

MEDS5420 Lecture 13

Using the UCSC Genome Browser

March 5, 2025

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 creators of UCSC genome browser: Jim Kent and David Haussler



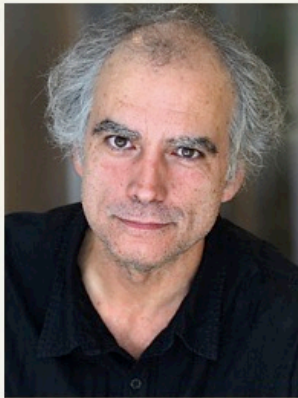
ABOUT US

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 manages the data of the human genome sequencing centers worldwide and the informatics associated with the data. The Bioinformatics Group participates in the project to produce, assemble, and annotate the human genome.

UCSC Genome Browser

The UCSC Genome Browser provides a comprehensive view of metazoan genome sequences. It offers a wide annotation in a web-based

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[Home](#) » [Speakers](#) » David Haussler



David Haussler

University of California, Santa Cruz



David Haussler is Scientific Director of the UCSC Genome Research Center 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, the International Human Genome Sequencing Consortium published the first publicly available draft of the human genome in 2001. Since then, there have been several large-scale projects, including the [Genome 10K Project](#), the [1000 Genomes Project](#), the [ENCODE Project](#), the [Human Cell Atlas](#), the [Genomic Data Commons](#), the [Genome Research 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



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



Our tools

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[More tools...](#)

Available genomes and info

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Genome Browser Gateway

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

Browse/Select Species

POPULAR SPECIES

 Human  Mouse  Rat  Zebrafish  Fruitfly  Worm  Yeast

Find Position

Human Assembly
Dec. 2013 (GRCh38/hg38) 

Position/Search Term

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

GO 

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)

Can't find a genome assembly?

REPRESENTED SPECIES



- Human
- Chimp
- Bonobo
- Gorilla
- Orangutan
- Gibbon
- Green monkey
- Crab-eating macaque
- Rhesus
- Baboon (anubis)
- Baboon (hamadryas)
- Proboscis monkey
- Golden snub-nosed monkey
- Marmoset
- Squirrel monkey
- Tarsier

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

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Genome Browser Gateway

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Browse/Select Species

POPULAR SPECIES

 Human  Mouse  Rat  Zebrafish  Fruitfly  Worm  Yeast

Find Position

Human Assembly
Dec. 2013 (GRCh38/hg38) 

Position/Search Term

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

GO 

Human Genome Browser - hg38 assembly

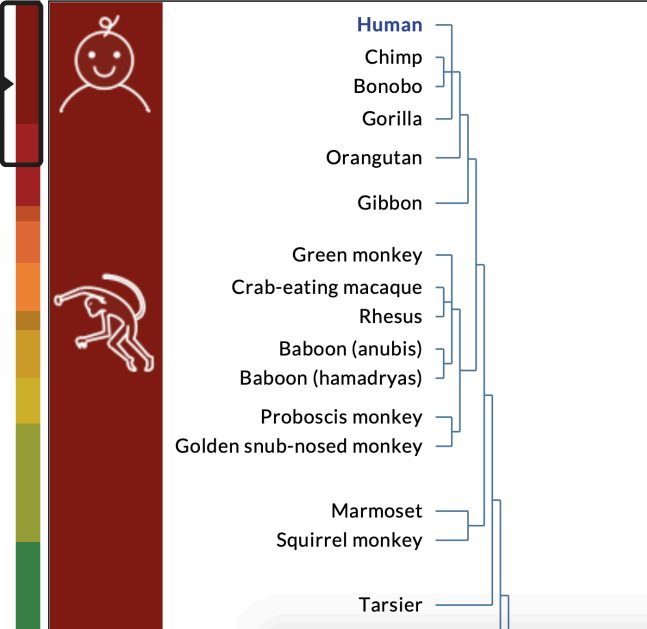
[view sequences](#)

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p13 (GCA_000001405.28)
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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

REPRESENTED SPECIES



Human
Chimp
Bonobo
Gorilla
Orangutan
Gibbon
Green monkey
Crab-eating macaque
Rhesus
Baboon (anubis)
Baboon (hamadryas)
Proboscis monkey
Golden snub-nosed monkey
Marmoset
Squirrel monkey
Tarsier



Homo sapiens
(Graphic courtesy of CBSE)

Browser view

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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. 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

Scale chr17: 8,170,000| 8,175,000| 8,180,000| 8,185,000| 8,190,000| 8,195,000| 8,200,000| hg38

Reference Assembly Fix Patch Sequence Alignments
GENCODE V38 (4 items filtered out)

Repeating Elements by RepeatMasker

move start < 2.0 > move end < 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.

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

Base Position

dense

Clone Ends

hide

GRC Incident

hide

RefSeq Acc

hide

P13 Updated Fix

Patches

pack

Exome Probesets

hide

Hg19 Diff

hide

Restr Enzymes

hide

P13 Updated Alt

Haplotypes

hide

FISH Clones

hide

INSDC

hide

Scaffolds

hide

Assembly

hide

Gap

hide

LiftOver & ReMap

hide

Short Match

hide

Centromeres

hide

GC Percent

hide

LRG Regions

hide

STS Markers

hide

Chromosome Band

hide

GRC Contigs

hide

Mappability

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

The screenshot displays the UCSC Genome Browser interface. At the top, a navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. A red arrow points to the 'UCSC' logo. Below the navigation bar, a search bar is visible with the text 'human Dec. 2013 (GRCh38/hg38) Assembly'. The main track view shows chromosome 17 (p13.1 to p13.1) with various tracks including TMEM107, SNORD118, RP11-599B13.7, MIR4521, BORCS6, and Repeating Elements by RepeatMasker. A detailed track view is shown below the main track, with a 'Mapping and Sequencing' section containing tracks for Base Position, Clone Ends, GRC Incident, RefSeq Acc, P13 Updated Fix, Patches, Exome Probesets, Hg19 Diff, Restr Enzymes, P13 Updated Alt, Haplotypes, FISH Clones, INSDC, Scaffolds, Assembly, Gap, LiftOver & ReMap, Short Match, Centromeres, GC Percent, LRG Regions, STS Markers, Chromosome Band, GRC Contigs, Mappability, and Genes and Gene Predictions. The 'Genes and Gene Predictions' section includes tracks for GENCODE V38, NCBI RefSeq, All GENCODE, CCDS, CRISPR Targets, and IKMC Genes. The interface also includes a 'move start' and 'move end' control at the bottom left and right, and a 'refresh' button at the bottom right.

UCSC Genome Browser

human Dec. 2013 (GRCh38/hg38) Assembly

chr17 (p13.1) p13.3 p13.2 p13.1 p13.1 p13.1

Scale chr17: 8,170,000 | 8,185,000 | 8,190,000 | 8,195,000 | 8,200,000

TMEM107
TMEM107
SNORD118
TMEM107
TMEM107
TMEM107
TMEM107
RP11-599B13.7
MIR4521
BORCS6
RP11-599B13.10

SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
RNA
Other
Unknown

Repeating Elements by RepeatMasker

hg38

Reference Assembly Fix Patch Sequence Alignments
GENCODE V38 (4 items filtered out)

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



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 Novocraft 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

Name	Last modified	Size	Description
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	2019-01-17 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 17:11	-	
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

UCSC 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 you use the **Table Browser** tool.

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**
- Variant 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. **server credits** page. Please acknowledge the contributor(s) of the data you use.

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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: Original Assembly: New Genome: New Assembly:

Minimum ratio of bases that must remap:

BED 4 to BED 6 Options

Allow multiple output regions: ☐

Minimum hit size in query:

Minimum chain size in target:

BED 12 Options

Min ratio of alignment blocks or exons that must map:

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

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

no file selected

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



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us



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

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

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

group: Genes and Gene Predictions track: GENCODE V38

table: knownGene describe table schema

Track type

Sub-table

Define region of interest

region: genome position chr17:8,164,338-8,204,114 lookup define regions

identifiers (names/accessions): paste list upload list

Choose fields or columns from table

Optional: Subset, combine, compare with another track

filter: create

intersection: create

Retrieve and display data

output format: BED - browser extensible data Send output to Galaxy GREAT

output filename: GENCODE_V38_intersect_XXX.bed (leave blank to keep output in browser)

file type returned: plain text gzip compressed

Name output file

Downloading DNA sequence from browser

UCSC Genome Browser on Human Dec

move <<< << < > >> >>> zoom

multi-region chr17:8,164,338-8,204,114 39,777 bp. gene, chrom

chr17 (p13.1) p13.3 p13.2 p13.1 17p12 17p11.2 17q11.2 17q12

Scale chr17: 8,170,000 8,175,000 10 kb 8,180,000

Reference Assembly GENCODE

TMEM107
TMEM107
SNORD118
TMEM107
TMEM107
TMEM107
RP11-599B13.7
MIR4521
BORCS6
RP11-599B13.10

SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
RNA
Other
Unknown

Repeating Elements by RepeatMasker

g38) Assembly 3x 10x 100x

Examples go examples

23.2 24.2 q24.3 q25.1 17q25.3

38 8,195,000 8,200,000

move start < 2.0 > move end < 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.

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

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
GGCCTTGATCTCTAAGACAAACAGGAACAGCTTCCTCCCTCCCCACCC
TGGCTTCCCAGGGCTCCGGGTGTGAGATCCTCCCCACTGCAGTGCCCC
ACCCGCTCCCCACAGAAGCCCGAGAGTGGCTCTGTCAACAGAGGTGTCA
TTTCCCAGCTGTCTGTGGGAGGTGAGTGAGCAGGGAATGTGTGTGCTGGG
TGTGGGAACCTCAGCCCAATCTAAGAGAAGATACTTTGGCTTCCTCCCC
TCAGAGGAGCAGCCGCTCCCTGGTCTTGTGCACTGACAGTCCCGGGTG
GCTCAGCCTATGTGATGAGAAAGAAAGAGCAGCTTCCACGGGGGTCTCA
GATCATGCTGTGAGATGCTGGCTCCTGCTTTTGGTCTTCAATGATTCC
TCTTTCTAGTCAGAGAACAAAGATGCCAAATTCAGCCTTTAAGTTCAA
AACCTCAGTGTCTGTCAAGGTATAAATAAGACATGGAGGATTGGAAGAG
GCAGGCACAGGAAGCCCTTCCGCCCCAGTTGGACACCCCTGCACAACTG
AGGGGAGCCTAGTGCAGAGCCAGACAAGACATTTGATGCTGGTTTGGGG
TGATGTGGAAGGGACAGAGCCCCAGATACACGGTCAAGGCCAGGGGTCGT
GCTATTGCTATTGGATCGTGGGGACGGCAGCAGCAGAGTAGAAATGAGGG
CATGTGTGACCCACGGAGATGAAGGGCCCAGGAGGATTCACTCAGAAAG
AGGACTCTCATCCAGCAGCCCTTCCACCCCACCCACCTAGGCTGTGG
CTCAGAGGAACCTCCCAAATTTAGATCAATGGTGGAGGTGGGAGAAGGAG
TGGGATGACGGAGTTCACCTGGAAGTCACTGAGAGAATGTTTTCTGCAGG
CAGGTAGAATGGAGACCCAAATAGAGGTAAGTTGAACAATAGAAAAATAA
TGTAATTTGCATAACTCAGATTTGGCTTCTACATGTACTGGCTTCGGGAAT
TGGCCAAATGATTTTCTAGGGCACACCCCCAAGACTCATTCAAAGGATGTA
GGACTCAAGGTGATGGTGATGTAGGCAACAGAGACCACACTTTCTTTTTC
TTTTTTTTTTCTTTTTTTTCTTTTTTGAGACAGAGTCTCTGTCTGTCAC
CCAGGCTGGAGTGCAATGGCGCATCTCTGCTCACTGCAAACTCCGCCTC
CCAGGTTACGCCATTCTCCTCCCTCAGCCTCCCGAGTAGCTGGGACTAC
AGGCGCCACCACCCGGCCCGGCTAATTTTTTGTATTTTAGTAGAGACA
GGGTTTACCCTGTTAGCCAGGTTGGTCTTGATCTCTGACCCCGTGATC
```

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

F

y align sequences to the genome

Genome 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

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

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
GGCCTTGATCTCTAAGACAAACAGGAACCACTTCTCCCTCCCCACCC
TGGCTTCCCAGGGCCTCCGGGTGTGAGATCCTCCCCACTGCAGTGCCCC
ACCCGCTCCCCACAGAAGCCCGGAGAGTGGCTCTGTCACCAGAGGTGTCA
TTTCCCAGCTGTCTGTGGGAGGTGAGTGAGCAGGGAATGTGTGTGCTGGG
TGTGGGAAGTCAAGCCCAATCTAAGAGAAGATACTTGGCTTCTCCCCC
TCAGAGGAGCAGCCGCGTCCCTGGTCTTGTGCACTGACAGTCCCGGGTG
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 [chr17:8164338-8164737](#) 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	+	7188760	7188781	22
browser details	hg38_dna	20	32	51	400	100.0%	chr1	+			
browser details	hg38_dna	20	196	215	400	100.0%	chr1	+			
browser details	hg38_dna	20	32	51	400	100.0%	chr1	+			

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 blue mark the boundaries of gaps in either sequence (often splice sites).

cDNA hg38_dna

```

GCTCTGATC TCTAAGACA ACAGAGACA GCTCTCTGC TCCCTCAC 50
TGCTTCCDA GGGCTCTCG GTGTGATC CTCCCTCAT GCAGTCC 100
ACCCCTCCC CACAGAGAC CGAGAGTGC CTCCTGACC AGAGGTGCA 150
TTTCCGACT CTCTGTGGA GTGTGATG CAGAGATCT GTTCTGTGG 200
TTGTGGAAT CAGCCCAATC TAAGAGAAGA TACTCTTGC TTCTTCCCC 250
TCAGAGAGC AGCCCTCTC CTGTCTCTG TGACTGTACA GTCCCGGTG 300
GCTCAGCTA TGTATGAGA AAGAAAGAG CAGCTTCCG GGGGTCTCA 350
GATCATGCT TGAGATGCT GCTCTCTCT TTTGTCTTC AAATGATTC 400

```

Genomic chr17 :

```

caaaagcagc ctaaagggtg caggaggaat tttaggcag gccctttgc 8164287
cctggggggg ggggtgctac tacatccctg gaagtgagag ggaagtgat 8164337
GCTCTGATC TCTAAGACA ACAGAGACA GCTCTCTGC TCCCTCAC 8164387
TGCTTCCDA GGGCTCTCG GTGTGATC CTCCCTCAT GCAGTCC 8164437
ACCCCTCCC CACAGAGAC CGAGAGTGC CTCCTGACC AGAGGTGCA 8164487
TTTCCGACT CTCTGTGGA GTGTGATG CAGAGATCT GTTCTGTGG 8164537
TTGTGGAAT CAGCCCAATC TAAGAGAAGA TACTCTTGC TTCTTCCCC 8164587
TCAGAGAGC AGCCCTCTC CTGTCTCTG TGACTGTACA GTCCCGGTG 8164637
GCTCAGCTA TGTATGAGA AAGAAAGAG CAGCTTCCG GGGGTCTCA 8164687
GATCATGCT TGAGATGCT GCTCTCTCT TTTGTCTTC AAATGATTC 8164737
tctttcagt caggagaa agatgcaaa ttcctggtt ttaggtcaa 8164787
aacctcagt gctctcagg gtataataa gacatgag agtggaag 8164837

```

Slide by Slide Alignment

Help

Missing a match?

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

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. go [examples](#)

chr17 (p13.1) p13.3 p13.2 p13.1 17p12 17p11.2 17p11.1 17p11 17p10 17p9.2 17p9.1 17p9 17p8.2 17p8.1 17p8 17p7.2 17p7.1 17p7 17p6.2 17p6.1 17p6 17p5.3

Scale chr17: 100 bases | hg38 8,164,500 | 8,164,550 | 8,164,600 | 8,164,650 | 8,164,700

hg38_dna

GENCODE V38
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 add custom tracks track hubs configure 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

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

Custom tracks

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

Display current tracks in their default order

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

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

100 bases hg38

Reference Assembly Fix Patch Sequence Alignments
Your Sequence from Blat Search

GENCODE V38
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 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

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 at [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

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:	☐
ATF1_ChIP_bed	ATF1_ChIP_bed	bed		7252908	chr1:	☐

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

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
ATF1_ChIP_10mil	ATF1_ChIP_10mil_bedGraph	bedGraph		8443869	chr11:
ATF1_ChIP_bed	ATF1_ChIP_bed	bed		7252908	chr1:

[Custom Tracks](#)
[My Sessions](#)
[Track Hubs](#)
[Track Collection Builder](#)
[Public Sessions](#)

tracks

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

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

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	☒	☐	Email
mm10_Srf_figure	2021-11-08	mm10	details	delete	☒	☐	Email
mm10_Twist2_supplemental	2021-11-08	mm10	details	delete	☒	☐	Email
mm10_sp3_figure	2021-11-08	mm10	details	delete	☒	☐	Email
mm10_Twist2_figure	2021-11-08	mm10	details	delete	☒	☐	Email
hg38_chr2_H1_more	2021-09-10	hg38	details	delete	☒	☐	Email
hg38_H1_chr2_DNase	2021-09-10	hg38	details	delete	☒	☐	Email
hg38_Plotr	2021-08-02	hg38	details	delete	☒	☐	Email
mm39_RBC_example	2021-07-27	mm39	details	delete	☒	☐	Email
mm39_Jurkat_example	2021-07-27	mm39	details	delete	☒	☐	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)

Enable sharing

Create sharing link in email

Save current
as:

Cruising the genome: Displays and Tracks

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

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_ 1 kb 5,290,000 5,290,500 5,291,000 5,291,500 hg38

ATF1_ChIP_10mil

ATF1_ChIP_bed

Drag to move

Highlight to zoom

ATF1_ChIP_bed

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

Repeating Elements by RepeatMasker

HBG2
CTD-264317.5
HBE1
HBE1

SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
RNA
Other
Unknown

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.

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

Double click in scale bar to zoom

Reverse direction of display

Polish the display for figure quality images

Reverse direction
of display

Track Display:

move start < 2.0 > move < 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.

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.

+	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

refresh

Available
display
tracks

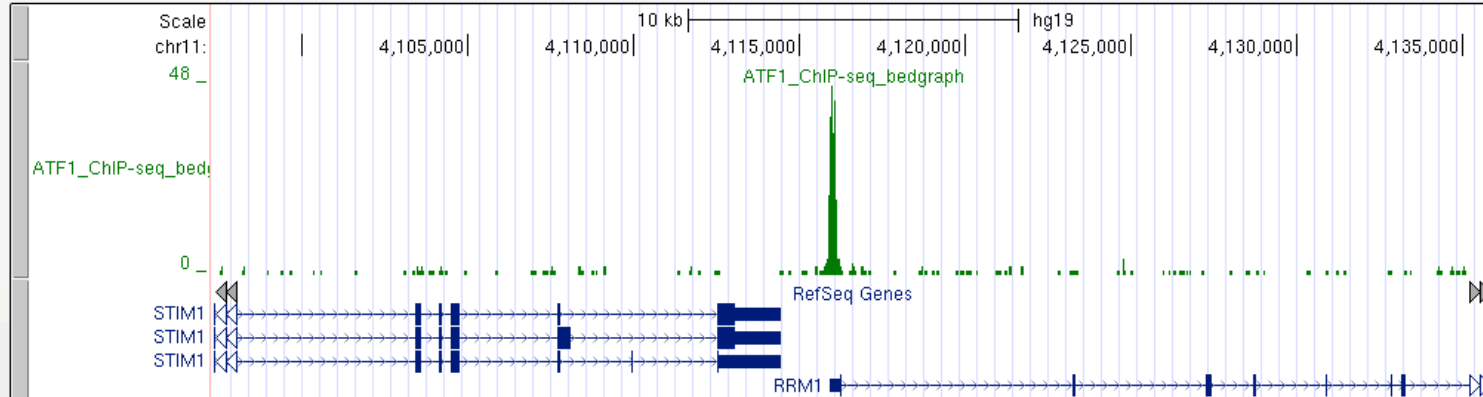
Track Display:

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 14.3 q21 22.1 q22.3 q23.3 q25



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.

move end

< 2.0 >

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

collapse all

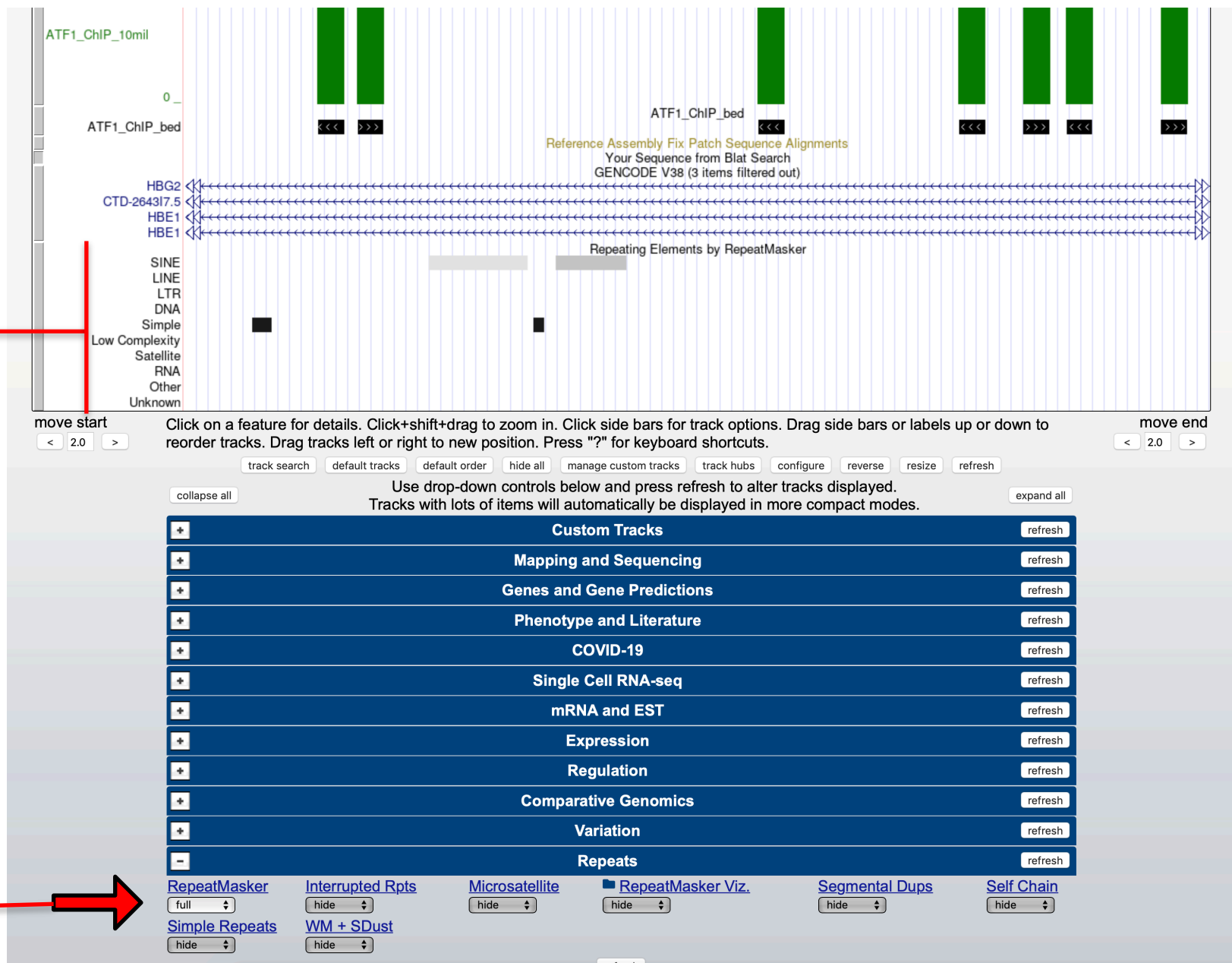
Use drop-down controls below and press refresh to alter tracks displayed.

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

expand all

Custom Tracks					
refresh					
Mapping and Sequencing					
refresh					
Genes and Gene Predictions					
refresh					
UCSC Genes	AceView Genes	CCDS	Ensembl Genes	EvoFold	
hide	hide	hide	hide	hide	
Exoniphy	GENCODE...	Geneid Genes	Genscan Genes	H-Inv 7.0	IKMC Genes Mapped
hide	hide	hide	hide	hide	hide
lincRNAs...	LRG Transcripts	MGC Genes	N-SCAN	Old UCSC Genes	ORFeome Clones
hide	hide	hide	hide	hide	hide
Other RefSeq	Pfam in UCSC Gene	Retroposed Genes	SGP Genes	SIB Genes	sno/miRNA
hide	hide	hide	hide	hide	hide
TransMap...	tRNA Genes	UCSC Alt Events	UniProt	Vega Genes	Yale Pseudo60
hide	hide	hide	hide	hide	hide

Track Display:



Configure Display

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

chr11 (p15.4) 1 p15.4 p15.1 14.3 14.1 11p15 11p12 11p11 12.1 13.4 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 < 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.

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.
Tracks with lots of items will automatically be displayed in compact modes.

collapse all expand all

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 Interrupted Rpts hide Microsatellite hide RepeatMasker Viz. hide Segmental Dups hide Self Chain hide

Simple Repeats WM + SDust hide

refresh

Configure Display Options

[Home](#) [Genomes](#) [Genome Browser](#) [Tools](#) [Mirrors](#) [Downloads](#) [My Data](#) [Projects](#) [Help](#) [About Us](#)

Configure Image

image width: pixels
label area width: characters
text size:
font:
style:
☒ 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: Groups:

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

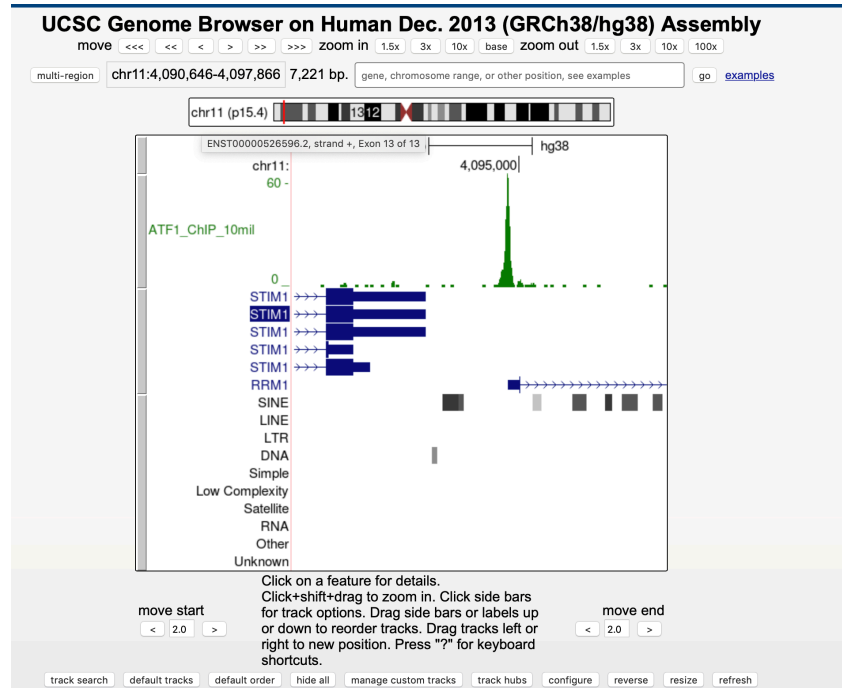
- ☒ Display chromosome ideogram above main graphic
- ☐ Show light blue vertical guidelines, or light red vertical window separators in multi-region view
- ☒ Display labels to the left of items in tracks
- ☐ Display description above each track
- ☒ Show track controls under main graphic
- ☐ Next/previous 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				



Configure Display: track order and options

The screenshot displays a genomic browser interface for chromosome 11 (p15.4). The main panel shows a genomic track with a 2 kb scale and a 4,095,000 position marker. The track is labeled "chr11:" and contains several tracks: STIM1 (blue), RRM1 (blue), ATF1_ChIP_10mil (green), SINE (black), LINE (black), LTR (black), DNA (black), Simple (black), Low Complexity (black), Satellite (black), RNA (black), Other (black), and Unknown (black). A red arrow points to the "ATF1_ChIP_10mil" track, with the text "Click to modify Settings (NEXT SLIDE)". Another red arrow points to the track list on the left, with the text "Drag tab to reorder".

Scale 2 kb | hg38 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

move start < 2.0 >

move end < 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.

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 ATF1_ChIP_bed

full hide

Configure Display: track order and options

ATF1_ChIP_10mil Track Settings

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

Display mode: Ex. Lower height to create space with multiple tracks

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) Ex. Log transform the data

Transform function: Transform data points by:

Windowing function: Smoothing window: pixels

Negate values: ☐

Draw y indicator lines: at y = 0.0: at y = Ex. Show mean, max, SD

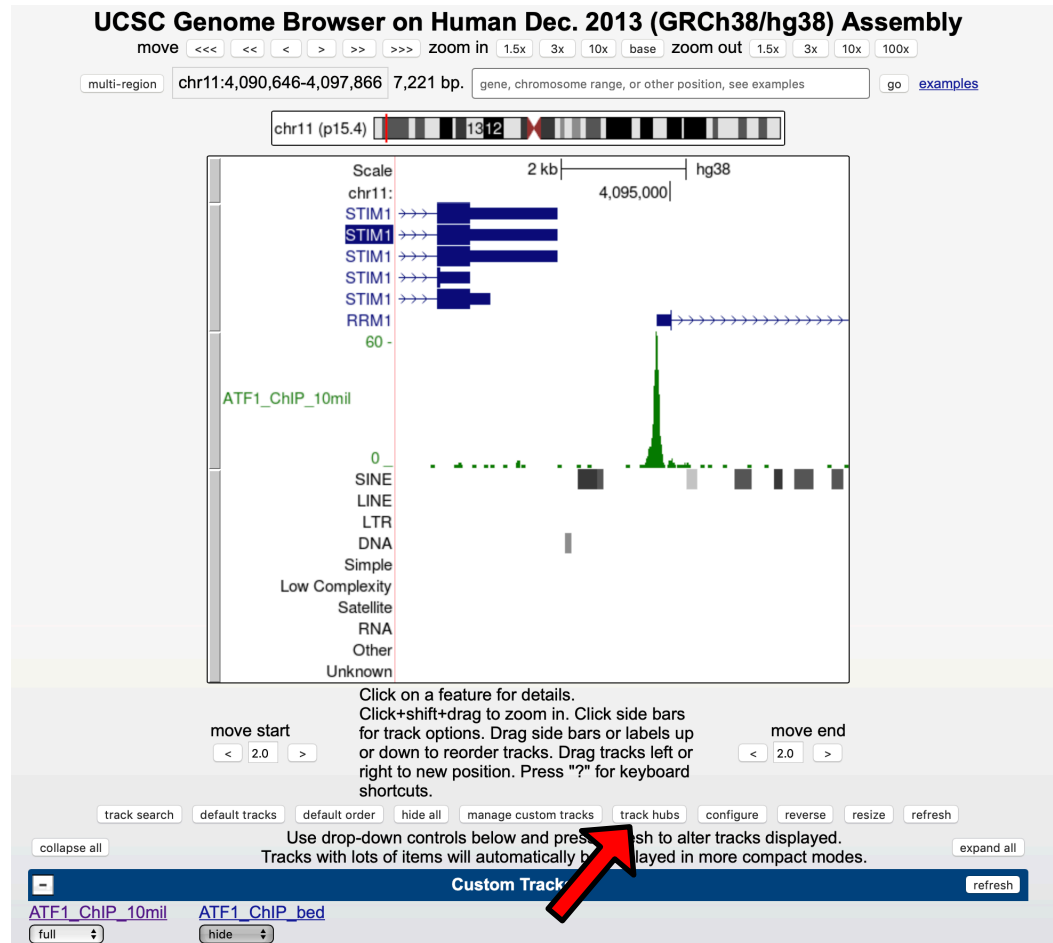
[Graph configuration help](#)

[View table schema](#)

Data last updated at UCSC: 2022-02-01

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



Track hubs: view public data

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[Genome Browser](#)
[Tools](#)
[Mirrors](#)
[Downloads](#)
[My Data](#)
[Projects](#)
[Help](#)
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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

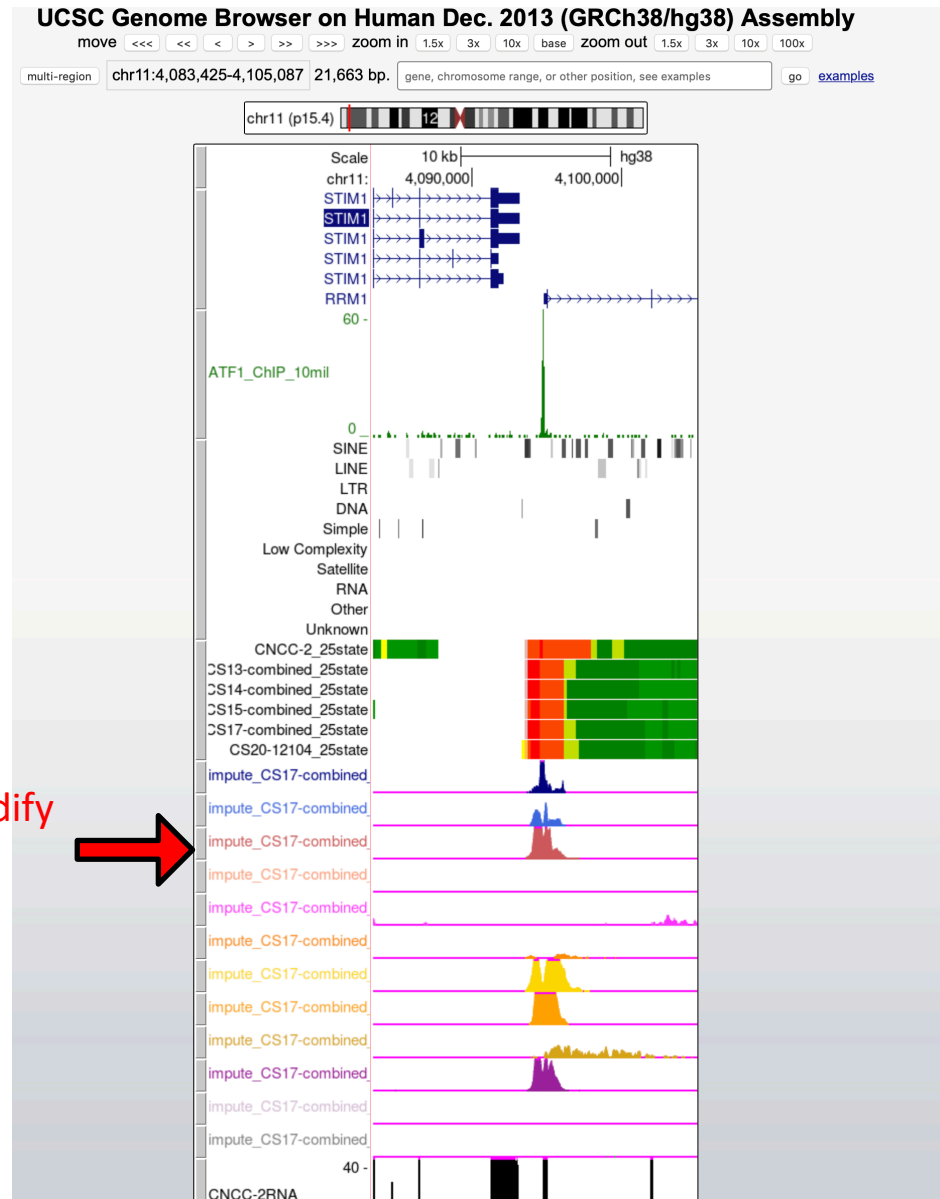
Track Hubs are created and maintained by external sources. UCSC is not responsible for their content.

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

Search terms: Assembly:

Display	Hub Name	Description	Assemblies Click to connect and browse directly
Connect	ALFA Hub	NCBI's Allele Frequency Aggregator (ALFA) allele frequency for variants in dbGaP studies.	hg19 , hg38
Connect	Bird Alignment (363 species)	Bird Alignment (363 species)	[+] Gallus_gallus , Acanthisitta_chloris...
Connect	Bird assemblies	Bird genome assemblies	[+] GCF_000699105.1 , GCF_000698965.1...
Connect	Blueprint Hub	Blueprint Epigenomics Data Hub	hg38
Connect	BrainEpigenomeHub	DNA methylation, chromatin accessibility, and gene expression data from NeuN flow-sorted human brain samples	hg19
Connect	Breast Cancer lncRNA	Breast Cancer lncRNA PMID 26236012	hg19
Connect	Broad Improved Canine Annotation v1	Broad Institute CanFam3 Improved Annotation Data v1	canFam3
Connect	C_elegans_isolates	C. elegans wild isolate assembly hub	[+] CB4856Princeton_JR-contig...
Connect	CADD	CADD Track for v1.3 to v1.6	hg19 , hg38
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
Connect	CEMT (CEEHRC)	Epigenomic Data tracks from BCGSC, Vancouver, B.C.	hg38 , hg19
Connect	CESAR Gene Mappings	Human Exons mapped by CESAR	[+] bosTau7 , ailMel1 , allMis1 , anoCar2 , calJac3...
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
Connect	Coloc segments	Colocalized segments of human genome for Roadmap cell types	hg19
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
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

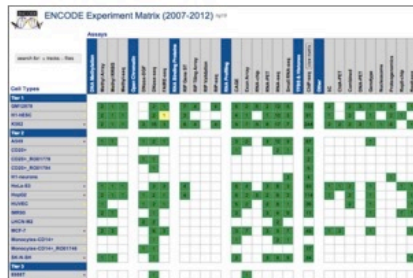
About

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.**

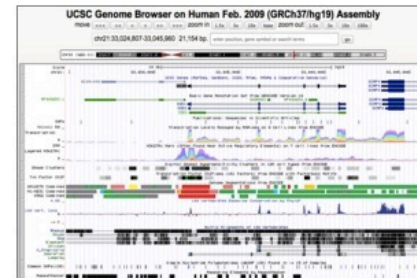
ENCODE results from 2013 and later are available from the ENCODE Project Portal, encodeproject.org. The ENCODE Project Portal also hosts ENCODE data from the first production phase, additional ENCODE access tools, and ENCODE project pages including up-to-date information about data releases, publications,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

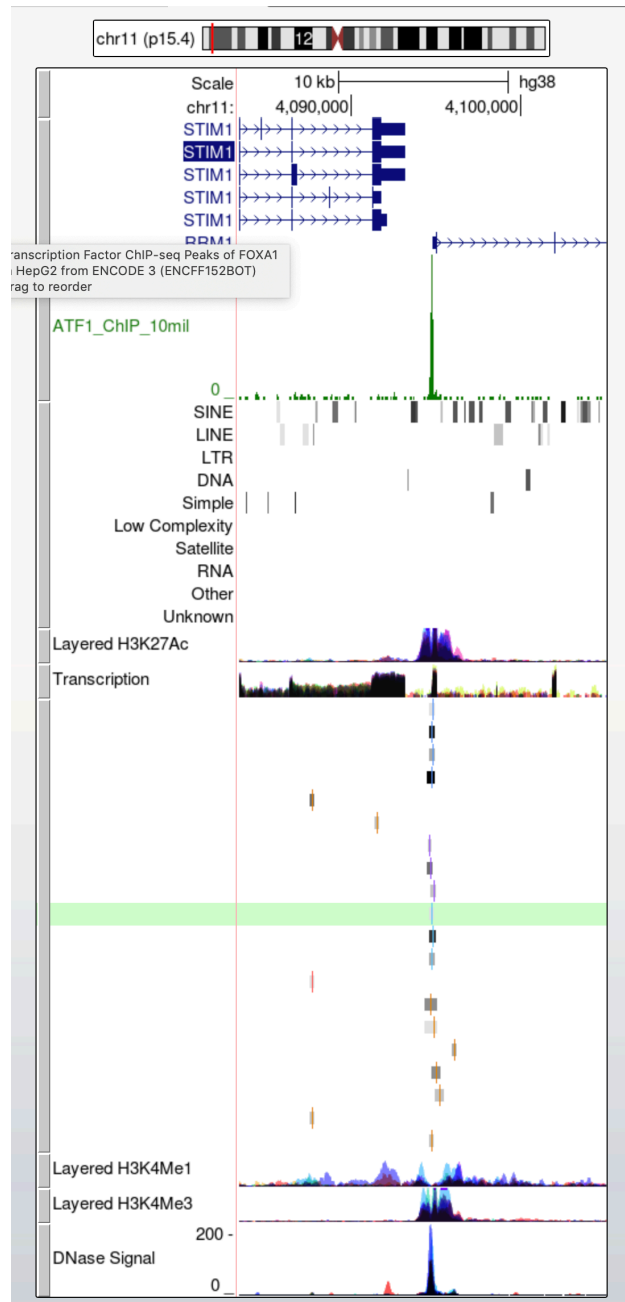
refresh

+

Repeats

refresh

ENCODE data browser



ENCODE experiment matrix

search for: ☒ tracks ☐ files

Assays

Cell Types

	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	view matrix	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/>