

Go to <https://genome.ucsc.edu/>, choose Human GRCh37/hg19 build



Genome Browser

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Our tools

- **Genome Browser**

interactively visualize genomic data

- **BLAT**

rapidly align sequences to the genome

- **Table Browser**

download data from the Genome Browser database

- **Variant Annotation Integrator**

get functional effect predictions for variant calls

- **Data Integrator**

combine data sources from the Genome Browser database

- **Gene Sorter**

find genes that are similar by expression and other metrics

- **Genome Browser in a Box (GBiB)**

run the Genome Browser on your laptop or server

- **In-Silico PCR**

rapidly align PCR primer pairs to the genome

- **LiftOver**

convert genome coordinates between assemblies

- **Track Hubs**

import and view external data tracks

[More tools...](#)

Enter query position in search bar, note there are different tracks below this screenshot

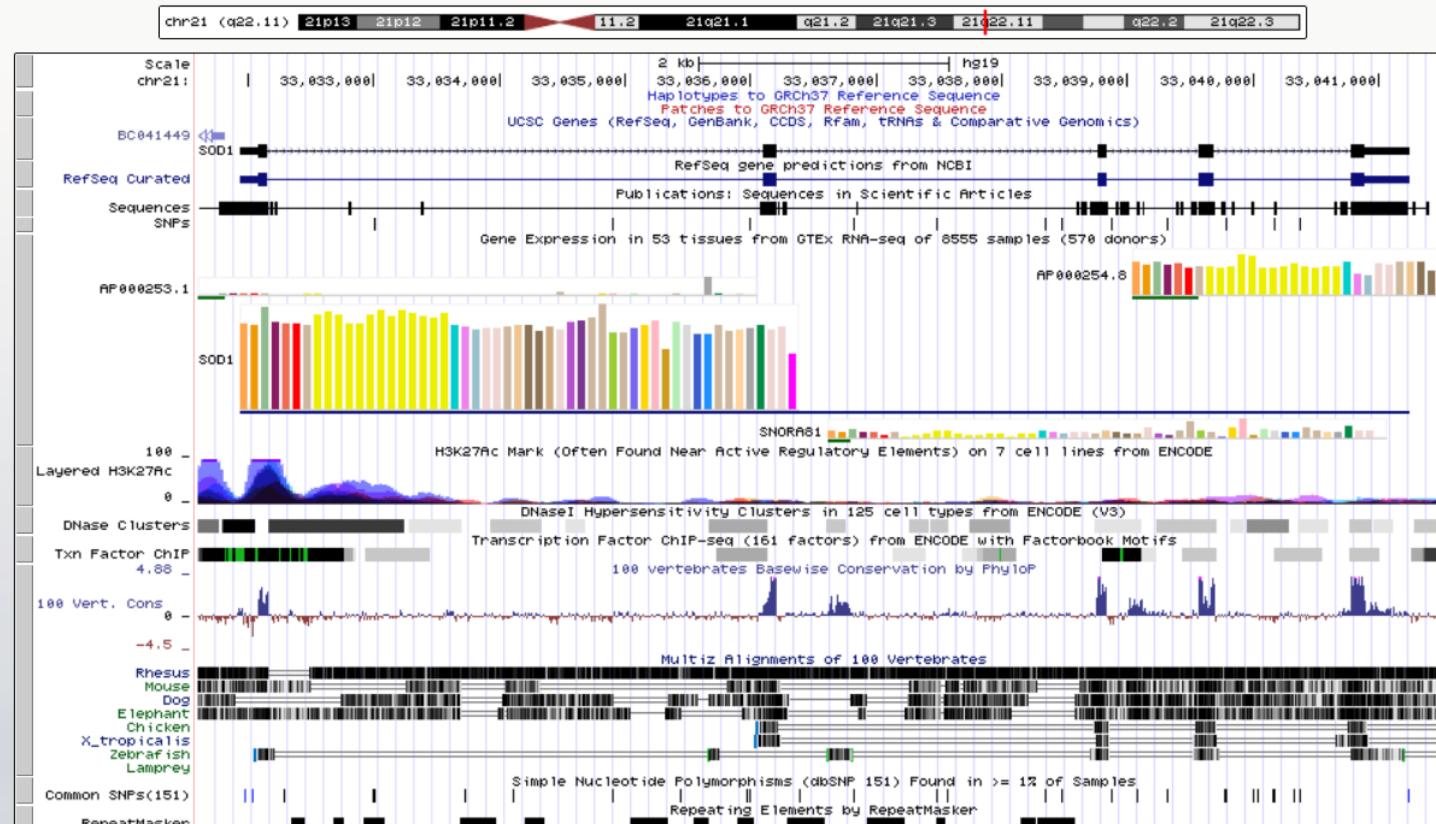
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UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr21:33,031,597-33,041,570 9,974 bp. enter position, gene symbol, HGVS or search terms

go



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. Drag tracks left or right to new position. Press "?" for keyboard shortcuts.

move end

< 2.0 >

[track search](#) [default tracks](#) [default order](#) [hide all](#) [add custom tracks](#) [track hubs](#) [configure](#) [multi-region](#) [reverse](#) [resize](#) [refresh](#)

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.

[collapse all](#)

[expand all](#)



Mapping and Sequencing

[refresh](#)

This track contains the DHS from ENCODE DNase-seq data we used in this class

Regulation

refresh

ENCODE Regulation... show ▲	GeneHancer Updated hide ▲	GTEx Combined eQTL hide ▲	GTEx Tissue eQTL hide ▲	CD34 DnaseI 18 hide ▲	CpG Islands... hide ▲
ENC Chromatin... hide ▲	ENC DNA Methyl... hide ▲	ENC DNase/FAIRE... show ▲	ENC Histone... hide ▲	ENC RNA Binding... hide ▲	ENC TF Binding... hide ▲
FSU Repli-chip hide ▲	Genome Segments hide ▲	NKI Nuc Lamina... 18 hide ▲	ORegAnno hide ▲	Stanf Nucleosome hide ▲	SUNY SwitchGear hide ▲
SwitchGear TSS 17 hide ▲	TFBS Conserved hide ▲	TS miRNA sites hide ▲	UCSF Brain Methyl hide ▲	UMMS Brain Hist hide ▲	UW Repli-seq hide ▲
Vista Enhancers hide ▲					

Click to configure this track, you can select the specific cell type/data type you are looking at

Duke DNasel HS Track Settings

[ENCODE at UCSC](#) [Downloads](#) [Subtracks](#) [Description](#) [Contact](#)



Open Chromatin by DNasel HS from ENCODE/OpenChrom(Duke University) ([^ENC DNase/FAIRE](#))

Maximum display mode: [Reset to defaults](#)

Select views ([help](#)):

[Peaks](#) [Density Signal](#) [Overlap Signal](#)

Select subtracks by treatment and cell line:

Cell Line		Treatment																				Cell Line	
<input type="checkbox"/>	All	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	All
GM12878 (Tier 1)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	GM12878 (Tier 1)
H1-hESC (Tier 1)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	H1-hESC (Tier 1)
K562 (Tier 1)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	K562 (Tier 1)
A549 (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	A549 (Tier 2)
B cells CD20+ RO01794 (Tier 2)	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	B cells CD20+ RO01794 (Tier 2)																		
HeLa-S3 (Tier 2)	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	HeLa-S3 (Tier 2)																		
HepG2 (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	HepG2 (Tier 2)
HUVEC (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	HUVEC (Tier 2)
IMR90 (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	IMR90 (Tier 2)
MCF-7 (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	MCF-7 (Tier 2)
Monocytes CD14+ (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Monocytes CD14+ (Tier 2)
SK-N-SH (Tier 2)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	SK-N-SH (Tier 2)
8988T	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	8988T

Use right mouse button to get the menu, you can change the display mode or configure this track

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

move [<<<] [<<] [<] [>] [>>] [>>>] zoom in [1.5x] [3x] [10x] [base] zoom out [1.5x] [3x] [10x] [100x]

chr22:42,510,977-42,510,986 10 bp. enter position, gene symbol, HGVS or search terms go

chr22 (q13.2) 22p13 22p12 22p11.2 22q11.21 11.23 22q12.1 q12.2 22q12.3 22q13.1 22q13.2 22q13.31 hg19

Scale chr22: 42,510,977| 42,510,978| 42,510,979| 42,510,980| 42,510,981| 42,510,982| 42,510,983| 42,510,984| 42,510,985| hg19
---> C T C T A C T C T T

NDUFA6-AS1 NDUFA6-AS1

Sequences SNPs 100 - Layered H3K27Ac

H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

DNase Clusters

Txn Factor ChIP

Click on a feature for details. Click or drag in the background to move start options. Drag side bars or labels up or down to reposition them. Press "?" for keyboard shortcuts.

track search default tracks default order hide all add custom

collapse all

Use drop-down controls below to change display modes. Tracks with lots of items will automatically switch to a more compact view.

Mapping a

Base Position GRC Patch Release Alt Haplotypes

18 deCODE

move end < 2.0 >

hide

dense

squish

pack

full

Configure DNase Clusters

Configure ENCODE Regulation track set...

View image

move end < 2.0 >

refresh expand all

BU ORCHID