

MEDS5420 Lec13

Using the UCSC Genome Browser

March 1, 2023

Lead creators of UCSC genome browser: Jim Kent and David Haussler



[email Jim](#)

Jim Kent's Web Page

I'm a research scientist at [UCSC](#). I work primarily on web tools to help understand the human genome. Before becoming a bioinformatician I got a PhD in biology working with the [Zahler lab](#). Before that I wrote computer art and animation programs. I live in Santa Cruz, CA and have three children, Mira, Tisa, and Maia.

Links to Stuff I Work On:

- [The UCSC Genome Browser](#) - also known as 'the golden path'.
- [Parasol](#) - A Job Control System for Computer Clusters. It's fast and it's free.
- [Papers](#) - PubMed index of my papers.
- [Presentations](#) - slides from presentations. Sadly no voice-over.
- [The Intronerator](#) - to look at C. elegans genes and splicing patterns.
- [cis-Site Seeker](#) - Look for regulatory regions in RNA or DNA sequences with the Improbizer.
- [Cross Species Alignments](#) - Program and some samples using the not yet famous WABA algorithm.
- [Commands](#) - Catalog of command line driven programs.
- [Source Code](#) - free for academic, non-profit or personal use.
- [Executables](#) - commonly requested compiled versions also free for academic, non-profit and personal use.

Other Useful Links


- [PubMed](#) - to search the scientific literature.
- [Blast](#) - homology searching.
- [Google Scholar](#) - search scientific literature the Google way.
- [UCSC Schedule of Classes](#) - er, when was that final?



<https://cbse.soe.ucsc.edu/people/kent>
<https://users.soe.ucsc.edu/~kent/>

<https://hausslergenomics.ucsc.edu/people/david-haussler/>

Lead creator of UCSC genome browser: Jim Kent

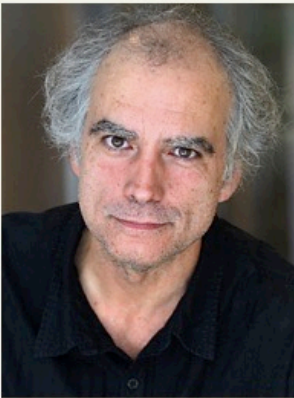


UNIVERSITY OF CALIFORNIA
SANTA CRUZ CENTER FOR BIOMOLECULAR
SCIENCE AND ENGINEERING

ABOUT US RESEARCH EDUCATION

Home

Jim Kent



Director, UCSC Genome Browser Project

Research Scientist, Department of Biomolecular Engineering, UC

Jim Kent

Research Projects

Jim Kent directs the genome browser assurance staff of the UCSC Genome Browser. He created the computer program that displays the human genome sequence and coordinates sequencing centers worldwide. He is also an informatics associated with the Bioinformatics Group participate in projects to produce, assemble, and annotate the human genome.

UCSC Genome Browser

The UCSC Genome Browser provides a comprehensive set of metazoan genome sequences. It also provides wide annotation in a web-based format.

START HERE EXPLORE RESEARCH TALKS STORIES CONTACT

Home » Speakers » David Haussler



David Haussler

University of California, Santa Cruz

   Share

David Haussler is Scientific Director of the Center for Genome Dynamics at the University of California Santa Cruz (UCSC). He is an Investigator of the Howard Hughes Medical Institute (HHMI). Haussler uses mathematical and computational biology to study the genomes of various organisms.

understanding disease and evolution. As part of the Human Genome Project, he contributed to the effort that published the first publicly available draft of the human genome. He has also led several large-scale projects, including the [Genome 10K Project](#), the [Genome Reference Consortium \(GRC\)](#), the [Genome Reference Consortium \(GRC\) Hub \(CGHub\)](#), and the [Global Alliance for Genomics and Health](#).

<https://www.ibiology.org/speakers/david-haussler/>

Some useful capabilities of the browser

- Some resources:
 - Genome build files (fasta format)
 - Converting genome coordinates between versions (e.g. hg19 to hg38)
 - Gene annotation files
 - Convert gene IDs from different sources (GENCODE-refSeq)
 - Obtaining DNA sequences from regions of interest
 - In-silico tools
 - BLAT- fast alignment of short sequences
 - PCR
- Custom tracks and resources:
 - Uploading custom data or annotations
 - Storing them in a user profile
 - Sharing / viewing track hubs
 - Configure Display for optimal clarity (e.g. for making figures)

UCSC homepage

UNIVERSITY OF CALIFORNIA
SANTA CRUZ

Genomics
Institute



Genome Browser



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us



Our tools

- **Genome Browser**
interactively visualize genomic data
- **COVID-19 Research**
use the SARS-CoV-2 genome browser and explore coronavirus datasets
- **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
- **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
- **REST API**
returns data in JSON format

[More tools...](#)

Click on Genomes

UNIVERSITY OF CALIFORNIA
SANTA CRUZ Genomics Institute UCSC **Genome Browser**

Home Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us



Our tools

- **Genome Browser**
interactively visualize genomic data
- **COVID-19 Research**
use the SARS-CoV-2 genome browser and explore coronavirus datasets
- **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
- **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
- **REST API**
returns data in JSON format

[More tools...](#)

Available genomes and info



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

Browse/Select Species

POPULAR SPECIES



Human



Mouse



Rat



Zebrafish



Fruitfly



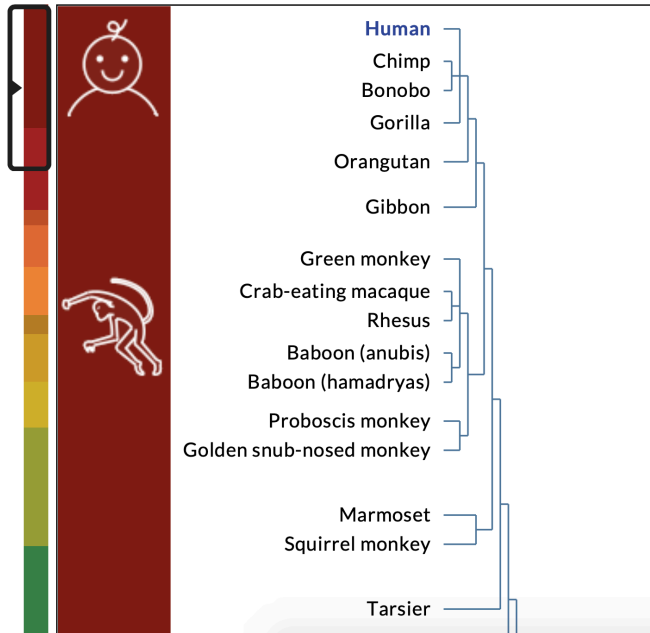
Worm



Yeast

[Can't find a genome assembly?](#)

REPRESENTED SPECIES




Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38) ▾



Position/Search Term

Current position: chr 1:1,300,932-3,320,931 

Human Genome Browser - hg38 assembly

[view sequences](#)

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p13 (GCA_000001405.28)
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 13
Assembly accession: [GCA_000001405.28](#)
NCBI Genome ID: [51](#) (Homo sapiens (human))
NCBI Assembly ID: [GCF_000001405.39](#) (GRCh38.p13, GCA_000001405.28)
BioProject ID: [PRJNA31257](#)



Homo sapiens
(Graphic courtesy of CBSE)

Search the assembly:

- **By position or search term:** Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. **More information**, including sample queries.
- **By gene name:** Type a gene name into the "search term" box. choose your gene

Click on the Genome Browser

UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute UCSC **Genome Browser Gateway**

Home Genomes **Genome Browser** Tools Mirrors Downloads My Data Projects Help About Us

Browse/Select Species

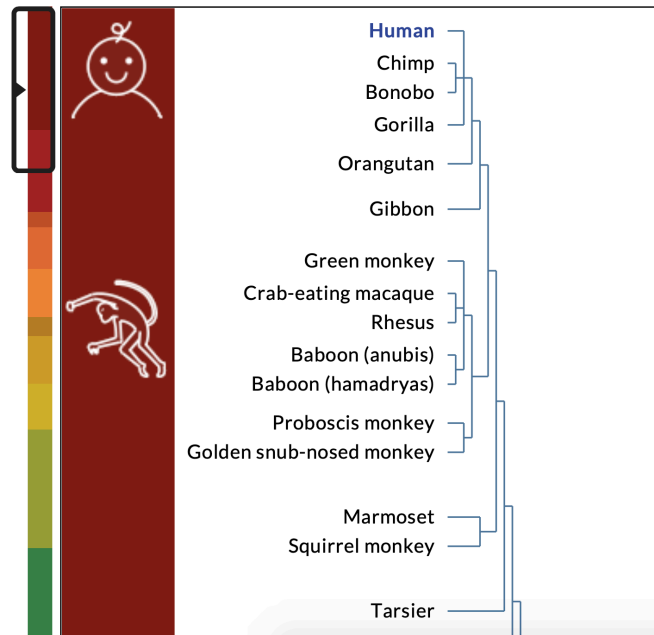
POPULAR SPECIES



Enter species, common name or assembly ID

[Can't find a genome assembly?](#)

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)



Position/Search Term

Enter position, gene symbol or search terms

Current position: chr1:1,300,932-3,320,931

Human Genome Browser - hg38 assembly

[view sequences](#)

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p13 (GCA_000001405.28)
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 13
Assembly accession: [GCA_000001405.28](#)
NCBI Genome ID: 51 (Homo sapiens (human))
NCBI Assembly ID: [GCF_000001405.39](#) (GRCh38.p13, GCA_000001405.28)
BioProject ID: [PRJNA31257](#)



Homo sapiens
(Graphic courtesy of CBSE)

Search the assembly:

- **By position or search term:** Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. **More information**, including sample queries.
- **By gene name:** Type a gene name into the "search term" box. choose your gene

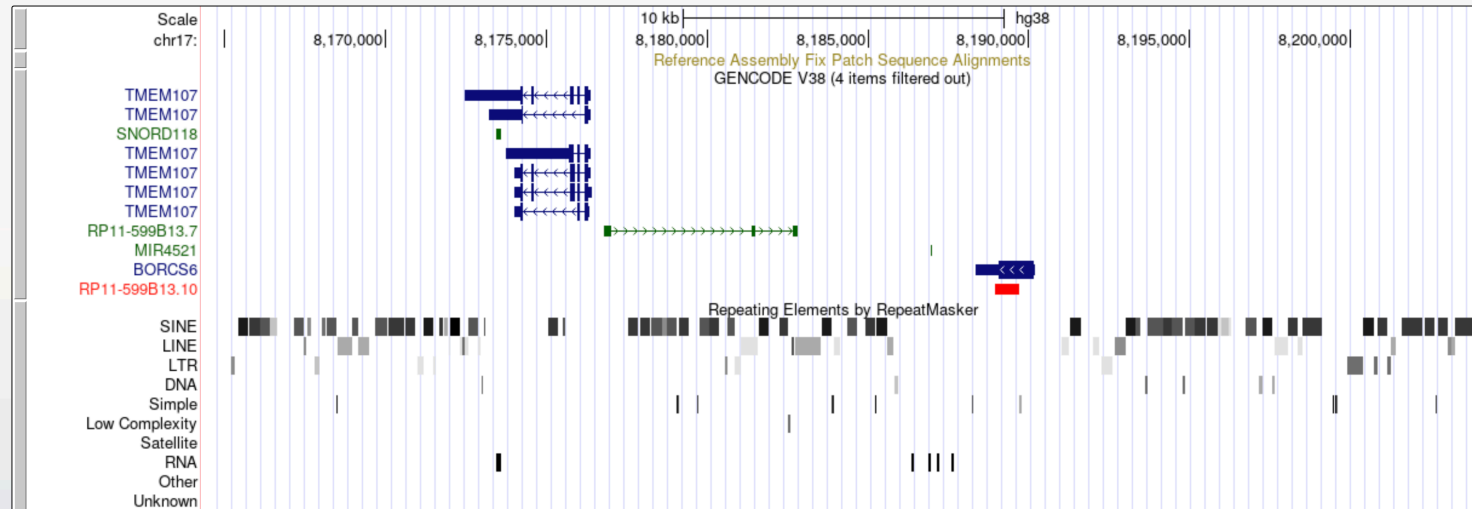
Browser view

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

multi-region chr17:8,164,338-8,204,114 39,777 bp. gene, chromosome range, or other position, see examples go examples

chr17 (p13.1) p13.3 p13.2 p13.1 17p12 17p11.2 17q11.2 17q12 21.2 q21.31 17q22 23.2 24.2 q24.3 q25.1 17q25.3



move start < 2.0 > Click on a feature for details. Click+shift+drag 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 reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. expand all Tracks with lots of items will automatically be displayed in more compact modes.

Mapping and Sequencing

Base Position dense ▾	P13 Updated Fix Patches pack ▾	P13 Updated Alt Haplotypes hide ▾	Assembly hide ▾	Centromeres hide ▾	Chromosome Band hide ▾
Clone Ends hide ▾	Exome Probesets hide ▾	FISH Clones hide ▾	Gap hide ▾	GC Percent hide ▾	GRC Contigs hide ▾
GRC Incident hide ▾	Hg19 Diff hide ▾	INSDC hide ▾	LiftOver & ReMap hide ▾	LRG Regions hide ▾	Mappability hide ▾
RefSeq Acc hide ▾	Restr Enzymes hide ▾	Scaffolds hide ▾	Short Match hide ▾	STS Markers hide ▾	

Genes and Gene Predictions

GENCODE V38 full ▾	NCBI RefSeq hide ▾	All GENCODE hide ▾	CCDS hide ▾	CRISPR Targets hide ▾	IKMC Genes Mapped hide ▾
---------------------------------------	---------------------------------------	---------------------------------------	--------------------------------	--	---

Browser view

UCSC Genome Browser navigation bar: Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, About Us

UCSC Genome Browser logo with a red arrow pointing to the 'Genome Data' menu.

Search bar: multi-region chr17:8,160,000

Assembly: hg38

Scale: chr17 (p13.1) | p13.3 | p13.2 | 17p13.1 | 17p13.2 | 17p13.3

Track list (left):

- TMEM107
- SNORD118
- RP11-599B13.7
- MIR4521
- BORCS6
- RP11-599B13.10
- SINE
- LINE
- LTR
- DNA
- Simple
- Low Complexity
- Satellite
- RNA
- Other
- Unknown

Main visualization area:

- Reference Assembly Fix Patch Sequence Alignments
- GENCODE V38 (4 items filtered out)
- Repeating Elements by RepeatMasker

Navigation controls: move start, < 2.0 >, move end, < 2.0 >

Track search, default tracks, default order, hide all, add custom tracks, track hubs, configure, reverse, resize, refresh

collapse all, expand all

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.

Mapping and Sequencing refresh

Base Position dense	P13 Updated Fix Patches pack	P13 Updated Alt Haplotypes hide	Assembly hide	Centromeres hide	Chromosome Band hide
Clone Ends hide	Exome Probesets hide	FISH Clones hide	Gap hide	GC Percent hide	GRC Contigs hide
GRC Incident hide	Hg19 Diff hide	INSDC hide	LiftOver & ReMap hide	LRG Regions hide	Mappability hide
RefSeq Acc hide	Restr Enzymes hide	Scaffolds hide	Short Match hide	STS Markers hide	

Genes and Gene Predictions refresh

GENCODE V38	NCBI RefSeq	All GENCODE	CCDS	CRISPR Targets	IKMC Genes Mapped
-------------	-------------	-------------	------	----------------	-------------------

Downloading Genomes and source code for utilities and browser




Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

Sequence and Annotation Downloads

This page contains links to sequence and annotation downloads for the genome assemblies featured in the UCSC Genome Browser. Downloads are also available via the Genome Browser [FTP server](#). For access to the most recent assembly of each genome, see the [current genomes](#) directory. To query and download data in JSON format, use our [JSON API](#). To view descriptions of annotations, use the "describe table schema" button in the [Table Browser](#). Previous versions of certain data are available from our [track archive](#). For data hosted in [Public Hubs](#) the files exist on external sites, with [GenArk](#) (Genome Archive) Public Hub species found [here](#).

All tables in the Genome Browser are freely usable for any purpose except as indicated in the README.txt files in the download directories. To view restrictions specific to a particular data set, click on the corresponding download link and review the README text. These data were contributed by many researchers, as listed on the Genome Browser [credits](#) page. Please acknowledge the contributor(s) of the data you use.

- 
- [Human](#)
 - [Mouse](#)
 - [Mammals](#) ▶
 - [Other vertebrates](#) ▶
 - [Deuterostomes](#) ▶
 - [Insects](#) ▶
 - [Nematodes](#) ▶
 - [Other genomes](#) ▶
 - [Other downloads](#) ▶

Source and utilities downloads

The source for the Genome Browser, Blat, liftOver and other utilities is free for non-profit academic research and for personal use. For information on commercial licensing, see the [Genome Browser](#) and [Blat](#) licensing requirements. The source and executables for several of these products can be downloaded or purchased from our [online store](#).

Mirroring the Genome Browser

Precompiled executable binaries are available for installing a local mirrored copy of the Genome Browser website on your web server, eliminating the need to compile the entire source tree.

- [Mirror instructions](#)
- [Build instructions](#)
- [Genome Browser hgcentral tables](#)
- [Genome Browser source code downloads](#) ▶

If you encounter difficulties with slow download speeds, try using [UDT Enabled Rsync](#) (UDR), which improves the throughput of large data transfers over long distances. The 32-bit and 64-bit versions can be downloaded [here](#).

Utilities

The [utilities directory](#) offers downloads of pre-compiled standalone binaries for:

- [LiftOver](#) (which may also be accessed via the [web version](#)). The over.chain liftOver conversion files are located in the individual assembly download sections.
- [Blat](#) ▶
- Other command-line utilities

All our command line tools can be obtained as pre-built binaries from our [downloads server](#). The following command can be used to copy all command line utilities into a directory with the correct permission bits set:

```
$ rsync -aP hgdownload.soe.ucsc.edu:/genome/admin/exe/linux.x86_64/ ./
```

Note about 'permission denied' error when downloading with curl or wget:

In order for your computer to run a freshly downloaded utility, you will need to update the file system permissions to allow your operating system to run the program. To make utilities usable, download a tool and turn on its 'executable' bit:


```
$ wget https://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/liftOver
```

```
$ chmod +x ./filePath/utility_name
```

Downloading Genomes

Human genome

Dec. 2013 (GRCh38/hg38)

- [Genome sequence files and select annotations \(2bit, GTF, GC-content, etc\)](#) ▼
-  ■ [Standard genome sequence files and select annotations \(2bit, GTF, GC-content, etc\)](#)
 - [Analysis set sequence files](#) (See: [What is the analysis set?](#))
- [Sequence data by chromosome](#)
- [Annotations](#) ▼
 - [SQL table dump annotations](#)
 - [Fileserver \(bigBed, maf, fa, etc\) annotations](#) Also see [Data Access](#)
- [SNP-masked fasta files](#) ▶
- [LiftOver files](#)
- [Pairwise alignments](#) ▶
- [Multiple alignments](#) ▶
- [Patches](#) ▶
- [Data archive](#)

Downloading Genomes and more

Top of page

Introduction

The Dec. 2013 assembly of the human genome (GRCh38 Genome Reference Consortium Human Reference 38), is called hg38 at UCSC. This directory contains the genome as released by UCSC, selected annotation files and updates. The directory "genes/" contains GTF/GFF files for the main gene transcript sets.

For more information about this assembly, see these NCBI resources:
<http://www.ncbi.nlm.nih.gov/genome/51>
<http://www.ncbi.nlm.nih.gov/genome/assembly/883148>
<http://www.ncbi.nlm.nih.gov/bioproject/31257>

These files are used by the UCSC Genome Browser for display and analysis. If you want to do analysis and show it later on the browser, it is usually easiest to run your analysis on the UCSC hg38 file. For most users, this will be the file "latest/hg38.fa.gz" in this directory. However, if you need a genome file for alignment or variant calling, please read the section "Analysis set" below.

The sequences of the main chromosomes are identical to the genome files distributed by NCBI and the EBI, but the sequence names are different. For example, the name of chromosome 1 is called "chr1" at UCSC, "NC_000001.11" at NCBI, and "1" at the EBI. Also, the lowercasing in the files is not exactly identical, as UCSC, NCBI and EBI run Repeatmasker with slightly different settings.

The NCBI accession of the UCSC hg38 genome is GCA_000001405.15. The version that includes the updates for patch release 13 GRCh38.p13 has the NCBI accession GCA_000001405.28.

Analysis set

The GRCh38 assembly contains more than just the chromosome sequences, but also a mitochondrial genome, unplaced sequences, centromeric sequences and alternates. To better capture variation in the human genome across the world it contains more copies of some loci than hg19. Some of these additions, like the EBV genome, are mostly relevant for genomic analysis, i.e. alignment. For an overview of the different types and reasons for the additions see <https://software.broadinstitute.org/gatk/documentation/article?id=11010>

This means that if you want to use the genome sequence for alignment and especially for variant calling, you should use the optimal genome file for your aligner. The genome file can make a big difference, especially for variant calling. In most cases, the authors of your alignment program will provide advice on which hg38 genome version to use and usually they recommend one of the files in our analysisSet/ directory, like the GATK link above. These special genome files sometimes remove the alternate sequences, sometimes they add decoys or change single nucleotides towards the major allele, but they never insert or delete sequences, so the annotation coordinates remain the same.

- for BWA see also <https://lh3.github.io/2017/11/13/which-human-reference-genome-to-use>
- for Novalign see its manual at <http://www.novocraft.com/userfiles/file/Novocraft.pdf>
- For Bowtie, see the different versions of the human genome that the Bowtie authors provide: <http://bowtie-bio.sourceforge.net/index.shtml>

Also see analysisSet/README.txt for further details

Patches

Like hg19, hg38 has been updated with patches since its release in 2013. GRC patch releases do not change any previously existing sequences; they simply add small, new sequences for fix patches or alternate haplotypes that correspond to specific regions of the main chromosome sequences (see below). For most users, the patches are unlikely to make a difference and may complicate the analysis as they introduce more duplication. If you want a version of the genome without these complexities, look at the analysisSet/ subdirectory.

The initial/ subdirectory contains files for the initial release of GRCh38, which includes the original alternate sequences (261) and no fix sequences.

The p11/ subdirectory contains files for GRCh38.p11 (patch release 11).

The p12/ subdirectory contains files for GRCh38.p12 (patch release 12).

The p13/ subdirectory contains files for GRCh38.p13 (patch release 13).

The "latest/" symbolic link points to the subdirectory for the most recent patch version.

Bottom of page

<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
Parent Directory		-	
analysisSet/	2021-10-07 16:48	-	
est.fa.gz	2020-09-09 11:27	1.5G	
est.fa.gz.md5	2020-09-09 11:27	44	
genes/	2021-12-09 03:03	-	
hg38.2bit	2015-04-30 16:16	797M	
hg38.agp.gz	2014-01-15 20:55	842K	
hg38.chrom.sizes	2013-12-24 21:06	11K	
hg38.chromAlias.txt	2021-10-06 13:44	27K	
hg38.chromFa.tar.gz	2014-01-23 17:18	938M	
hg38.chromFaMasked.tar.gz	2014-01-23 17:10	487M	
hg38.fa.align.gz	2014-01-08 23:43	2.4G	
hg38.fa.gz	2014-01-15 21:14	938M	
hg38.fa.masked.gz	2014-01-15 21:24	487M	
hg38.fa.out.gz	2014-01-15 20:56	172M	
hg38.gc5Base.bw	2013-12-24 21:28	1.6G	
hg38.gc5Base.wib	2019-01-17 14:50	591M	
hg38.gc5Base.wig.gz	2010-01-17 14:50	11M	
hg38.gc5Base.wigVarStep.gz	2013-12-24 21:14	1.5G	
hg38.trf.bed.gz	2014-01-15 20:56	7.9M	
initial/	2021-10-07 16:50	-	
latest/	2021-10-07 16:57	-	
md5sum.txt	2021-10-06 14:07	667	
mrna.fa.gz	2020-09-09 11:08	372M	
mrna.fa.gz.md5	2020-09-09 11:08	45	
p11/	2021-10-07 16:51	-	
p12/	2021-10-07 16:51	-	
p13/	2021-10-07 16:53	-	
refMrna.fa.gz	2020-09-09 11:28	89M	
refMrna.fa.gz.md5	2020-09-09 11:28	48	
upstream1000.fa.gz	2020-09-09 11:29	11M	
upstream1000.fa.gz.md5	2020-09-09 11:29	53	
upstream2000.fa.gz	2020-09-09 11:29	20M	
upstream2000.fa.gz.md5	2020-09-09 11:29	53	
upstream5000.fa.gz	2020-09-09 11:30	52M	
upstream5000.fa.gz.md5	2020-09-09 11:30	53	
xenoMrna.fa.gz	2020-09-09 11:19	6.7G	
xenoMrna.fa.gz.md5	2020-09-09 11:19	49	
xenoRefMrna.fa.gz	2020-09-09 11:27	255M	
xenoRefMrna.fa.gz.md5	2020-09-09 11:27	52	

FASTA formatted genome

We use this for input in bedtools

Descriptions of file content are in the middle

Converting genome coordinates



Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

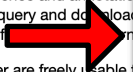
Sequence and Annotation Downloads

This page contains links to sequence and annotation **current genomes** directory. To query and download data hosted in **Public Hubs** the first time.

All tables in the Genome Browser are freely usable. These data were contributed by many researchers.

- Human
- Mouse
- Mammals
- Other vertebrates

- Blat
- Table Browser
- In-Silico PCR
- LiftOver
- Variation Annotation Integrator
- Gene Sorter
- Data Integrator
- Genome Graphs
- Gene Interactions
- Other Tools



Assemblies featured in the UCSC Genome Browser. Downloads are also available via the Genome Browser **FTP server**. For access to the most recent assembly of each genome, see the **JSON API**. To view descriptions of annotations, use the "describe table schema" button in the **Table Browser**. Previous versions of certain data are available from our **track archive**. For (Archive) Public Hub species found **here**.

described in the README.txt files in the download directories. To view restrictions specific to a particular data set, click on the corresponding download link and review the README text. Please acknowledge the contributor(s) of the data you use.

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Lift Genome Annotations

This tool converts genome coordinates and genome annotation files between assemblies. The input data can be pasted into the text box or uploaded from a file. For more information, please see our [LiftOver documentation](#). If a pair of assemblies cannot be selected from the pull-down menus, a sequential lift may still be possible. For example, to lift from mm9 to mm39, lift from Mouse mm9 to mm10 and then from mm10 to mm39.

Specify original genome

Specify new genome

Original Genome:

Human

Original Assembly:

Dec. 2013 (GRCh38/hg38)

New Genome:

Human

New Assembly:

Feb. 2009 (GRCh37/hg19)

Minimum ratio of bases that must remap:

0.95

BED 4 to BED 6 Options

Allow multiple output regions:

Minimum hit size in query:

0

Minimum chain size in target:

0

BED 12 Options

Min ratio of alignment blocks or exons that must map:

1

If thickStart/thickEnd is not mapped, use the closest mapped base:

Paste in data below, one position per line. You can use the [BED format](#) (e.g. "chr4 100000 100001", 0-based) or the format of the position box ("chr4:100,001-100,001", 1-based). See the [documentation](#).

Paste in .bed format data or upload file

Submit

Clear

Or upload data from a file ([BED](#) or chrN:start-end in plain text format):

Choose File no file selected

Submit File

Command Line Tool

To lift genome annotations locally on Linux systems, download the [liftOver](#) executable and the appropriate [chain file](#). Run *liftOver* with no arguments to see the usage message.

Downloading annotation tracks: gene lists



- Blat
- In-Silico PCR
- Table Browser**
- LiftOver
- Gene Sorter
- Variant Annotation Integrator

Tools

Genome Browser

Interactively visualize genomic data

COVID-19 Research

Use the SARS-CoV-2 genome browser and explore coronavirus datasets

Table Browser

Use this tool to retrieve and export data from the Genome Browser annotation track database. You can limit retrieval based on data attributes and intersect or merge with data from another track, or retrieve DNA sequence covered by a track. [More...](#)

Select dataset

clade: genome: assembly:
group: track:
table: [describe table schema](#)

Track type

Sub-table

Define region of interest

region: genome position

identifiers (names/accessions):

Choose fields or columns from table

Optional: Subset, combine, compare with another track

filter:

intersection:

Retrieve and display data

output format: Send output to Galaxy GREAT

output filename: (leave blank to keep output in browser)

Name output file

file type returned: plain text gzip compressed

Downloading DNA sequence from browser

The screenshot displays the UCSC Genome Browser interface for Human Decoding (hg38) Assembly. The main track shows a genomic region on chromosome 17 (p13.1 to q11.2) with a scale of 10 kb. A red arrow points to the 'DNA' option in the 'PDF/PS' dropdown menu. The interface includes navigation controls (move, zoom), track labels (TMEM107, SNORD118, RP11-599B13.7, MIR4521, BORCS6, RP11-599B13.10), and a footer with instructions: 'Click on a feature for details. Click+shift+drag 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.' The footer also includes a 'refresh' button and the text 'Mapping and Sequencing'.

Downloading DNA from browser

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Get DNA in Window (hg38/Human)

Get DNA for

Position

Note: This page retrieves genomic DNA for a single region. If you would prefer to get DNA for many items in a particular track, or get DNA with formatting options based on gene structure (introns, exons, UTRs, etc.), try using the [Table Browser](#) with the "sequence" output format. You can also use the [REST API](#) with the `/getData/sequence` endpoint function to extract sequence data with coordinates.

Sequence Retrieval Region Options:

Add extra bases upstream (5') and extra downstream (3') **Options to get flanking DNA as well**

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

Sequence Formatting Options:

All upper case.
 All lower case. **Options for case and masking of repeats**
 Mask repeats: to lower case to N
 Reverse complement (get '-' strand sequence)

Note: The "Mask repeats" option applies only to "get DNA", not to "extended case/color options".

Fasta output



```
>hg38_dna range=chr17:8164338-8204114 5'pad=0 3'pad=0 strand=+ repeatMasking=none
GGCCTTGATCTCTAAGACAAAACAGGAACCCAGCTTCCCTCCCACCCACCC
TGGCTTCCCAGGGCCTCCGGGTGTGAGATCCTCCCACCTGCAGTGGCCC
ACCCGCTCCCACAGAAGCCGGAGAGTGGCTCTGTCCACAGAGGTGTCA
TTTCCCAGCTGTCTGTGGGAGGTGAGTGAGCAGGGAAATGTGTGTGCTGGG
TGTGGGAACCTCAGCCCAATCTAAGAGAAGATACTTTGGCTTCCCTCCC
TCAGAGGAGCAGCCGCTCCCTGGTCTTGTGCACTGCAGTCCCAGGGTGTG
GCTCAGCCTATGTGATGAGAAAAGAAAGAGCAGCTTCCACGGGGTCTCA
GATCATGCTGTGAGATGCTGGCTCCTGCTTTTGGTCTTCAAAATGATTC
TCTTTCTAGTCAGAGAACAAGATGCCAAATTCAGCCTTTTAAAGTTCAA
AACCTCAGTGTCTGTGAGGGTATAAATAAGACATGGAGGATTTGGAAGAG
GCAGGCACAGGAAGCCCTTCCGCCCCAGTTGGACACCCTGCACTAACTG
AGGGGAGCCTAGTGCAGAGCCAGACAAGACATTTGATGCTGGTTTGGGG
TGATGTGGAAGGGACAGAGCCCCAGATACACGGTCAAGGCCAGGGTTCGT
GCTATTGCTATTGGATCGTGGGACGGCAGCAGCAGAGTAGAAATGAGGG
CATGTGTGACCCACGGAGATGAAGGGCCAGGAGGATTCATCTCAGAAAG
AGGACTCTCATCCAGCAGCCCTTCCCACCCACCCACCTAGGCTGTGG
CTCAGAGGAACCTCCCAAATTTAGATCAATGGTGGAGGTGGGAGAAGGAG
TGGGATGACGGAGTTCACCTGGAAGTACTGAGAGAAATGTTTTCTGCAGG
CAGGTAGAATGGAGACCCAAATAGAGGTAAGTTGAACAATAGAAAAATAA
TGTATTTGCATAACTCAGATTTGGCTTCTACATGTACTGGCTTCGGGAAT
TGGCCAATGATTTTTCTAGGGCACACCCCAAGACTCATTCAAAGGATGTA
GGACTCAAGGTGATGGTGTAGTGGCAACAGAGACCACACTTTCTTTTTC
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTCTCTGTCTGTCAC
CCAGGCTGGAGTGCAATGGCCGATCTCTGCTCACTGCAAACTCCGCCCTC
CCAGGTTACGCCATTTCTCCTCCCTCAGCCTCCCGAGTAGCTGGACTAC
AGGCGCCACCACCCGGCCCGGCTAATTTTTTGTATTTTGTAGTAGAGACA
GGTTTTACCGTGTAGCCAGGGTGGTCTTGATCTCCTGACCCCGTGATC
```

Fast DNA search: BLAT



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

Blat

In-Silico PCR

Table Browser

LiftOver

Gene Sorter

Variant Annotation
Integrator

Data Integrator

Genome Graphs

Gene Interactions

Other Tools

Tools

Genome Browser

actively visualize genomic data

COVID-19 Research

the SARS-CoV-2 genome browser and explore coronavirus datasets

BLAT

align sequences to the genome

Table Browser

load data from the Genome Browser database

Variant Annotation Integrator

functional effect predictions for variant calls

Data Integrator

combine data sources from the Genome Browser database

■ Genome Browser in a Box (GBiB)

run the Genome Browser on your laptop or server

Fast DNA search with BLAT

Human BLAT Search

BLAT Search Genome

Genome: Search all

Human

Assembly:

Dec. 2013 (GRCh38/hg38)

Query type:

BLAT's guess

Sort output:

query,score

Output type:

hyperlink

```
>hg38_dna range=chr17:8164338-8204114 5'pad=0 3'pad=0 strand=+ repeatMasking=none
GGCCTTGATCTCTAAGACAAACAGGAACCCAGCTTCCTCCCTCCCCACCC
TGGCTTCCCAGGGCCTCCGGGTGTGAGATCCTCCCCACTGCAGTGCCCC
ACCCGCTCCCCACAGAAGCCCGGAGAGTGGCTCTGTACCAGAGGTGTCA
TTTCCCAGCTGTCTGTGGGAGGTGAGTGAGCAGGGAATGTGTGCTGGG
TGTGGAACTCAGCCCAATCTAAGAGAAGATACTTTGGCTTCTCCCC
TCAGAGGAGCAGCCGCGTCCCTGGTCTTGTGACTGACAGTCCCGGGTG
GCTCAGCCTATGTGATGAGAAAGAAAAGAGCAGCTTCCACGGGGGTCTCA
GATCATGCTGTGAGATGCTGGCTCCTGCTTTTGGTCTTCAAATGATTCC
```

Paste Sequence. Use fasta format for more than 1 sequence

All Results (no minimum matches)

Submit

I'm feeling lucky

Clear

About BLAT

BLAT on DNA is designed to quickly find sequences of 95% and greater similarity of length 25 bases or more. It may miss more divergent or shorter sequence alignments. It will find perfect sequence matches of 20 bases. BLAT on proteins finds sequences of 80% and greater similarity of length 20 amino acids or more. In practice DNA BLAT works well on primates, and protein BLAT on land vertebrates.

BLAT is not BLAST. DNA BLAT works by keeping an index of the entire genome in memory. The index consists of all overlapping 11-mers stepping by 5 except for those heavily involved in repeats. The index takes up about 2 gigabytes of RAM. RAM can be further reduced to less than 1 GB by increasing step size to 11. The genome itself is not kept in memory, allowing BLAT to deliver high performance on a reasonably priced Linux box. The index is used to find areas of probable homology, which are then loaded into memory for a detailed alignment. Protein BLAT works in a similar manner, except with 4-mers rather than 11-mers. The protein index takes a little more than 2 gigabytes.

BLAT was written by [Jim Kent](#). Like most of Jim's software, interactive use on this web server is free to all. Sources and executables to run batch jobs on your own server are available free for academic, personal, and non-profit purposes. Non-exclusive commercial licenses are also available. See the [Kent Informatics](#) website for details.

For more information on the graphical version of BLAT, click the Help button on the top menu bar or see the Genome Browser [FAQ](#).

Kent WJ. [BLAT - the BLAST-like alignment tool](#). Genome Res. 2002 Apr;12(4):656-64. PMID: 11932250

BLAT Search Results

Fast DNA search with BLAT

Go back to [chr17:8164338-8164734](#) in the Genome Browser

Custom track name:

Custom track description:

[Build a custom track with these results](#)

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	hg38_dna	400	1	400	400	100.0%	chr17	+	8164338	8164737	400
browser details	hg38_dna	25	29	54	400	100.0%	chr19	-	10310700	10310726	27
browser details	hg38_dna	25	349	379	400	88.9%	chr1	+	247443829	247443858	30
browser details	hg38_dna	25	15	49	400	89.3%	chr1	+	204244803	204244836	34
browser details	hg38_dna	23	34	58	400	96.0%	chr14	-	20262748	20262772	25
browser details	hg38_dna	23	321	344	400	100.0%	chr1	-	59157007	59157032	26
browser details	hg38_dna	23	42	65	400	100.0%	chr14	+	72549910	72549939	30
browser details	hg38_dna	22	34	58	400	96.0%	chr6	-	166516416	166516441	26
browser details	hg38_dna	22	32	56	400	95.9%	chr13	+	51135725	51135753	29
browser details	hg38_dna	21	32	52	400	100.0%	chr10	-	5966101	5966121	21
browser details	hg38_dna	20	26	47	400	95.5%	chr18	-	44760280	44760301	22
browser details	hg38_dna	20	367	386	400	100.0%	chr15	+	93348003	93348022	20
browser details	hg38_dna	20	360	381	400	95.5%	chr11	+	71338003	71338021	20
browser details	hg38_dna	20	32	51	400	100.0%	chr1	+	71338003	71338021	20
browser details	hg38_dna	20	196	215	400	100.0%	chr1	+	71338003	71338021	20
browser details	hg38_dna	20	32	51	400	100.0%	chr1	+	71338003	71338021	20

Alignment of hg38_dna and chr17:8164338-8164737

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light mark the boundaries of gaps in either sequence (often splice sites).

cDNA hg38_dna

```

GGCTGTGC TACTAGACAA ACAGGAACA GCTCTGTGC TCCGCCACC 50
TGGTTCOCA GGGCTCCCG GGTGTGATC CTCGCCACT GCAGTCCCC 100
ACCCCTCCC CACAGAGGC CGAGAGTGG CTCGTCCAC AGAGGTCCA 150
TTTCCAGCT CTCGTGTGG CAGAGATGT CTCGTCCGG 200
TGTGGAACT CAGCCAAATC TAGAGAGA TACTCTTGC TTCCCTCCC 250
TCAGAGAGC ACCCCCTCC CTGCTCTTG TCACTTACA GTCCCGGTG 300
GCTACGCTA TGTATGATA AAGAAAGAG CAGCTTCCA GGGGTCTCA 350
GATCATGCT TGAATGCTG GCTCTGCTT TTTGTCTTC AANAATTC 400
    
```

Genomic chr17 :

```

caaaqaagc ctaaaggtg caggagcat tttagcagc gcccttggc 8164287
cctgggggg ggtgcttac taatccctg gaagtgcaq ggaggtgat 8164337
GGCTGTGC TACTAGACAA ACAGGAACA GCTCTGTGC TCCGCCACC 8164387
TGGTTCOCA GGGCTCCCG GGTGTGATC CTCGCCACT GCAGTCCCC 8164437
ACCCCTCCC CACAGAGGC CGAGAGTGG CTCGTCCAC AGAGGTCCA 8164487
TTTCCAGCT CTCGTGTGG CAGAGATGT CTCGTCCGG 8164537
TGTGGAACT CAGCCAAATC TAGAGAGA TACTCTTGC TTCCCTCCC 8164587
TCAGAGAGC ACCCCCTCC CTGCTCTTG TCACTTACA GTCCCGGTG 8164637
GCTACGCTA TGTATGATA AAGAAAGAG CAGCTTCCA GGGGTCTCA 8164687
GATCATGCT TGAATGCTG GCTCTGCTT TTTGTCTTC AANAATTC 8164737
cctgggggg ggtgcttac taatccctg gaagtgcaq ggaggtgat 8164787
aaacctcagt gctgtcagg gtataaataa gacatggagt attgqaag 8164837
    
```

chr17:8164338-8164737

Help

Missing a match?

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

chr17:8164338-8164737 400 bp

Scale chr17: 8,164,400 | 8,164,450 | 8,164,500 | 8,164,550 | 8,164,600 | 8,164,650 | 8,164,700

hg38_dna

GENCODE V38
Repeating Elements by RepeatMasker

move start < 2.0 > move end

Use drop-down controls below and press refresh to alter tracks displayed.

→ "Your Sequence From Blat Search"
Matched region shown as track in browser

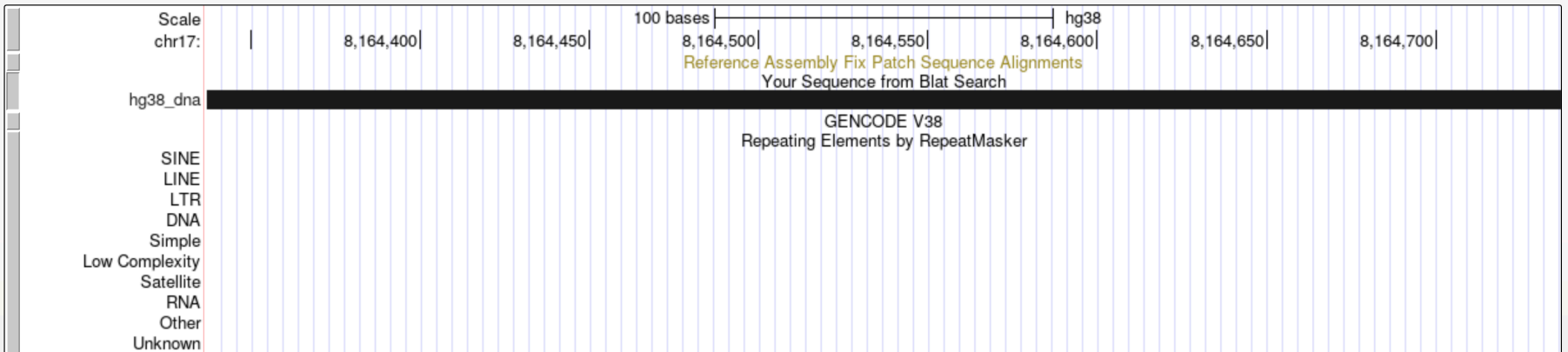
Custom tracks

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

multi-region chr17:8,164,338-8,164,737 400 bp. gene, chromosome range, or other position, see examples go [examples](#)

chr17 (p13.1) p13.3 p13.2 17p13.1 17p12 17p11.2 17q11.2 17q12 21.2 q21.31 17q22 23.2 24.2 q24.3 q25.1 17q25.3



move start < 2.0 > Click on a feature for details. Click+shift+drag 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 reverse resize refresh

collapse all

Use drop-down controls to show and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

expand all

Custom tracks: uploading

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Add Custom Tracks

clade genome assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigBarChart](#), [bigChain](#), [bigGenePred](#), [bigInteract](#), [bigLolly](#), [bigMaf](#), [bigPsl](#), [bigWig](#), [BAM](#), [barChart](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [CRAM](#), [GFE](#), [GTF](#), [hic](#), [interact](#), [MAE](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats.

You can paste just a URL to the file, without a "track" line, for bigBed, bigWig, bigGenePred, BAM and VCF.

- To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#).

Examples are [here](#). If you do not have web-accessible data storage available, please see the [Hosting](#) section of the Track Hub Help documentation.

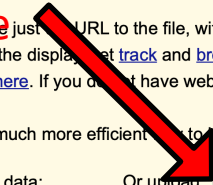
Please note a much more efficient way to load data is to use [Track Hubs](#), which are loaded from the [Track Hubs Portal](#) found in the menu under My Data.

Paste URLs or data: Or upload: no file selected

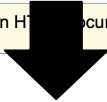
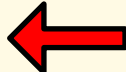
Optional track documentation: Or upload: no file selected

Click [here](#) for an HTML document template that may be used for Genome Browser track descriptions.

Select File



upload



Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Manage Custom Tracks

genome: Human assembly: Dec. 2013 (GRCh38/hg38) [hg38]

Name	Description	Type	Doc	Items	Pos	delete
ATF1_ChIP_10mil	ATF1_ChIP_10mil_bedGraph	bedGraph		8443869	chr11	<input type="checkbox"/>
ATF1_ChIP_bed	ATF1_ChIP_bed	bed		7252908	chr1	<input type="checkbox"/>

view in

Managing Custom Tracks

This section provides a brief description of the columns in custom track management table. For more details about managing custom tracks, see the Genome Browser [User's Guide](#).

- Name** - a hyperlink to the update page where you can edit your track data.
- Description** - the value of the "description" attribute from the track line, if present. If no description is included in the input file, this field contains the track name.
- Type** - the track type, determined by the Browser based on the format of the data.
- Doc** - displays "Y" (Yes) if a description page has been uploaded for the track; otherwise the field is blank.
- Items** - the number of data items in the custom track file. An item count is not displayed for tracks lacking individual items (e.g. wiggle format data).
- Pos** - the default chromosomal position defined by the track file in either the browser line "position" attribute or the first data line. Clicking this link opens the Genome Browser or Table Browser at the specified position (note: only the chromosome name is shown in this column). The Pos column remains blank if the track lacks individual items (e.g. wiggle format data) and the browser line "position" attribute hasn't been set.

Custom tracks: saving and sharing

Manage Custom Tracks

genome: Human assembly: Dec. 2013 (GRCh38/hg38) [hg38]

Name	Description	Type	Doc	Items	Pos
ATF1_ChIP_10mil	ATF1_ChIP_10mil_bedGraph	bedGraph		8443869	chr1:
ATF1_ChIP_bed	ATF1_ChIP_bed	bed		7252908	chr1:

Managing Custom Tracks

This section provides a brief description of the columns in custom track management table. For more details about managing custom tracks, see the Genome Browser [User's Guide](#).

Sign in or register

Welcome Mike Guertin

Your Account Information

Username: Mike Guertin
[Change password](#)
[Sign out](#)

Session Management

See the [Sessions User's Guide](#) for more information about this tool. See the [Session Gallery](#) for example sessions.
[Click here to reset](#) the browser user interface settings to their defaults.

My Sessions

Show entries

session name (click to load)	created on	assembly	view/edit details	delete this session	share with others?	post in public listing?	send to mail
hg38_ATF1_ChIP_RRM1	2022-01-21	hg38	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_Srf_figure	2021-11-08	mm10	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_Twist2_supplemental	2021-11-08	mm10	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_sp3_figure	2021-11-08	mm10	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_Twist2_figure	2021-11-08	mm10	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
hg38_chr2_H1_more	2021-09-10	hg38	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
hg38_H1_chr2_DNase	2021-09-10	hg38	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
hg38_Ploir	2021-08-02	hg38	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm39_RBC_example	2021-07-27	mm39	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm39_Jurkat_example	2021-07-27	mm39	details	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email

Showing 1 to 10 of 174 entries

Previous 2 3 4 5 ... 18 Next

Save Settings

Save current settings as named session:

name: allow this session to be loaded by others

Save current settings to a local file:

file: file type returned: plain text gzip compressed (ignored if output file is blank)

(leave file blank to get output in browser window)

Save current as:

Enable sharing

Create sharing link in email

Cruising the genome: Displays and Tracks

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

multi-region chr11:5,289,521-5,291,937 2,417 bp. gene, chromosome range, or other position, see examples go examples Search for gene

Current location ← chr11 (p15.4) | 1 p15.4 | p15.1 | 14.3 | 14.1 | 11p13 | 11p12 | p11.2 | 12.1 | q13.4 | 11q14.1 | 14.3 | q21 | q22.1 | 11q22.3 | q23.3 | 24.2 | q25

Scale chr11: 3_ | 5,290,000 | 1 kb | 5,291,500 | hg38 | 5,291,500 |

ATF1_ChIP_10mil

ATF1_ChIP_bed

Reference Assembly Fix Patch Sequence Alignments
Your Sequence from Blat Search
GENCODE V38 (3 items filtered out)

Repeating Elements by RepeatMasker

move start < 2.0 > Click on a feature for details. Click+shift+drag 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 manage custom tracks track hubs configure reverse resize refresh

collapse all 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. expand all

Polish the display for figure quality images

Reverse direction of display

Double click in scale bar to zoom

Track Display:

move start < 2.0 > Click on a feature for details. Click+shift+drag 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 < 2.0 >

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. expand all
Tracks with lots of items will automatically be displayed in more compact modes.

<input type="checkbox"/>	Custom Tracks	<input type="button" value="refresh"/>
<input type="checkbox"/>	Mapping and Sequencing	<input type="button" value="refresh"/>
<input type="checkbox"/>	Genes and Gene Predictions	<input type="button" value="refresh"/>
<input type="checkbox"/>	Phenotype and Literature	<input type="button" value="refresh"/>
<input type="checkbox"/>	COVID-19	<input type="button" value="refresh"/>
<input type="checkbox"/>	Single Cell RNA-seq	<input type="button" value="refresh"/>
<input type="checkbox"/>	mRNA and EST	<input type="button" value="refresh"/>
<input type="checkbox"/>	Expression	<input type="button" value="refresh"/>
<input type="checkbox"/>	Regulation	<input type="button" value="refresh"/>
<input type="checkbox"/>	Comparative Genomics	<input type="button" value="refresh"/>
<input type="checkbox"/>	Variation	<input type="button" value="refresh"/>
<input type="checkbox"/>	Repeats	<input type="button" value="refresh"/>

Available
display
tracks

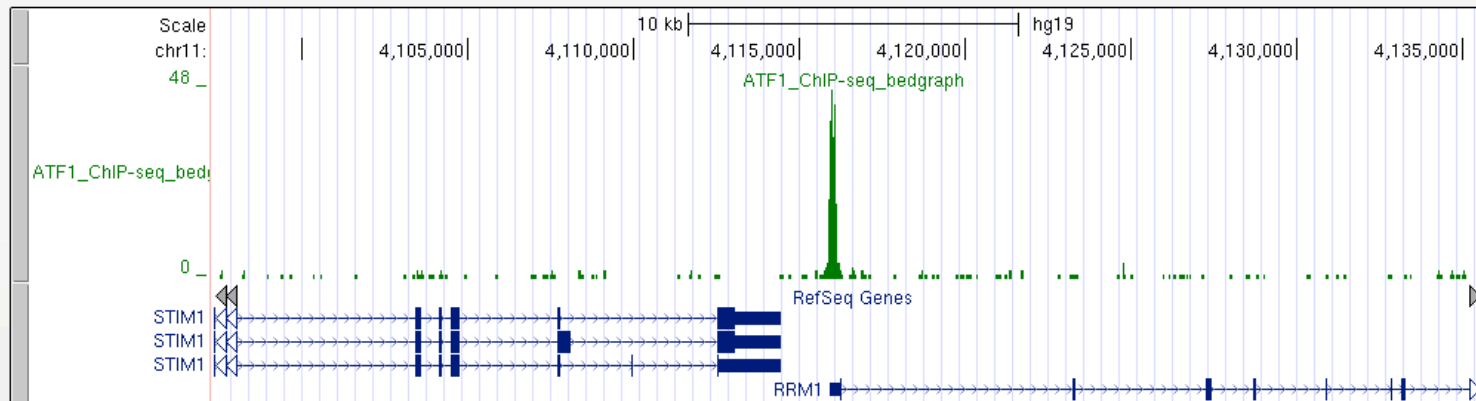
Track Display:

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

chr11:4,097,329-4,135,918 38,590 bp. enter position, gene symbol or search terms go

chr11 (p15.4) 15.4 15.1 p13 11p12 11.2 13.4 11q14.1 14.3q21 22.1 q22.3 q23.3 q25



move start 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. move end

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

Use drop-down controls below and press refresh to alter tracks displayed.

collapse all Tracks with lots of items will automatically be displayed in more compact modes. expand all

Custom Tracks refresh

Mapping and Sequencing refresh

Genes and Gene Predictions refresh

UCSC Genes hide	Ensembl Genes hide	EvoFold hide
Exoniphy hide	GENCODE... hide	IKMC Genes Mapped hide
lincRNAs... hide	LRG Transcripts hide	ORFeome Clones hide
Other RefSeq hide	Pfam in UCSC Gene hide	SIB Genes hide
TransMap... hide	tRNA Genes hide	Yale Pseudo60 hide

UCSC Genes hide

- hide
- dense
- squish
- pack
- full

AceView Genes hide

CCDS hide

Ensembl Genes hide

Geneid Genes hide

Genscan Genes hide

H-Inv 7.0 hide

MGC Genes hide

N-SCAN hide

Old UCSC Genes hide

Retroposed Genes hide

SGP Genes hide

UCSC Alt Events hide

UniProt hide

Vega Genes hide

Track Display:

The screenshot displays a genomic track interface. At the top, there are tracks for **ATF1_ChIP_10mil** and **ATF1_ChIP_bed**, with green vertical bars representing ChIP-seq signal. Below these are tracks for **Reference Assembly Fix Patch Sequence Alignments** and **Your Sequence from Blat Search GENCODE V38 (3 items filtered out)**. The main track shows **Repeating Elements by RepeatMasker** with grey bars. Other tracks include **HBG2**, **CTD-2643|7.5**, **HBE1**, **SINE**, **LINE**, **LTR**, **DNA**, **Simple**, **Low Complexity**, **Satellite**, **RNA**, **Other**, and **Unknown**.

Navigation and control elements include:

- move start** and **move end** buttons with zoom controls (2.0).
- Buttons for **track search**, **default tracks**, **default order**, **hide all**, **manage custom tracks**, **track hubs**, **configure**, **reverse**, **resize**, and **refresh**.
- Instructions: "Click on a feature for details. Click+shift+drag 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." and "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."
- A list of track categories with expand/collapse icons and refresh buttons:
 - Custom Tracks
 - Mapping and Sequencing
 - Genes and Gene Predictions
 - Phenotype and Literature
 - COVID-19
 - Single Cell RNA-seq
 - mRNA and EST
 - Expression
 - Regulation
 - Comparative Genomics
 - Variation
 - Repeats
- Individual track controls for **RepeatMasker**, **Interrupted Rpts**, **Microsatellite**, **RepeatMasker Viz.**, **Segmental Dups**, **Self Chain**, **Simple Repeats**, and **WM + SDust**, each with a dropdown menu and a refresh button.

A red arrow points from the left side of the interface towards the **RepeatMasker** track control.

Configure Display

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

chr11:5,289,973-5,291,937 1,965 bp. gene, chromosome range, or other position, see examples

chr11 (p15.4) p15.4 p15.1 14.3 14.1 11p15 11p12 p11.2 12.1 p13.4 11q14.1 14.3 q21 q22.1 11q22.3 q23.3 24.2 q25

Scale chr11: 1 | 500 bases | hg38 | 5,290,500 | 5,291,000 | 5,291,500

ATF1_ChIP_10mil

ATF1_ChIP_bed

Reference Assembly Fix Patch Sequence Alignments
Your Sequence from Blat Search
GENCODE V38 (3 items filtered out)

HBG2
CTD-26437.5
HBE1
HBE1

Repeating Elements by RepeatMasker

SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
RNA
Other
Unknown

move start < 2.0 > move end

Click on a feature for details. Click+shift+drag 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.

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

collapse all expand all

Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in compact modes.

- Custom Tracks refresh
- Mapping and Sequencing refresh
- Genes and Gene Predictions refresh
- Phenotype and Literature refresh
- COVID-19 refresh
- Single Cell RNA-seq refresh
- mRNA and EST refresh
- Expression refresh
- Regulation refresh
- Comparative Genomics refresh
- Variation refresh
- Repeats refresh

RepeatMasker full hide
Interrupted Rpts hide
Microsatellite hide
RepeatMasker Viz. hide
Segmental Dups hide
Self Chain hide
Simple Repeats hide
WM + SDust hide

refresh

Configure Display Options

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Configure Image

submit

image width: 1000 pixels

label area width: 20 characters

text size: 12

font: Helvetica

style: Normal

- Display chromosome ideogram above main graphic
- Show light blue vertical guidelines, or light red vertical window separators in multi-region view
- Display labels to the left of items in tracks
- Display description above each track
- Show track controls under main graphic
- Next/previous item navigation
- Next/previous exon navigation
- Show exon numbers
- Enable highlight with drag-and-select (if unchecked, drag-and-select always zooms to selection)

Configure Tracks on UCSC Genome Browser: Human Dec. 2013 (GRCh38/hg38)

Tracks: track search hide all show all default Groups: collapse all expand all

Control track and group visibility more selectively below.

Custom Tracks		hide all	show all	default	submit
ATF1_ChIP_10mil	full	ATF1_ChIP_10mil_bedGraph			
ATF1_ChIP_bed	hide	ATF1_ChIP_bed			

- Mapping and Sequencing hide all show all default submit
- Genes and Gene Predictions hide all show all default submit
- Phenotype and Literature hide all show all default submit
- COVID-19 hide all show all default submit
- Single Cell RNA-seq hide all show all default submit
- mRNA and EST hide all show all default submit
- Expression hide all show all default submit
- Regulation hide all show all default submit
- Comparative Genomics hide all show all default submit
- Variation hide all show all default submit
- Repeats hide all show all default submit

Configure Display: Clarity

Configure Image

submit

image width: 600 pixels

label area width: 20 characters

text size: 14

font: Helvetica

style: Normal

- Display chromosome ideogram above main graphic
- Show light blue vertical guidelines, or light red vertical window separators in multi-region view
- Display labels to the left of items in tracks
- Display description above each track
- Show track controls under main graphic
- Next/previous item navigation
- Next/previous exon navigation
- Show exon numbers
- Enable highlight with drag-and-select (if unchecked, drag-and-select always zooms to selection)

Configure Tracks on UCSC Genome Browser: Human Dec. 2013 (GRCh38/hg38)

Tracks: track search hide all show all default Groups: collapse all expand all

Control track and group visibility more selectively below.

Custom Tracks hide all show all default submit

ATF1_ChIP_10mil	full	ATF1_ChIP_10mil_bedGraph
ATF1_ChIP_bed	hide	ATF1_ChIP_bed



UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

multi-region chr11:4,090,646-4,097,866 7,221 bp. gene, chromosome range, or other position, see examples go examples

chr11 (p15.4) hg38

ENST00000526596.2, strand +, Exon 13 of 13

chr11: 60 - 4,095,000

ATF1_ChIP_10mil

STIM1

RRM1

SINE

LINE

LTR

DNA

Simple

Low Complexity

Satellite

RNA

Other

Unknown

Click on a feature for details.
Click+shift+drag 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 start < 2.0 > move end < 2.0 >

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

Configure Display: track order and options

chr11 (p15.4) | 1312 | hg38

Scale 2 kb | 4,095,000

chr11:
STIM1
STIM1
STIM1
STIM1
STIM1
RRM1
60 -
ATF1_ChIP_10mil
0 -
SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
RNA
Other
Unknown

Drag tab to reorder

Click to modify Settings (NEXT SLIDE)

Click on a feature for details.
Click+shift+drag 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 start < 2.0 > move end < 2.0 >

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

collapse all expand all

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.

Custom Tracks refresh

ATF1_ChIP_10mil full
ATF1_ChIP_bed hide

Configure Display: track order and options

ATF1_ChIP_10mil Track Settings

ATF1_ChIP_10mil_bedGraph ([^All Custom Tracks](#))

Display mode:

Type of graph:

Track height: pixels (range: 11 to 128)

Data view scaling: Always include zero:

Vertical viewing range: min: max: (range: 0 to 1000)

Transform function: Transform data points by:

Windowing function: Smoothing window: pixels

Negate values:

Draw y indicator lines: at y = 0.0: at y =

[Graph configuration help](#)

[View table schema](#)

Data last updated at UCSC: 2022-02-01

Ex. Lower height to create space with multiple tracks

Ex. Log transform the data

Ex. Show mean, max, SD

These are all track line settings that can be set when you upload data.
You can upload without any settings and then modify them here

Track hubs: view public data

The image shows a screenshot of the UCSC Genome Browser interface. At the top, there is a navigation bar with links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. Below this, the main content area displays a track hub visualization for chromosome 11 (hg38). The track is titled "chr11 (p15.4)" and shows a scale from 4,094,000 to 4,096,000. The visualization consists of a vertical column of red and blue squares, representing data points for different tracks. A red arrow points to the "Track Hubs" option in the "My Data" dropdown menu. The dropdown menu also includes "Custom Tracks", "My Sessions", "Track Collection Builder", and "Public Sessions".

UCSC Genome Browser Custom Tracks My Sessions Track Hubs Track Collection Builder Public Sessions

chr11 (p15.4) 4,094,000 4,094,500 4,095,000 4,095,500 4,096,000

Scale chr11: 1 Kb hg38

Track hubs: view public data

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Track Data Hubs

Public Hubs My Hubs Hub Development

Track data hubs are collections of external tracks that can be added to the UCSC Genome Browser. Click **Connect** to attach a hub and red show up in the hub's own blue bar track group under the browser graphic. For more information, including [where to host your track hub](#), s

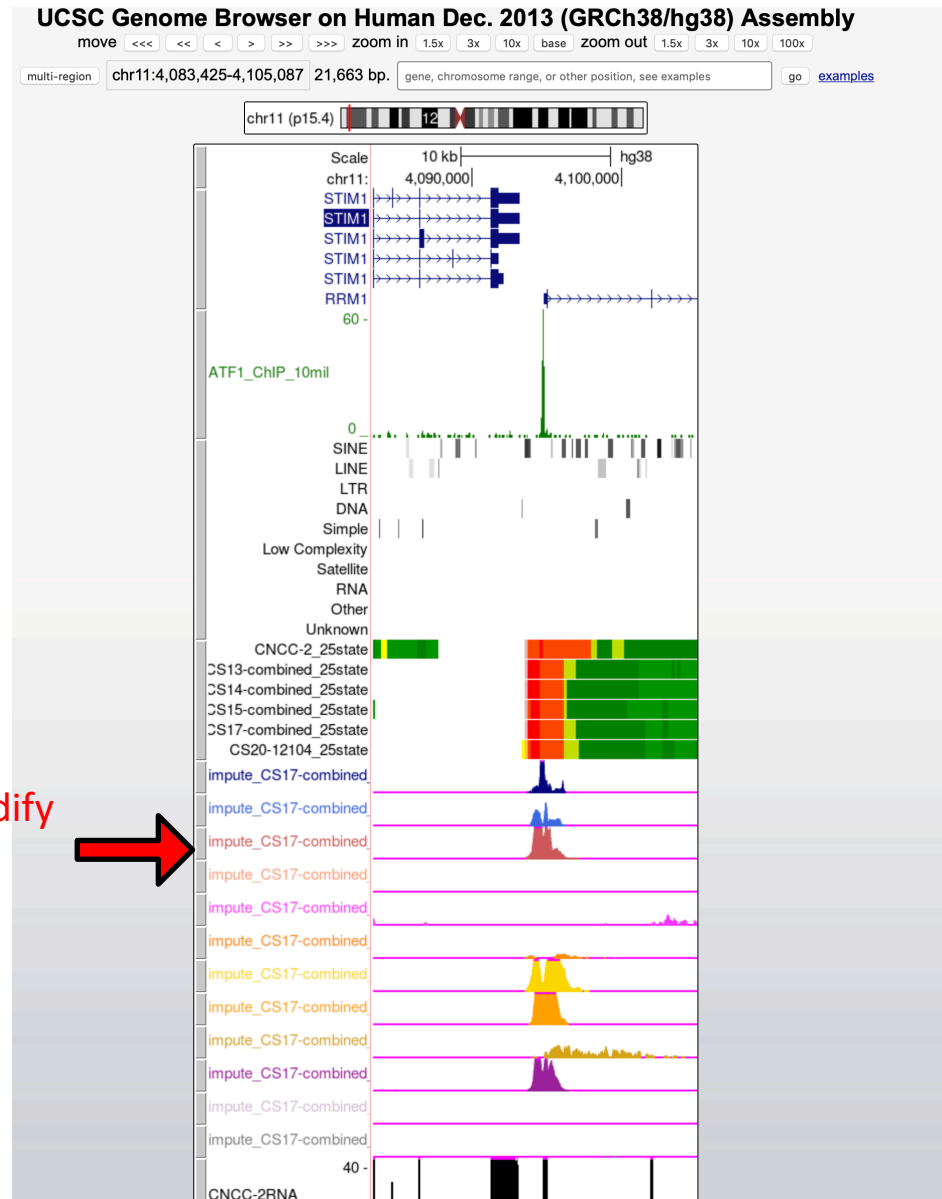
Track Hubs are created and maintained by external sources. UCSC is not responsible for their content.

The list below can be filtered on words in the hub description pages or by assemblies.

Search terms: Assembly:

Display	Hub Name	Description	Assemblies <small>Click to connect and browse directly</small>
<input type="button" value="Connect"/>	ALFA Hub	NCBI's Allele Frequency Aggregator (ALFA) allele frequency for variants in dbGaP studies.	hg19 , hg38
<input type="button" value="Connect"/>	Bird Alignment (363 species)	Bird Alignment (363 species)	[+] Gallus_gallus , Acanthisitta_chloris...
<input type="button" value="Connect"/>	Bird assemblies	Bird genome assemblies	[+] GCF_000699105.1 , GCF_000698965.1...
<input type="button" value="Connect"/>	Blueprint Hub	Blueprint Epigenomics Data Hub	hg38
<input type="button" value="Connect"/>	BrainEpigenomeHub	DNA methylation, chromatin accessibility, and gene expression data from NeuN flow-sorted human brain samples	hg19
<input type="button" value="Connect"/>	Breast Cancer lncRNA	Breast Cancer lncRNA PMID 26236012	hg19
<input type="button" value="Connect"/>	Broad Improved Canine Annotation v1	Broad Institute CanFam3 Improved Annotation Data v1	canFam3
<input type="button" value="Connect"/>	C_elegans_isolates	C. elegans wild isolate assembly hub	[+] CB4856Princeton_JR-contig...
<input type="button" value="Connect"/>	CADD	CADD Track for v1.3 to v1.6	hg19 , hg38
<input type="button" value="Connect"/>	Cancer Genomics Tracks	TCGA and ICGC Cancer Mutations, TCGA Expression, Immune Epitopes Database (IEDB), Cancer Immunity Peptides Database, Dienstmann Variant/Cancer database, CIVIC, MyCancerGenome.org, OncoKB	hg19
<input type="button" value="Connect"/>	CEMT (CEEHRC)	Epigenomic Data tracks from BCGSC, Vancouver, B.C.	hg38 , hg19
<input type="button" value="Connect"/>	CESAR Gene Mappings	Human Exons mapped by CESAR	[+] bosTau7 , ailMel1 , allMis1 , anoCar2 , calJac3...
<input type="button" value="Connect"/>	ChIP-seq data track HUBs from MSC cells from GSE79815	ChIP-seq data from the publication "Epigenetic plasticity drives adipogenic and osteogenic differentiation of marrow-derived mesenchymal stem cells" (10.1074/jbc.M116.736538) from GEO record GSE79815	mm9
<input type="button" value="Connect"/>	Coloc segments	Colocalized segments of human genome for Roadmap cell types	hg19
<input type="button" value="Connect"/>	Cotney Lab Human Craniofacial Epigenomics	Human Embryonic Craniofacial Tissue Epigenomic Data and Chromatin State Segmentations from the Cotney Lab at UConn Health	hg19 , mm9 , hg38
<input type="button" value="Connect"/>	Cotney Lab Human Embryonic Heart Hub	Human Embryonic Heart Tissue Epigenomic and Transcriptomic Data from the Cotney Lab at UConn Health	hg19 , hg38

Track hubs: view public data



ENCODE data is available from several organisms



Encyclopedia of DNA Elements at UCSC 2003 - 2012

Human Data at UCSC

Downloads

Experiment Matrix

Search

Genome Browser
(hg19)

Experiment List

Cell Types

Mouse Data at UCSC

Downloads

Experiment Matrix

Search

Genome Browser
(mm9)

Experiment List

Cell Types

Metadata Terms

Registered Variables

Antibodies

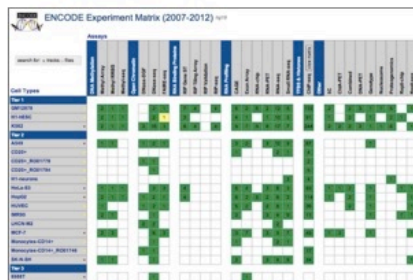
About

The [Encyclopedia of DNA Elements \(ENCODE\) Consortium](#) is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive parts list of functional elements in the human genome, including elements that act at the protein and RNA levels, and regulatory elements that control cells and circumstances in which a gene is active.

UCSC coordinated data for the ENCODE Consortium from its inception in 2003 (Pilot phase) to the end of the first 5 year phase of whole-genome data production in 2012. All data produced by ENCODE investigators and the results of ENCODE analysis projects from this period are hosted in the UCSC Genome browser and database. Explore ENCODE data using the image links below or via the left menu bar. **All ENCODE data at UCSC are freely available for download and analysis.**

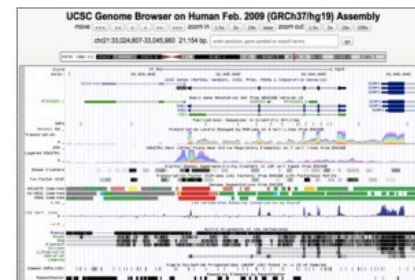
ENCODE results from 2013 and later are available from the ENCODE Project Portal, [encodeproject.org](#). The ENCODE Project Portal also hosts ENCODE data from the first production phase, additional ENCODE access tools, and ENCODE project pages including up-to-date information about data releases, publications, and upcoming tutorials.

Explore ENCODE data at UCSC



Experiment matrix

View ENCODE data in the UCSC Genome Browser



Preloaded browser tracks

ENCODE data tracks

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

[track search](#) [default tracks](#) [default order](#) [hide all](#) [manage custom tracks](#) [track hubs](#) [configure](#) [reverse](#) [resize](#) [refresh](#)

[collapse all](#)

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.

[expand all](#)

Custom Tracks [refresh](#)

[ATF1_ChIP_10mil](#) [ATF1_ChIP_bed](#)
[full](#) [hide](#)

+ **Cotney Lab Human Craniofacial Epigenomics** [disconnect](#) [refresh](#)

+ **Mapping and Sequencing** [refresh](#)

+ **Genes and Gene Predictions** [refresh](#)

+ **Phenotype and Literature** [refresh](#)

+ **COVID-19** [refresh](#)

+ **Single Cell RNA-seq** [refresh](#)

+ **mRNA and EST** [refresh](#)

+ **Expression** [refresh](#)

- **Regulation** [refresh](#)

[ENCODE cCREs](#) [hide](#) [ENCODE Regulation](#) [hide](#) [CpG Islands](#) [hide](#) [GeneHancer](#) [hide](#) [GTEx cis-eQTLs](#) [hide](#) [Hi-C and Micro-C](#) [hide](#)

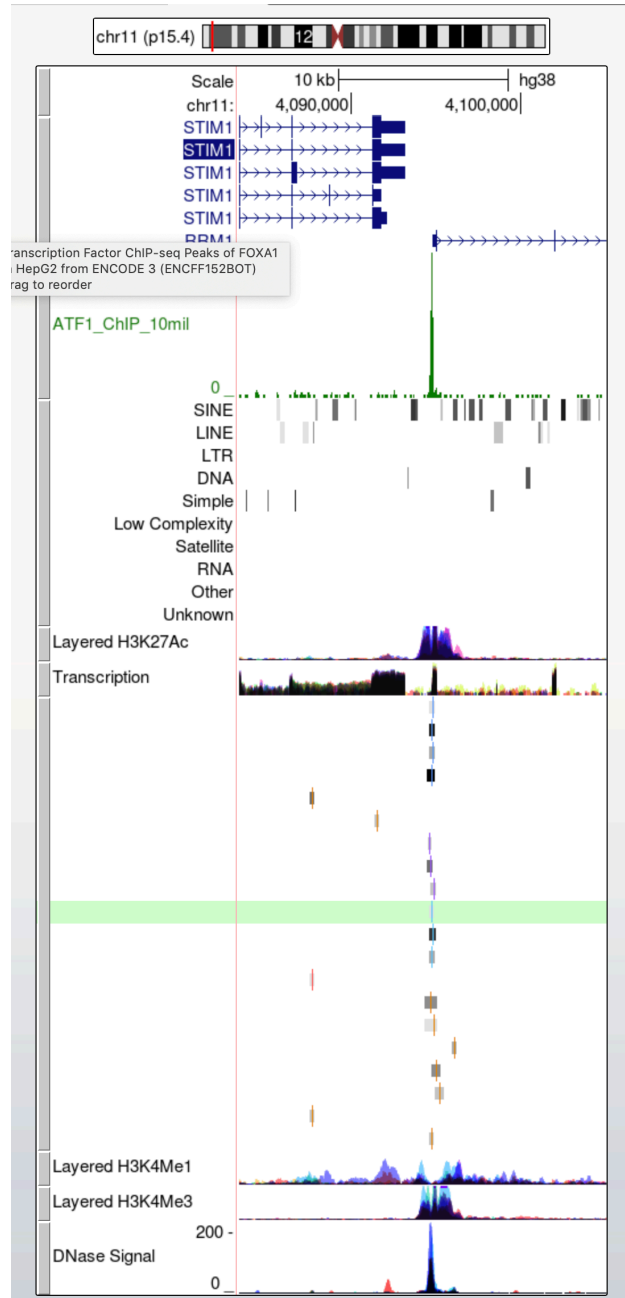
New [JASPAR Transcription Factors](#) [hide](#) [ORegAnno](#) [hide](#) [RefSeq Func Elems](#) [hide](#)

+ **Comparative Genomics** [refresh](#)

+ **Variation** [refresh](#)

+ **Repeats** [refresh](#)

ENCODE data browser



ENCODE experiment matrix

search for: tracks files

Assays

Cell Types

Cell Type	DNA Methylation	Methyl Array	Methyl RRBS	Open Chromatin	DNase-DGF	DNase-seq	FAIRE-seq	RNA Binding Proteins	RIP Gene ST	RIP Tiling Array	RIP Validation	RIP-seq	RNA Profiling	CAGE	Exon Array	RNA-chip	RNA-PET	RNA-seq	Small RNA-seq	TFBS & Histones	CHIP-seq	Other	5C	ChIA-PET	Combined	DNA-PET	Genotype	Nucleosome	Proteogenomics	Repli-chip	Repli-seq						
Tier 1																																					
GM12878	1	1		2	1		7	4		4		6	2	6	2	12	5		133		2		2	3	1	1	5					1					
H1-hESC	1	1		2	1		3					4	1		1	10	3		91		1		2		1		2	1									
K562	1	1		3	16	3		6	4		4		9	7	9	6	17	7		224		2	2	2	3	1	1	6					1				
Tier 2																																					
A549	1	1		1	2	1							3	2		3	10	9		87						1											
CD20+													1			2	1		4																		
CD20+_RO01778				1	1														2																		
CD20+_RO01794					1														5																		
H1-neurons																	3		4										1								
HeLa-S3	1	1		3	3		4					6	4		3	8	3		93		1	1	2		1			1	1								
HepG2	1	1		1	2	1		4					6	2	5	2	8	3		114		1		2		1								1			
HUVEC	1			1	2	1							5	2		2	8	1		36			2		1									1			
IMR90	1	1		1									3			3	4	9		11					1				1	1							
LHCN-M2				2	2												2																				
MCF-7	1	3		8	3								3	7		3	5	7		49		1	3			1									1		
Monocytes-CD14+				1									1			2	1																				
Monocytes-CD14+_RO01746				1	1														17																		
SK-N-SH	1	1		1									3			3	4	9		34																1	
Tier 3																																					

Can view in browser or download raw and processed data

Resources / links

Browser:

- <http://www.sciencedirect.com/science/article/pii/S0888754308000451>
- <http://genome.ucsc.edu/training/vids/>
- <http://www.nature.com/scitable/ebooks/guide-to-the-ucsc-genome-browser-16569863>

ENCODE:

- <http://genome.ucsc.edu/ENCODE/index.html>
- <http://www.genome.gov/encode/>