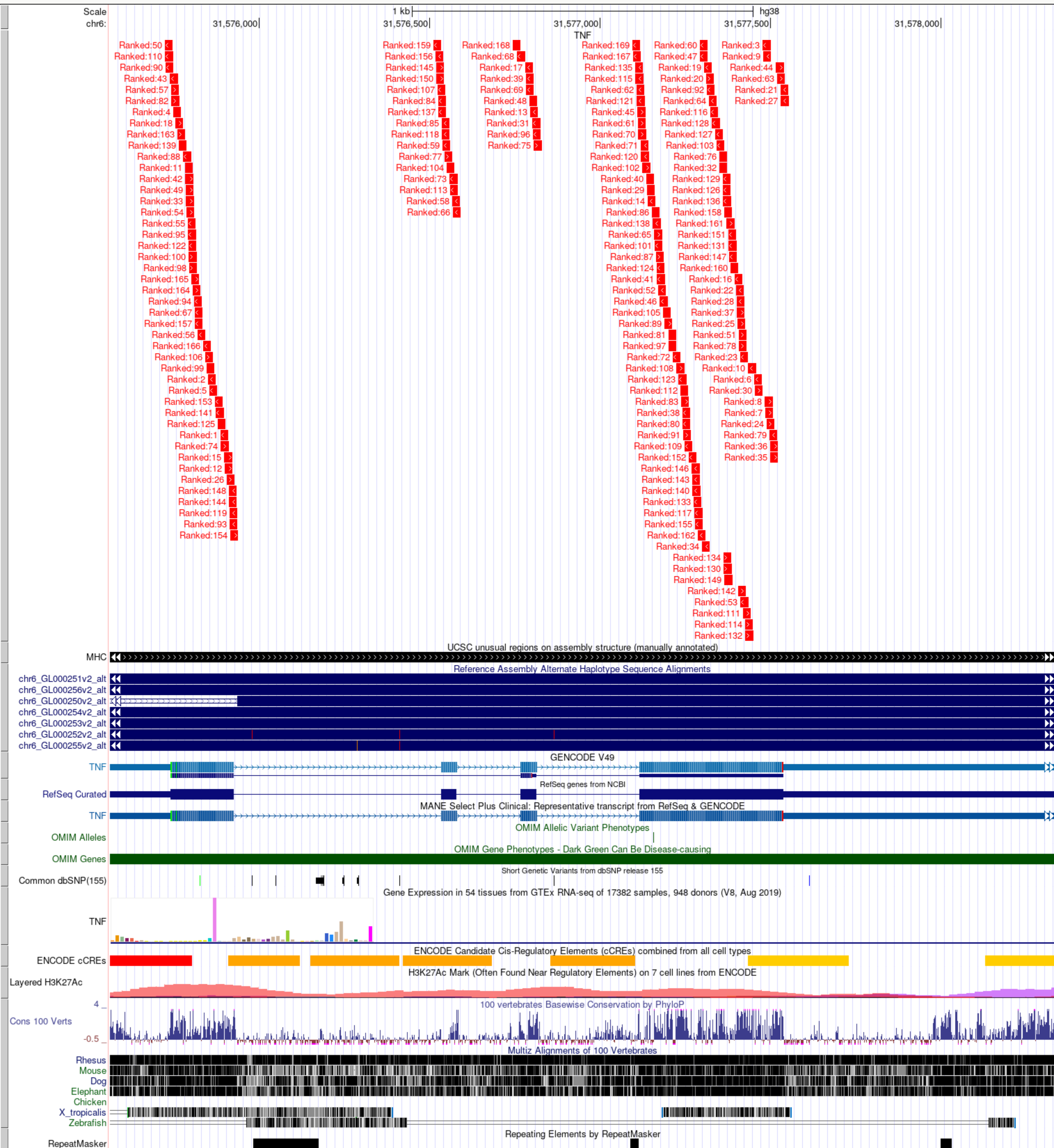
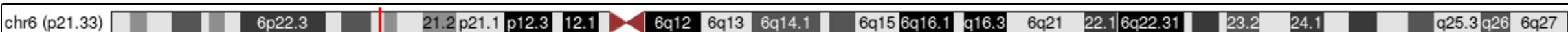


UCSC Genome Browser on Human (GRCh38/hg38)

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

Multi-region chr6:31,575,564-31,578,335 2,772 bp. [gene, chromosome range, search terms, help pages, see examples](#) [Search](#) [Examples](#)



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

-

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 ▾	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 <small>show</small>	AlphaMissense <small>hide</small>	CADD 1.6 <small>hide</small>	CADD 1.7 <small>hide</small>	Cancer Gene Expr <small>hide</small>	CIVIC <small>hide</small>	ClinGen <small>hide</small>	ClinGen CNVs <small>hide</small>
ClinVar Variants <small>hide</small>	Constraint scores <small>hide</small>	Coriell CNVs <small>hide</small>	COSMIC <small>hide</small>	COSMIC Regions <small>hide</small>	COVID Data <small>hide</small>	DECIPHER <small>hide</small>	Deleteriousness Predictions <small>hide</small>
Development Delay <small>hide</small>	Dosage Sensitivity <small>hide</small>	G2P Project <small>hide</small>	GenCC <small>hide</small>	Gene Interactions <small>hide</small>	GeneReviews <small>hide</small>	GWAS Catalog <small>hide</small>	HGMD public <small>hide</small>
LOVD Variants <small>hide</small>	MITOMAP [No data-chr6]	Orphanet <small>hide</small>	PanelApp <small>hide</small>	REVEL Scores <small>hide</small>	SNPedia <small>hide</small>	Splicing Impact <small>hide</small>	TCGA Pan-Cancer <small>hide</small>
UniProt Variants <small>hide</small>	Variants in Papers <small>hide</small>						

Variation Hide group Refresh

dbSNP 155

pack

1000 Genomes

hide

Updated Array

Probesets

hide

dbSNP Archive

hide

dbVar Common Struct

Var

hide

GVV Struct Var

hide

Genome In a Bottle

hide

gnomAD Variants

hide

New Long-read Variants

hide

Platinum Genomes

hide

-

Human Pangenome - HPRC

Hide group

Refresh

[Multiple Alignment](#)
[Pairwise Alignments](#)
[Rearrangements](#)
[Short Variants](#)

-

RNA and Transcriptome

Hide group

Refresh

[Human ESTs](#)
[Human mRNAs](#)
[New Long-read Transcripts](#)
[Other ESTs](#)
[Other mRNAs](#)
[SIB Alt-Splicing](#)
[Spliced ESTs](#)

[-] Expression Hide group Refresh

[GTEx Gene V8](#)
[GTEx RNA-Seq Coverage](#)
[Affy Archive](#)
[EPDnew Promoters](#)
[GNF Atlas 2](#)
[19 GTEx Gene](#)
[GTEx Transcript](#)
[GWIPS-viz Riboseq](#)

hide

Single Cell RNA-seq

Hide group

Refresh

Regulation

Hide group

Refresh

ENCODE cCREs

dense

ENCODE Regulation

show

CpG Islands

hide

FANTOM5

hide

GeneHancer

hide

GTEx cis-eQTLs

hide

Hi-C and Micro-C

hide

JASPAR Transcription Factors

hide

ORegAnno

hide

RefSeq Func Elems

hide

ReMap ChIP-seq

hide

VISTA Enhancers

hide

-
Comparative Genomics

Hide group
Refresh

UCSC 100 Vertebrates

full

Zoonomia 241 Placent

hide

UCSC 30 Primates

hide

Primate Chain/Net

hide

Placental Chain/Net

hide

Vertebrate Chain/Net

hide

CHM13 alignments

hide

Hiller Lab 470 Mammals

hide

New

Unusually Conserved

hide

Zoonomia+Primates

447

hide

Repeats Hide group Refresh

[RepeatMasker](#) [Interrupted Rpts](#) [Microsatellite](#) [NuMTs Sequence](#) [RepeatMasker Viz.](#) [Segmental Dups](#) [Self Alignment](#) [Simple Repeats](#)
 dense ▾ hide ▾ hide ▾ hide ▾ hide ▾ hide ▾ hide ▾ hide ▾
[WM + SDust](#)
 hide ▾

Refresh