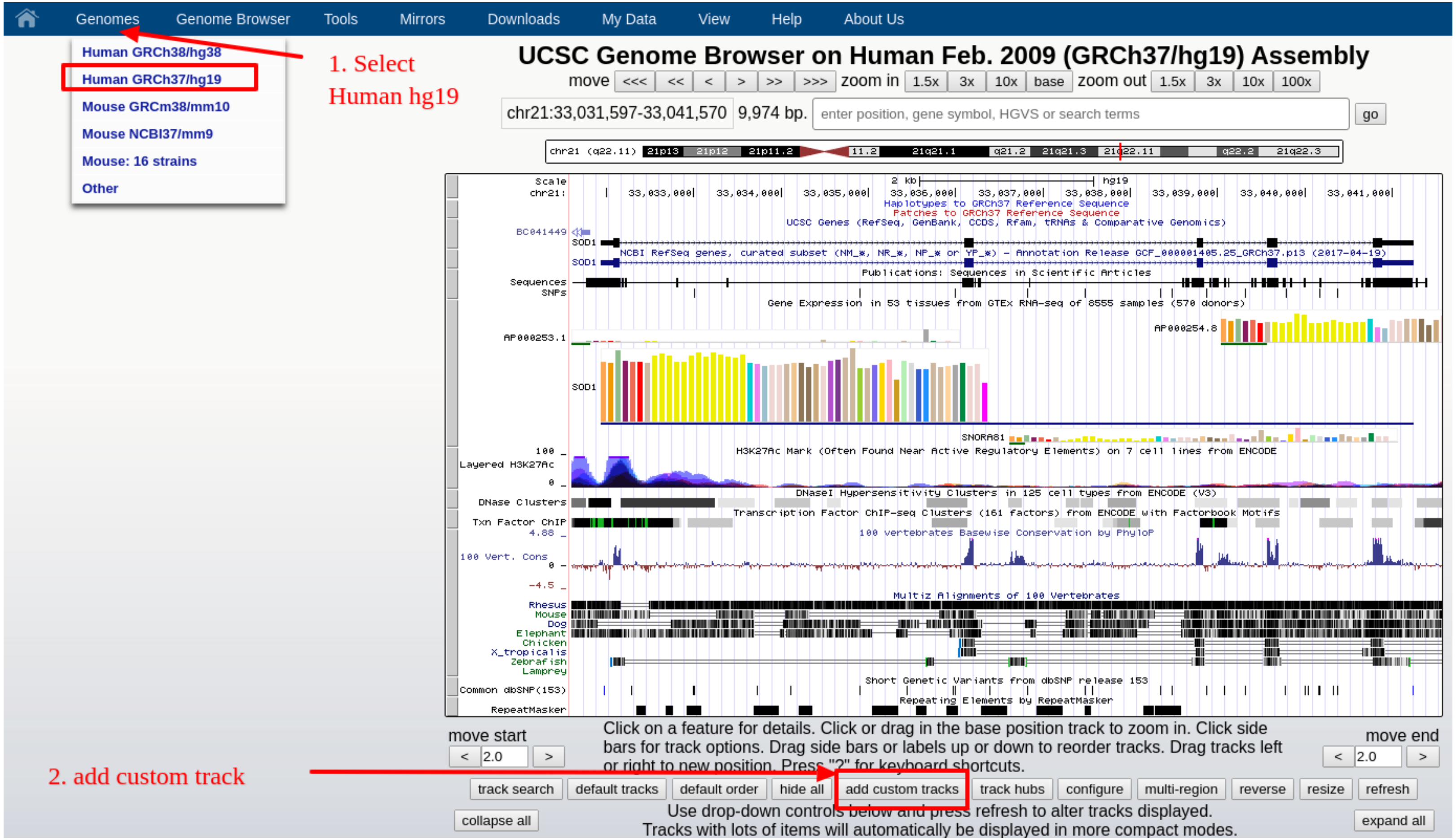
Add custom track to genome browser



1. Select Human hg19

2. add custom track

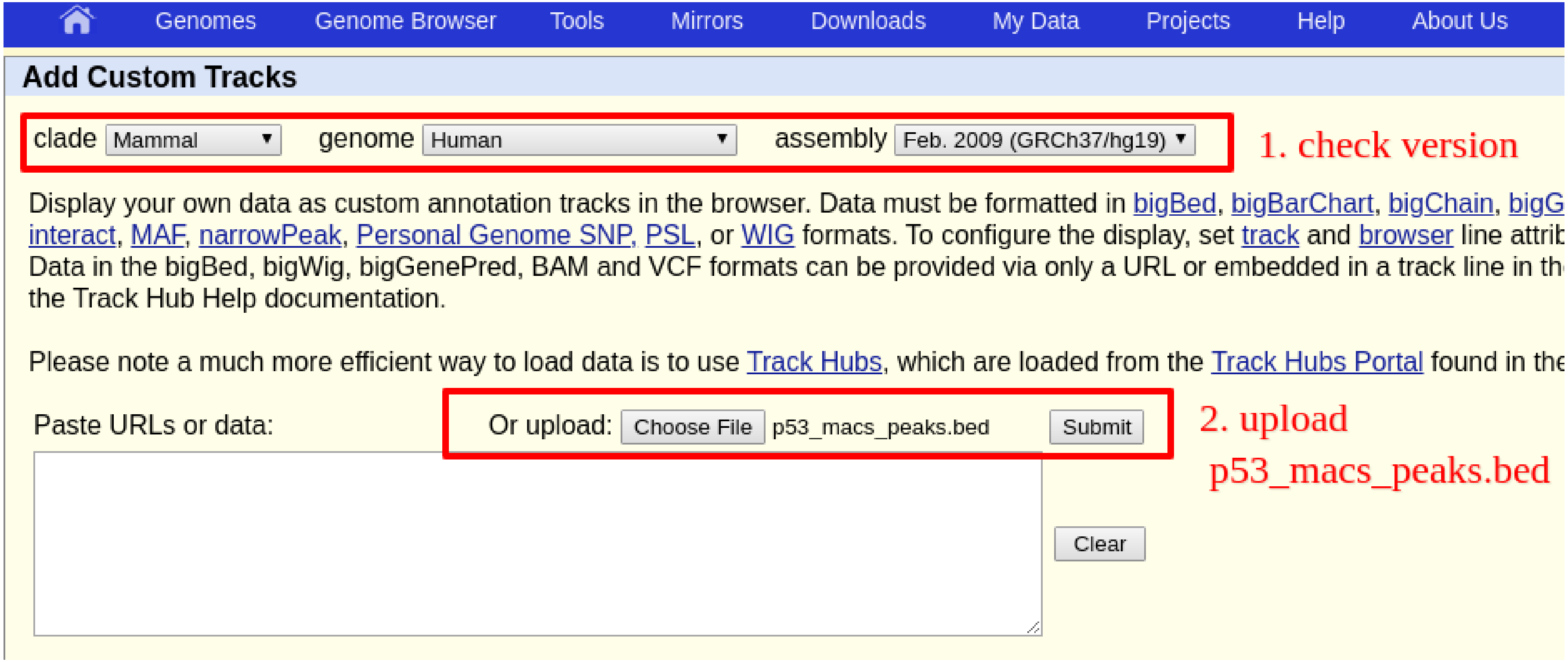
UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr21:33,031,597-33,041,570 9,974 bp.

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 "?" for keyboard shortcuts.

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



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

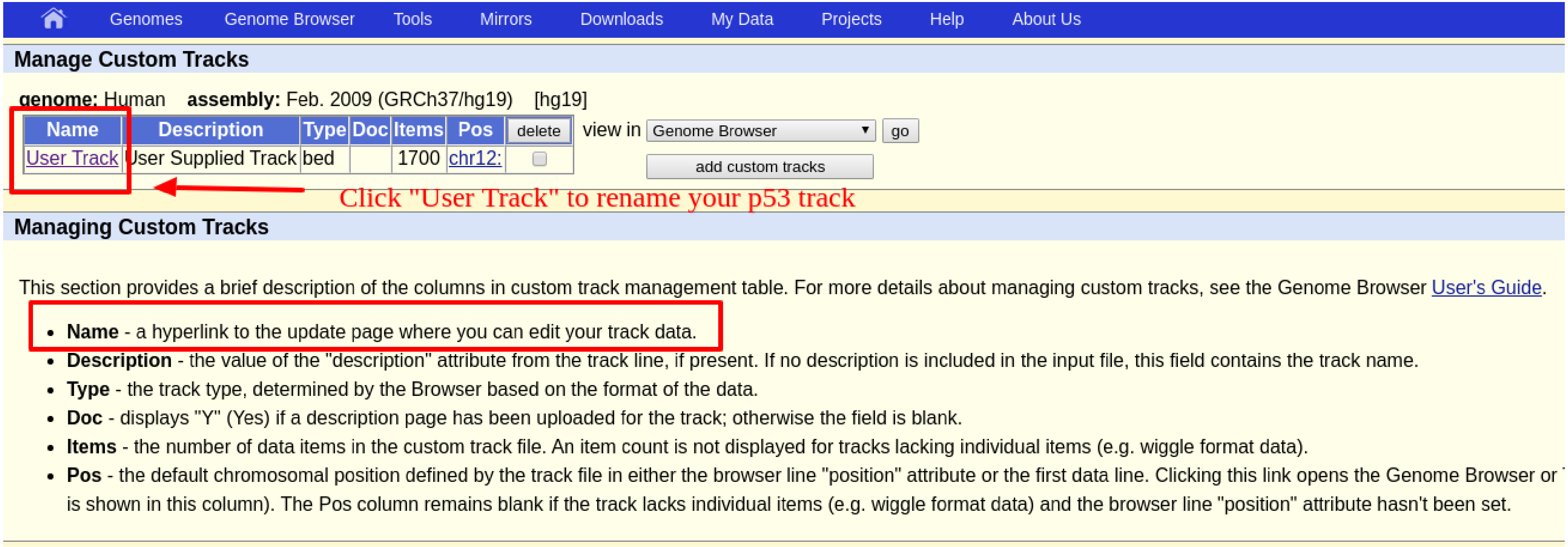
Paste URLs or data:

Or upload: p53_macs_peaks.bed

1. check version

2. upload p53_macs_peaks.bed

Rename custom track



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:	☐

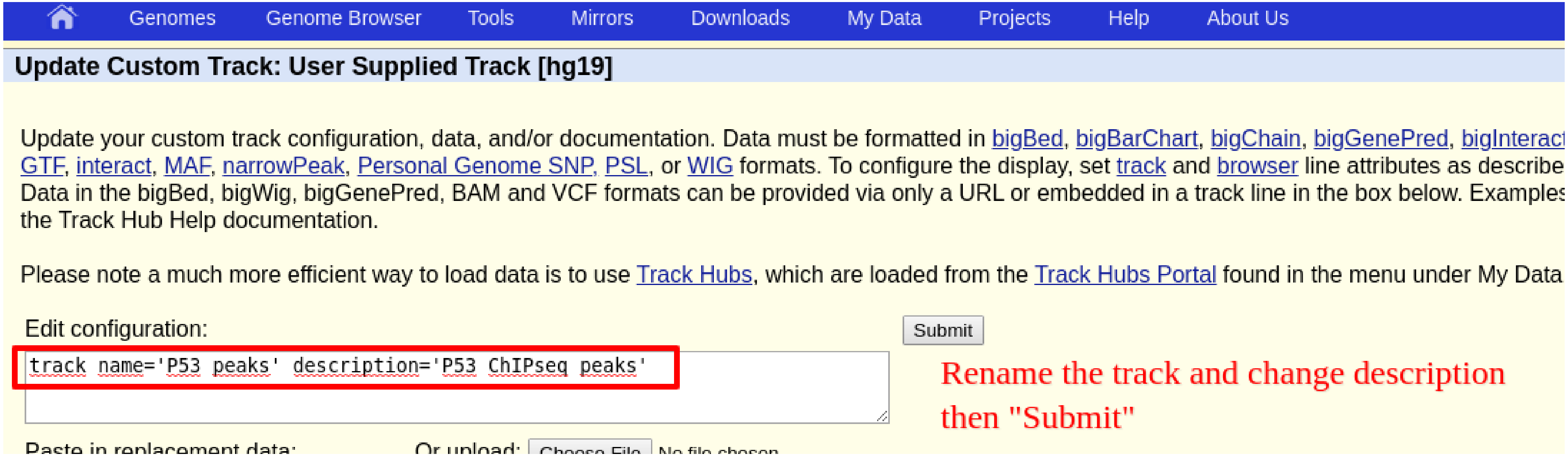
Click "User Track" to rename your p53 track

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



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, bigInterac
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.

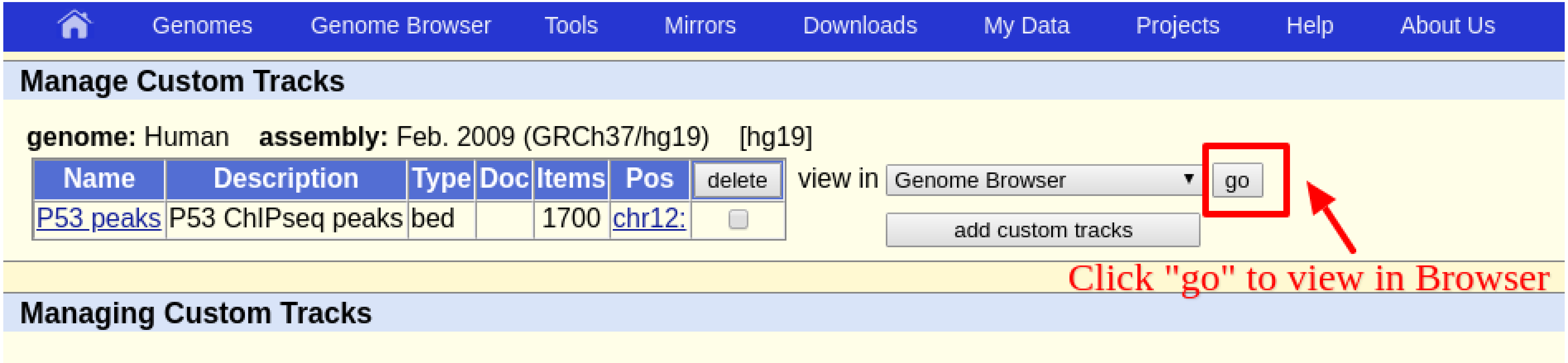
Please note a much more efficient way to load data is to use Track Hubs, which are loaded from the Track Hubs Portal found in the menu under My Data

Edit configuration:

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

Rename the track and change description then "Submit"

View custom track in genome browser



Manage Custom Tracks

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

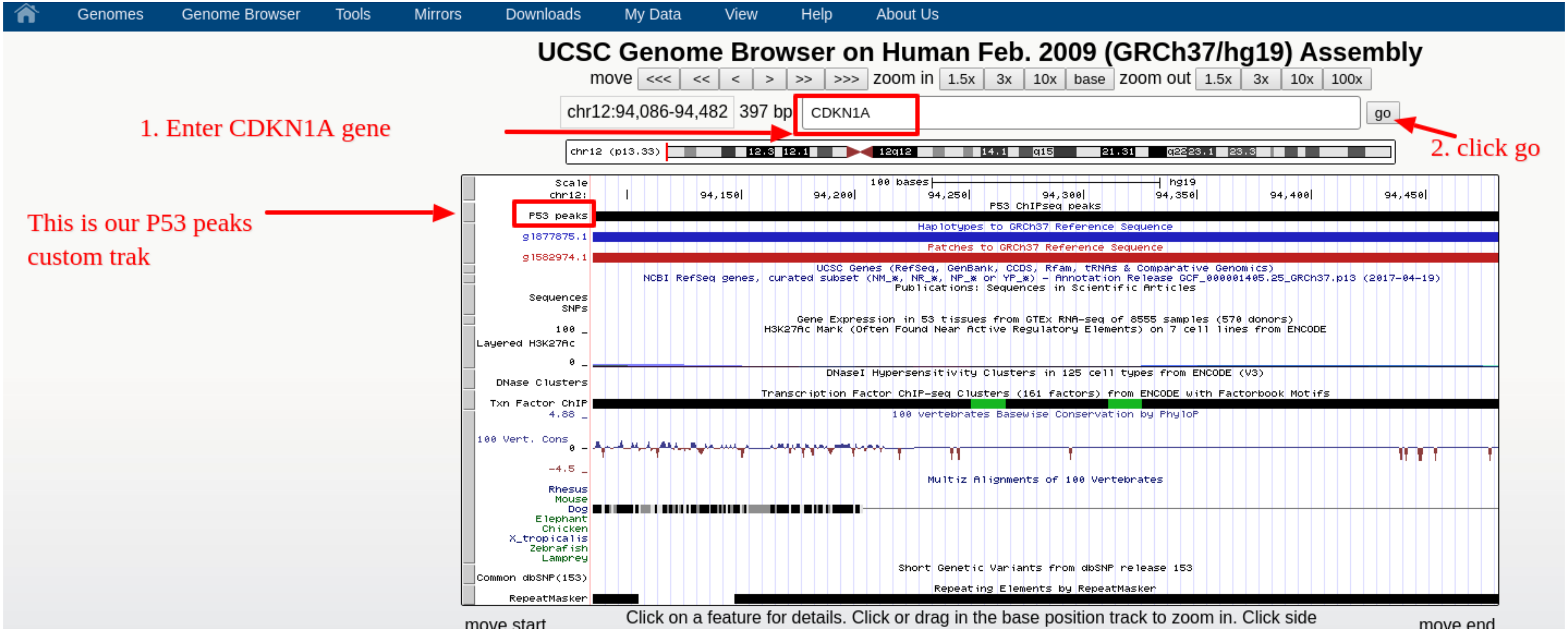
Name	Description	Type	Doc	Items	Pos	delete
P53 peaks	P53 ChIPseq peaks	bed		1700	chr12:	☐

view in: Genome Browser

Click "go" to view in Browser

Managing Custom Tracks

View custom track and CDKN1A in genome browser



1. Enter CDKN1A gene

2. click go

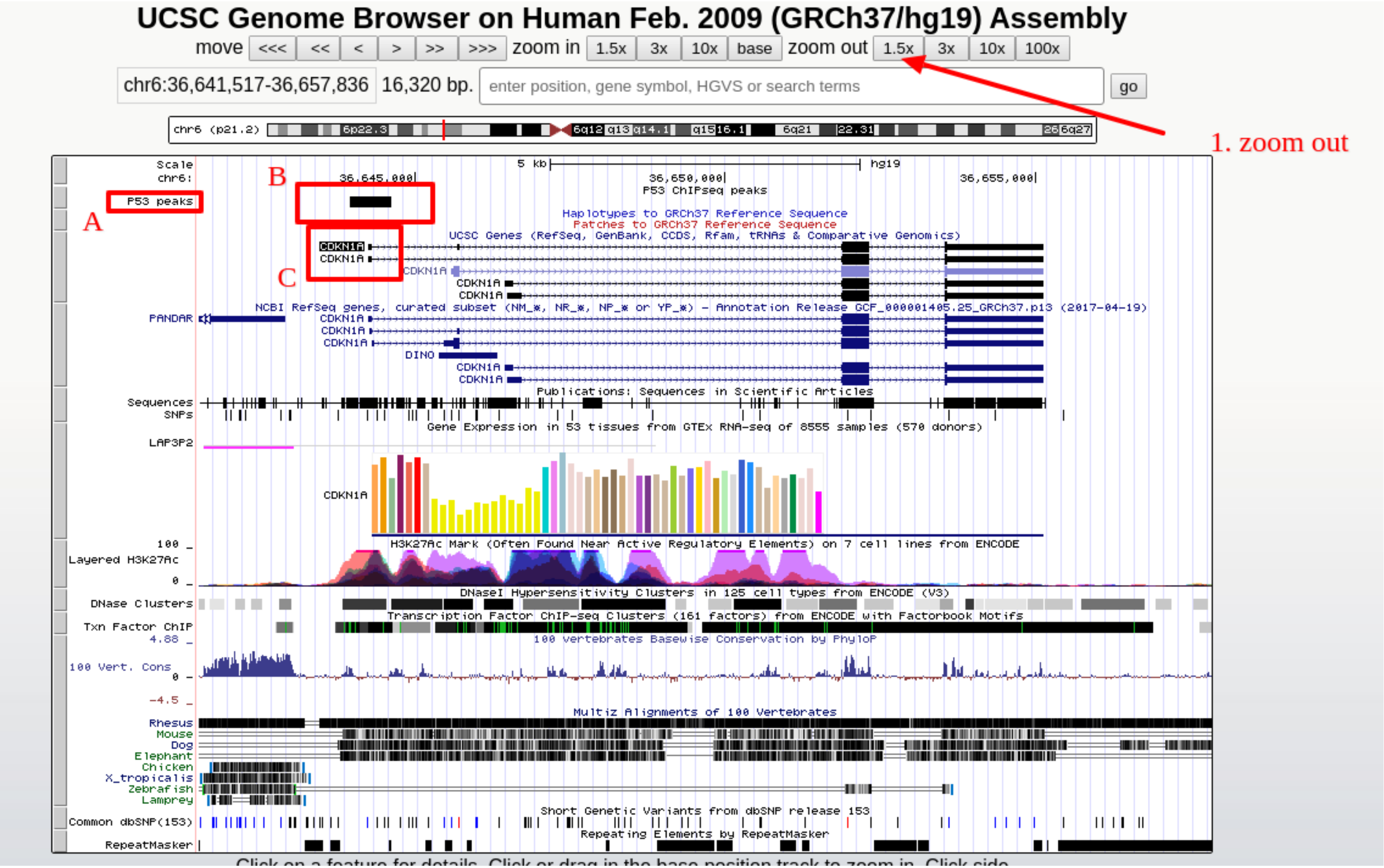
This is our P53 peaks custom trak

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

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

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

View custom track and CDKN1A in genome browser

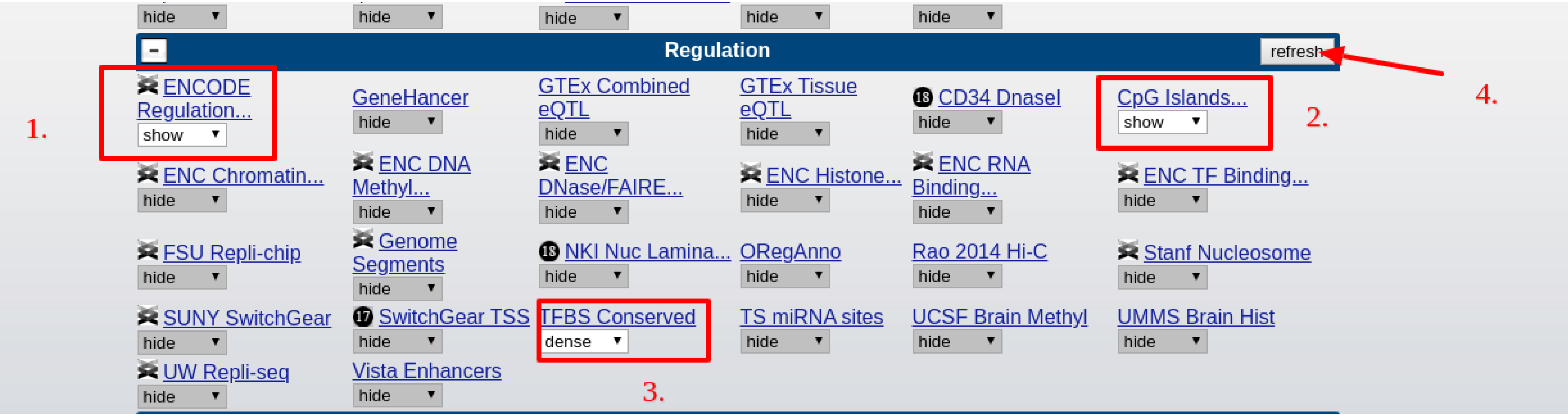


A: P53 ChIP peak track

B: P53 ChIP peak

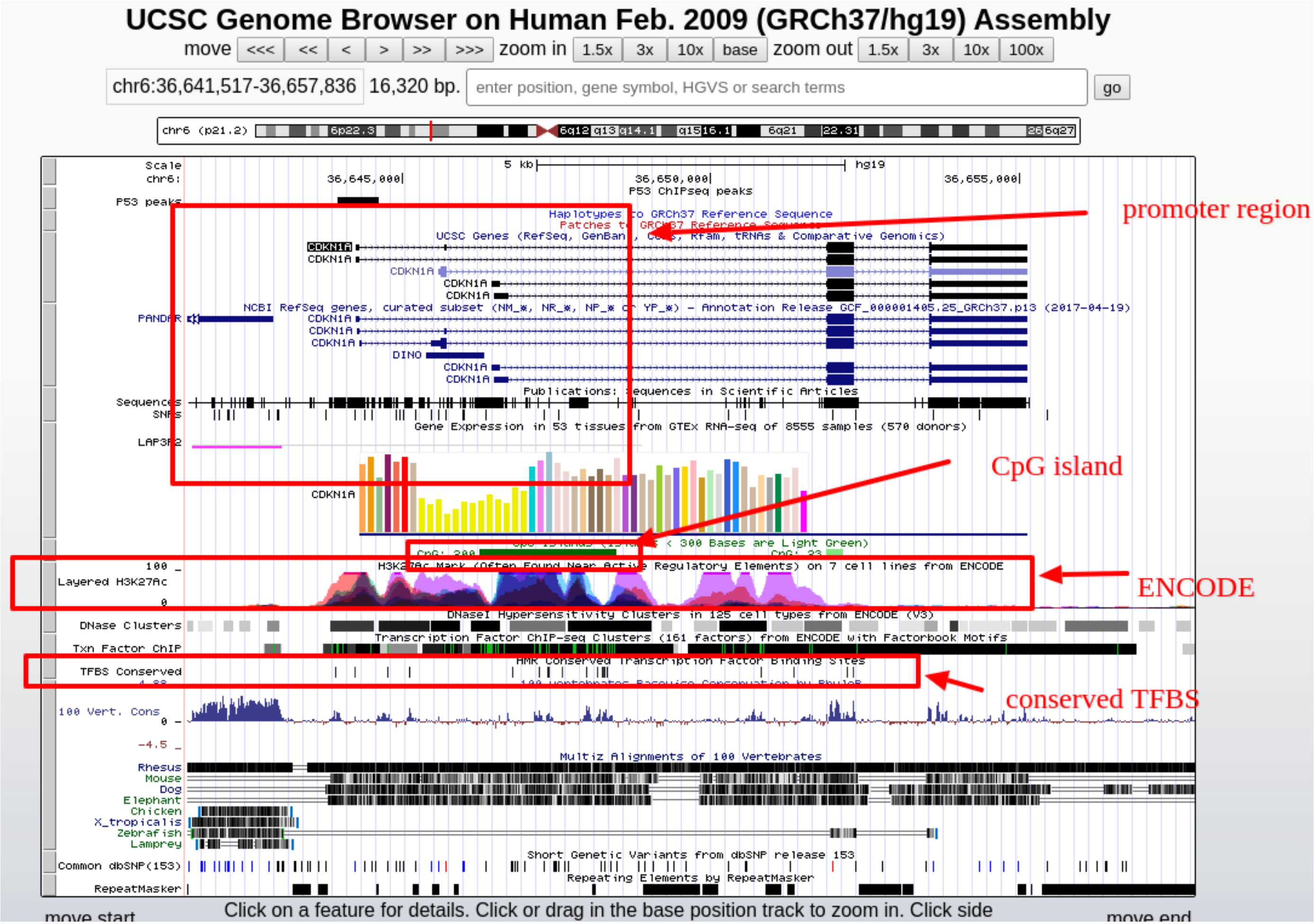
C: Transcription start site / promoter region of CDKN1A

Select regulation tracks in genome browser



ENCODE Regulation... show
GeneHancer hide
GTEx Combined eQTL hide
GTEx Tissue eQTL hide
18 CD34 DnaseI hide
CpG Islands... show
ENC Chromatin... hide
ENC DNA Methyl... hide
ENC DNase/FAIRE... hide
ENC Histone... hide
ENC RNA Binding... hide
ENC TF Binding... hide
FSU Repli-chip hide
Genome Segments hide
18 NKI Nuc Lamina... hide
ORegAnno hide
Rao 2014 Hi-C hide
Stanf Nucleosome hide
SUNY SwitchGear hide
17 SwitchGear TSS hide
TFBS Conserved dense
TS miRNA sites hide
UCSF Brain Methyl hide
UMMS Brain Hist hide
UW Repli-seq hide
Vista Enhancers hide

Select regulation tracks in genome browser



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

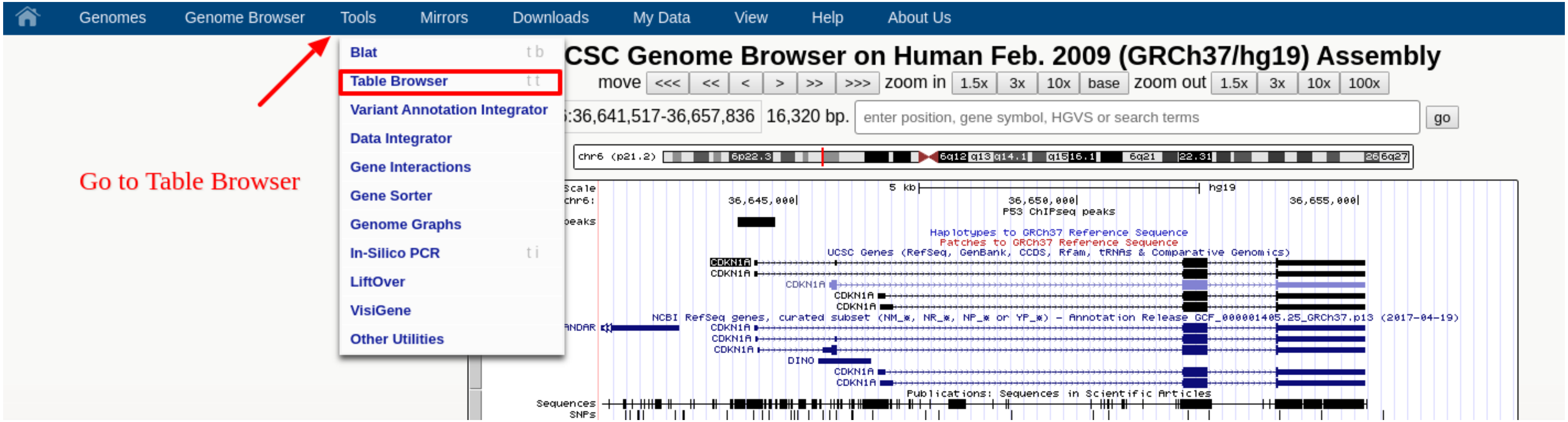
promoter region

CpG island

ENCODE

conserved TFBS

Use Table Browser to generate intersections



Go to Table Browser

Use Table Browser to generate intersection

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

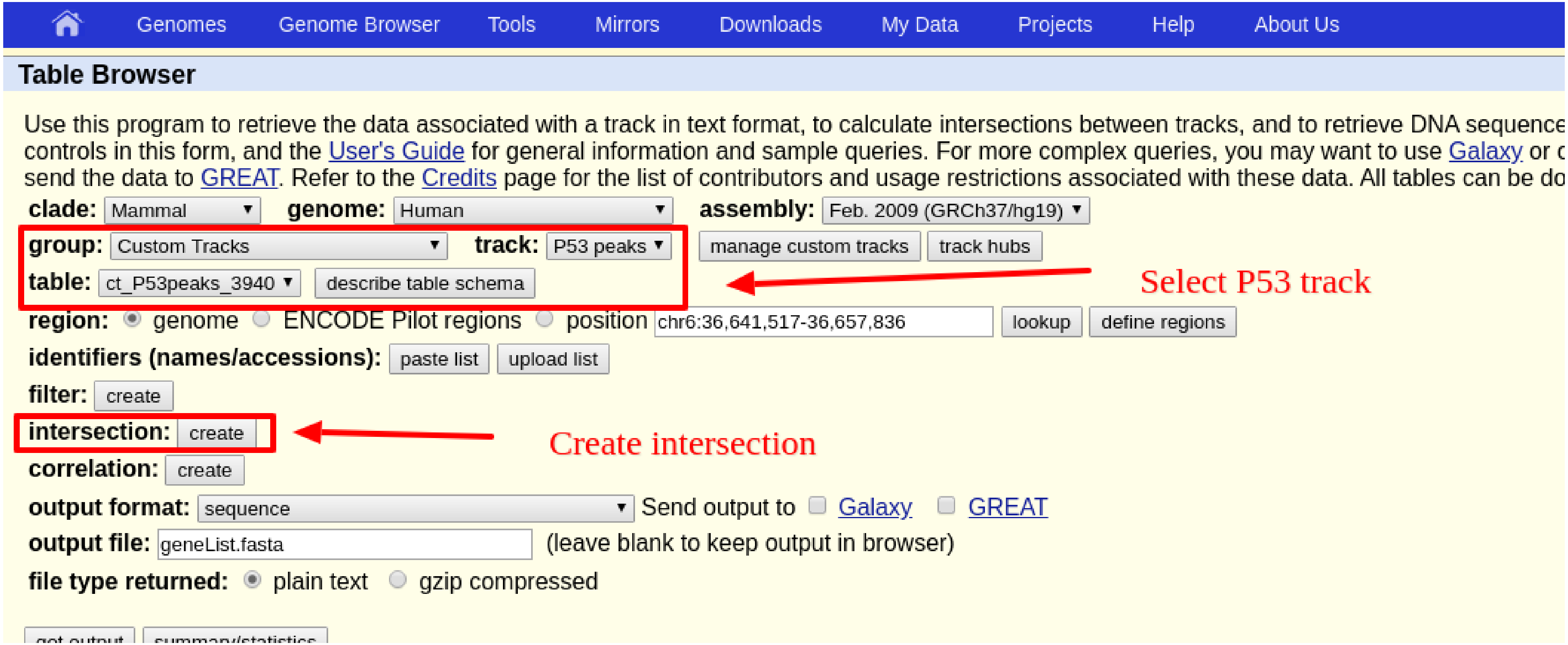


Table Browser

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

group: Custom Tracks **track:** P53 peaks

table: ct_P53peaks_3940

region: ● genome ○ ENCODE Pilot regions ○ position chr6:36,641,517-36,657,836

identifiers (names/accessions):

filter:

intersection:

correlation:

output format: sequence Send output to ☐ Galaxy ☐ GREAT

output file: geneList.fasta (leave blank to keep output in browser)

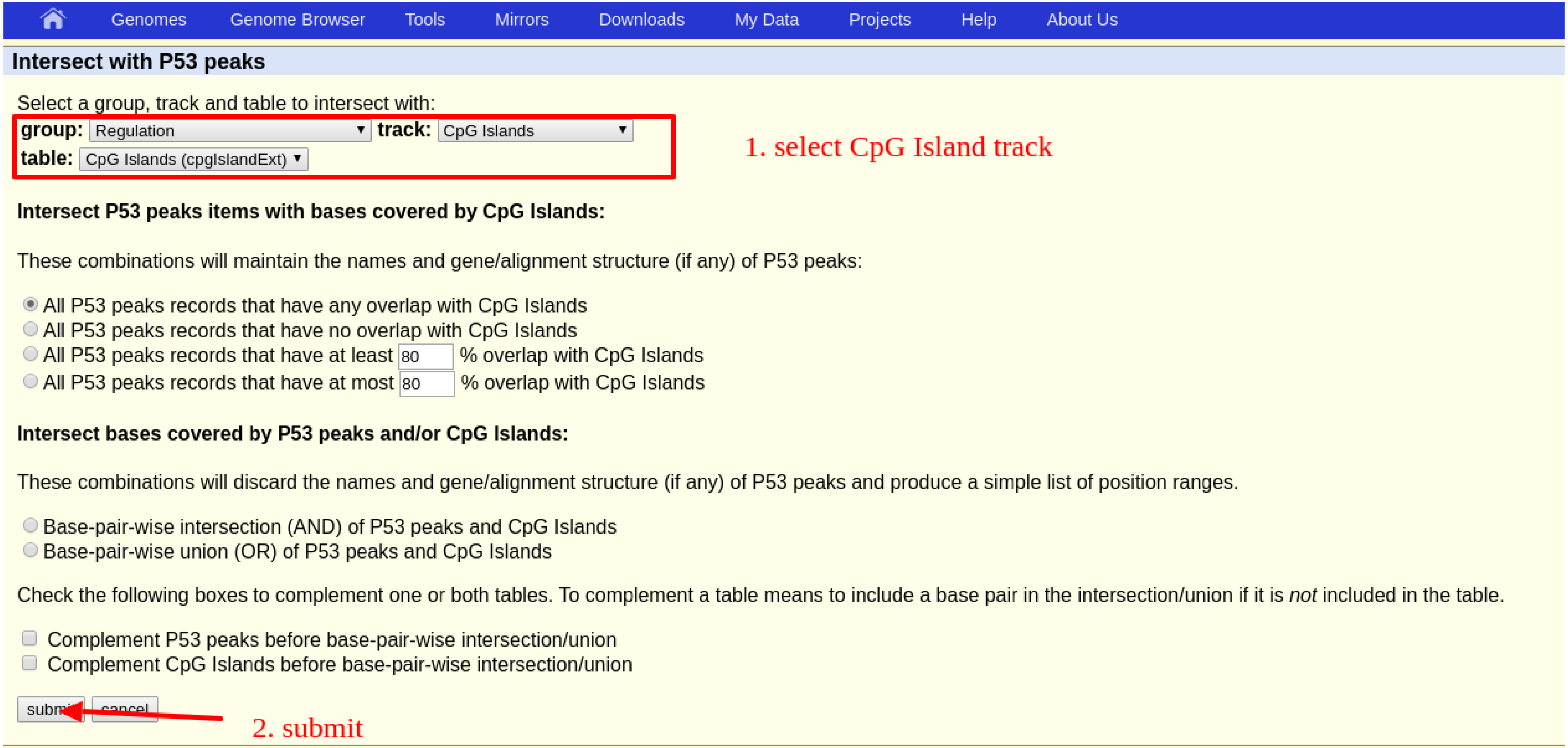
file type returned: ● plain text ○ gzip compressed

Select P53 track

Create intersection

Use Table Browser to generate intersection

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



Intersect with P53 peaks

Select a group, track and table to intersect with:

group: Regulation **track:** CpG Islands
table: CpG Islands (cpgIslandExt)

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 80 % overlap with CpG Islands
○ All P53 peaks records that have at most 80 % 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

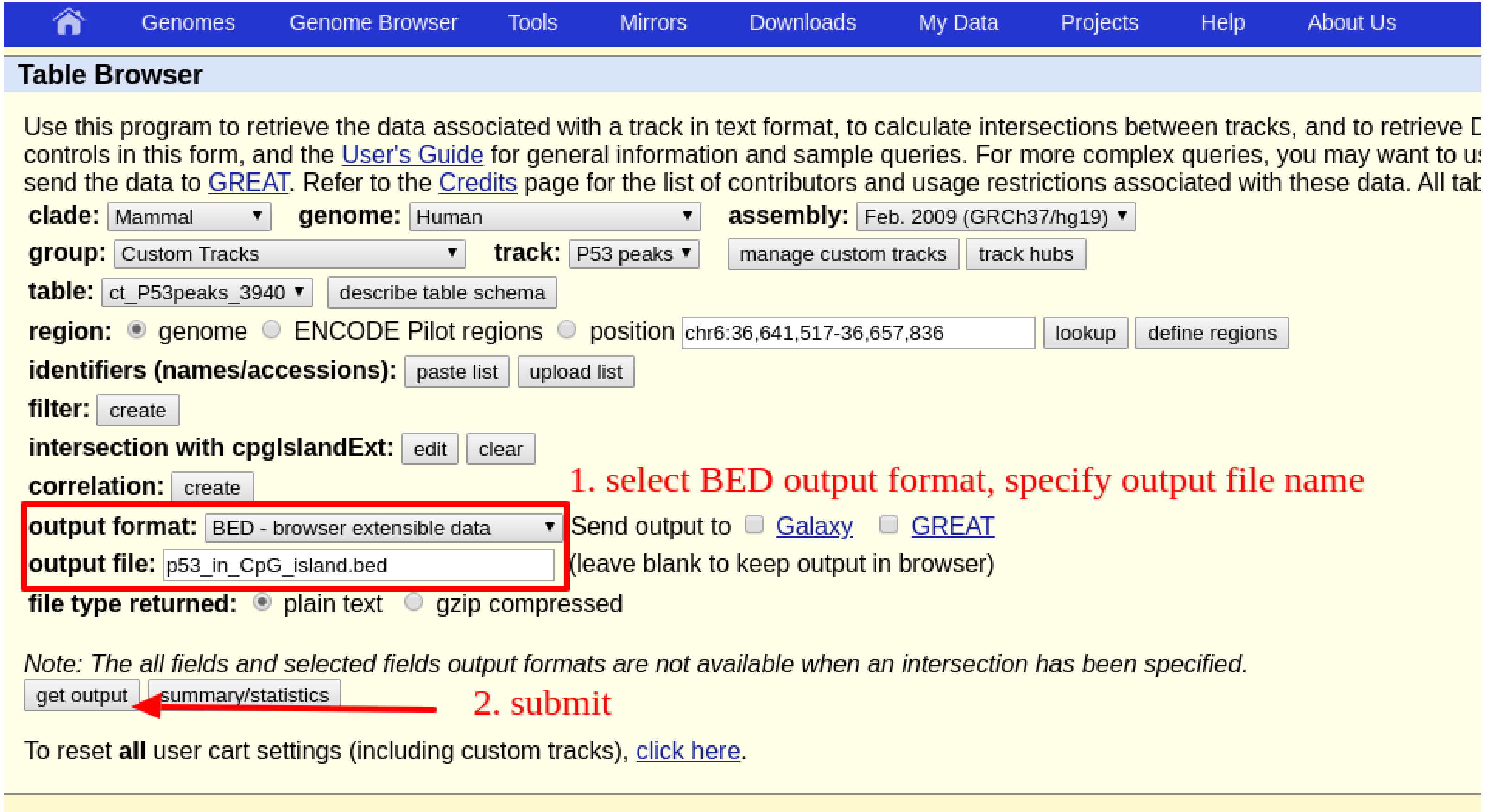


Table Browser

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 us
send the data to GREAT. Refer to the Credits page for the list of contributors and usage restrictions associated with these data. All tab

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

1. select BED output format, specify output file name

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.

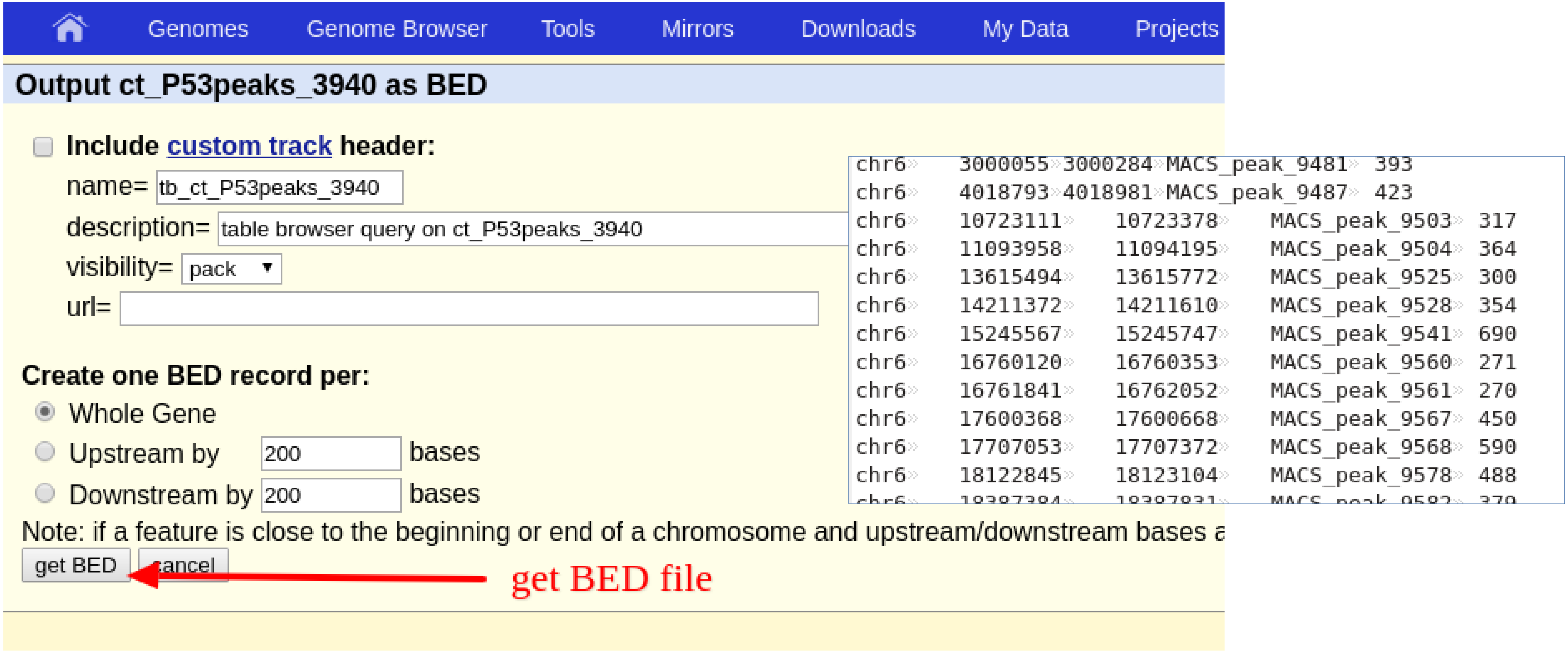
get output summary/statistics

2. submit

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

Use Table Browser to generate intersection

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



Output ct_P53peaks_3940 as BED

☐ **Include custom track header:**

name= tb_ct_P53peaks_3940

description= table browser query on ct_P53peaks_3940

visibility= pack

url=

Create one BED record per:

● Whole Gene

○ Upstream by 200 bases

○ Downstream by 200 bases

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases a

```
chr6	3000055	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
```

get BED file

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)