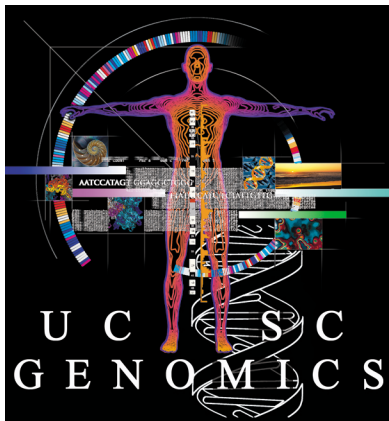



Visualizing ENCODE Data in the UCSC Genome Browser



Pauline Fujita, Ph.D.
UCSC Genome Bioinformatics Group

Training Resources

genome@soe.ucsc.edu

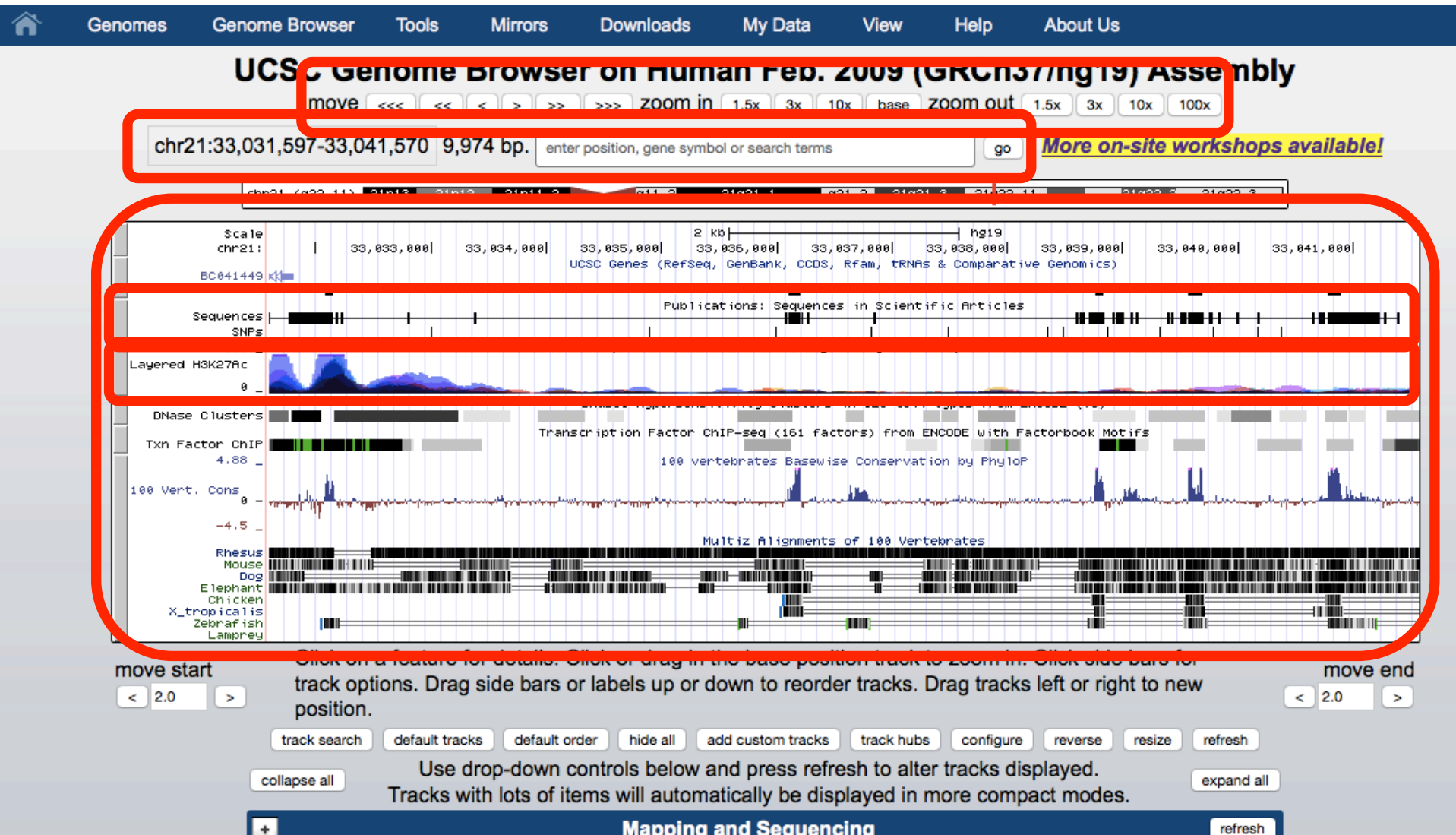
- Genomewiki: genomewiki.ucsc.edu
- Mailing list archives:
genome.ucsc.edu/FAQ/
- Training page:
genome.ucsc.edu/training.html
- Twitter  @GenomeBrowser
- Tutorial videos: YouTube channel
- Open Helix: openhelix.com/ucsc

Outline

- Browser Basics
- Tools for finding ENCODE data
- Annotating a BED file: RNAseq example
- Annotating a VCF file
- Track Hubs: What are they? How do I make one?
- Exercises

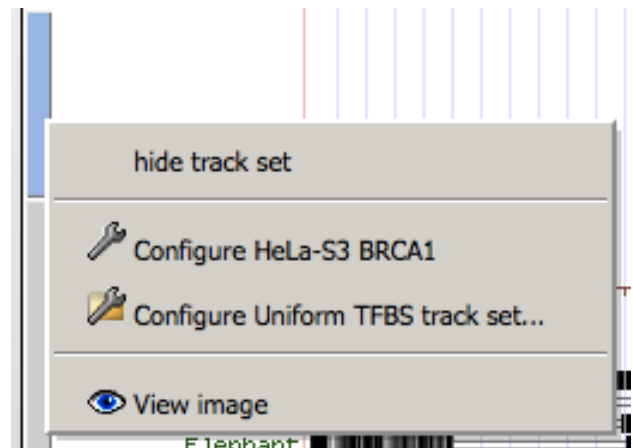
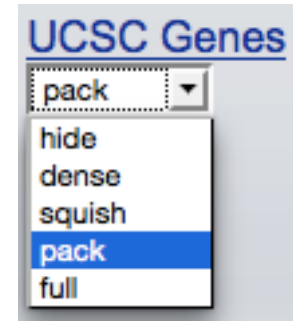
Basic Navigation: Main Display

genome.ucsc.edu/cgi-bin/hgTracks?db=hg19



Display Configuration

- Visibility:
hide, dense, squish, pack, full
- Track ordering: drag and drop
- Drag and zoom/highlighting
- Configuration page
- Right click menu



How to find more info

The screenshot shows a genomic browser interface. At the top, a track labeled 'RepeatMasker' is visible, with a red box highlighting a vertical bar. Below it, a track labeled 'UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)' is shown, with a red box highlighting a blue bar representing a gene. A text box labeled 'Item Description' points to this bar. Below the tracks, there is a section titled 'Mapping and Sequencing' and another titled 'Genes and Gene Predictions'. In the 'Genes and Gene Predictions' section, the 'UCSC Genes' link is highlighted with a red box, and a text box labeled 'Track Description' points to it. The interface includes various controls such as 'move start', 'track search', 'default tracks', 'default order', 'hide all', 'add custom tracks', 'track hubs', 'configure', 'reverse', and 'use all'. There are also instructions: 'Click on a feature for details. Click or drag in the browser to zoom in. Click side track options. Drag side bars or labels up or down to change position.' and 'Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes'.

RepeatMasker

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

Item Description

Track Description

move start

track search default tracks default order hide all add custom tracks track hubs configure reverse

Mapping and Sequencing

Genes and Gene Predictions

UCSC Genes RefSeq Genes AceView Genes CCDS Ensembl Genes

Exoniphy GENCODE... Geneid Genes Genscan Genes H-Inv 7.0

More info: Track Description

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

UCSC Genes Track Settings

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics) ([▲All Genes and Gene Predictions tracks](#))

Display mode:

Label: ☒ gene symbol ☐ UCSC Known Gene ID ☐ UniProt Display ID ☐ OMIM ID

Show: ☒ non-coding genes ☒ splice variants

Color track by codons: [Help on codon coloring](#)

Show codon numbering: ☐

[View table schema](#)

Data last updated: 2013-06-14

Description

The UCSC Genes track is a set of gene predictions based on data from RefSeq, GenBank, CCDS, Rfam, and the [tRNA Genes](#) track. The track includes both protein-coding genes and non-coding RNA genes. Both types of genes can produce non-coding transcripts, but non-coding RNA genes do not produce protein-coding transcripts. This is a moderately conservative set of predictions. Transcripts of protein-coding genes require the support of one RefSeq RNA, or one GenBank RNA sequence plus at least one additional line of evidence. Transcripts of non-coding RNA genes require the support of one Rfam or tRNA prediction. Compared to RefSeq, this gene set has generally about 10% more protein-coding genes, approximately four times as many putative non-coding genes, and about twice as many splice variants.

More info: Item Description

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

Human Gene SCAF4 (uc002ypd.2) Description and Page Index

Description: Homo sapiens SR-related CTD-associated factor 4 (SCAF4), transcript variant 1, mRNA.

RefSeq Summary (NM_020706): This gene likely encodes a member of the arginine/serine-rich splicing factor family. A similar protein in Rat appears to bind the large subunit of RNA polymerase II and provide a link between transcription and pre-mRNA splicing. Alternatively spliced transcript variants have been described. [provided by RefSeq, Feb 2009].

Transcript (Including UTRs)

Position: chr21:33,043,313-33,104,431 **Size:** 61,119 **Total Exon Count:** 20 **Strand:** -

Coding Region

Position: chr21:33,043,712-33,104,005 **Size:** 60,294 **Coding Exon Count:** 20

Page Index	Sequence and Links	UniProtKB Comments	CTD	Gene Alleles	RNA Structure
Protein Structure	Other Species	GO Annotations	mRNA Descriptions	Other Names	Model Information
Methods					

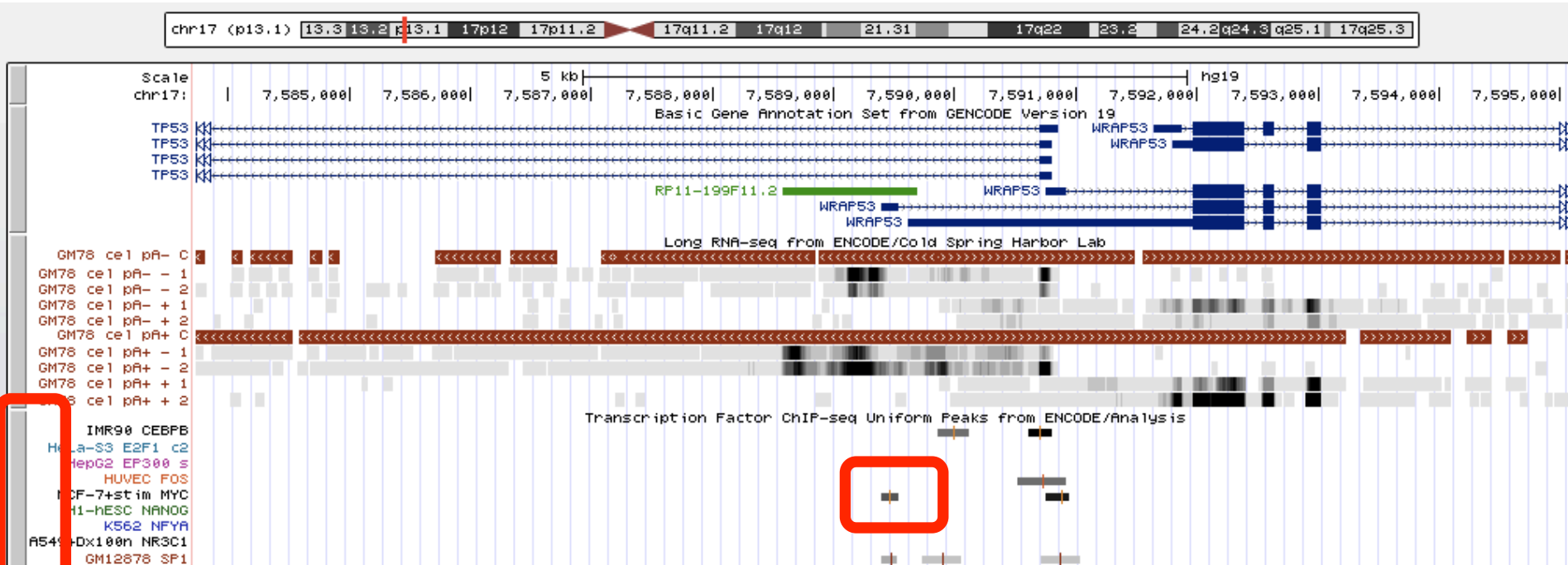
Data last updated: 2013-06-14

☐ Sequence and Links to Tools and Databases

Genomic Sequence (chr21:33,043,313-33,104,431)			mRNA (may differ from genome)		Protein (1147 aa)
Gene Sorter	Genome Browser	Protein FASTA	VisiGene	Table Schema	BioGPS
CGAP	Ensembl	Entrez Gene	ExonPrimer	GeneCards	GeneNetwork
Gepis Tissue	H-INV	HGNC	HPRD	Jackson Lab	Lynx
MOPED	neXtProt	OMIM	PubMed	Stanford SOURCE	UniProtKB

☐ Comments and Description Text from UniProtKB

ENCODE



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

Regulation

refresh

ENCORE Regulation...

hide

ENC Histone...

hide

ENC RNA Binding...

hide

ENC TF Binding...

show

ENC Chromatin...

hide

FSU Repli-chip

hide

ENC DNA Methyl...

hide

Genome Segments

hide

ENC DNase/FAIRE...

hide

NKI Nuc Lamina...

hide

ENCODE: Super-track Settings

Regulation refresh

ENCODE Regulation... hide	CD34 DnaseI hide	CpG Islands... hide	ENC Chromatin... hide	ENC DNA Methyl... hide	ENC DNase/FAIRE... hide
ENC Histone... hide	ENC RNA Binding... hide	ENC TF Binding... show	FSU Repli-chip hide	Genome Segments hide	NKI Nuc Lamina... hide

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

ENC TF Binding Super-track Settings



ENCODE Transcription Factor Binding Tracks ([All Regulation tracks](#))

Display mode: show Submit



All

☒ dense [Uniform TFBS](#)

☐ hide [HAIB TFBS](#)

☐ hide [SYDH TFBS](#)

☐ hide [UChicago TFBS](#)

☐ hide [UTA TFBS](#)

☐ hide [UW CTCF Binding](#)

Transcription Factor ChIP-seq Uniform Peaks from ENCODE/Analysis ENCODE March 2012 Freeze

Transcription Factor Binding Sites by ChIP-seq from ENCODE/HAIB

Transcription Factor Binding Sites by ChIP-seq from ENCODE/Stanford/Yale/USC/Harvard

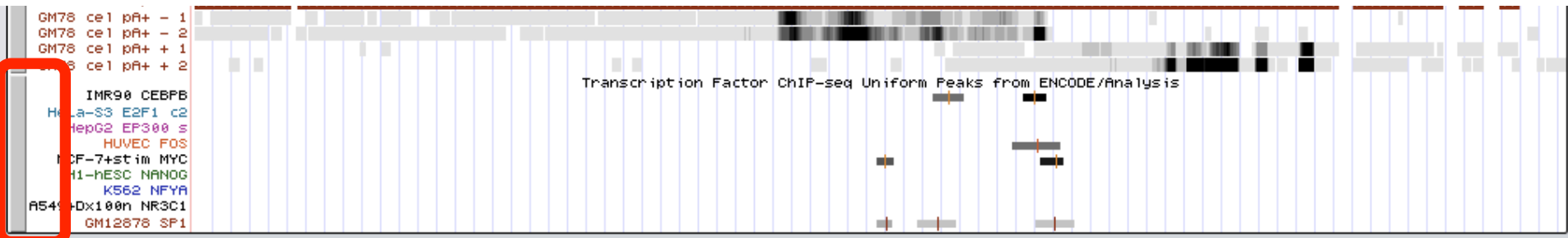
Transcription Factor Binding Sites by Epitope-Tag from ENCODE/UChicago

Open Chromatin TFBS by ChIP-seq from ENCODE/Open Chrom(UT Austin) ENCODE July 2011 Freeze

CTCF Binding Sites by ChIP-seq from ENCODE/University of Washington

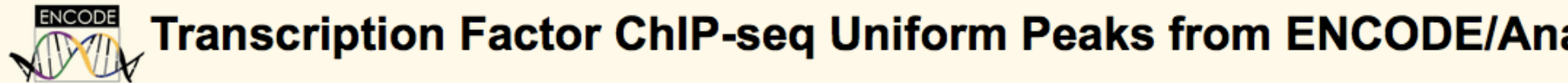
Description

ENCODE: Track Settings



Uniform TFBS Track Settings

[ENCODE](#) [Downloads](#) [Subtracks↓](#) [Description↓](#) [Contact↓](#)



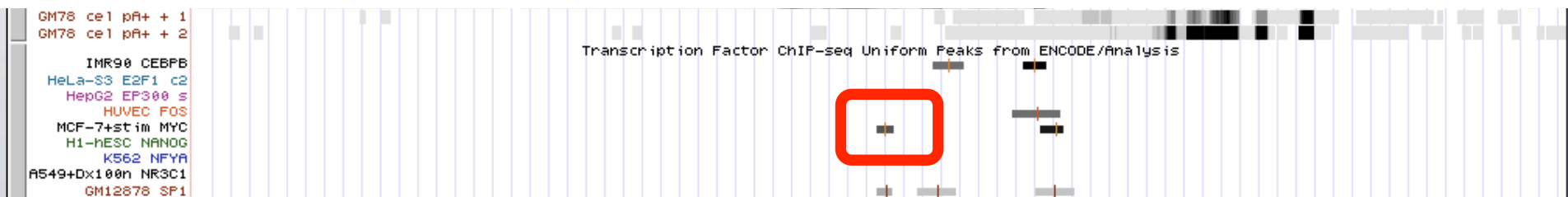
Display mode: dense Submit Cancel [Reset to defaults](#)

Score range: min: (0 to 1000)

Select subtracks by cell line and factor: (help)

[illegible]

ENCODE: Item Details



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.

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

MCF-7 (serum_stimulated) TFBS Uniform Peaks of c-Myc from ENCODE/UT-A/Analysis

Position: [chr17:7589391-7589530](#)

Peak point: 7589461

Score: 688

Signal value: 107.768

Q-value (FDR): 4.212

View table: [schema](#), [downloads](#), [metadata](#) ▾

[Go to Uniform TFBS track controls](#)

Data version: ENCODE Mar 2012 Freeze

Data last updated: 2013-04-12

Description

This track represents a comprehensive set of human transcription factor binding sites based on ChIP-seq experiments generated by production in the ENCODE Consortium from the inception of the project in September 2007, through the March 2012 internal data freeze. The track represents

ENCODE Tools

UCSC Genome Bioinformatics

Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Session - FAQ - Help

- Genome Browser
- Ebola
- Blat
- Table Browser
- Gene Sorter
- In Silico PCR
- Genome Graphs
- Galaxy
- VisiGene
- Utilities
- Downloads
- Release Log
- Custom Tracks
- Cancer Browser
- Microbial Genomes
- ENCODE**

About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides portals to [ENCODE](#) data at UCSC (2003 to 2012) and to the [Neandertal](#) project. Download or purchase the Genome Browser source code, or the Genome Browser in a Box ([GBiB](#)) at our [online store](#).

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the [UC Santa Cruz Genomics Institute](#) and the Center for Biomolecular Science and Engineering ([CBSE](#)) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#).

The Genome Browser project team relies on public funding to support our work. Donations are welcome -- we have many more ideas than our funding supports! If you have ideas, drop a comment in our [suggestion box](#).

[DONATE NOW](#)

News



[News Archives](#) ►

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the [genome-announce](#) mailing list. Please see our [blog](#) for posts about Genome Browser tools, features, projects and more.

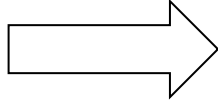
03 March 2015 - Use UDR for Quick Sizable Downloads

The UCSC Genome Browser is pleased to share a download protocol to use when downloading large sets of files from our download servers: **UDR (UDT Enabled Rsync)**. UDR utilizes rsync as the transport mechanism, but sends the data over the UDT protocol, which enables huge amounts of data to be downloaded efficiently over long distances.

Protocols like http, ftp and rsync can have a problem in that the further away the download source is from the user, the slower the speed becomes. Protocols like UDT/UDR allow for many UDP packets to be sent in batch, thus allowing for much higher transmit speeds over long distances. UDR will be especially useful for users who are downloading from places that are far away from California. The US East Coast and the international community will likely see much higher download speeds by using UDR rather than rsync, http or ftp. [Read more](#).

ENCODE

ENCODE



genome.ucsc.edu/ENCODE/



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)

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.

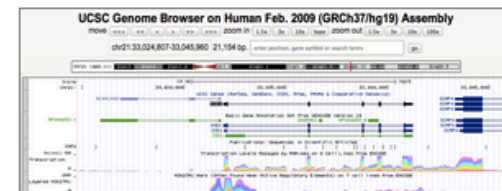
UCSC coordinated data for the ENCODE Consortium from its inception in 2003 (Pilot phase) to the end of the first 5 year phase of whole-genome data production in 2012. All data produced by ENCODE investigators and the results of ENCODE analysis projects from this period are hosted in the UCSC Genome browser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



ENCODE: Experiment Matrix

search for: ☒ tracks ☐ files

Cell Types

Assays

DNA Methylation	Methyl Array	Methyl RRBS	Open Chromatin	DNase-DGF	DNase-seq	FAIRE-seq	RNA Binding Proteins	RIP Gene ST	RIP Tiling Array	RIP Validation	RIP-seq	RNA Profiling	CAGE	Exon Array	RNA-chip	RNA-PET	RNA-seq	Small RNA-seq	TFBS & Histones	ChIP-seq	Other
Tier 1																					
GM12878	1	1			2	1		7	4		4		6	2	6	2	12	5		133	
H1-hESC	1	1			2	1		3					4	1		1	10	3		91	
K562	1	1		3	16	3		6	4		4		9	7	9	6	17	7		224	
Tier 2																					
A549	1	1		1	2	1							3	2		3	10	9		87	
CD20+													1				2	1		4	
CD20+_RO01778				1	1															2	
CD20+_RO01794					1															5	
H1-neurons																		3		4	
HeLa-S3	1	1			3	3		4					6	4		3	8	3		93	
HepG2	1	1		1	2	1		1					6	2	5	2	2	2		114	

view matrix

ENCODE: Experiment Summary



ENCODE Experiment Summary hg19 2007 - 2012

search for: ☒ tracks ☐ files

Genome Annotation	
GENCODE	4
Mappability	10
ORChID	1
Total: 3	15

All Experiments		view matrix by cell line
5C	13	
CAGE	78	
ChIA-PET	8	
ChIP-seq	1479	
Combined	26	
DNA-PET	6	
DNase-DGF	56	
DNase-seq	219	
Exon Array	158	
FAIRE-seq	37	
Genotype	64	
Methyl Array	62	

ChIP-seq Experiments		view matrix by cell line
ARID3A	2	
ATF1	1	
ATF2	2	
ATF3	7	
BACH1	2	
BATF	1	
BCL11A	3	
BCL3	3	
BCLAF1	2	
BDP1	2	
BRCA1	4	

ENCODE: Track Search

Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly

Search

Advanced

Track Name: contains

and Description: contains

and Group: is

and Data Format: is

ENCODE terms

+ and is among [Antibody or target protein](#)

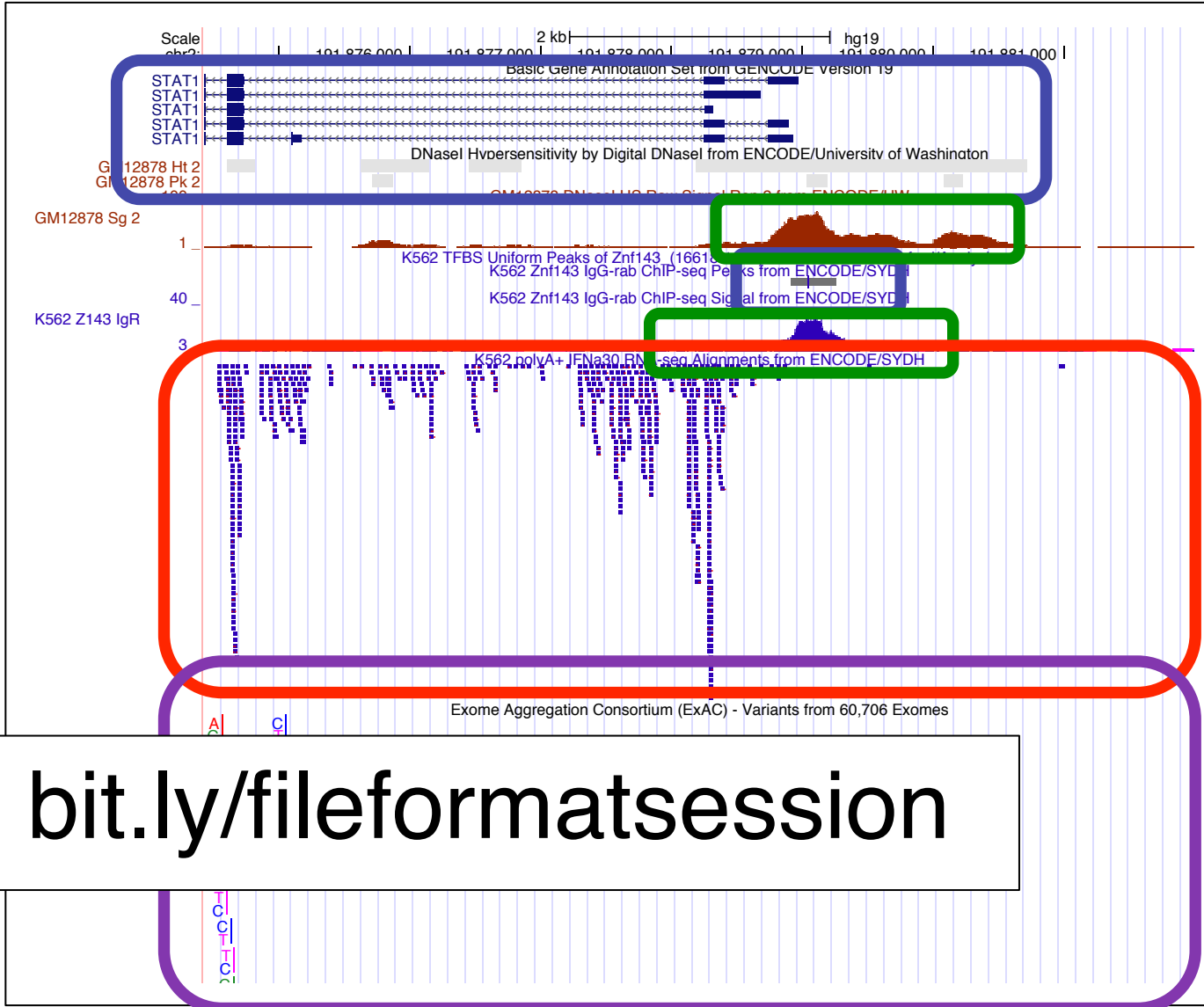
+ and is among

[return to browser](#)

(12 of 12 selected)

+ -	Visibility	Track Name	Sort: <input checked="" type="radio"/> by Relevance <input type="radio"/> Alphabetically <input type="radio"/> by Hierarchy
<input checked="" type="checkbox"/>	pack ▾	GM12878 BRCA1	GM12878 TFBS Uniform Peaks of BRCA1_(A300-000A) from ENCODE/Stanford/Analysis ▾
<input checked="" type="checkbox"/>	pack ▾	H1-hESC BRCA1	H1-hESC TFBS Uniform Peaks of BRCA1_(A300-000A) from ENCODE/Stanford/Analysis ▾
<input checked="" type="checkbox"/>	pack ▾	HeLa-S3 BRCA1	HeLa-S3 TFBS Uniform Peaks of BRCA1_(A300-000A) from ENCODE/Stanford/Analysis ▾
<input checked="" type="checkbox"/>	pack ▾	HepG2 BRCA1 Display track details	HepG2 TFBS Uniform Peaks of BRCA1_(A300-000A) from ENCODE/Stanford/Analysis ▾
<input checked="" type="checkbox"/>	pack ▾	GM12878 BRC1 IgM	GM12878 BRCA1 IgG-mus ChIP-seq Peaks from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	full ▾	GM12878 BRC1 IgM	GM12878 BRCA1 IgG-mus ChIP-seq Signal from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	pack ▾	H1ES BRC1 IgR	H1-hESC BRCA1 IgG-rab ChIP-seq Peaks from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	full ▾	H1ES BRC1 IgR	H1-hESC BRCA1 IgG-rab ChIP-seq Signal from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	pack ▾	HeLa BRC1 IgR	HeLa-S3 BRCA1 IgG-rab ChIP-seq Peaks from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	full ▾	HeLa BRC1 IgR	HeLa-S3 BRCA1 IgG-rab ChIP-seq Signal from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	pack ▾	HEPG BRC1 IgR	HEPG2 BRCA1 IgG-rab ChIP-seq Peaks from ENCODE/SYDH ▾
<input checked="" type="checkbox"/>	full ▾	HEPG BRC1 IgR	HEPG2 BRCA1 IgG-rab ChIP-seq Signal from ENCODE/SYDH ▾

File Formats



BED

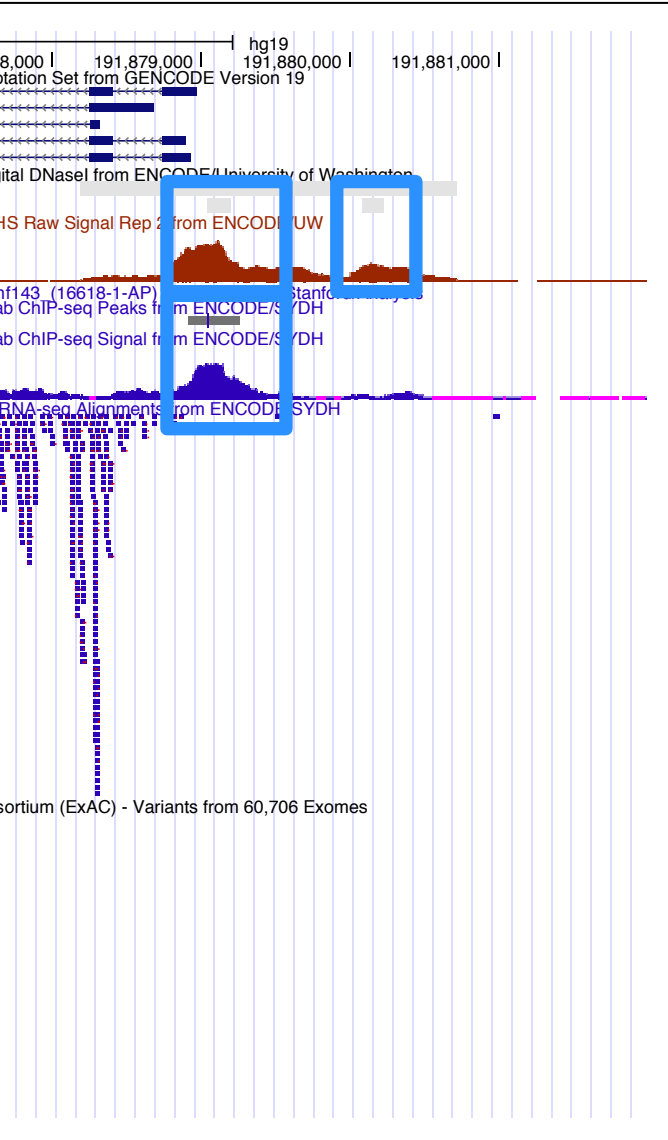
wig(gle)

BAM

VCF

bit.ly/fileformatsession

File Formats



BED

Positional annotations. (ex. Regions w/: enriched ChIP-seq signal for TF binding, Δ I methylation, splice jxns from RNA-seq)

wig(gle)

Continuous signal data. # of reads (ex. DNase I HS and ChIP-seq signals)

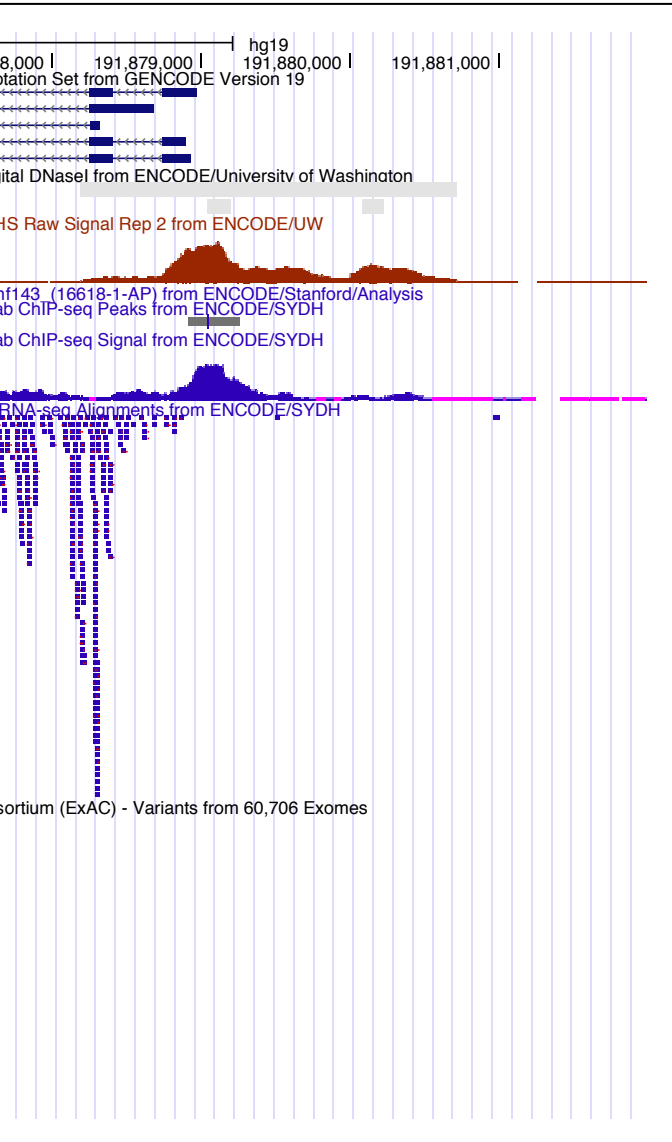
BAM

Alignments of seq. reads, mapped to genome (ex. RNA-seq alignments)

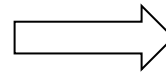
VCF

Variation data: SNPs, indels, Copy Number Variants, Structural Variants (ex. ExAC data)

Indexed File Formats

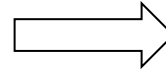


BED



bigBed

wig(gle)



bigWig

BAM

VCF

Indexed File Formats

- Only displayed portions of files transferred to UCSC
- Display large files (would time out)
- File + index on your web-accessible server (http, https, or ftp)
- Faster display
- More user control

File Formats

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

Add Custom Tracks

clade genome assembly

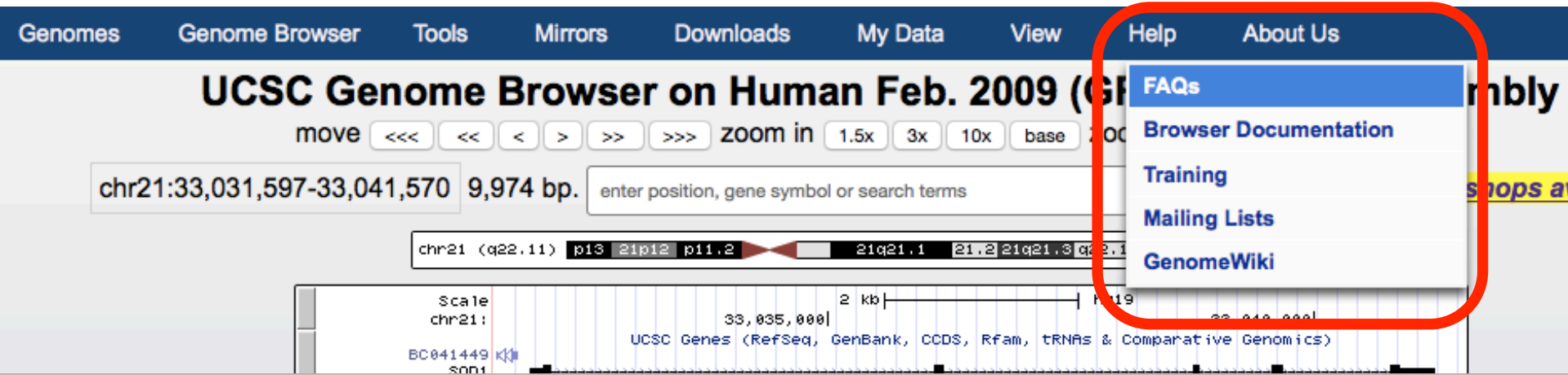
Display your own data as custom annotation tracks in the browser. Data must be formatted in [BED](#), [bigBed](#), [bedGraph](#), [GFF](#), [GTF](#), [WIG](#), [bigWig](#), [MAF](#), [BAM](#), [BED detail](#), [Personal Genome SNPs](#), [VCF](#), [broadPeak](#), [narrowPeak](#), or [PSL](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Publicly available custom tracks are listed [here](#). Examples are [here](#).

Paste URLs or data:

Or upload:

No file selected.

File Formats



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

UCSC Genome Browser on Human Feb. 2009 (GRCh37)

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

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

chr21 (q22.11) p13 p12 p11.2 21q21.1 21.2 21q21.3 q22.1

Scale chr21: 33,035,000 2 kb

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

BC041449 SOD1

UCSC Genome Bioinformatics

Home - Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Session - Help

FAQ Table of Contents

This page contains responses to questions frequently asked by our user community and subscribers to the [Genome Browser mailing list](#).

- [Display Problems](#)
- [Assembly Releases and Versions](#)
- [Data and Downloads](#)
- [Genome Browser Tracks](#)
- [Custom Annotation Tracks](#)
- [Data File Formats](#)

- [Blat](#)
- [ENCODE Resources and FAQ](#)

File Formats

UCSC Genome Bioinformatics

[Home](#) - [Genomes](#) - [Blat](#) - [Tables](#) - [Gene Sorter](#) - [PCR](#) - [VisiGene](#) - [Session](#) - [Help](#)

Frequently Asked Questions: Data File Formats

General formats:

- [Axt format](#)
- [BAM format](#)
- [BED format](#)
- [BED detail format](#)
- [bedGraph format](#)
- [bigBed format](#)
- [bigGenePred table format](#)
- [bigWig format](#)

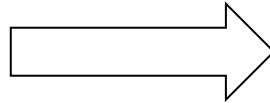
ENCODE-specific formats:

- [ENCODE broadPeak format](#)
- [ENCODE gappedPeak format](#)
- [ENCODE narrowPeak format](#)
- [ENCODE pairedTagAlign format](#)
- [ENCODE peptideMapping format](#)
- [ENCODE RNA elements format](#)
- [ENCODE tagAlign format](#)

File Formats

www.encodeproject.org/help/file-formats/

Help



File formats

ENCODE Data ▾ Methods ▾ About ENCODE ▾ Help ▾ Search ENCODE 🔍 Sign In

Common File Formats the ENCODE Consortium

Getting started
REST API
File formats
Tutorials
Contact

Overview

The ENCODE consortium uses several file formats to store, display, and disseminate data:

- **FASTQ**: a text-based format for storing nucleotide sequences (reads) and their quality scores. [1]
- **BAM**: The Sequence Alignment/Mapping (SAM) format is a text-based format for storing read alignments against reference sequences and it is interconvertible with the binary BAM format. [2]
- **bigWig**: The bigWig format is an indexed binary format for rapid display of continuous and dense data in the UCSC Genome Browser.
- **bigBed**: The bigBed format is also an indexed binary format for rapid display of annotation items such as a linked collection of exons or the binding peaks of a transcription factor.

These file formats were originally designed to be generic and flexible. As the ENCODE consortium is a collaborative effort, the consortium has made several specifications on the file formats to facilitate data archival, presentation, and distribution, as well as integrative analysis on the data. The consortium considers FASTQ as the basic file format for archival purpose and thus the FASTQ format's specifications aim to preserve the raw

Custom Tracks

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group genome assembly position search term

Mammal Human Feb. 2009 (GRCh37/hg19) chr17:7,583,734-7,595,119 enter position, gene symbol or search terms submit

[Click here to reset](#) the browser user interface settings to their defaults. [More on-site workshops available!](#)

track search **add custom tracks** track hubs configure tracks and display

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

UCSC Genome Browser on Human Feb 9) Assembly

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

chr17:7,583,734-7,595,119 11,386 bp. enter position, gene symbol or search term

Custom Tracks

chr17 (p13.1) 13.3 13.2 13.1 17p12 17p11.2 17q11.2 17q12 21.31 17q22 23.2 24.2q24.3 q25.1 17q25.3

Scale chr17: 5 kb hg19

TP53 TP53 TP53 TP53

Basic Gene Annotation Set from GENCODE Version 19

WRAP53 WRAP53

RP11-199F11.2

move start < 2.0 > move end < 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.

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

Use drop-down controls below to alter tracks displayed

Custom Tracks

genome.ucsc.edu/cgi-bin/hgCustom

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

Add Custom Tracks

clade genome assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [BED](#), [bigBed](#), [bedGraph](#), [GFF](#), [GTF](#), [WIG](#), [bigWig](#), [MAF](#), [BAM](#), [BED detail](#), [Personal Genome SNP](#), [VCF](#), [broadPeak](#), [narrowPeak](#), or [PSL](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Publicly available custom tracks are listed [here](#). Examples are [here](#).

Paste URLs or data:

Or upload:

No file selected.

BED format

[Index](#)

BED format provides a flexible way to define the data lines that are displayed in an annotation track. BED lines have three required fields and nine additional optional fields. The number of fields per line must be consistent throughout any single set of data in an annotation track. The order of the optional fields is binding: lower-numbered fields must always be populated if higher-numbered fields are used.

If your data set is BED-like, but it is very large and you would like to keep it on your own server, you should use the [bigBed](#) data format.

The first three required BED fields are:

1. **chrom** - The name of the chromosome (e.g. chr3, chrY, chr2_random) or scaffold (e.g. scaffold10671).
2. **chromStart** - The starting position of the feature in the chromosome or scaffold. The first base in a chromosome is numbered 0.
3. **chromEnd** - The ending position of the feature in the chromosome or scaffold. The *chromEnd* base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as *chromStart*=0, *chromEnd*=100, and span the bases numbered 0-99.

The 9 additional optional BED fields are:

4. **name** - Defines the name of the BED line. This label is displayed to the left of the BED line in the Genome Browser window when the track is

Custom Tracks

genome.ucsc.edu/cgi-bin/hgCustom

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

Add Custom Tracks

clade genome assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [BED](#), [bigBed](#), [bedGraph](#), [GFF](#), [GTF](#), [WIG](#), [bigWig](#), [MAF](#), [BAM](#), [BED detail](#), [Personal Genome SNP](#), [VCF](#), [broadPeak](#), [narrowPeak](#), or [PSL](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Publicly available custom tracks are listed [here](#). Examples are [here](#).

Paste URLs or data:

Or upload:

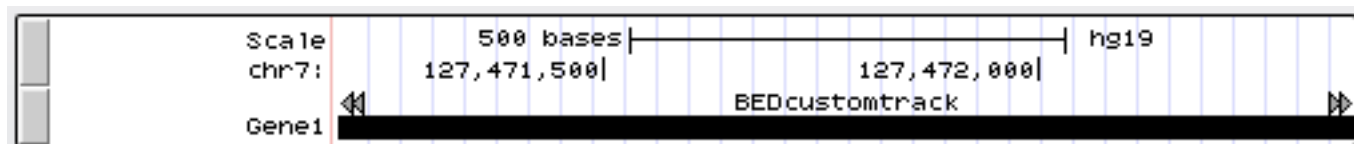
No file selected.

```
track name="BED_custom_track"
chr7 127471196 127472363 Gene1
```

Optional track documentation:

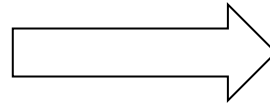
Or upload:

No file selected.

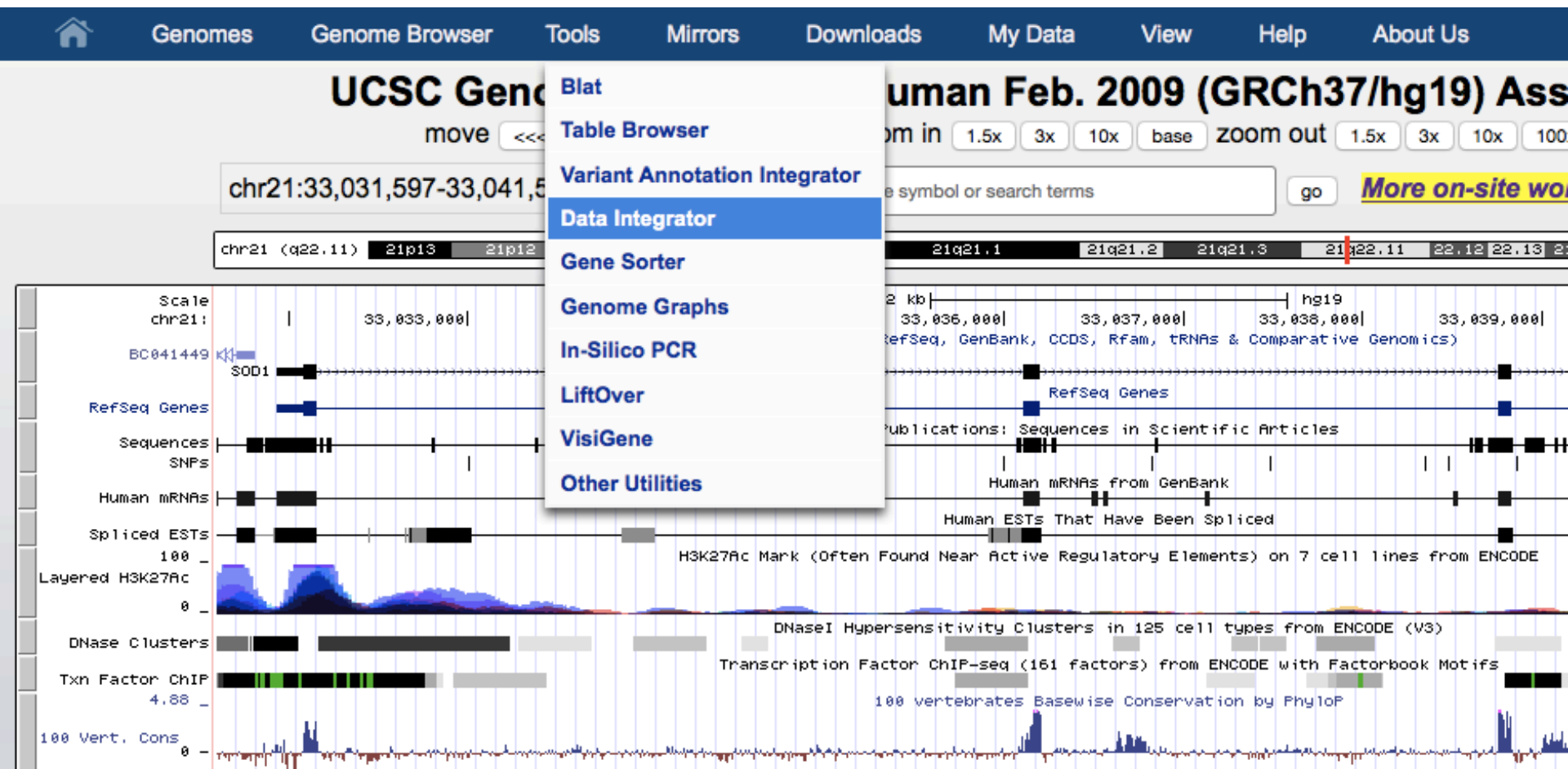


Annotating your data: BED

Tools



Data Integrator



Data Integrator

genome.ucsc.edu/cgi-bin/hgIntegrator

Data Integrator

Select Genome Assembly and Region

group

genome

assembly

Mammal

Human

Feb. 2009 (GRCh37/hg19)

region to annotate

position or search term

chr21:33031597-33041570

Configure Data Sources

↓ SYDH_TFBS [View table schema](#)

↓ GENCODE Genes V19 - Basic [View table schema](#)

Add Data Source

track group

track

view

subtrack

Genes and Gene Predictions

GENCODE Genes V19...

Genes...

Basic (wgEncodeGencodeBasicV19)

[View table schema](#)

get more data:

Output Options

☐ Send output to file

Data Integrator

Data Integrator Undo Redo

Select **Choose Fields** ✕

group
Mamm

region
positi

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↑ SY
↑ G

Add **Basic**

track
Gene
[View](#)

get m
track

Outp

☐ S
Cho
Get

Using

SYDH_TFBS
Set all Clear all

<input checked="" type="checkbox"/> chrom	Reference sequence chromosome or scaffold
<input checked="" type="checkbox"/> chromStart	Start position in chromosome
<input checked="" type="checkbox"/> chromEnd	End position in chromosome
<input checked="" type="checkbox"/> name	Name of item.
<input checked="" type="checkbox"/> score	Score (0-1000)
<input type="checkbox"/> strand	+ or - for strand

Basic
Set all Clear all

<input checked="" type="checkbox"/> name	Name of gene (usually transcript_id from GTF)
<input type="checkbox"/> chrom	Reference sequence chromosome or scaffold
<input type="checkbox"/> strand	+ or - for strand
<input type="checkbox"/> txStart	Transcription start position
<input type="checkbox"/> txEnd	Transcription end position
<input type="checkbox"/> cdStart	Coding region start
<input type="checkbox"/> cdEnd	Coding region end
<input type="checkbox"/> exonCount	Number of exons
<input type="checkbox"/> exonStarts	Exon start positions
<input type="checkbox"/> exonEnds	Exon end positions
<input type="checkbox"/> score	score
<input checked="" type="checkbox"/> name2	Alternate name (e.g. gene_id from GTF)
<input type="checkbox"/> cdStartStat	enum('none','unk','incmpl','cmpl')

Data Integrator

Data Integrator Undo Redo

Select Genome Assembly and Region

group

genome

assembly

Mammal

Human

Feb. 2009 (GRCh37/hg19)

region to annotate

position or search term

chr21:33031597-33041570

Configure Data Sources

↓ SYDH_TFBS [View table schema](#)

↓ GENCODE Genes V19 - Basic [View table schema](#)

Add Data Source

track group

track

view

subtrack

Genes and Gene Predictions

GENCODE Genes V19...

Genes...

Basic (wgEncodeGencodeBasicV19)

[View table schema](#) Add

get more data:

track hubs custom tracks

Output Options

☐ Send output to file

Choose fields...

Get output

Using the Data Integrator

Data Integrator

```
#ct_SYDHTFBS_4733.chrom ct_SYDHTFBS_4733.chromStart
ct_SYDHTFBS_4733.chromEnd ct_SYDHTFBS_4733.name ct_SYDHTFBS_4733.score
wgEncodeGencodeBasicV19.name wgEncodeGencodeBasicV19.name2
```

chr21	33031473	33032186	.	608	ENST00000449339.1	
AP000253.1						
chr21	33031473	33032186	.	608	ENST00000270142.6	SOD1
chr21	33031473	33032186	.	608	ENST00000389995.4	SOD1
chr21	33031473	33032186	.	608	ENST00000470944.1	SOD1

Annotating your VCF file

1. Make a VCF custom track
2. Go to the Variant Annotation Integrator
3. Choose your track
4. Add annotations

Remotely Hosted Custom Tracks

- Put data file (bigBed/bigWig/BAM/VCF, etc) in internet accessible location
- Must have: 1. track info, 2. bigDataUrl
- VCF example:

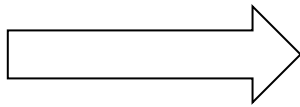
```
track type=vcfTabix  
name="VCF_Example"  
description="VCF Ex. 1: 1000 Genomes phase 1  
interim SNVs"  
bigDataUrl=  
http://hgwdev.cse.ucsc.edu/~pauline/presentations/  
vcfExample.vcf.gz
```

Variant Annotation Integrator

- Upload pgSnp or VCF custom track
- Associate UCSC annotations with your uploaded variant calls
- Add dbSNP info if dbSNP identifier found
- Select custom track and VAI options

Variant Annotation Integrator

Tools



Variant Annotation Integrator

The screenshot displays the UCSC Genome Browser interface. The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. The 'Tools' menu is open, and the 'Variant Annotation Integrator' option is highlighted with a red circle. The main content area shows the 'Human Feb. 2009 (GRCh37/hg19) Assembly' with a zoomed-in view of chromosome 21. The position track shows coordinates from 33,031,596 to 33,041,000. Below the position track, there are tracks for RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics, and H2A.2 Histone Mods by ChIP-seq Peaks from ENCODE/Broad. The bottom of the interface includes a 'move start' and 'move end' section with a zoom level of 2.0, and a row of buttons: track search, default tracks, default order, hide all, manage custom tracks, track hubs, configure, reverse, resize, and refresh.

Variant Annotation Integrator

genome.ucsc.edu/cgi-bin/hgVai

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

Variant Annotation Integrator

Select Genome Assembly and Region

clade	genome	assembly
<input type="text" value="Mammal"/>	<input type="text" value="Human"/>	<input type="text" value="Feb. 2009 (GRCh37/hg19)"/>

region to annotate

Select Variants

If you have more than one custom track or hub track in [pgSnp](#) or [VCF](#) format, please select the one you wish to annotate:

variants:

maximum number of variants to be processed:

[manage custom tracks](#)[track hubs](#)

To reset **all** user cart settings (including custom tracks), [click here](#).

Select Genes

The gene predictions selected here will be used to determine the effect of each variant on genes, for example intronic, missense, splice site, intergenic, etc.

Select Regulatory Annotations

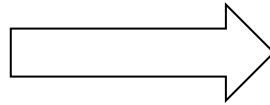
The annotations in this section provide predicted regulatory regions based on various experimental data. When a variant overlaps an annotation, a consequence term [regulatory region variant](#) will be assigned. Follow the links to description pages that explain how each dataset was constructed. A significant portion of the genome and it may be desirable to filter these annotations by cell type and/or score in order to avoid an overabundance of annotations.

Track Data Hubs

- Remotely hosted
- Data persistence
- File formats:
bigBED, bigWig, BAM, VCF
- Track organization:
groups, supertracks
- multiWigs
- Assembly hubs

Track Hubs

My Data



Track Hubs

Human (*Homo sapiens*) Genome Browser Gateway

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group

genome

assembly

position

search term

Mammal

Human

Feb. 2009 (GRCh37/hg19)

chr17:7,583,734-7,595,119

enter position, gene symbol or search terms

submit

[Click here to reset](#) the browser user interface settings to their defaults.

[More on-site workshops available!](#)

track search

add custom tracks

track hubs

configure tracks and display

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Genome Browser

Tools

Mirrors

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View

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UCSC Genome Browser on Human Feb

19) Assembly

move

<<<

<<

<

>

>>

>>>

zoom in

1.5x

3x

10x

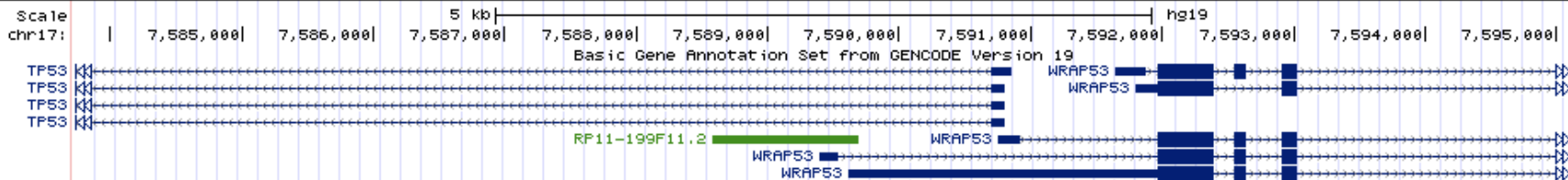
100x

chr17:7,583,734-7,595,119 11,386 bp.

enter position, gene symbol or search terms

[on-site workshops available!](#)

chr17 (p13.1) 13.3 13.2 13.1 17p12 17p11.2 17q11.2 17q12 21.31 17q22 23.2 24.2q24.3 q25.1 17q25.3



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

add custom tracks

track hubs

configure

reverse

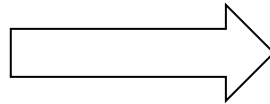
resize

refresh

Track Hubs

genome.ucsc.edu/cgi-bin/hgHubConnect

My Data



Track Hubs



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Track Data Hubs

Track data hubs are collections of external tracks that can be imported into the UCSC Genome Browser. Hub tracks show up under the label bar on the main browser page, as well as on the configure page. For more information, see the [User's Guide](#). To import a public hub "Connect" button below.

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

Public Hubs

My Hubs

Enter search terms to find in public track hub description pages:

Search Public Hubs

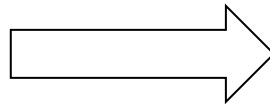
Clicking Connect redirects to the gateway page of the selected hub's default assembly.

Display	Hub Name	Description	Assemblies
Connect	Roadmap Epigenomics Data Complete Collection at Wash U VizHub	Roadmap Epigenomics Human Epigenome Atlas Data Complete Collection, VizHub at Washington University in St. Louis	hg19
		UMassMed H3K4me3 ChIP-seq data for	

My Hubs

genome.ucsc.edu/cgi-bin/hgHubConnect

My Data



Track Hubs



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Track Data Hubs

Track data hubs are collections of external tracks that can be imported into the UCSC Genome Browser. Hub tracks show up under the hub's own blue label bar on the main browser page, as well as on the configure page. For more information, see the [User's Guide](#). To import a public hub click its "Connect" button below.

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

Public Hubs

My Hubs

URL:

Add Hub

No Unlisted Track Hubs

Contact genome@soe.ucsc.edu to add a public hub.

Make Your Own Track Hub

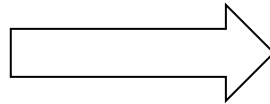
You will need:

- Data (compressed binary index formats: bigBed, bigWig, BAM, VCF)
- Text files to define properties of the track hub
- Internet-enabled web/ftp server
- *Assembly Hubs:*
a twoBit sequence file

Track Hubs

genome.ucsc.edu/cgi-bin/hgHubConnect

My Data



Track Hubs



myHub/ - directory containing track hub files



hub.txt - a short description of hub properties



genomes.txt - list of genome assemblies included



hg19/ - directory of data for the hg19 human assembly



Data files! BAM, bigBed, bigWig, VCF

An Example Assembly Hub

An Arabidopsis hub:

*[http://genome-test.cse.ucsc.edu/
~pauline/hubs/Plants/hub.txt](http://genome-test.cse.ucsc.edu/~pauline/hubs/Plants/hub.txt)*



Acknowledgements

UCSC Genome Browser team

- David Haussler – co-PI
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- Bob Kuhn – Associate Director, Outreach – co-PI
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Engineering

Angie Hinrichs
Kate Rosenbloom
Hiram Clawson
Galt Barber
Brian Raney
Max Haeussler

QA, Docs, Support

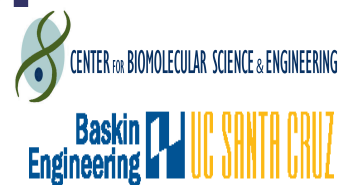
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Sys-admins

Jorge Garcia
Erich Weiler
Gary Moro



THE GB TEAM



UNIVERSITY OF CALIFORNIA
SANTA CRUZ

THE ORIGINAL
AUTHORITY ON
QUESTIONING
AUTHORITY

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QB3 (UCBerkeley, UCSF, UCSC)

California Institute for Regenerative Medicine (CIRM)

Genotype-Tissue Expression Project (GTex)



genome.ucsc.edu

THANK YOU!

Exercises

1. Load example BED and VCF tracks via url
2. Look at custom track data by pasting url into a web browser.
3. Annotate the TFBS custom track using the Data Integrator.
4. Annotate the VCF custom track using the Variant Annotation Integrator.

Exercise 1

Load example BED and VCF tracks via url

1. Go to the Custom tracks menu
 - My Data -> Custom Tracks
2. Input this url: <http://bit.ly/customtracks> (note that you must include the "http" part of this url or you will get an error) and click [submit].
3. Click the [Go to genome browser] button.
4. Once in the main Browser, jump to this position:
 - chr21:33,034,804-33,037,719
5. See if you can drag your 2 custom tracks to the top of the display

Exercise 2

Exploring your BED and VCF tracks

1. Now that you have 2 custom tracks loaded, take a look at the data by pasting that same url into a web browser:
2. These custom tracks are actually data copied from some existing tracks, see if you can find them, turn them on, and observe that the original tracks and custom tracks look the same in the browser:
 - Track 1 (BED format): Group (Regulation), Super Track (ENC TF Binding), Track (SYDH TFBS)
 - Track 2 (VCF format): Group (Variation), Track (1000G Ph1 Vars)
3. Navigate to this position for best comparison (esp. for the VCF track): chr21:33,034,804-33,037,719

Exercise 3

Annotate your BED with the Data Integrator

1. Go to the Data Integrator
2. Once there select:
 1. Region to annotate: chr21:33031597-33041570
 2. Add data source: group (custom tracks), track (SYDH...) [click add]
3. Now choose which annotations you want to add by [add]ing more tracks to the list – ex:
 1. *Find the genes that overlap with your regions:* group (Genes and Gene Prediction), track (GENCODE V19), view (Genes), subtrack (Basic) [add]
 2. *Find the SNPs that overlap with your regions:* group (Variation), track (Common SNPs) [add]

Choose which fields to include in your output:

Output options -> Choose fields [Done] -> [get output]

Exercise 4

Annotate your VCF with the Variant Annotation Integrator

1. Go to the Variant Annotation Integrator
 - Tools -> V.A.I.
2. Select your custom track of variants:
 - Variants: “VCF Ex. 1...”
3. Now choose which annotations you want to add:
 - To determine which gene regions your variants fall into, select a gene track (Select Genes = “Basic Gene Annotation Set... GENCODE”)
 - Add regulatory annotations: Under “Select Regulatory Annotations” click the “+” button to choose which TFs to include (or select none to include all binding sites)

Bonus Material!

Where to search

genome.ucsc.edu/cgi-bin/hgGateway

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(Homo sapiens) Genome Browser Gateway

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group	genome	assembly	position	search term	
normal	Human	Feb. 2009 (GRCh37/hg19)	chr21:33,031,597-33,041,570	brc	submit

[Click here to reset](#) the browser user interface settings to their defaults. **[More on-site workshops available!](#)**

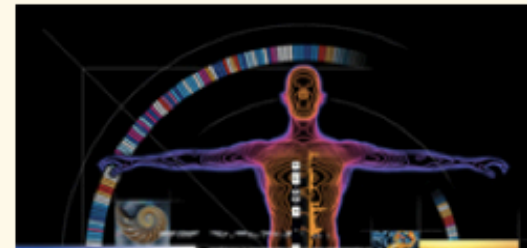
[track search](#) [add custom tracks](#) [track hubs](#) [configure tracks and display](#)

Genome Browser – hg19 assembly ([sequences](#))

February 2009 human reference sequence (GRCh37) was produced by the [Genome Reference Consortium](#). For more information about this assembly, see [GRCh37](#) in the NCBI Assembly database.

Position queries

A position can be specified by the accession number of a sequenced genomic clone, or



Where to search

genome.ucsc.edu/cgi-bin/hgGateway

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(Homo sapiens) Genome Browser Gateway

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group	genome	assembly	position	search term
mmal	Human	Feb. 2009 (GRCh37/hg19)	chr21:33,031,597-33,041,570	brc

[Click here to reset](#) the browser user interface settings to their defaults. [More](#)

[track search](#) [add custom tracks](#) [track hubs](#) [configure tracks](#)

Genome Browser – hg19 assembly ([sequences](#))


February 2009 human reference sequence (GRCh37) was produced by the [Genome Reference Consortium](#). For more information about this assembly, see [GRCh37](#) in the NCBI Assembly database.

Position queries

BRCA1 (Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant 2, mRNA.)

BRCA2 (Homo sapiens breast cancer 2, early onset (BRCA2), mRNA.)

BRCC3 (Homo sapiens BRCA1/BRCA2-containing complex, subunit 3 (BRCC3), transcript variant 1, mRNA.)



Where to search: Main Browser

genome.ucsc.edu/cgi-bin/hgTracks

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

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

1,196,312-41,277,500 81,189 bp

go [More on-site workshop](#)

chr17 (q21.31) 13

Scale chr17: 41,210,000

BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1

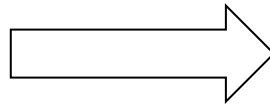
SMAD1 (Homo sapiens SMAD family member 1 (SMAD1), transcript variant 1, mRNA.)
SMAD2 (Homo sapiens SMAD family member 2 (SMAD2), transcript variant 2, mRNA.)
SMAD3 (Homo sapiens SMAD family member 3 (SMAD3), transcript variant 1, mRNA.)
SMAD4 (Homo sapiens SMAD family member 4 (SMAD4), mRNA.)
SMAD5 (Homo sapiens SMAD family member 5 (SMAD5), transcript variant 3, mRNA.)
SMAD5-AS1 (Homo sapiens SMAD5 antisense RNA 1 (SMAD5-AS1), non-coding RNA.)
SMAD6 (Homo sapiens SMAD family member 6 (SMAD6), transcript variant 1, mRNA.)
SMAD7 (Homo sapiens SMAD family member 7 (SMAD7), transcript variant 1, mRNA.)
SMAD9 (Homo sapiens SMAD family member 9 (SMAD9), transcript variant a, mRNA.)

BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1

ChIP-seq of GM12878 - ENCSR000DZS (Target - BRCA1)

Public Hubs

My Data



Track Hubs

Human (*Homo sapiens*) Genome Browser Gateway

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group

genome

assembly

position

search term

Mammal

Human

Feb. 2009 (GRCh37/hg19)

chr17:7,583,734-7,595,119

enter position, gene symbol or search terms

submit

[Click here to reset](#) the browser user interface settings to their defaults.

[More on-site workshops available!](#)

track search

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track hubs

configure tracks and display

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UCSC Genome Browser on Human Feb

19) Assembly

move

<<<

<<

<

>

>>

>>>

zoom in

1.5x

3x

10x

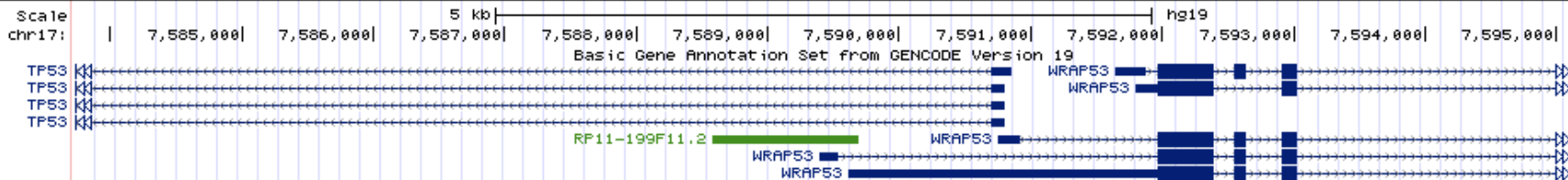
100x

chr17:7,583,734-7,595,119 11,386 bp.

enter position, gene symbol or search terms

[on-site workshops available!](#)

chr17 (p13.1) 13.3 13.2 13.1 17p12 17p11.2 17q11.2 17q12 21.31 17q22 23.2 24.2q24.3 q25.1 17q25.3



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

add custom tracks

track hubs

configure

reverse

resize

refresh

Where to search

genome.ucsc.edu/cgi-bin/hgHubConnect

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Track Data Hubs

Track data hubs are collections of external tracks that can be imported into the UCSC Genome Browser. Hub tracks show up under their own blue label bar on the main browser page, as well as on the configure page. For more information, see the [User's Guide](#). To import a hub click its "Connect" button below.

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

[Public Hubs](#)[My Hubs](#)

Enter search terms to find in public track hub description pages:

Clicking Connect redirects to the gateway page of the selected hub's default assembly.

Display	Hub Name	Description	Assemblies
<input type="button" value="Connect"/>	Roadmap Epigenomics Data Complete Collection at Wash U VizHub	Roadmap Epigenomics Human Epigenome Atlas Data Complete Collection, VizHub at Washington University in St. Louis	hg19
<input type="button" value="Connect"/>	Cancer genome polyA site &	An in-depth map of polyadenylation sites in cancer from matched genotypes	hg19

Track search

Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

(Homo sapiens) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
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group genome assembly position search term

normal Human Feb. 2009 (GRCh37/hg19) chr21:33,031,597-33,041,570 brc submit

[Click here to reset](#) the browser user interface settings to their defaults. **More on-site workshops available!**

track search add custom tracks track hubs configure tracks and display

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UCSC Genome Browser on Human Feb. 2009

move <<< << < > >> >>> zoom in 1.5x 3x 10x

chr17:41,196,312-41,277,500 81,189 bp. enter position, gene symbol or search term

chr17 (q21.31) 13.1 17p12 17p11.2 q11.2 17q12 17q22 24.3 25.1 q25.3

Scale chr17: 41,210,000 41,220,000 41,230,000 41,240,000 41,250,000 41,260,000 41,270,000

20 kb hg19 Basic Gene Annotation Set from GENCODE Version 19

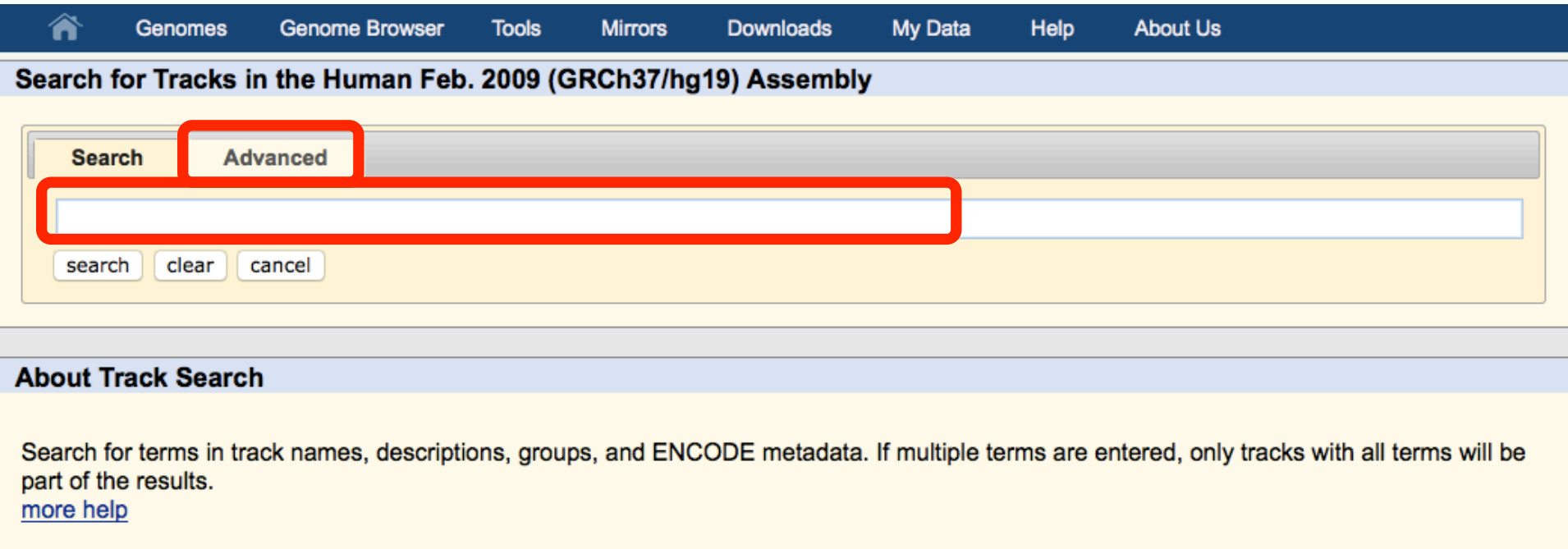
move start < 2.0 >

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 add custom tracks track hubs configure reverse resize refresh

Track search



The screenshot shows the 'Track Search' interface. At the top is a dark blue navigation bar with a home icon and links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. Below this is a light blue header bar with the text 'Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly'. The main search area has a yellow background and contains two tabs: 'Search' and 'Advanced'. The 'Advanced' tab is selected and highlighted with a red box. Below the tabs is a large white search input field, also highlighted with a red box. Underneath the input field are three buttons: 'search', 'clear', and 'cancel'. Below the search area is a light blue section titled 'About Track Search'. This section contains a paragraph explaining the search criteria and a link to 'more help'.

Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly

Search Advanced

search clear cancel

About Track Search

Search for terms in track names, descriptions, groups, and ENCODE metadata. If multiple terms are entered, only tracks with all terms will be part of the results.

[more help](#)

Track search

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

Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly

Search

Advanced

Track Name:

contains

and Description:

contains

and Group:

is

and Data Format:

is

[ENCODE terms](#)

and

H1-hESC

[Cell, tissue or DNA sample](#)

and

[Antibody or target protein](#)

☐

Visibility

☐

Track Name

☐

[GM12878](#)

GM12878 Methylation 450K Bead Array from ENCODE/HAIB

☐

[H1-hESC](#)

H1-hESC Methylation 450K Bead Array from ENCODE/HAIB

(0 of 2 selected)

About Track Search