UCSC Genome Browser Home - Mozilla Firefox

File Edit View History Bookmarks Tools Help

(1) http://genome.ucsc.edu/

ChIA-PET Graphs Track Settings | HEMOGLOBIN--BETA LOCUS; HBB - ... | UCSC Genome Browser Home | Ay/Bi 199: Methods of Computation... | Table of Contents — April 2011, 21... | Eichler alkan nature genetic reveiw ... | Vi Cheat Sheet

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UCSC Genome Bioinformatics

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

Genome Browser

About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides portals to the ENCODE and Neandertal projects.

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Human (*Homo sapiens*) Genome Browser Gateway

Pick the proper genome and assembly (i.e. human hg19, mouse mm9)

(3)

The UCSC Genome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
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clade	genome	assembly	position or search term	gene	image width	
Mammal	Human	Feb. 2009 (GRCh37/hg19)	chr11:5,246,669-5,246,972		800	submit

(4)

Click here to reset the browser user interface settings to their defaults.

track search | add custom tracks | configure tracks and display | clear position

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

slide left or right — move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x — zoom in and out

move to a position or search for a gene — position/search chr19:45,805,400-45,852,009 gene jump clear size 46,610 bp. configure — change size and attributes of picture

chr19 (q13.32) 19p13.3 19p13.2 p13.11 19p12 19q12 q13.11 13.12 19q13.2 13.32 q13.33 13.42 13.43 — where you are on the chromosome

chromosome and bp location. Each base pair (bp) on a chromosome gets a number from left to right

Scale chr19: 45810000 45815000 45820000 45825000 45830000 45835000 45840000 45845000 45850000 — 10 kb

UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics

MARK4 MARK4 CKM KLC3 KLC3 KLC3 KLC3

exons — <-<-<- means direction of transcription

gene name (click on it and it will take you to an info page on that gene)

thin exons are untranslated

RefSeq Genes

mRNA's (this view is toggled to "squish" instead of the default "dense")

Human mRNAs from GenBank

Spliced ESTs — Human ESTs That Have Been Spliced

conservation (higher = more conserved)

Mammal Cons — Placental Mammal Basewise Conservation by PhyloP (4 / -4)

conservation to specific species (dark is more conserved; ===== means a gap)

Multiz Alignments of 46 Vertebrates: Rhesus, Mouse, Dog, Elephant, Opossum, Chicken, X_tropicalis, Zebrafish

SNPs (131) — Simple Nucleotide Polymorphisms (dbSNP build 131)

RepeatMasker — Repeating Elements by RepeatMasker

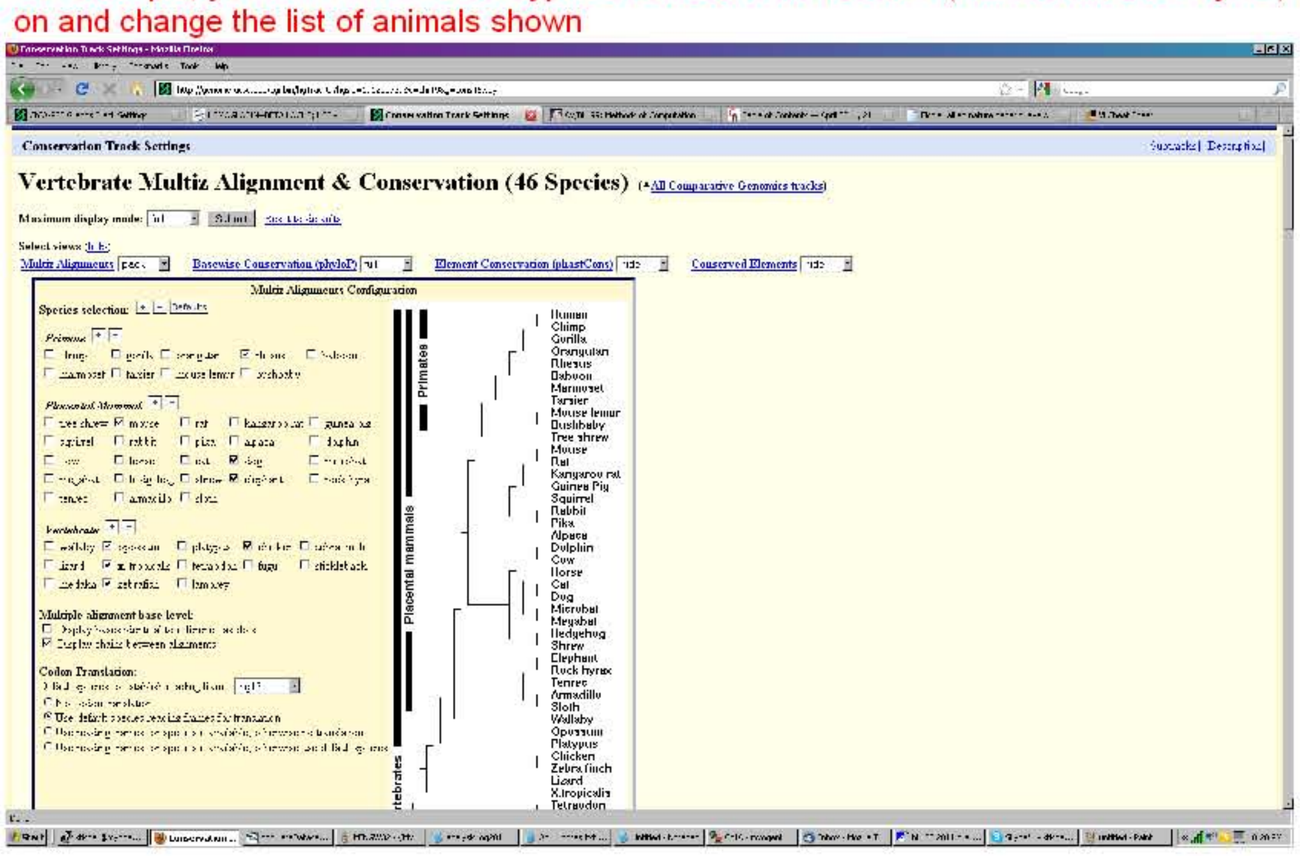
move start < 2.0 > — Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. — move end < 2.0 >

track search | default tracks | default order | hide all | add custom tracks | configure | reverse | refresh

collapse all — 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. — expand all

Mapping and Sequencing Tracks (refresh)

Base Position: dense	Chromosome Band: hide	STS Markers: hide	FISH Clones: hide	Recomb Rate: hide	Map Contigs: hide
Assembly: hide	GRC Map Contigs: hide	Gap: hide	BAC End Pairs: hide	Fosmid End Pairs: hide	GC Percent: hide
GRC Patch Release: hide	Hg18 Diff: hide	NCBI Incident: hide	Short Match: hide	Restr Enzymes: hide	Wiki Track: hide

All of the tracks you see (and more) are listed down here. Toggle them on and/or click on the blue names to turn on sub-tracks and to specialize the view. When you are done with modifications, press "refresh" or "submit"

For example, you can turn different types of conservation scores (PhastCons vs. PhyloP) on and change the list of animals shown