2</a> hide	<a href="#">Affy U95</a> hide
<a href="#">Agilent Array</a> hide	<a href="#">Allen Brain</a> hide	<a href="#">Bertone Yale TAR</a> hide	<input checked="" type="checkbox"/> <a href="#">Caltech RNA-seq</a> hide	<input checked="" type="checkbox"/> <a href="#">CSHL Long RNA-seq</a> hide	<input checked="" type="checkbox"/> <a href="#">CSHL Sm RNA-seq</a> hide
<a href="#">GIS PET RNA</a> hide	<a href="#">GNF Atlas 2</a> hide	<a href="#">GNF Ratio</a> hide	<input checked="" type="checkbox"/> <a href="#">Helicos RNA-seq</a> hide	<a href="#">Illumina WG-6</a> hide	<input checked="" type="checkbox"/> <a href="#">RIKEN CAGE Loc</a> hide
<a href="#">Sestan Brain</a> hide	<input checked="" type="checkbox"/> <a href="#">UW Affy Exon</a> hide	<a href="#">Affy Txn...</a> hide			
- Regulation refresh					
<input checked="" type="checkbox"/> <a href="#">Broad Histone</a> dense	<a href="#">CpG Islands</a> hide	<a href="#">EIO/JCVINAS</a> hide	<a href="#">Eponine TSS</a> hide	<a href="#">FirstEF</a> hide	<a href="#">GIS ChIP-PET</a> hide
<input checked="" type="checkbox"/> <a href="#">HAIB Methyl-seq</a> hide	<input checked="" type="checkbox"/> <a href="#">HAIB Methyl27</a> hide	<input checked="" type="checkbox"/> <a href="#">HAIB TFBS</a> hide	<input checked="" type="checkbox"/> <a href="#">NHGRI Bi-Pro</a> hide	<input checked="" type="checkbox"/> <a href="#">NHGRI NRE</a> [No data-chr8]	<input checked="" type="checkbox"/> <a href="#">Open Chromatin</a> hide
<a href="#">ORegAnno</a> hide	<input checked="" type="checkbox"/> <a href="#">SUNY RBP</a> hide	<a href="#">SwitchGear TSS</a> hide	<a href="#">TFBS Conserved</a> hide	<a href="#">TS miRNA sites</a> hide	<input checked="" type="checkbox"/> <a href="#">UW DNaseI HS</a> hide
<input checked="" type="checkbox"/> <a href="#">UW Histone</a> hide	<a href="#">Vista Enhancers</a> hide	<input checked="" type="checkbox"/> <a href="#">Yale TFBS</a> hide	<a href="#">7X Reg Potential</a> hide	<a href="#">FOX2 CLIP-seq</a> hide	<a href="#">LLUCSD TAF1...</a> hide
<a href="#">NKI Nuc Lamina...</a> hide	<a href="#">Nucleosome Occupancy...</a> hide	<a href="#">Uppsala ChIP...</a> hide			
+ Comparative Genomics refresh					
+ Neandertal Assembly and Analysis refresh					
+ Variation and Repeats refresh					





## Broad Histone Track Settings

# ENCODE Histone Modifications by Broad Institute ChIP-seq

Maximum display mode:   [Reset to defaults](#)

Select views ([help](#)):

[Peaks](#)

**Signal Configuration**

Type of graph:  [Graph configuration help](#)

Track height:  pixels (range: 16 to 100)

Vertical viewing range: min:  max:  (range: 0 to 15647)

Data view scaling: use vertical viewing range setting  Always include zero:

Transform function: Transform data points by:

Windowing function:  Smoothing window:  pixels

Draw y indicator lines: at y = 0.0:  at y =

Select subtracks by cell line and antibody:

<input type="checkbox"/> All	Cell Line	GM12878	H1-hESC	HepG2	HMEC	HSMM	HUVEC	K562	NHEK	NHLF	Cell Line	All
	Antibody	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Antibody	
	<a href="#">CTCF</a>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K4me1</a>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K4me2</a>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K4me3</a>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K9ac</a>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K9me1</a>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K27ac</a>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K27me3</a>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>
	<a href="#">H3K36me3</a>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		<input type="checkbox"/>



List subtracks:  only selected/visible  all

<u>Cell Line</u> <sup>↓1</sup>	<u>Antibody</u> <sup>↓2</sup>	<u>Views</u> <sup>↓3</sup>			<u>Restricted Until</u>	
<input checked="" type="checkbox"/>	GM12878	CTCF	Peaks	ENCODE Histone Mods, Broad ChIP-seq Peaks (CTCF, GM12878) ...	<a href="#">schema</a>	2009-10-05
<input checked="" type="checkbox"/>	GM12878	CTCF	Signal	ENCODE Histone Mods, Broad ChIP-seq Signal (CTCF, GM12878) ...	<a href="#">schema</a>	2009-10-05
<input checked="" type="checkbox"/>	GM12878	H3K4me1	Peaks	ENCODE Histone Mods, Broad ChIP-seq Peaks (H3K4me1, GM12878) ...	<a href="#">schema</a>	2009-10-05
<input checked="" type="checkbox"/>	GM12878	H3K4me1	Signal	ENCODE Histone Mods, Broad ChIP-seq Signal (H3K4me1, GM12878) ...	<a href="#">schema</a>	2009-10-05
<input type="checkbox"/>	GM12878	H3K4me2	Peaks	ENCODE Histone Mods, Broad ChIP-seq Peaks (H3K4me2, GM12878) ...	<a href="#">schema</a>	2009-10-05

<input type="checkbox"/>	NHLF	H4K20me1	Signal	ENCODE Histone Mods, Broad ChIP-seq Signal (H4K20me1, NHLF) ...	<a href="#">schema</a>	2010-06-28
<input type="checkbox"/>	NHLF	Input Control	Signal	ENCODE Histone Mods, Broad ChIP-seq Signal (NHLF control) ...	<a href="#">schema</a>	2010-06-29

24 of 177 selected

Submit

[Downloads](#)

**Data version:** through the ENCODE Jan 2010 Freeze

## RESTRICTED

until	File	Size	Submitted	Details
2009-10-05	<a href="#">wgEncodeBroadChIPseqPeaksGm12878Ctcf.broadPeak.gz</a>	363K	2009-01-05	cell=GM12878; dataType=ChipSeq; antibody=CTCF; lab=Broad; type
2009-10-05	<a href="#">wgEncodeBroadChIPseqRawDataRep1Gm12878Ctcf.fastq.gz</a>	774M	2009-01-05	cell=GM12878; dataType=ChipSeq; antibody=CTCF; lab=Broad; type
2009-10-05	<a href="#">wgEncodeBroadChIPseqRawDataRep2Gm12878Ctcf.fastq.gz</a>	517M	2009-01-05	cell=GM12878; dataType=ChipSeq; antibody=CTCF; lab=Broad; type
2009-10-05	<a href="#">wgEncodeBroadChIPseqRawDataRep3Gm12878Ctcf.fastq.gz</a>	513M	2009-01-05	cell=GM12878; dataType=ChipSeq; antibody=CTCF; lab=Broad; type

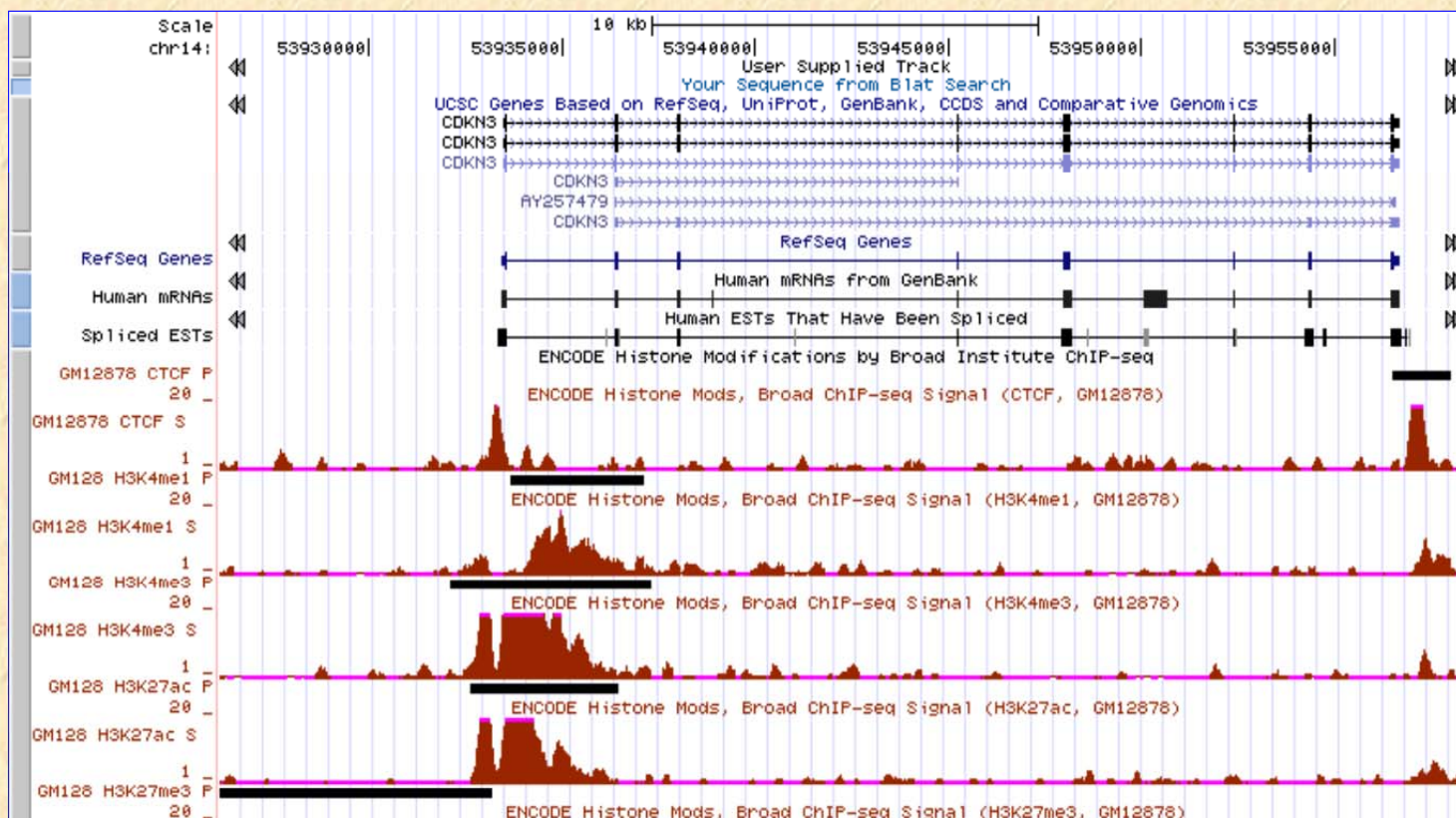
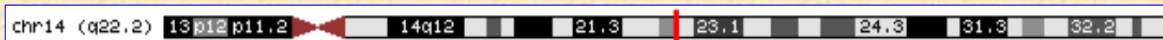




# UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr14:53,926,128-53,958,540 gene  jump clear size 32,413 bp. configure





# References



OpenHelix: <http://www.openhelix.com/ucsc/>

[MIT library: Bioinformatics Tutorial Series](http://libguides.mit.edu/bits)

<http://libguides.mit.edu/bits>

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[The UCSC Genome Browser database: update 2010](#). *Nucleic Acids Res.* 2010 Jan;38(Database issue):D613-9. Epub 2009 Nov 11.

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UCSC Genome Browser Wiki site:

[http://genomewiki.ucsc.edu/index.php/Main\\_Page](http://genomewiki.ucsc.edu/index.php/Main_Page)