

UCSC Genome Browser on Human (GRCh38/hg38)

Move

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Zoom in

1.5x

3x

10x

Base

Zoom out

1.5x

3x

10x

100x

New to the Genome Browser? See our short (2-3 minute) guided tutorial. All tutorials can be found in the top blue bar menu under **Help > Interactive Tutorial**.

Start tutorial

Don't show again

Multi-region

chr17:7,668,401-7,687,550

19,150 bp.

gene, chromosome range, search terms, help pages, see examples

Search

Examples

chr17 (p13.1)

17p13.3

17p13.2

17p13.1

17p12

17p11.2

17q11.2

17q12

17q21.2

17q21.31

21.32

21.33

17q22

q23.2

q24.2

17q24.3

17q25.1

17q25.3



Collapse all

Track search

Highlight

Hide all

Manage custom tracks

Configure

Reverse

Resize

Expand all

Custom Tracks

Hide group

Refresh

CHOPCHOP

pack

Mapping and Sequencing

Hide group

Refresh

Base Position dense	Assembly hide	Assembly Tracks hide	Centromeres hide	Chromosome Band hide	Clone Ends hide	Exome Probesets hide	Gap hide
GC Percent hide	GRC Incident hide	P14 GRC Patches pack	Hg19 Diff hide	INSDC hide	LiftOver & ReMap hide	LRG Regions hide	Mappability hide
Updated Problematic Regions show	Recomb Rate hide	RefSeq Acc hide	Restr Enzymes hide	Short Match hide			

Genes and Gene Predictions

Hide group

Refresh

Updated GENCODE V49 pack	NCBI RefSeq dense	CCDS hide	CRISPR Targets hide	GENCODE Archive hide	Updated GENCODE Versions hide	Updated HGNC hide	19 IKMC Genes Mapped hide
LRG Transcripts hide	MANE pack	MGC/ORFeome Genes hide	Non-coding RNA hide	Other RefSeq hide	Pfam in GENCODE hide	Prediction Archive hide	Pseudogenes hide
RetroGenes V9 hide	TransMap V5 hide	UCSC Alt Events hide	UniProt hide				

Phenotypes, Variants, and Literature

Hide group

Refresh

OMIM show	AlphaMissense hide	CADD 1.6 hide	CADD 1.7 <div>hide</div>	Cancer Gene Expr <div>hide</div>	CIViC <div>hide</div>	ClinGen <div>hide</div>	ClinGen CNVs <div>hide</div>
ClinVar Variants <div>hide</div>	Constraint scores <div>hide</div>	19 Coriell CNVs <div>hide</div>	COSMIC <div>hide</div>	COSMIC Regions <div>hide</div>	COVID Data <div>hide</div>	DECIPHER <div>hide</div>	New Deleteriousness Predictions <div>hide</div>
Development Delay <div>hide</div>	Dosage Sensitivity <div>hide</div>	New G2P Project <div>hide</div>	GenCC <div>hide</div>	Gene Interactions <div>hide</div>	GeneReviews <div>hide</div>	GWAS Catalog <div>hide</div>	HGMD public <div>hide</div>
LOVD Variants <div>hide</div>	MITOMAP <div>hide</div>	Orphanet <div>hide</div>	Updated PanelApp <div>hide</div>	19 REVEL Scores <div>hide</div>	SNPedia <div>hide</div>	Updated Splicing Impact <div>hide</div>	TCGA Pan-Cancer <div>hide</div>
UniProt Variants <div>hide</div>	Updated Variants in Papers <div>hide</div>						

Variation

Hide group

Refresh

dbSNP 155 pack	1000 Genomes <div>hide</div>	Updated Array Probesets <div>hide</div>	dbSNP Archive <div>hide</div>	dbVar Common Struct Var <div>hide</div>	DGV Struct Var <div>hide</div>	Genome In a Bottle <div>hide</div>	gnomAD Variants <div>hide</div>
New Long-read Variants <div>hide</div>	Platinum Genomes <div>hide</div>						

Human Pangenome - HPRC

Hide group

Refresh

Multiple Alignment <div>hide</div>	Pairwise Alignments <div>hide</div>	Rearrangements <div>hide</div>	Short Variants <div>hide</div>
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RNA and Transcriptome

Hide group

Refresh

Human ESTs <div>hide</div>	Human mRNAs <div>hide</div>	New Long-read Transcripts <div>hide</div>	Other ESTs <div>hide</div>	Other mRNAs <div>hide</div>	SIB Alt-Splicing <div>hide</div>	Spliced ESTs <div>hide</div>
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Expression

Hide group

Refresh

GTEx Gene V8 pack	GTEx RNA-Seq Coverage <div>hide</div>	Affy Archive <div>hide</div>	EPDnew Promoters <div>hide</div>	GNF Atlas 2 <div>hide</div>	19 GTEx Gene <div>hide</div>	GTEx Transcript <div>hide</div>	GWIPS-viz Riboseq <div>hide</div>
New MaveDB Experiments <div>hide</div>	miRNA Tissue Atlas <div>hide</div>	Single Cell Expression <div>hide</div>					

Single Cell RNA-seq

Hide group

Refresh

Regulation

Hide group

Refresh

ENCODE cCREs <div>dense</div>	ENCODE Regulation <div>show</div>	CpG Islands <div>hide</div>	FANTOM5 <div>hide</div>	GeneHancer <div>hide</div>	GTEx cis-eQTLs <div>hide</div>	Hi-C and Micro-C <div>hide</div>	JASPAR Transcription Factors <div>hide</div>
OREgAnno <div>hide</div>	RefSeq Func Elems <div>hide</div>	ReMap ChIP-seq <div>hide</div>	VISTA Enhancers <div>hide</div>				

Comparative Genomics

Hide group

Refresh

UCSC 100 Vertebrates <div>full</div>	Zoonomia 241 Placent <div>hide</div>	UCSC 30 Primates <div>hide</div>	Primate Chain/Net <div>hide</div>	Placental Chain/Net <div>hide</div>	Vertebrate Chain/Net <div>hide</div>	CHM13 alignments <div>hide</div>	Hiller Lab 470 Mammals <div>hide</div>
New Unusually Conserved <div>hide</div>	Zoonomia+Primates 447 <div>hide</div>						

Repeats

Hide group

Refresh

RepeatMasker <div>dense</div>	Interrupted Rpts <div>hide</div>	Microsatellite <div>hide</div>	NuMTs Sequence <div>hide</div>	RepeatMasker Viz. <div>hide</div>	Segmental Dups <div>hide</div>	Self Alignment <div>hide</div>	Simple Repeats <div>hide</div>
WM + SDust <div>hide</div>							

Refresh