UCSC Genome Browser on Human (GRCh37/hg19)

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

Multi-region chr17:7,571,739-7,590,808 19,070 bp. gene, chromosome range, search terms, help pages, see examples Search Examples

Collapse all | Track search | Highlight | Hide all | Add custom tracks | Configure | Reverse | Resize | Expand all

Mapping and Sequencing

Refresh

Genes and Gene Predictions

Refresh

Updated GENCODE V48lift37 (hide)	NCBI RefSeq (dense)	Genes Archive (hide)	CCDS (hide)	CRISPR Targets (hide)	Ensembl Genes (hide)	FoldFold (hide)
Exoniphy (hide)	Updated GENCODE Versions (hide)	H-Inv 7.0 (hide)	Updated HGNC (hide)	IMC Genes Mapped (hide)	lncRNAs (hide)	LRG Transcripts (hide)
MGC/ORFeome Genes (hide)	Other RefSeq (hide)	Pfam in GENCODE (hide)	Prediction Archive (hide)	Retrogenes (hide)	snoRNA/miRNA (hide)	TransMap V5 (hide)
tRNA Genes (hide)	UCSC AB Events (hide)	UniProt (hide)	Vega Genes (hide)	Yale Pseudo60 (hide)		

Phenotypes, Variants, and Literature

Refresh

OMIM (show)	Publications (dense)	AlphaMissense (hide)	CADD 1.6 (hide)	CADD 1.7 (hide)	CIVIC (hide)	ClinGen (hide)
ClinGen CNVs (hide)	ClinVar Variants (hide)	Constraint scores (hide)	Curated CNVs (hide)	COSMIC (hide)	COSMIC Regions (hide)	COVID Data (hide)
Updated DECIPHER (hide)	New Deleteriousness Predictions (hide)	Development Delay (hide)	Dosage Sensitivity (hide)	GAD View (hide)	GenCC (hide)	Gene Interactions (hide)
GeneReviews (hide)	GWAS Catalog (hide)	Haploinsufficiency (hide)	HGMD public (hide)	Lens Patents (hide)	LOVD Variants (hide)	MGI Mouse QTL (hide)
MITOMAP [No data-chr17]	Orphanet (hide)	Updated PanelApp (hide)	Polygenic Risk Scores (hide)	REVEL Scores (hide)	RGD Human QTL (hide)	RGD Rat QTL (hide)
SNPedia (hide)	Splicing Impact (hide)	UniProt Variants (hide)	Updated Variants in Papers (hide)	Web Sequences (hide)		

Variation

Refresh

dbSNP 155 (back)	1000G Archive (hide)	Updated Array Probesets (hide)	dbSNP Archive (hide)	dbVar Common Struct Var (hide)	denovo-db (hide)	DGV Struct Var (hide)
EVS Variants (hide)	ExAC (hide)	Genome In a Bottle (hide)	Genome Variants (hide)	GIS DNA PET (hide)	gnomAD (hide)	HAIB Genotype (hide)
HapMap SNPs (hide)	HGDP Allele Freq (hide)	Platinum Genomes (hide)				

RNA and Transcriptome

Refresh

CGAP SAGE (hide)	Gene Bounds (hide)	H-Inv (hide)	Human ESTs (hide)	Human mRNAs (hide)	Human RNA Editing (hide)	Other ESTs (hide)
Other mRNAs (hide)	Poly(A) (hide)	PolyA-Seq (hide)	SIB Alt-Splicing (hide)	Spliced ESTs (hide)	UniGene (hide)	

Expression

Refresh

GTEx Gene V8 (back)	Allen Brain (hide)	Burge RNA-seq (hide)	CSHL Small RNA-seq (hide)	ENC Exon Array (hide)	ENC ProtGeno (hide)	ENC RNA-seq (hide)
EPDnew Promoters (hide)	Affy Archive (hide)	GIS RNA PET (hide)	GNF Atlas 2 (hide)	GTEx Gene (hide)	GTEx Transcript (hide)	GWIPS-viz Riboseq (hide)
Illumina WG-6 (hide)	PeptideAtlas (hide)	qPCR Primers (hide)	RIKEN CAGE Loc (hide)	Sestan Brain (hide)		

Regulation

Refresh

ENCODE Regulation (show)	CD34 Dnase1 (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 (hide)	Genome Segments (hide)	GTEx Combined eQTL (hide)
GTEx Tissue eQTL (hide)	JASPAR Transcription Factors (hide)	NKI Nuc Lamina (hide)	OReganno (hide)	Rao 2014 Hi-C (hide)	ReMap ChIP-seq (hide)	Stanf Nucleosome (hide)
SUNY SwitchGear (hide)	SwitchGear TSS (hide)	TFBS Conserved (hide)	TS miRNA Targets (hide)	UCSF Brain Methyl (hide)	UMMS Brain Hist (hide)	UW Repli-seq (hide)
Updated VISTA Enhancers (hide)						

Comparative Genomics

Refresh

Conservation (full)	Cons 46-Way (hide)	Cons Indels MmCf (hide)	Evo Cpg (hide)	GERP (hide)	phastBias qBGC (hide)	Primate Chain/Net (hide)
Placental Chain/Net (hide)	Vertebrate Chain/Net (hide)	CHM13 alignments (hide)				

Neandertal Assembly and Analysis

Refresh

Denisova Assembly and Analysis

Refresh

Repeats

Refresh

RepeatMasker (dense)	Interrupted Rpts (hide)	Microsatellite (hide)	NumtS Sequence (hide)	Segmental Dups (hide)	Self Alignment (hide)	Simple Repeats (hide)
WM + SDust (hide)						

Refresh