

MEDS5420 Lec13

Using the UCSC Genome Browser

March 1, 2023

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



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.

[email Jim](#)

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/>

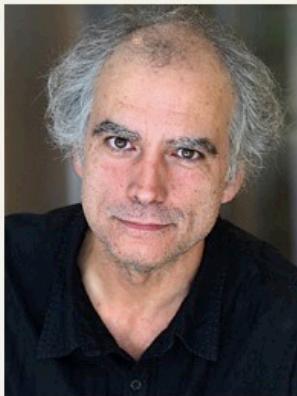
Lead creator of UCSC genome browser: Jim Kent



ABOUT US RESEARCH EDUCATION

Home

Jim Kent



Director, UCSC Genome Browser Project

Research Scientist, Department of Biomolecular Engineering, UC

Jim Kent

Research Projects

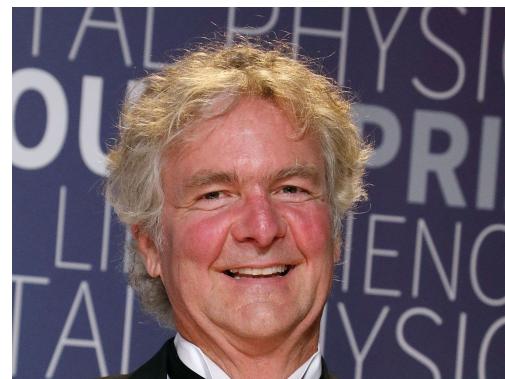
Jim Kent directs the genome bioinformatics staff of the UCSC Genome Bioinformatics Group. He created the computer program that produced the first draft of the human genome sequence. He leads a network of sequencing centers worldwide and manages the informatics associated with the Bioinformatics Group participation in international projects to produce, assemble, and annotate genomes.

UCSC Genome Browser

The UCSC Genome Browser provides access to all sequenced eukaryotic and metazoan genome sequences. It provides genome-wide annotation in a web-based interface.

START HERE EXPLORE RESEARCH TALKS STORIES C

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



David Haussler

University of California, Santa Cruz

Share

David Haussler is Scientific Director of the University of California Santa Cruz (UCSC) Computation Institute and Investigator of the Howard Hughes Medical Institute (HHMI). Haussler uses mathematical and computational biology to study the genomes of plants, animals, and viruses.

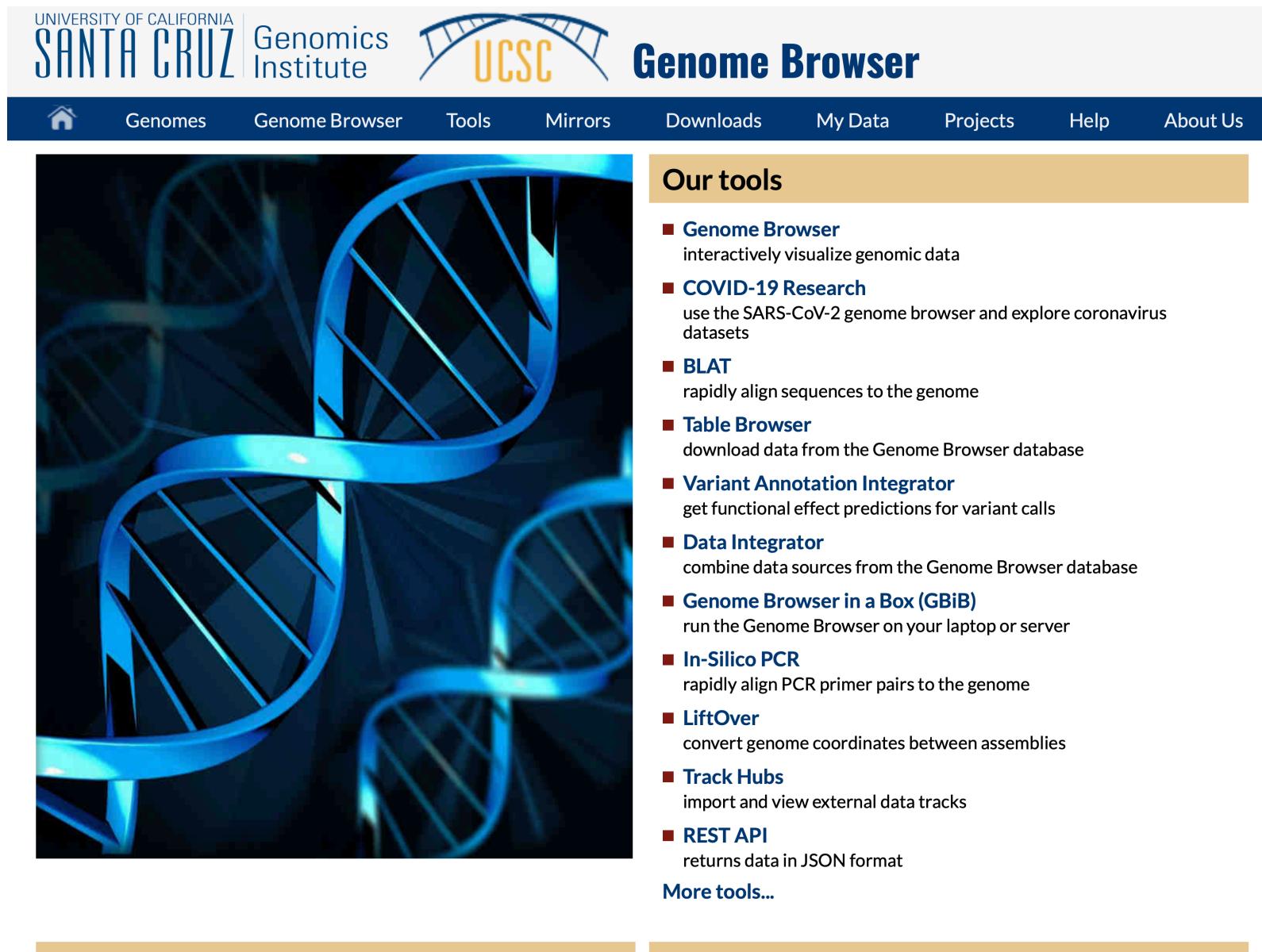
understanding disease and evolution. As part of the Human Genome Project, he was one of the leaders of the team that published the first publicly available draft of the human genome. He has also led several large-scale projects, including the [Genome 10K Project](#), the [Conservation Genomics Hub \(CGHub\)](#), 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



The image shows the homepage of the UCSC Genome Browser. At the top left is the University of California Santa Cruz Genomics Institute logo. To its right is the UCSC logo, which features a blue arch with the letters "UCSC" in yellow. The main title "Genome Browser" is displayed prominently in blue text. Below the title is a navigation bar with links: Home (represented by a house icon), Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. A large, stylized blue DNA double helix graphic is on the left side of the page. On the right, there is a section titled "Our tools" containing a list of various genomic analysis tools.

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



The screenshot shows the UCSC Genome Browser homepage. At the top left is the University of California Santa Cruz Genomics Institute logo. To its right is the UCSC logo. The main title "Genome Browser" is centered above a navigation bar. The navigation bar includes links for Home, Genomes (which has a red arrow pointing to it), Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below the navigation bar is a large blue background image of DNA helixes. To the right of the image is a yellow box titled "Our tools" containing a list of various genomic analysis tools.

Genome Browser

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**
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returns data in JSON format

[More tools...](#)

Available genomes and info

UNIVERSITY OF CALIFORNIA
SANTA CRUZ Genomics Institute



Genome Browser Gateway

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

Browse/Select Species

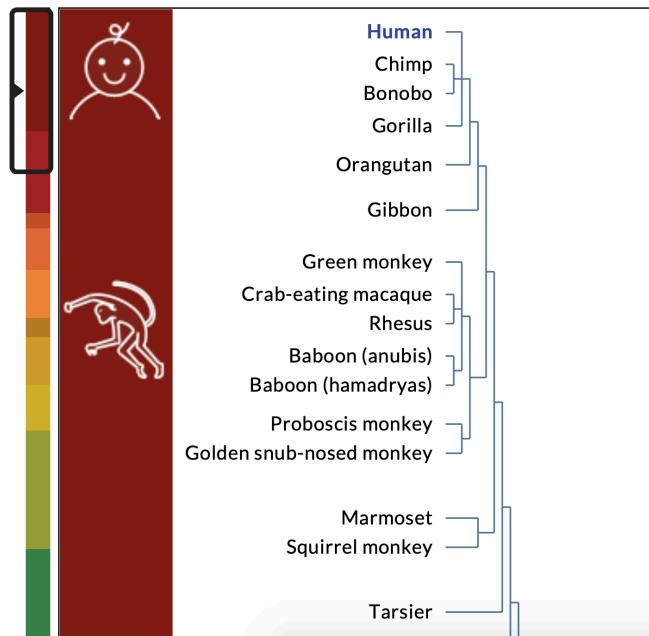
POPULAR SPECIES



Enter species, common name or assembly ID

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

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

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)

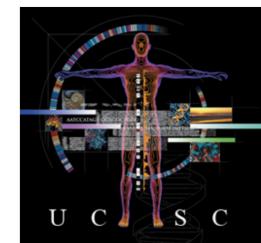
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 13

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

Click on the Genome Browser

UNIVERSITY OF CALIFORNIA
SANTA CRUZ Genomics Institute 

Genome Browser Gateway

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

Browse/Select Species

POPULAR SPECIES

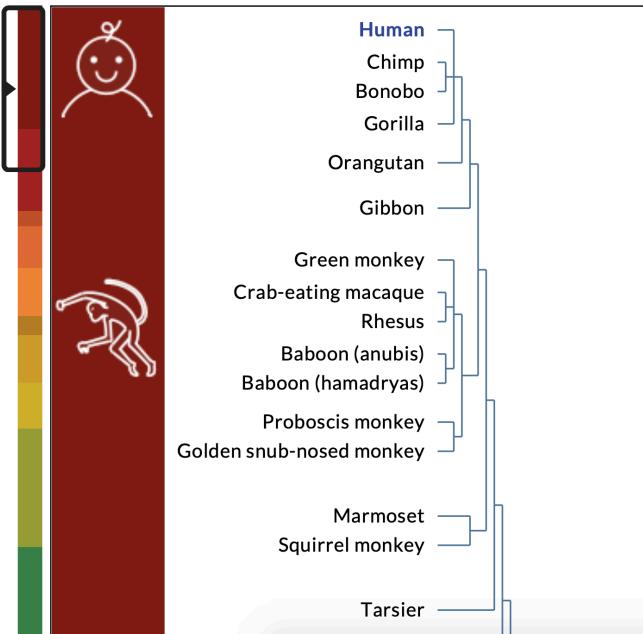


Human Mouse Rat Zebrafish Fruitfly Worm Yeast

Enter species, common name or assembly ID

[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

Find Position

Human Assembly
Dec. 2013 (GRCh38/hg38)

Position/Search Term
Enter position, gene symbol or search terms

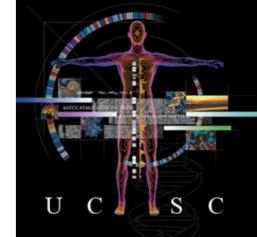
Current position: chr1:1,300,932-3,320,931 

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)

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

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 chr17:8,164,338-8,204,114 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

Scale chr17: | 8,170,000| 8,175,000| 10 kb 8,180,000| 8,185,000| 8,190,000| hg38 8,195,000| 8,200,000| Reference Assembly Fix Patch Sequence Alignments GENCODE V38 (4 items filtered out)

TMEM107
TMEM107
SNORD11B
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

move start 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 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 P13 Updated Fix Patches Haplotypes Assembly Centromeres Chromosome Band

Clone Ends hide FISH Clones Gap GC Percent GRC Contigs

GRC Incident hide Hg19 Diff INSDC LiftOver & ReMap LRG Regions Mappability

RefSeq Acc hide Restr Enzymes Scaffolds Short Match STS Markers

refresh

Genes and Gene Predictions

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

full hide hide hide hide hide hide

Browser view

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

UCSC

move <<< <<

multi-region chr17:8,16...

chr17 (p13.1) p13.3 p13.2 17p13.1 17p13.2

Scale chr17: 8,170,000

TMEM107
TMEM107
SNORD11B
TMEM107
TMEM107
TMEM107
TMEM107
RP11-599B13.7
MIR4521
BORCS6
RP11-599B13.10

SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
RNA
Other
Unknown

Human Dec. 2013 (GRCh38/hg38) Assembly

hg38

Reference Assembly Fix Patch Sequence Alignments Gencode V38 (4 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 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.

refresh

Mapping and Sequencing

Base Position P13 Updated Fix Patches P13 Updated Alt Haplotypes Assembly Centromeres Chromosome Band

Clone Ends Exome Probesets FISH Clones Gap GC Percent GRC Contigs

GRC Incident Hg19 Diff INSDC LiftOver & ReMap LRG Regions Mappability

RefSeq Acc Restr Enzymes Scaffolds Short Match STS Markers

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

refresh

refresh

Downloading Genomes and source code for utilities and browser

UCSC 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 Brower, Blat, liftOver and other utilities is free for non-profit academic research and for personal use. For information on commercial licensing, see the [Genome Brower](#) 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 Brower

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

- [Mirror instructions](#)
- [Build instructions](#)
- [Genome Brower hgcentral tables](#)
- [Genome Brower 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

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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 "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 Novoalign 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 additions and/or patches of external sequences 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.

FASTA formatted genome

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	

We use this for input in bedtools

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 data for the [current genomes](#) directory. To query and download data from other 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 [UCSC Genome Browser](#). Previous versions of certain data are available from our [track archive](#). For more information about the [UCSC Genome Browser](#), see the [UCSC Genome Browser](#).

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

Human
Mouse
Mammals
Other vertebrates

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 [UCSC Genome Browser](#). Previous versions of certain data are available from our [track archive](#). For more information about the [UCSC Genome Browser](#), see the [UCSC Genome Browser](#).

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 more information about the [UCSC Genome Browser](#), see the [UCSC Genome Browser](#).

located 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. User credits page. Please acknowledge the contributor(s) of the data you use.

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

Original Genome: Human
Original Assembly: Dec. 2013 (GRCh38/hg38)

Specify new genome

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

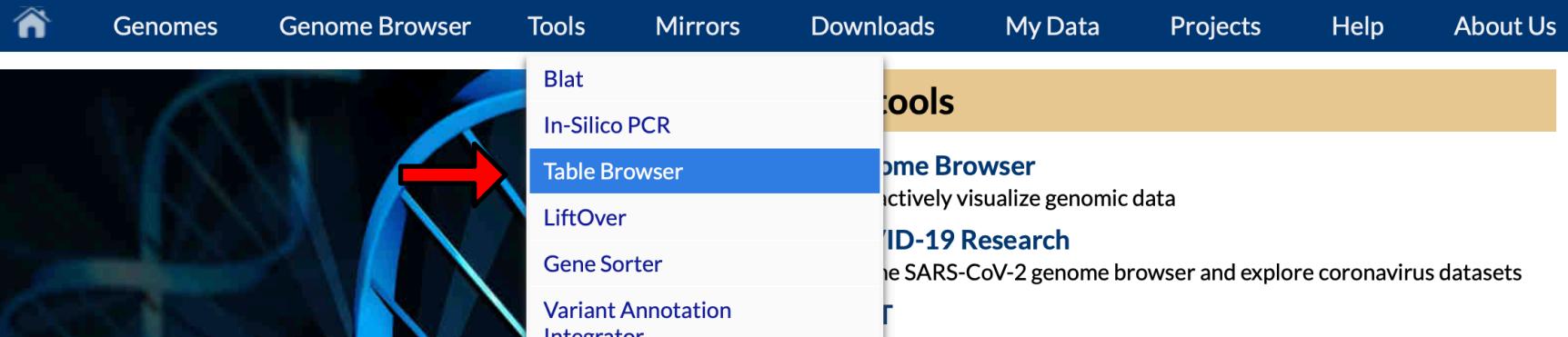
Or upload data from a file ([BED](#) or chrN:start-end in plain text format):

Choose File no file selected Submit File

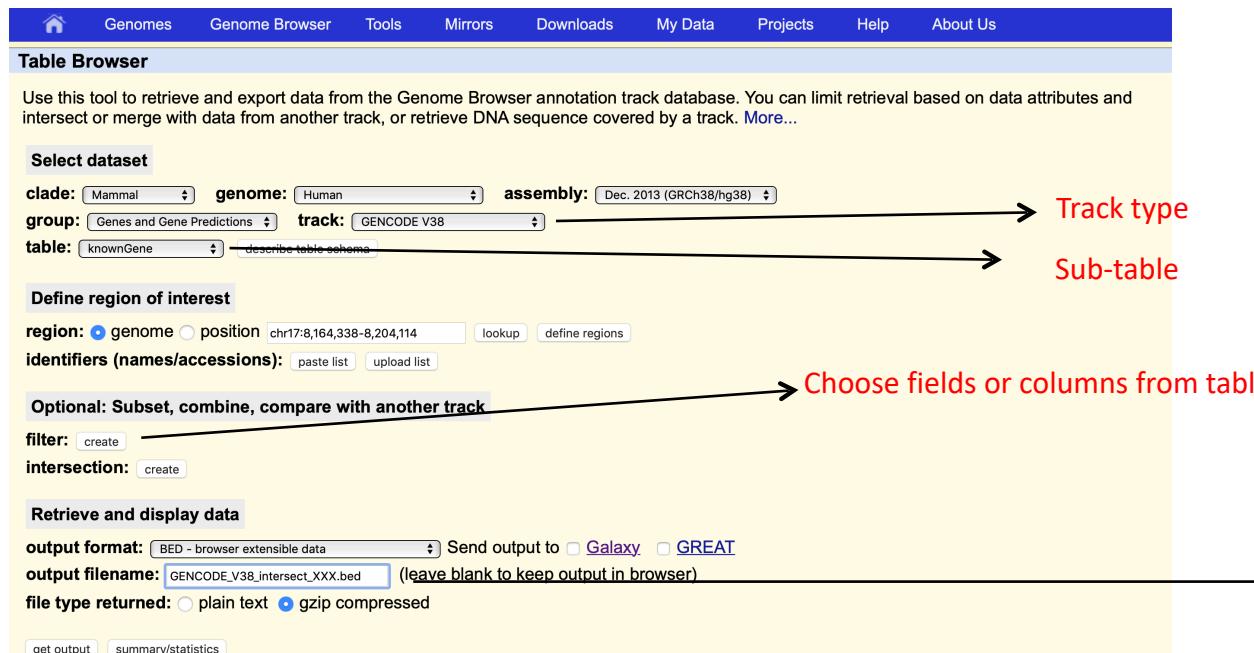
Command Line Tool

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



The screenshot shows the UCSC Genome Browser homepage. The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. On the left, there's a decorative image of a DNA double helix. The 'Tools' menu is open, showing options like Blat, In-Silico PCR, Table Browser (which is highlighted with a blue background), LiftOver, Gene Sorter, Variant Annotation Integrator, and others. To the right of the tools menu, there's a brief introduction to the Table Browser and a mention of COVID-19 Research.



The screenshot shows the UCSC Table Browser interface. At the top, there's a navigation bar with links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below that, the 'Table Browser' section is active. It includes a brief introduction and a 'Select dataset' section with dropdown menus for clade (Mammal), genome (Human), assembly (Dec. 2013 (GRCh38/hg38)), group (Genes and Gene Predictions), track (GENCODE V38), and table (knownGene). A 'describe table schema' link is also present. Red arrows point from the text labels 'Track type' and 'Sub-table' to the assembly and table dropdowns respectively. Below this, there's a 'Define region of interest' section with a 'region' dropdown (set to genome, chr17:8,164,338-8,204,114), a 'lookup' button, and a 'define regions' link. A 'filter' button is also shown. Red arrows point from the text labels 'Optional: Subset, combine, compare with another track' and 'Choose fields or columns from table' to the optional subset/combine button and the filter button respectively. At the bottom, there's a 'Retrieve and display data' section with an 'output format' dropdown (BED - browser extensible data), a 'Send output to' checkbox (Galaxy), a 'GREAT' checkbox, an 'output filename' input field (GENCODE_V38_intersect_XXX.bed), and a 'file type returned' checkbox (plain text, gzip compressed). A red arrow points from the text label 'Name output file' to the output filename input field.

Downloading DNA sequence from browser

Genomes Show DNA sequence in view Tools Mirrors Downloads My Data View Help About Us

UCSC Genome Browser on Human Reference Assembly (hg38)

move <<< << < > >> zoom

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

chr17 (p13.1) p13.3 p13.217 p13.1 17p12 17p11.2 17q11.2 17q12 17q21 17q25.3

Scale chr17: 8,170,000 | 8,175,000 | 8,180,000 | 10 kb Reference Assembly GENCODE

TMEM107
TMEM107
SNORD11B
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

PDF/PS

DNA v d

In Other Genomes (Convert)
In External Tools
Ensembl
NCBI

Configure Browser c f
Multi-Region
Default Tracks d t
Default Track Order d o
Remove all highlights h c
Reset All User Settings c r

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 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.

< 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 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

refresh

Mapping and Sequencing

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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 chr17:8,164,338-8,204,114

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.
 Mask repeats: to lower case to N
 Reverse complement (get '-' strand sequence)

Options for case and masking of repeats

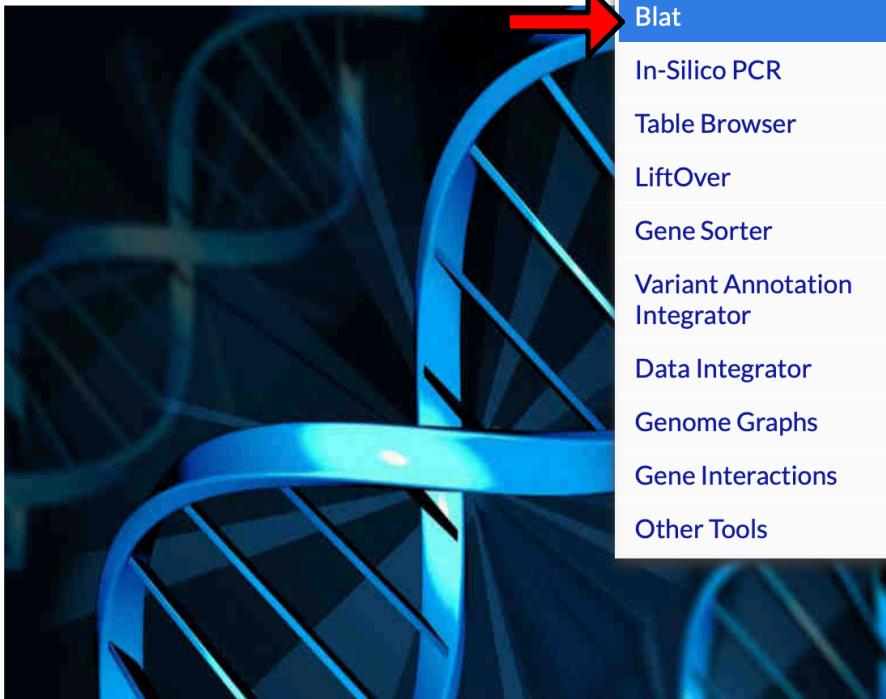
Note: The "Mask repeats" option applies only to "get DNA", not to "extended case/color options".

Fasta output



```
>hg38_dna range=chr17:8164338-8204114 5'pad=0 3'pad=0 strand=+ repeatMasking=none
GGCCTTGATCTTAAGACAAACAGGAACCGAGCTTCTCCCTCCCCACCC
TGGCTTCCCAGGGCTCGGGTGTGAGATCTCCCTCACTGCAGTGCCTC
ACCCGCTCCCCACAGAACGCCGGAGAGTGGCTCTGTCACCAGAGGTGTCA
TTGGGAACTCAGCCCAATCTAAAGAGAGATACTCTGGCTTCTCCCC
TGTGGAAACTCTGGCTCTGTCAGGGTATAAAAGACATGGAGGATTGGAAGAG
TCAGAGGAGCAGCCGCTCCCTGGCTCTGTGACTGACAGTCCGGGTG
GCTCAGGCTATGTGATGAGAAAAGAGCAGCTTCACGGGGTCTCA
GATCATGCTGTGAGATGCTGGCTCTGGCTTTGGCTTCTCAAATGATTCC
TCTTTCTACTCAGAGAACAAAGATGCCAAATTCCACGCTTTAAGTC
AACCCCTCAGTGTCTGTCAGGGTATAAAAGACATGGAGGATTGGAAGAG
GCAGGGCACAGGAACGCCCTCCGCCAGTTGGACACCTTGCACACTAAG
AGGGAGGCTTAGTCAGAGCCAGACAAAGACATTGATGCTGGTTGGGG
TGATGTTGAAGGGACAGAGCCCCAGATACAGGTCAAGGCCAGGGTCTG
GCTATTGCTATTGGATCTGGGGACGCCAGCAGCAGAGTAGAAATGAGGG
CATGTGTGACCCACGGAGATGAAGGGGCCAGGAGGATTCATCTCAGAAAG
AGGACTCTCATCCAGCACCCCCCTCCCCACCCACCTAGCTGTG
CTCAGAGGAACCTCCCAAATTAGATCAATGGTGGAGGTGGAGAAGGAG
TGGATGACGGACTTACCTGGAAAGTGACTGAGGAATGTTTCTGCAGG
CAGGTAGAATGGAGACCCAAATAGAGGTAAGTTGAAACAATAGAAAAATAA
TGTATTGCTAACTCAGATTGGCTTCTACATGTACTGGCTTGGGAAAT
TGGCCAATGATTCTAGGGCACACCCCAAGACTCATTCAAAGGATGTA
GGACTCAAGGTGATGGTGTAGGGCAACAGAGACCAACTTCTTTTC
TTTTTTTTCTTTTTCTTTTGAGACAGACTCTGTCTGTCAC
CCAGGCTGGAGTGCATGGCGCAGTCTGCTCACTGCAAACCTCCGCTC
CCAGGTCAACGCCATTCTCCCTCAAGCCCTCCCGAGTAGCTGGGACTAC
AGGCCGCCAACCCGGCGGCTAAATTGTTGATTTTAGTAGAGAGACA
GGGTTCACCGTGTAGCCAGGGTGTCTGATCTCTGACCCCGTGTAC
```

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

Interactively visualize genomic data

SARS-CoV-2 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

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

Human BLAT Search

BLAT Search Genome

Genome: Search all

Assembly:

Query type:

Sort output:

Output type:

```
>hg38_dna range=chr17:8164338-8204114 5'pad=0 3'pad=0 strand=+ repeatMasking=none
GGCCTTGATCTCTAAAGACAAACAGGAACCAGCTCCCTCCCCACCC
TGGCTTCCCAGGGCCTCGGGTGTGAGATCCTCCCCACTGCAGTCCCC
ACCCGCTCCCCACAGAACGCCGGAGAGTGGCTCTGTCACCAGAGGTGTCA
TTTCCCAGCTGTCTGTGGGAGGTGAGTGAGCAGGAAATGTGTGTGCTGG
TGTGGGAACTCAGCCCAATCTAAAGAGAAGATACTTGGCTTCTCCCCC
TCAGAGGAGCAGCCGCGTCCCTGGCTCTGTGCACTGACAGTCCCAGGTG
GCTCAGCCTATGTGATGAGAAAGAAAAGAGCAGCTTCCACGGGGGTCTCA
GATCATGCTGTGAGATGCTGGCTCTGCTTTGGTCTCAAATGATTCC|
```

Paste Sequence. Use fasta format for
more than 1 sequence

 All Results (no minimum matches)

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](#).

BLAT Search Results

Fast DNA search with BLAT

Go back to [chr17:8164388-8204114](#) in the Genome Browser

Custom track name: blat hg38_dna

Custom track description: blat on hg38_dna

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	100.0%	chr17	+	8164338	8164737	400
browser	details	hg38_dna	25	29	54	100.0%	chr19	-	10310700	10310726	26
browser	details	hg38_dna	25	349	379	88.9%	chr1	+	247443829	247443858	30
browser	details	hg38_dna	25	15	49	89.3%	chr1	+	204244803	204244836	34
browser	details	hg38_dna	23	34	58	96.0%	chr14	-	20262748	20262772	25
browser	details	hg38_dna	23	321	344	100.0%	chr1	-	59157007	59157032	26
browser	details	hg38_dna	23	42	65	100.0%	chr14	+	72549910	72549939	30
browser	details	hg38_dna	22	34	58	96.0%	chr6	-	166516416	166516441	26
browser	details	hg38_dna	22	32	56	95.9%	chr13	+	51135725	51135753	29
browser	details	hg38_dna	21	32	52	100.0%	chr10	-	5966101	5966121	21
browser	details	hg38_dna	20	26	47	95.5%	chr18	-	44760280	44760301	22
browser	details	hg38_dna	20	367	386	100.0%	chr15	+	93348003	93348022	20
browser	details	hg38_dna	20	360	381	95.5%	chr11	+	7422660	7422671	11
browser	details	hg38_dna	20	32	51	100.0%	chr1	+	Alignment of hg38_dna and chr17:8164338-8164737		
browser	details	hg38_dna	20	196	215	100.0%	chr1	+	Click on links in the frame to the left to navigate through the alignment. Matching bases in chr17 are highlighted in blue.		
browser	details	hg38_dna	20	32	51	100.0%	chr1	+	Mark the boundaries of gaps in either sequence (often splice sites).		

Alignment of hg38 dna and chr17:8164338-816473

Click on links in the frame to the left to navigate through the alignments. You can also mark the boundaries of gaps in either sequence (often splice sites).

cDNA hg38 dna

GCCGTTGATC	TCTAAAGACCA	ACAGGACCCA	GCTTCCTCCC	TCCCCCACCC	5
TGGCGTTCCTCA	GGGGCTTCGG	GTTGTGATGC	CCTCCGGAACT	GAAGTGCTCCG	10
ACCGGGCTTC	CACAGGACGC	GGAGGAGGTT	CTCTGTCATC	AGAGGATGTC	15
TTTCGGCTACTG	GTCTGGTGGG	GTTGATGAGT	CAGGGGGGCTG	GTGGCTGCTG	20
TGTGGGCTGCTG	GGGGGGGGGG	GGGGGGGGGG	TTTAACTTAA	GGGGGGGGGG	25
GGGGGGGGGG	ACGGCGCTTC	CGGGGGGGGG	TTTAACTTAA	GGGGGGGGGG	30
GCTCCCTTA	TGTGGTGGAA	AAAAGAAAGA	GGGGGGGGGG	GGGGGGGGGG	35
GATGCGCTCC	TGGAGGCGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	40

Section 1.17

→ “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| 100 bases | hg38
hg38_dna 8,164,500| 8,164,550| 8,164,600| 8,164,650| 8,164,700|
Reference Assembly Fix Patch Sequence Alignments
Your Sequence from Blat Search
GENCODE V38
Repeating Elements by RepeatMasker

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 move end < 2.0 >
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.



Custom tracks: uploading

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

Add Custom Tracks

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

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](#), [GFF](#), [GTF](#), [hic](#), [interact](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats.

Select File You can paste just the 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](#).

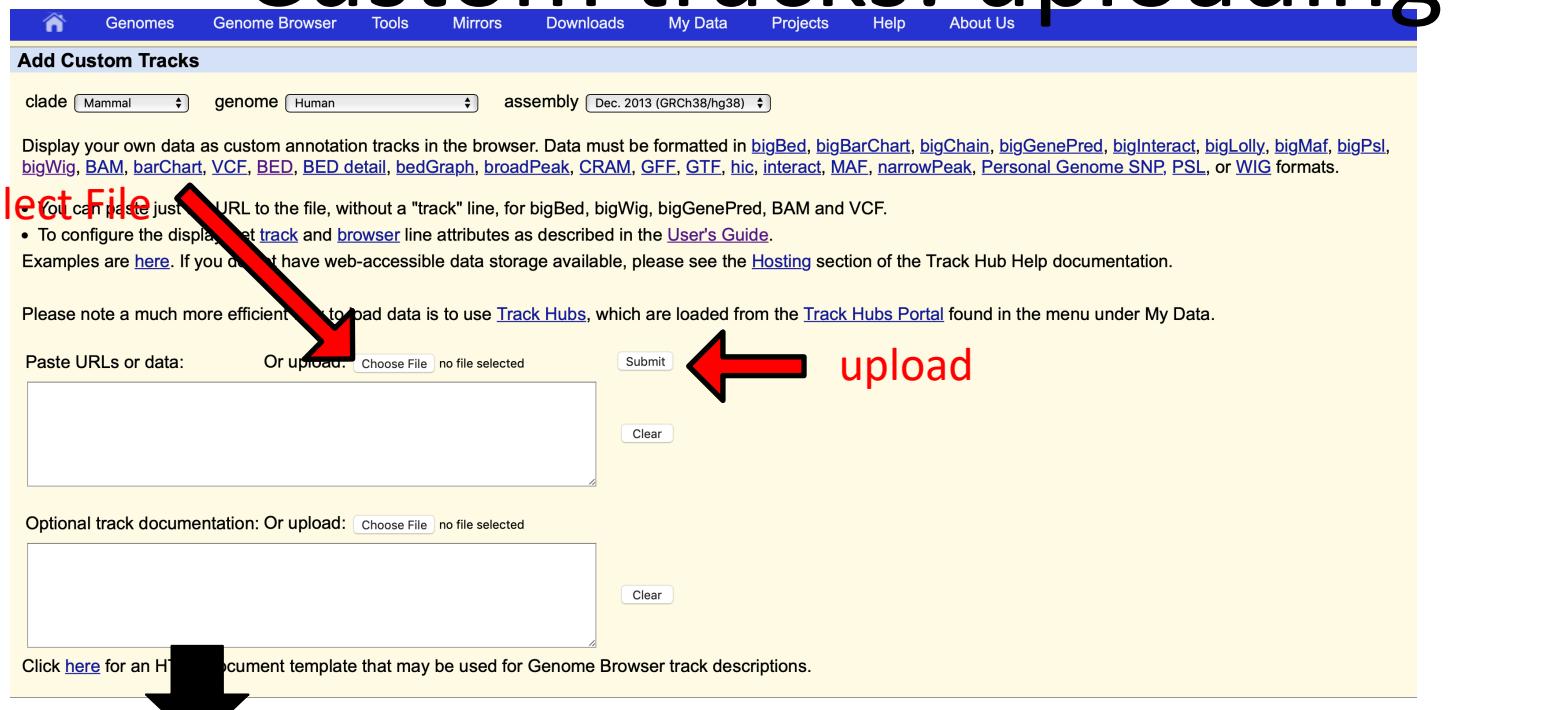
Examples are [here](#). If you don't have web-accessible data storage available, please see the [Hosting](#) section of the Track Hub Help documentation.

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: Choose File no file selected Submit Clear

Optional track documentation: Or upload: Choose File no file selected Clear

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



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 [Genome Browser](#) go add custom 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](#).

- 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.

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Custom tracks: saving and sharing

The screenshot shows the top navigation bar of the Genome Browser with various links like Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. A red arrow points to the 'My Data' link, which has a dropdown menu. The 'Custom Tracks' option is highlighted in the dropdown menu.

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:

Custom Tracks
My Sessions
Track Hubs
Track Collection Builder
Public Sessions

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 10 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	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_Srf_figure	2021-11-08	mm10	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_Twist2_supplemental	2021-11-08	mm10	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_sp3_figure	2021-11-08	mm10	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm10_Twist2_figure	2021-11-08	mm10	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
hg38_chr2_H1_more	2021-09-10	hg38	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
hg38_H1_chr2_DNase	2021-09-10	hg38	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
hg38_Piotr	2021-08-02	hg38	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm39_RBC_example	2021-07-27	mm39	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
mm39_Jurkat_example	2021-07-27	mm39	details	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email

Search:

Enable sharing

Create sharing link in email

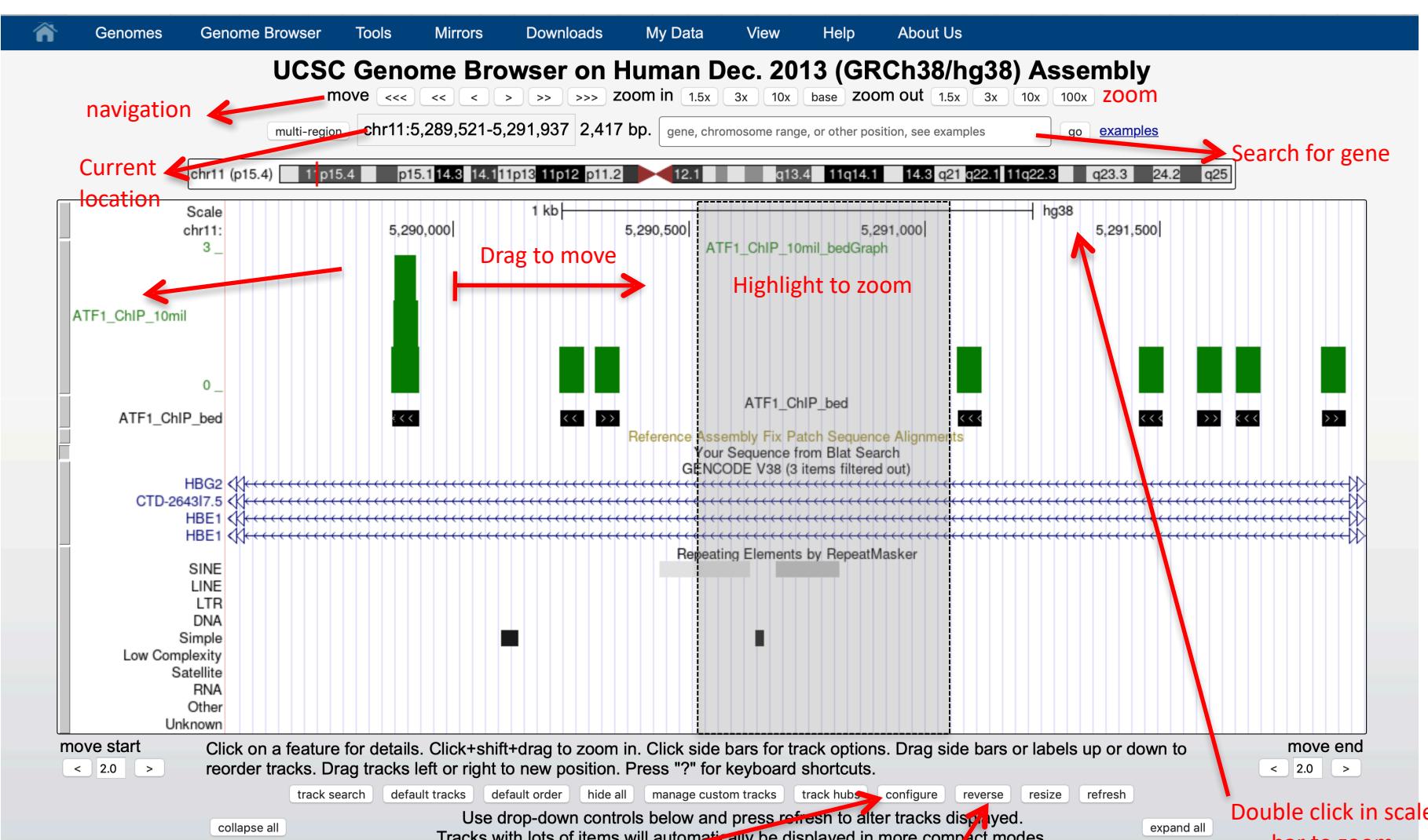
Save current as:

Save Settings

Save current settings as named session:
name: hg38_ATF1_beds 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)

Cruising the genome: Displays and Tracks



Track Display:

move start 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.

< 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

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

This screenshot shows a track display interface with a sidebar on the left containing the text "Available display tracks". The main area displays a list of genomic tracks, each represented by a blue card with a plus sign icon, a track name, and a "refresh" button. The tracks listed are: 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, and Repeats. There are also buttons for "move start" and "move", "track search", "default tracks", "default order", "hide all", "manage custom tracks", "track hubs", "configure", "reverse", "resize", "refresh", "collapse all", and "expand all". A message at the top indicates that users can click on features for details, use keyboard shortcuts, and drag tracks to reorder them.

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

Scale chr11: 48 hg19 10 kb 4,105,000 4,110,000 4,115,000 4,120,000 4,125,000 4,130,000 4,135,000

ATF1_ChIP-seq_bedgraph

RefSeq Genes

STIM1 RRM1

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

< 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

Mapping and Sequencing

Genes and Gene Predictions

UCSC Genes (hide) Exoniphy (hide) lincRNAs... (hide) Other RefSeq (hide) TransMap... (hide) tRNA Genes (hide)

GENCODE... (hide) LRG Transcripts (hide) Pfam in UCSC Gene (hide) Retroposed Genes (hide) UCSC Alt Events (hide)

Geneid Genes (hide) MGC Genes (hide) N-SCAN (hide) UniProt (hide)

Genscan Genes (hide) H-Inv 7.0 (hide) Old UCSC Genes (hide)

EvoFold (hide) IKMC Genes Mapped (hide) ORFeome Clones (hide)

sno/miRNA (hide) Yale Pseudo60 (hide)

refresh refresh

+

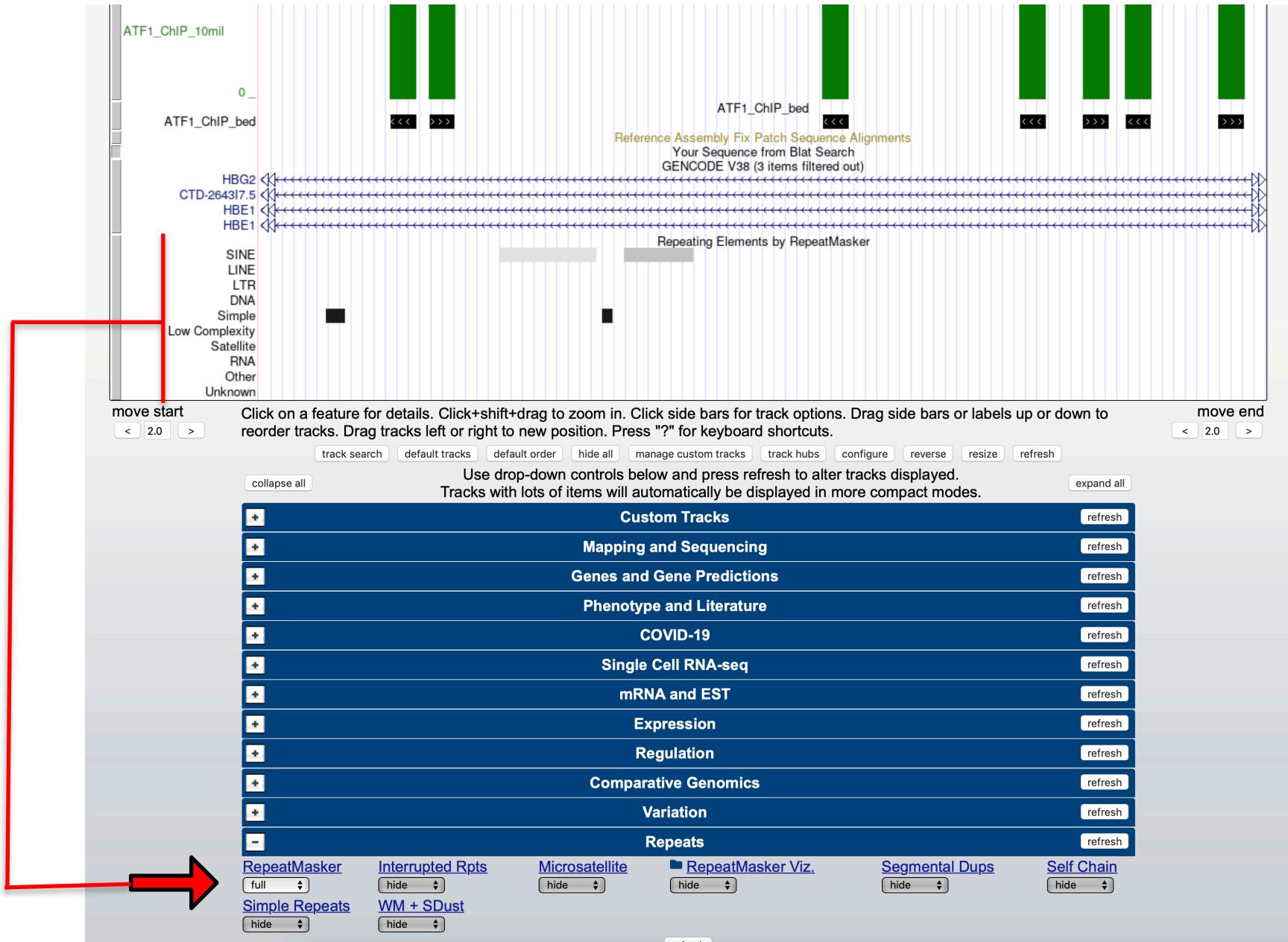
+

-

hide dense squish pack full

26

Track Display:



Configure Display

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 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 p15.114.3 14.1 11p13 11p12 p11.2 12.1 q13.4 q14.1 14.3 q21 q22.1 11q22.3 q23.3 24.2 q25

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

ATF1_ChIP_10mil

ATF1_ChIP_bed

HBG2 CTD-264317.5 HBE1 HBE1

SINE LINE LTR DNA Simple Low Complexity Satellite RNA Other Unknown

Reference Assembly Fix Patch Sequence Alignments Your Sequence from BLAST Search GENCODE V38 (3 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 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

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

RepeatMasker

Interrupted Rpts

Microsatellite

RepeatMasker Viz.

Segmental Dups

Self Chain

full hide WM + SDust hide

Simple Repeats hide

refresh

28

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
 Show track controls under main graphic
 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)

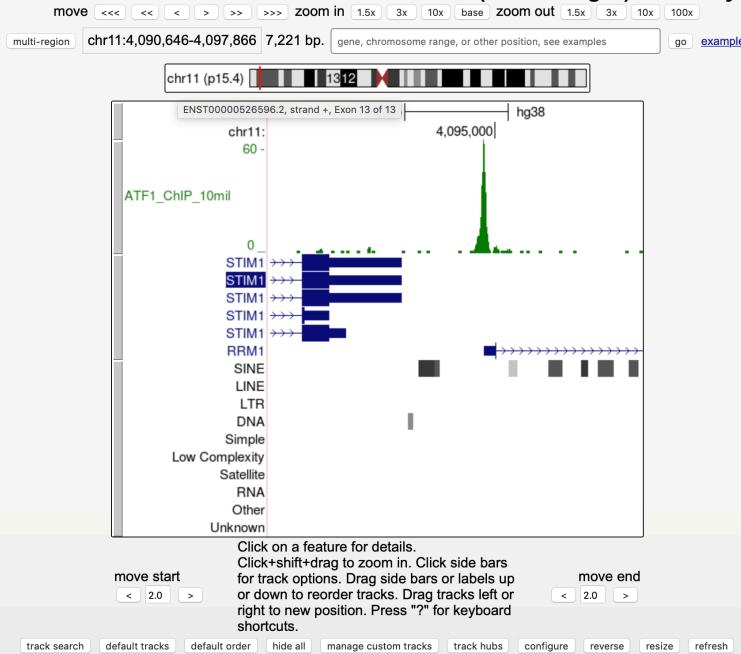
Configure Tracks on UCSC Genome Browser: Human Dec. 2013 (GRCh38/hg38)

Tracks: track search hide all show all default Groups: collapse all expand all
Control track and group visibility more selectively below.

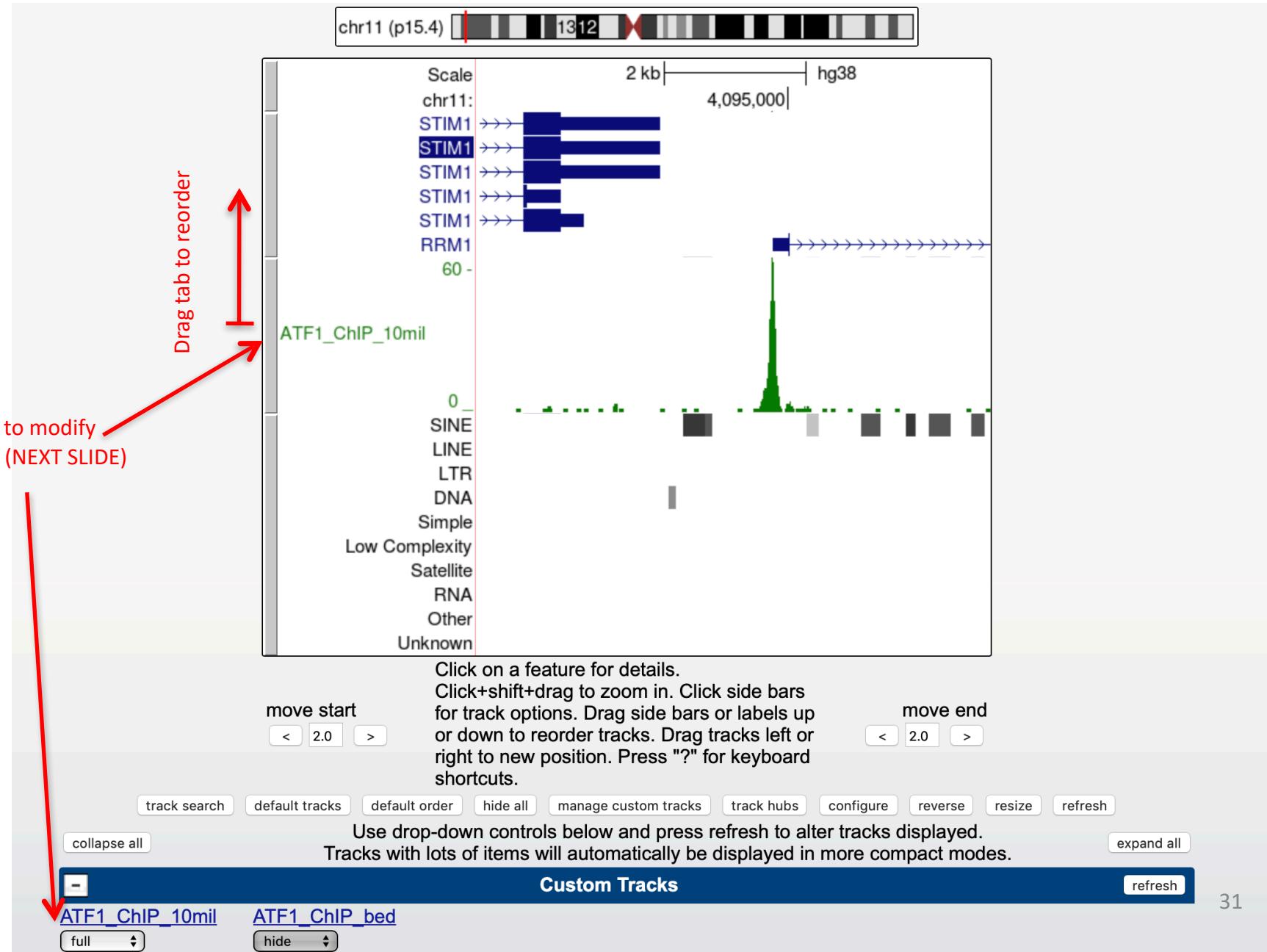
Custom Tracks	hide all	show all	default	submit
ATF1_ChIP_10mil	full		ATF1_ChIP_10mil_bedGraph	
ATF1_ChIP_bed	hide		ATF1_ChIP_bed	



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



Configure Display: track order and options



Configure Display: track order and options

The screenshot shows the 'ATF1_ChIP_10mil Track Settings' page. The main title is 'ATF1_ChIP_10mil_bedGraph' with a link to 'All Custom Tracks'. Below the title are several configuration options:

- Display mode:** full (dropdown), Submit, Remove custom track, Update custom track. A red arrow points to the 'Update custom track' button with the text 'Ex. Lower height to create space with multiple tracks'.
- Type of graph:** bar (dropdown).
- Track height:** 128 pixels (range: 11 to 128).
- Data view scaling:** auto-scale to data view (dropdown), Always include zero: ON (dropdown).
- Vertical viewing range:** min: 0, max: 1000 (range: 0 to 1000).
- Transform function:** Transform data points by: NONE (dropdown). A red arrow points to this dropdown with the text 'Ex. Log transform the data'.
- Windowing function:** maximum (dropdown).
- Smoothing window:** OFF (dropdown) pixels.
- Negate values:**
- Draw y indicator lines:** at y = 0.0: OFF (dropdown), at y = 1000: OFF (dropdown). A red arrow points to this section with the text '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

The screenshot shows the UCSC Genome Browser interface. A red arrow points to a context menu that has appeared over the 'Track Hubs' option in the top navigation bar. The menu items are: Custom Tracks, My Sessions, Track Hubs (which is highlighted), Track Collection Builder, and Public Sessions. The main genome browser window displays a genomic track for chromosome 11, specifically the p15.4 region. The scale at the top indicates positions from 4,094,000 to 4,096,000. The track itself consists of numerous small blue and red arrows pointing in various directions, likely representing RNA-seq or ChIP-seq data.

Track hubs: view public data

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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](#), see the [FAQ](#).

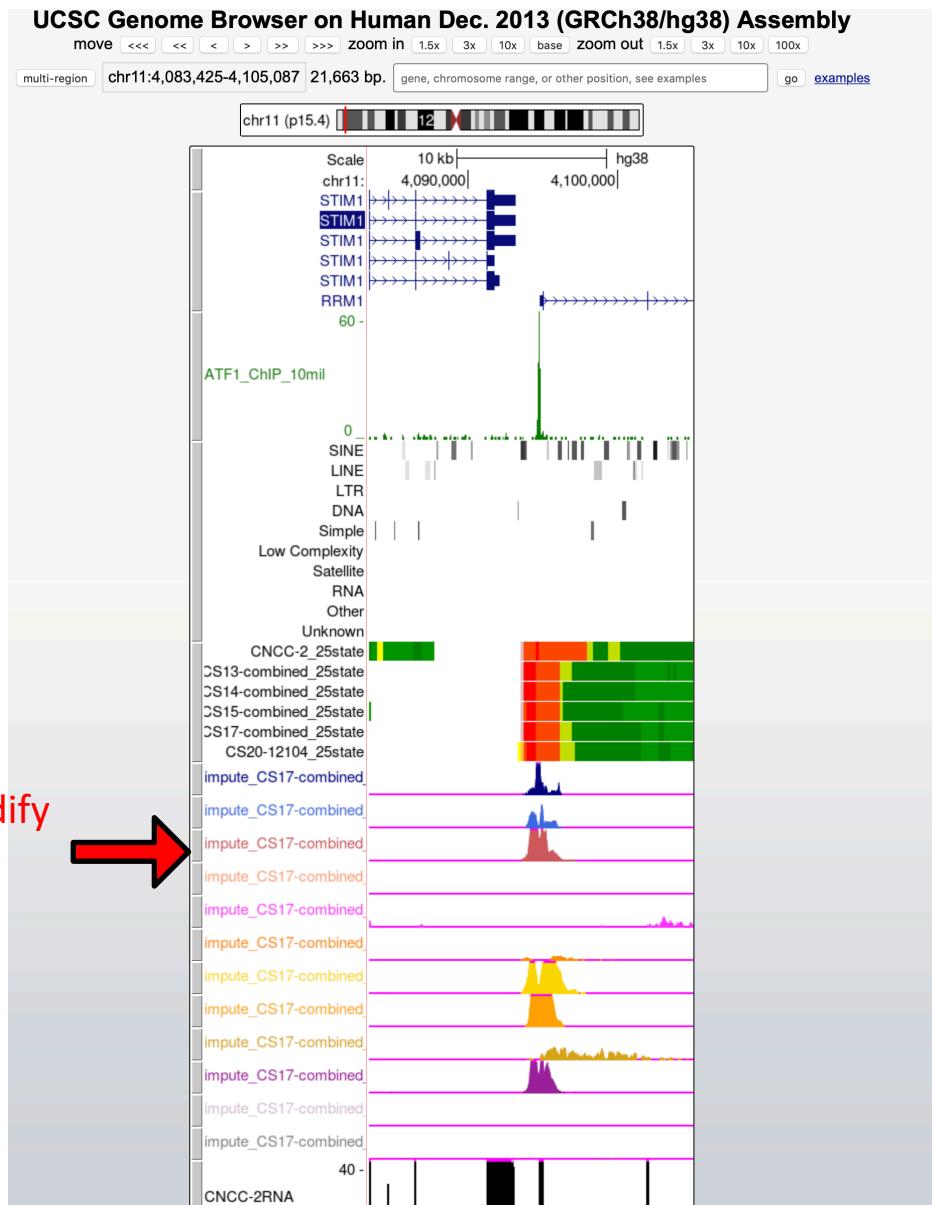
Track Hubs are created and maintained by external sources. UCSC is not responsible for their content.

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

Search terms: Assembly:

Display	Hub Name	Description	Assemblies
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 , ailMe1 , ailMis1 , 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



Click to modify
settings

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.

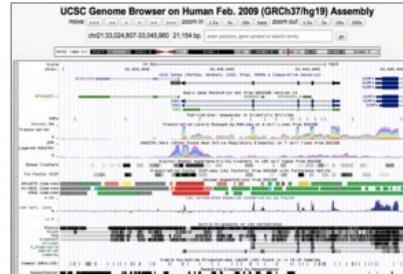
UCSC coordinated data for the ENCODE Consortium from its inception in 2003 (Pilot phase) to the end of the first 5 year phase of whole-genome data production in 2012. All data produced by ENCODE investigators and the results of ENCODE analysis projects from this period are hosted in the UCSC Genome browser 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



View ENCODE data in the UCSC Genome Browser



Experiment matrix

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

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.

refresh

Custom Tracks

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 ENCODE Regulation hide

New JASPAR Transcription Factors

hide

CpG Islands hide

ORegAnno hide

RefSeq Func Elms hide

GeneHancer GTEX cis-eQTLs hide

Hi-C and Micro-C hide

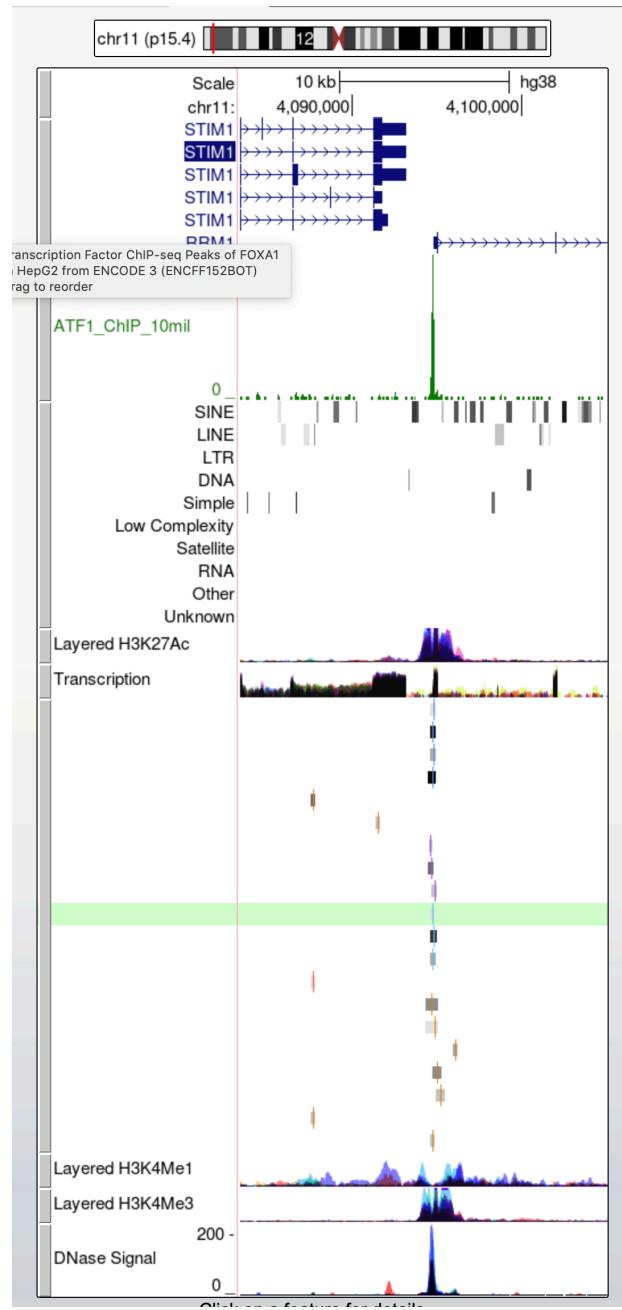
Comparative Genomics refresh

Variation refresh

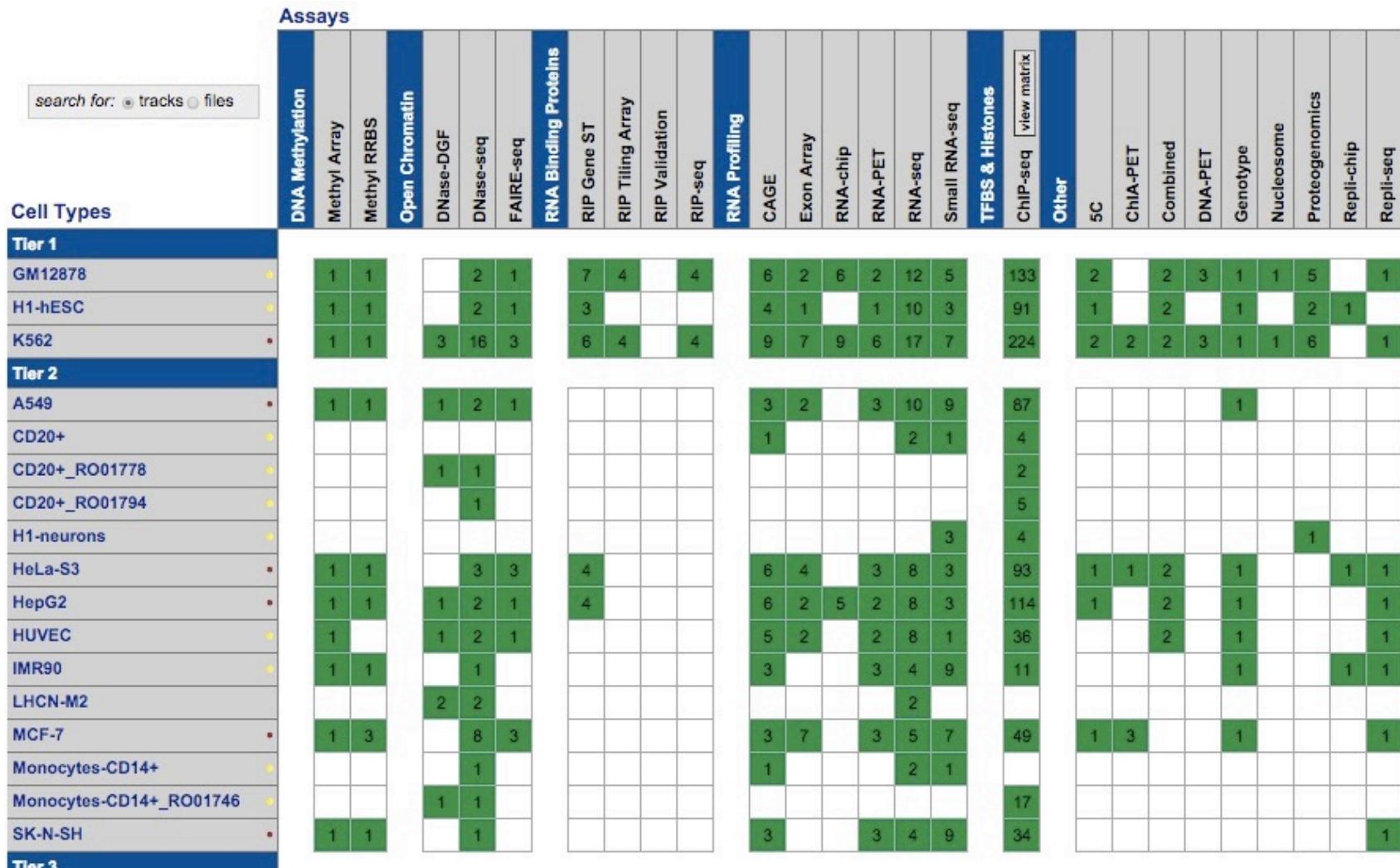
Repeats refresh



ENCODE data browser



ENCODE experiment matrix



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/>