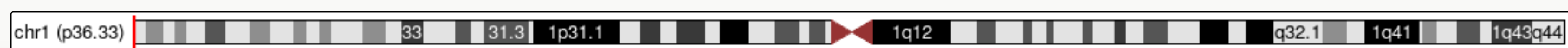


UCSC Genome Browser on Human (GRCh37/hg19)

Move <<< << < > >> >>> Zoom in 1.5x 3x 10x Base Zoom out 1.5x 3x 10x 100x

Multi-region chr1:233 538 247 337 13 800 bp gene, chromosome, range, search, terms, help, pages, see, examples Search Examples



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Mapping and Sequencing

Genes and Gene Predictions

Updated GENCODE V48lift37 <small>(dense)</small>	NCBI RefSeq <small>(hide)</small>	Genes Archive <small>(hide)</small>	CCDS <small>(hide)</small>	CRISPR Targets <small>(hide)</small>	Ensembl Genes <small>(hide)</small>	EvoFold <small>(hide)</small>	Exoniphy <small>(hide)</small>
Updated GENCODE Versions <small>(hide)</small>	H-Inv 7.0 <small>(hide)</small>	Updated HGNC <small>(hide)</small>	IKMC Genes Mapped <small>(hide)</small>	lincRNAs <small>(hide)</small>	LRG Transcripts <small>(hide)</small>	MGC/ORFeome Genes <small>(hide)</small>	Other RefSeq <small>(hide)</small>
Pfam in GENCODE <small>(hide)</small>	Prediction Archive <small>(hide)</small>	Retroposed Genes <small>(hide)</small>	sno/miRNA <small>(hide)</small>	TransMap V5 <small>(hide)</small>	tRNA Genes <small>(hide)</small>	UCSC Alt Events <small>(hide)</small>	UniProt <small>(hide)</small>
Vega Genes <small>(hide)</small>	Yale Pseudo60 <small>(hide)</small>						

Phenotypes Variants and Literature

OMIM

show

ClinVar Variants

hide

Development Delay

hide

HGMD public

hide

REVEL Scores

hide

Publications

dense

Constraint scores

hide

Dosage Sensitivity

hide

Lens Patents

hide

RGD Human QTL

hide

RGD Rat QTL

hide

AlphaMissense

hide

Coriell CNVs

hide

GAD View

hide

LOVD Variants

hide

18 RGD Human QTL

hide

18 RGD Rat QTL

hide

CADD 1.6

hide

COSMIC

hide

GenCC

hide

18 MGI Mouse QTL

hide

SNPedia

hide

CADD 1.7

hide

COSMIC Regions

hide

Gene Interactions

hide

New MITOMAP

[No data-chr1]

Splicing Impact

hide

CIVIC

hide

COVID Data

hide

GeneReviews

hide

Orphanet

hide

UniProt Variants

hide

ClinGen

hide

Updated DECIPHER

hide

GWAS Catalog

hide

Updated PanelApp

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Updated Variants in Papers

hide

ClinGen CNVs

hide

New Deleteriousness Predictions

hide

Haploinsufficiency

hide

Polygenic Risk Scores

hide

Web Sequences

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Variation

[dbSNP 155](#) [1000G Archive](#) [Updated](#) [Array](#) [dbSNP Archive](#) [dbVar Common](#) [denovo-db](#) [DGV Struct Var](#) [EVS Variants](#)
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[hide](#) [hide](#) [15](#) [hide](#) [hide](#) [hide](#) [16](#) [hide](#) [hide](#) [hide](#)

RNA and Transcriptome									
CGAP SAGE	Gene Bounds	H-Invy	Human ESTs	Human mRNAs	Human RNA Editing	Other ESTs	Other mRNAs		Refresh
Poly(A)	PolyA-Seq	SIB Alt-Splicing	Spliced ESTs	UniGene					

Expression							
GTEX Gene V8	Allan Brain	Burge RNA-seq	CSHL Small	ENC Exon Array	ENC ProtGeno	ENC RNA-seq	EPDnew Promoters

hide

Affy Archive

hide

GIS RNA PET

hide

GNF Atlas 2

hide

GTEX Gene

hide

GTEX Transcript

hide

GWIPS-viz Riboseq

hide

18 Illumina WG-6

hide

PeptideAtlas

hide

qPCR Primers

hide

RIKEN CAGE Loc

hide

18 Sestan Brain

hide

Regulation

Refresh

ENCORE Regulation

show

18 CD34 Dnasel

hide

CpG Islands

hide

ENC Chromatin

hide

ENC DNA Methyl

hide

ENC DNase/FAIRE

hide

ENC Histone

show

ENC RNA Binding

hide

ENC TF Binding

hide

FANTOM5

hide

FSU Repli-chip

hide

GeneHancer

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Genome Segments

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GTEX Combined eQTL

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GTEX Tissue eQTL

hide

JASPAR Transcription Factors

hide

hide

[TS miRNA Targets](#)
[UCSF Brain Methylation](#)
[UMMS Brain Hist](#)
[UW Repli-seq](#)
[Updated VISTA Enhancers](#)

18 = GERP

Conservation

hide

Cons. 3-way

hide

Cons. Indels

hide

Evo Cpg

hide

Indels

hide

gBGC

hide

Phylogenetic Chain/Net

hide

Phylogenetic Chain/Net

hide

Vertebrate Chain/Net

hide

CHM13 alignments

hide

Neandertal Assembly and Analysis

Refresh

Assembly