


Add custom track to genome browser

The screenshot displays the UCSC Genome Browser interface for Human GRCh37/hg19. The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. A red arrow points to the 'Genomes' link, which has opened a dropdown menu. In this menu, 'Human GRCh37/hg19' is highlighted with a red box. A red text label '1. Select Human hg19' is positioned next to this menu.

The main content area shows the 'UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly'. It includes a search bar with the coordinates 'chr21:33,031,597-33,041,570' and a zoom level of '9,974 bp.'. Below the search bar is a track for 'chr21 (q22.11)' showing various genomic features. These tracks include: 'SOD1' gene model, 'NCBI RefSeq genes', 'Publications: Sequences in Scientific Articles', 'Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (570 donors)', 'SNORA81', 'H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE', 'DNase I Hypersensitivity Clusters in 125 cell types from ENCODE (V3)', 'Transcription Factor ChIP-seq Clusters (161 factors) from ENCODE with Factorbook Motifs', '100 vertebrates Basewise Conservation by PhyloP', 'Multiz Alignments of 100 Vertebrates', 'Short Genetic Variants from dbSNP release 153', and 'Repeating Elements by RepeatMasker'.

At the bottom of the interface, there is a 'move start' and 'move end' section with a zoom level of '2.0'. A red arrow points to the 'add custom tracks' button in the track search bar. A red text label '2. add custom track' is positioned next to this button. Below the track search bar, there is a note: 'Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "2" for keyboard shortcuts.' and another note: '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.'

Add custom track to genome browser

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Add Custom Tracks

clade Mammal ▼ genome Human ▼ assembly Feb. 2009 (GRCh37/hg19) ▼

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigBarChart](#), [bigChain](#), [bigG interact](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attri

Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in 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

Paste URLs or data:

Or upload: Choose File p53_macs_peaks.bed Submit

Clear

1. check version

2. upload
p53_macs_peaks.bed

Rename custom track

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Manage Custom Tracks

genome: Human assembly: Feb. 2009 (GRCh37/hg19) [hg19]

Name	Description	Type	Doc	Items	Pos	delete
User Track	User Supplied Track	bed		1700	chr12:	<input type="checkbox"/>

view in


Click "User Track" to rename your p53 track

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 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.

Rename custom track

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Update Custom Track: User Supplied Track [hg19]

Update your custom track configuration, data, and/or documentation. Data must be formatted in [bigBed](#), [bigBarChart](#), [bigChain](#), [bigGenePred](#), [bigInteract](#), [GTF](#), [interact](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as describe Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples 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

Edit configuration:


`track name='P53 peaks' description='P53 ChIPseq peaks'`

Paste in replacement data:

Or upload: No file chosen

Rename the track and change description then "Submit"

View custom track in genome browser

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Manage Custom Tracks

genome: Human assembly: Feb. 2009 (GRCh37/hg19) [hg19]

Name	Description	Type	Doc	Items	Pos	delete
P53 peaks	P53 ChIPseq peaks	bed		1700	chr12:	<input type="checkbox"/>

view in Genome Browser ▼ go

add custom tracks

Click "go" to view in Browser

Managing Custom Tracks

View custom track and CDKN1A in genome browser

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

chr12:94,086-94,482 397 bp CDKN1A go

1. Enter CDKN1A gene

2. click go

This is our P53 peaks custom trak

Scale chr12: | 94,150 | 94,200 | 100 bases | hg19 94,250 | 94,300 | 94,350 | 94,400 | 94,450 |

P53 peaks

g15677875.1

g1562974.1

Haplotypes to GRCh37 Reference Sequence

Patches to GRCh37 Reference Sequence

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

NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or YP_*) - Annotation Release GCF_000001405.25_GRCh37.p13 (2017-04-19)

Publications: Sequences in Scientific Articles

Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (570 donors)

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

DNaseI Hypersensitivity Clusters in 125 cell types from ENCODE (V3)

Transcription Factor ChIP-seq Clusters (161 factors) from ENCODE with Factorbook Motifs

100 vertebrates Basewise Conservation by PhyloP

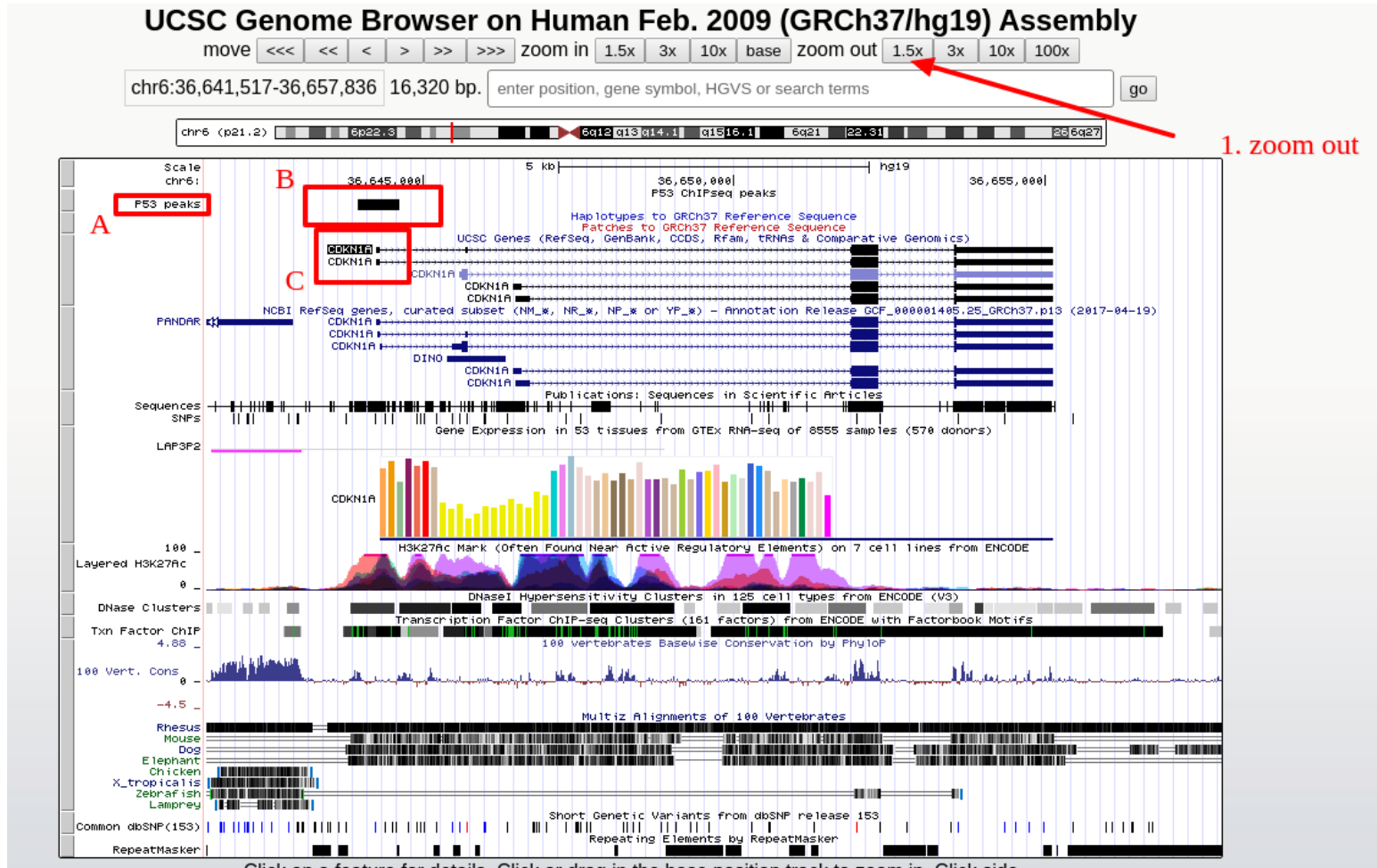
Multiz Alignments of 100 Vertebrates

Short Genetic Variants from dbSNP release 153

Repeating Elements by RepeatMasker

move start Click on a feature for details. Click or drag in the base position track to zoom in. Click side move end

View custom track and CDKN1A in genome browser



A: P53 ChIP peak track

B: P53 ChIP peak

C: Transcription start site / promoter region of CDKN1A

Select regulation tracks in genome browser

The screenshot displays a genome browser interface with a 'Regulation' section. The interface includes a grid of tracks, each with a 'hide' button. The tracks are organized into columns. The first column contains tracks like 'ENCODE Regulation...', 'ENC Chromatin...', 'FSU Repli-chip', 'SUNY SwitchGear', and 'UW Repli-seq'. The second column contains 'GeneHancer', 'ENC DNA Methyl...', 'Genome Segments', 'SwitchGear TSS', and 'Vista Enhancers'. The third column contains 'GTEx Combined eQTL', 'ENC DNase/FAIRE...', 'NKI Nuc Lamina...', 'TFBS Conserved', and 'Vista Enhancers'. The fourth column contains 'GTEx Tissue eQTL', 'ENC Histone...', 'ORegAnno', 'TS miRNA sites', and 'Vista Enhancers'. The fifth column contains 'CD34 DnaseI', 'ENC RNA Binding...', 'Rao 2014 Hi-C', 'UCSF Brain Methyl', and 'Vista Enhancers'. The sixth column contains 'CpG Islands...', 'ENC TF Binding...', 'Stanf Nucleosome', and 'UMMS Brain Hist'. A 'refresh' button is located in the top right corner of the 'Regulation' section. Red boxes and numbers 1-4 highlight specific features: 1. ENCODE Regulation... show button, 2. CpG Islands... show button, 3. TFBS Conserved dense dropdown, 4. refresh button.

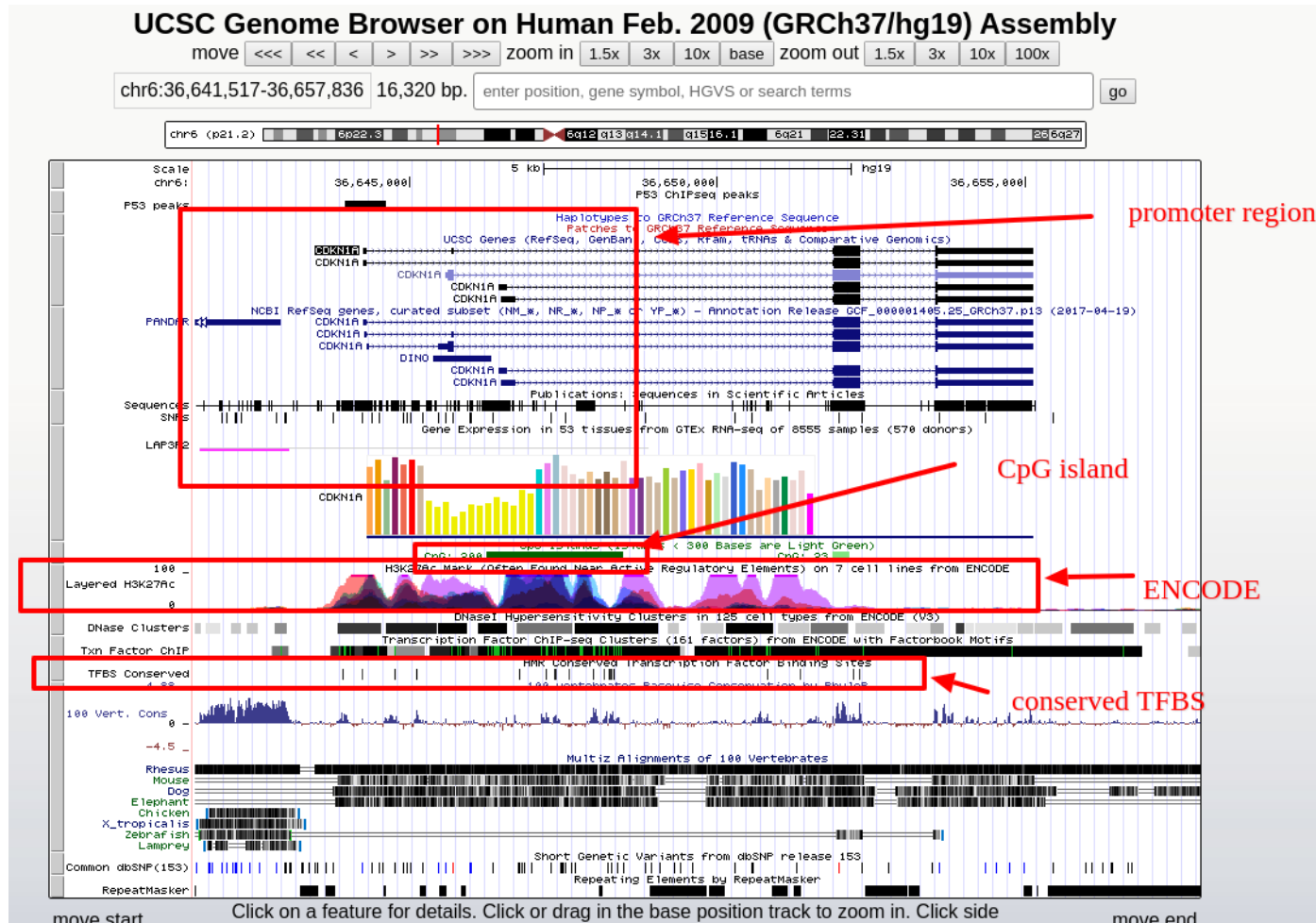
1. ENCODE Regulation... show

2. CpG Islands... show

3. TFBS Conserved dense

4. refresh

Select regulation tracks in genome browser



Use Table Browser to generate intersections

Go to Table Browser

The screenshot displays the CSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly. 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 'Table Browser' is highlighted with a red box and a red arrow. Other tools listed include Blat, Variant Annotation Integrator, Data Integrator, Gene Interactions, Gene Sorter, Genome Graphs, In-Silico PCR, LiftOver, VisiGene, and Other Utilities. The main content area shows a genomic track for chromosome 6 (p21.2) with a 5 kb scale. It displays various annotations including P53 ChIPseq peaks, Haplotypes to GRCh37 Reference Sequence, Patches to GRCh37 Reference Sequence, UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics), NCBI RefSeq genes, and Publications: Sequences in Scientific Articles. The CDKN1A gene is prominently featured in the track.

Use Table Browser to generate intersection to find overlap of TP53 peaks with CpG site or DNase cluster

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence controls in this form, and the [User's Guide](#) for general information and sample queries. For more complex queries, you may want to use [Galaxy](#) or send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be do

clade: genome: assembly:

group: track:

table:

region: ☒ genome ☐ ENCODE Pilot regions ☐ position

identifiers (names/accessions):

filter:

intersection: ← Create intersection

correlation:

output format: Send output to ☐ [Galaxy](#) ☐ [GREAT](#)

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

file type returned: ☒ plain text ☐ gzip compressed

Use Table Browser to generate intersection to find overlap of TP53 peaks with CpG site or DNase cluster

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Intersect with P53 peaks

Select a group, track and table to intersect with:

group: **track:**
table:

1. select CpG Island track

Intersect P53 peaks items with bases covered by CpG Islands:

These combinations will maintain the names and gene/alignment structure (if any) of P53 peaks:

- ☒ All P53 peaks records that have any overlap with CpG Islands
- ☐ All P53 peaks records that have no overlap with CpG Islands
- ☐ All P53 peaks records that have at least % overlap with CpG Islands
- ☐ All P53 peaks records that have at most % overlap with CpG Islands

Intersect bases covered by P53 peaks and/or CpG Islands:

These combinations will discard the names and gene/alignment structure (if any) of P53 peaks and produce a simple list of position ranges.

- ☐ Base-pair-wise intersection (AND) of P53 peaks and CpG Islands
- ☐ Base-pair-wise union (OR) of P53 peaks and CpG Islands

Check the following boxes to complement one or both tables. To complement a table means to include a base pair in the intersection/union if it is *not* included in the table.

- ☐ Complement P53 peaks before base-pair-wise intersection/union
- ☐ Complement CpG Islands before base-pair-wise intersection/union

2. submit

Use Table Browser to generate intersection to find overlap of TP53 peaks with CpG site or DNase cluster

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Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve controls in this form, and the [User's Guide](#) for general information and sample queries. For more complex queries, you may want to send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tracks are controlled by the [User's Guide](#).

clade: Mammal **genome:** Human **assembly:** Feb. 2009 (GRCh37/hg19)

group: Custom Tracks **track:** P53 peaks [manage custom tracks](#) [track hubs](#)

table: ct_P53peaks_3940 [describe table schema](#)

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr6:36,641,517-36,657,836 [lookup](#) [define regions](#)

identifiers (names/accessions): [paste list](#) [upload list](#)

filter: [create](#)

intersection with cpGislandExt: [edit](#) [clear](#)

correlation: [create](#)

output format: BED - browser extensible data [Send output to](#) ☐ [Galaxy](#) ☐ [GREAT](#)

output file: p53_in_CpG_island.bed (leave blank to keep output in browser)

file type returned: ☒ plain text ☐ gzip compressed

Note: The all fields and selected fields output formats are not available when an intersection has been specified.

[get output](#) [summary/statistics](#)

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

1. select BED output format, specify output file name

2. submit

Use Table Browser to generate intersection

to find overlap of TP53 peaks with CpG site or DNase cluster

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Output ct_P53peaks_3940 as BED

☐ Include [custom track](#) header:
name=
description=
visibility=
url=

Create one BED record per:
☒ Whole Gene
☐ Upstream by bases
☐ Downstream by bases

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are specified, the feature will be truncated to fit within the specified range.

get BED file

chr6»	30000055»	3000284»	MACS_peak_9481»	393
chr6»	4018793»	4018981»	MACS_peak_9487»	423
chr6»	10723111»	10723378»	MACS_peak_9503»	317
chr6»	11093958»	11094195»	MACS_peak_9504»	364
chr6»	13615494»	13615772»	MACS_peak_9525»	300
chr6»	14211372»	14211610»	MACS_peak_9528»	354
chr6»	15245567»	15245747»	MACS_peak_9541»	690
chr6»	16760120»	16760353»	MACS_peak_9560»	271
chr6»	16761841»	16762052»	MACS_peak_9561»	270
chr6»	17600368»	17600668»	MACS_peak_9567»	450
chr6»	17707053»	17707372»	MACS_peak_9568»	590
chr6»	18122845»	18123104»	MACS_peak_9578»	488
chr6»	18387384»	18387831»	MACS_peak_9582»	370

How many P53 peaks have an overlap with CpG islands (count lines in resulting BED file)

How many P53 peaks have an overlap with DNase sites (you can do this similar to the way you did with CpG islands)