WashU Epigenome Browser Tutorial

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Notes:

- To follow along with this tutorial, use instructions marked by ➢. We have provided screenshots for guidance (ordered by bracketed alphabets: [A], [B], …)
- Click in the order of the numbered circles on the screenshots to follow this tutorial.



Official site: https://epigenomegateway.wustl.edu/browser/

AWS mirror: https://epigenomegateway.org/browser/

1. Getting started with the Epigenome Browser

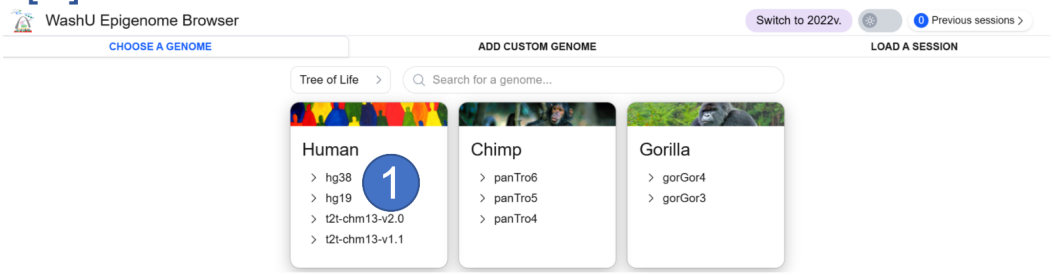
1.1. Load the browser

- Access the browser at https://epigenomegateway.wustl.edu/browser

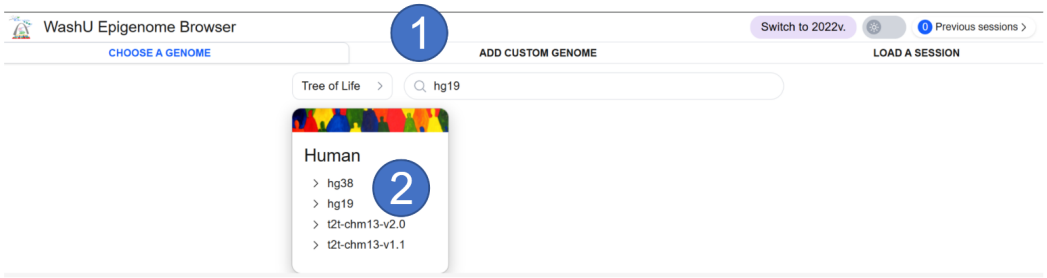
1.2. Select the genome assembly of interest

- In this tutorial, please select Human hg19.
- [A] Click on hg19 located top left
- [B] type hg19 into the search bar and the genome with hg19 will appear at the top and then click on hg19

[A]



[B]

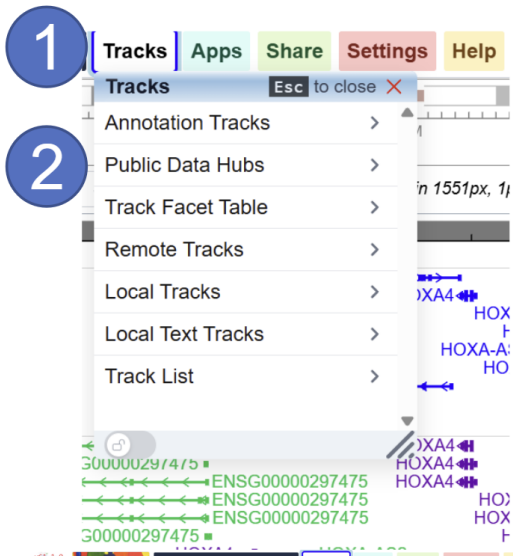


2. Loading data on the Epigenome Browser

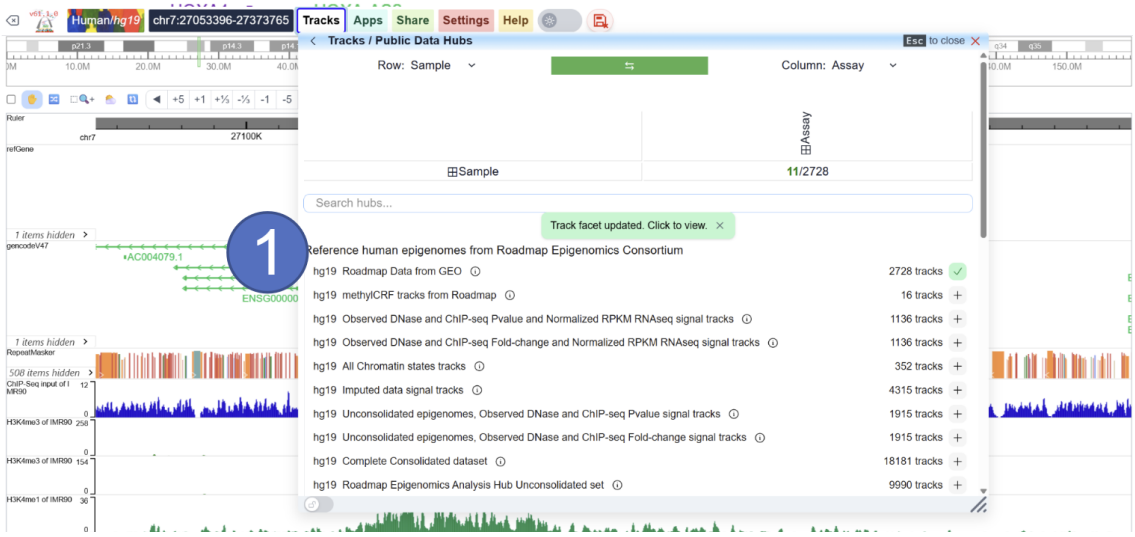
2.1. Data hubs: A data hub is a collection of tracks/datasets that can be viewed on the browser.

- [A] Click on the Tracks -> Public Data Hubs (21 available) to view all the available public datasets on the Epigenome Browser.
- [B] Choose the first hub named Roadmap Data from GEO, Click the Add button. Exit the data hub section by clicking on the X at the top-right of the floating window.

[A]



[B]



Data visualization (linear)

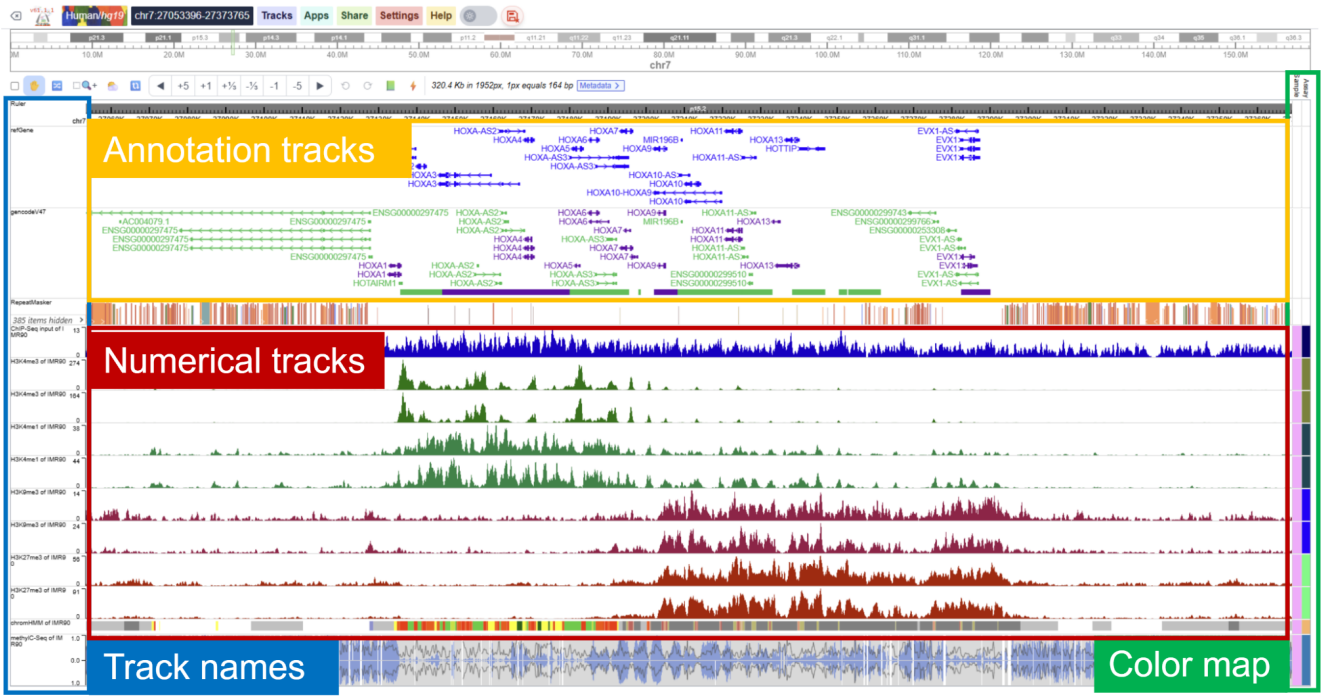
Visualizations are displayed as Tracks in each row:

Numerical tracks represent the density of reads from sequencing experiments aligned to the genome assembly.

Annotation tracks represent the annotation of a genomic segment of the genome assembly.

In the screenshot below:

- Track names for each track are listed on the left-hand side of the track itself.
- On the right-hand side of the tracks is a color map, which represents the metadata for the tracks.
- Above the numerical tracks are annotation tracks, including annotations of genes and transposable elements.



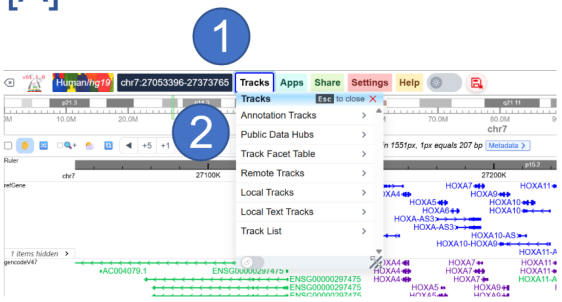
2.2. Searching for datasets on the Epigenome Browser

2.2.1. Facet table: The facet table organizes all the loaded datasets into a table, to allow the user to search for datasets using metadata terms. Here, rows represent samples and columns represent assay types. Cells with numbers represent the number of datasets. For example, the cell with numbers: 11/602 - here, 11 represents the number of datasets currently loaded on the browser, while 602 represents the total number of datasets available.

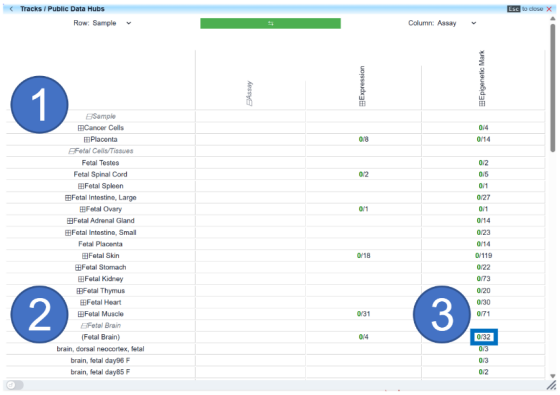
- [A] To display the facet table click on the Tracks menu, and then click on the Track Facet Table box.
- [B] This will generate the facet table. To add more datasets, click on Fetal Cells/Tissues and then select Fetal Brain. Click on the cell corresponding to the Epigenetic Mark column and the Fetal Brain row to list the datasets in this category.

- [C] To select data, click the Add button of H3K9me3 of Fetal Brain and H3K4me3 of Fetal Brain.
- To exit this floating window, click on the X at the top-right of the window.

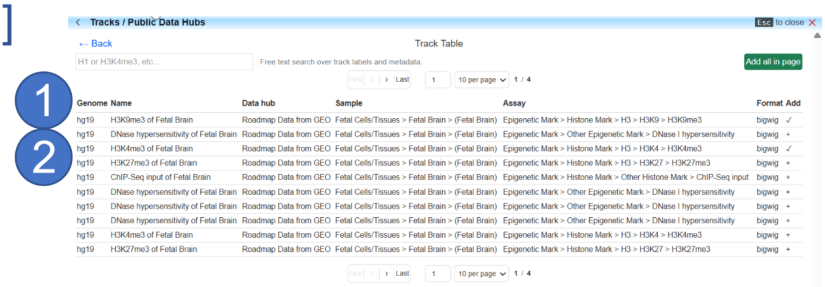
[A]



[B]

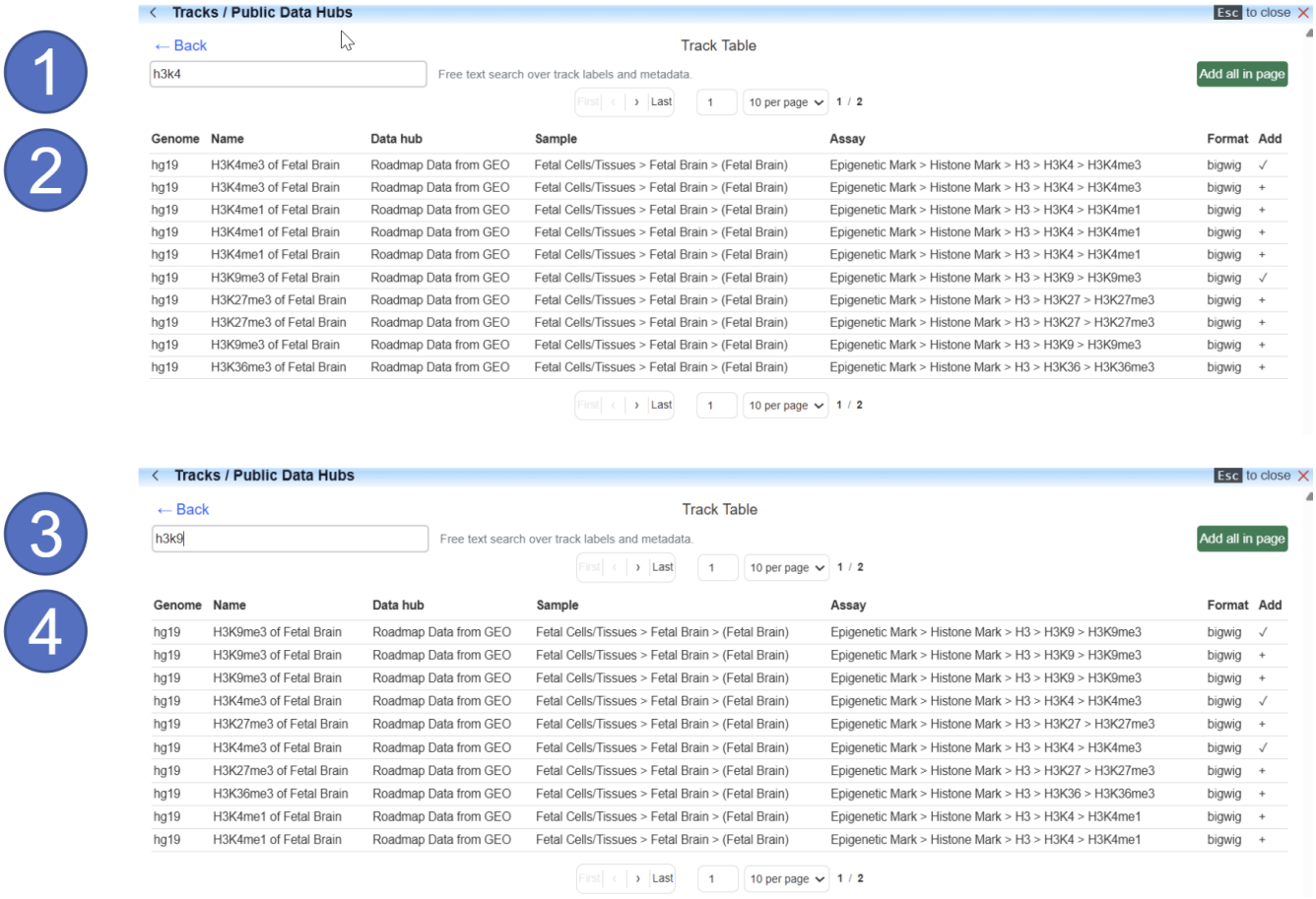


[C]



2.2.2. Searching for track in track table

- Click on the cell at Fetal Brain row and Epigenetic Mark column on the facet table.
- This will list all the dataset under these 2 metadata terms. Type h3k4 in the box under Name header. Add the track H3K4me3 of Fetal Brain.
- Repeat this process to add one more replicate track for H3K9me3 of Fetal Brain.
- Click on the X at the top-right of the window to get back to the browser.



2.3. Configuring the Epigenome Browser

2.3.1. Changing the height of tracks

- To select multiple tracks, hold down the shift-key and click on the names of the 4 Fetal Brain tracks that were just added. Right-click on the yellow-highlighted track names. This will bring the configuration window.
- Change the value in Height option to increase/decrease the height of the tracks to your preference.

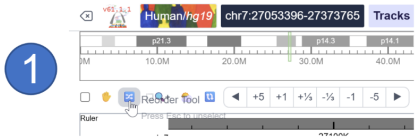


- Click outside this floating box to get back to the browser.
- To de-select the 4 tracks, right-click on the yellow-highlighted track names and select Deselect 4 tracks.

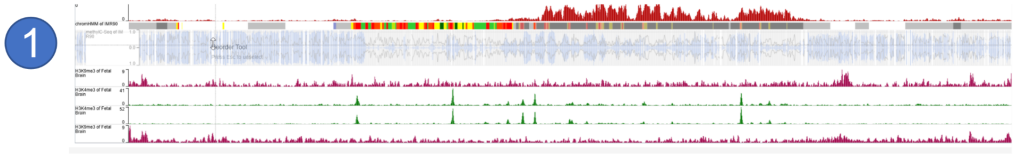
2.3.2. Re-ordering tracks

- Using the Re-order tool
- [A] Choose the Re-order tool.
- [B] Drag the methylC track to one track up.

[A]



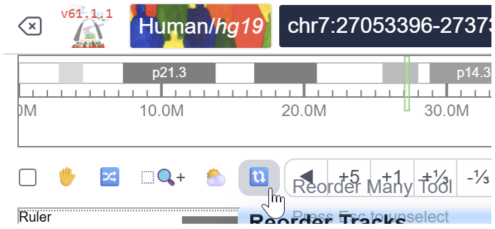
[B]

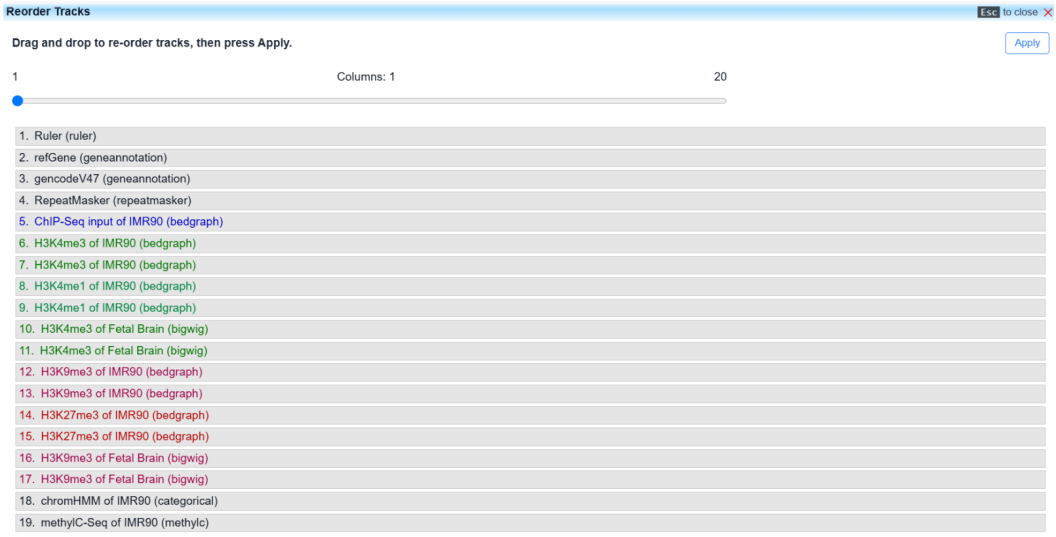


[C]



- Using the reorder many





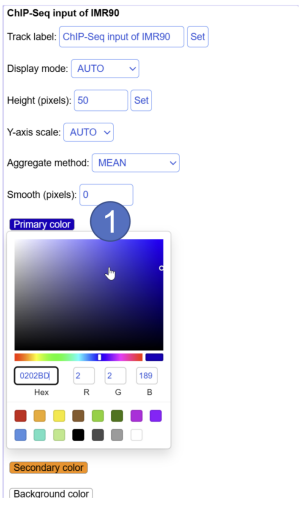
2.3.3. Changing the color of tracks

- [A] Right Click on the Chip-Seq input of IMR90 track.
- [B] In the Configure menu, click on the Primary color button and then select the color of your choice to change the color of the track.

[A]



[B]



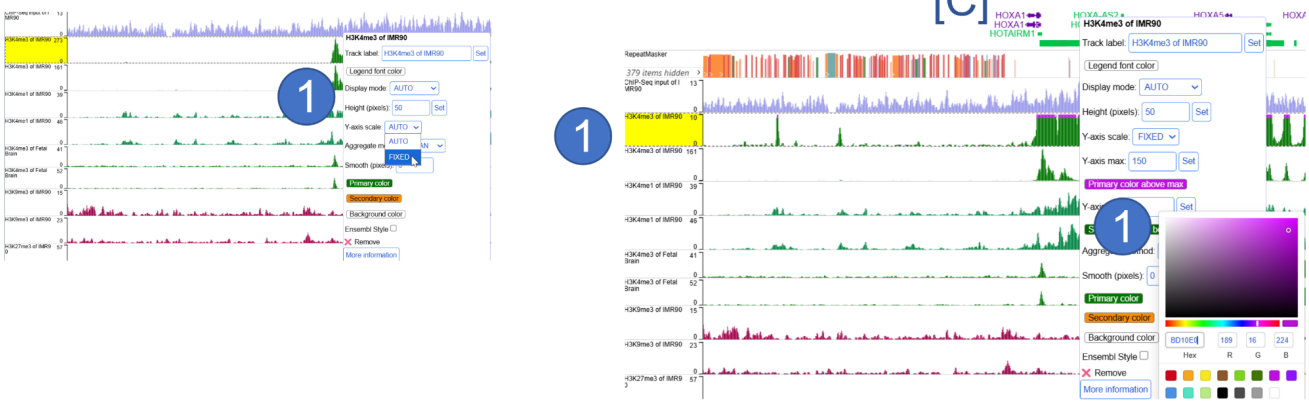
- Click outside this floating box to get back to the browser.

2.3.4. Changing the y-axis scale for tracks

- [A] Right-click on one H3K4me3 track.

- [B] Click on the Y-axis scale drop-down menu and then click FIXED. This will generate text boxes to enter the y-axis range. Enter 150 in the max text-box. Click on Set to change the y-axis scale.
- [C] Click on the button labeled Primary color above max. This will generate a floating window with color options; change the color to any color of your choice.

[A] [B] [C]



- Click anywhere outside the Configure box to get back to the browser.

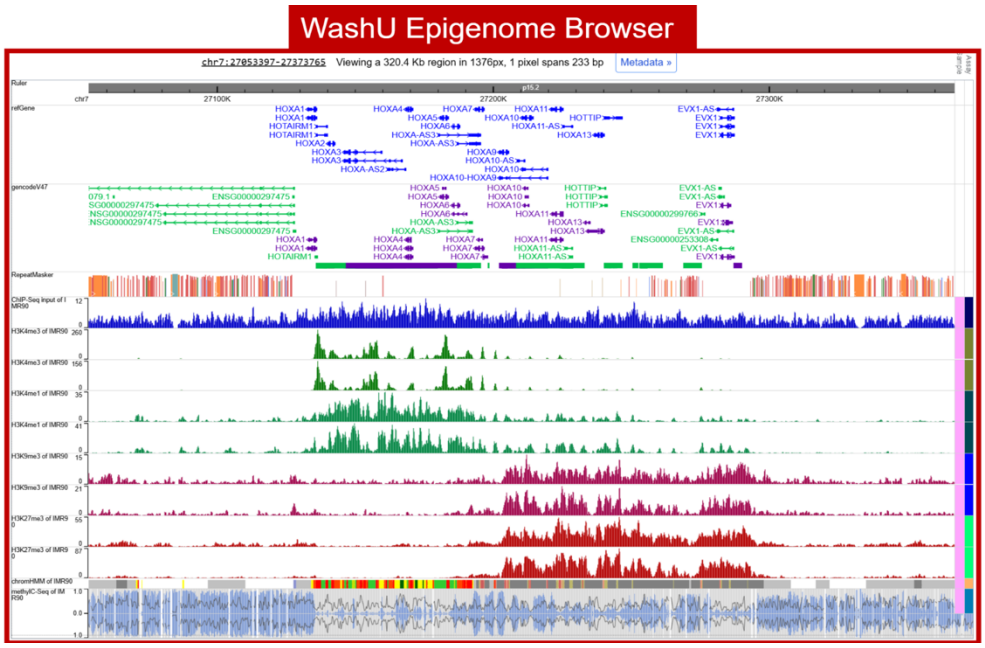
3. Navigating the Epigenome Browser

3.1. Layout of the Epigenome Browser



3.1.1. Epigenome Browser

- This region contains the data tracks aligned to the genome, overlaid on gene annotations and other annotations customized by the user.



3.2. Navigating the genome on the Epigenome Browser

3.2.1. Navigation Search

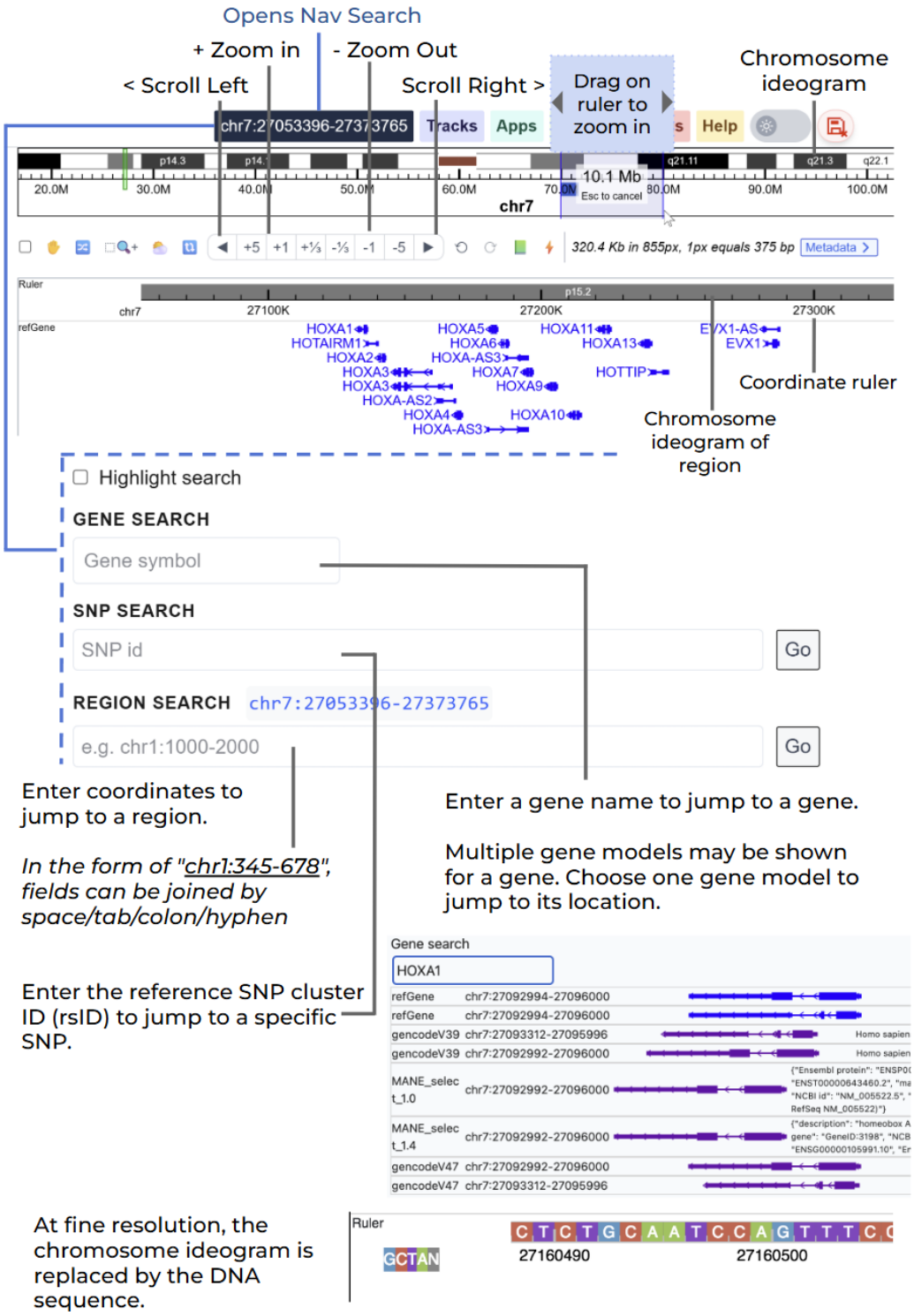
- Alternatively, click on the navigation box to enter the genomic coordinates of the region of interest. Click on Go to move to the new region.
- The Search Box can also perform the same functions as the navigation box, it allows the user to enter a new genomic coordinate, search for genes, or snp

3.2.2. Genome Navigator

- Use mouse scroll to view a larger or smaller part of the ruler
- Mouse over the region and scroll up to zoom in that specific area
- Left click and drag to view that region

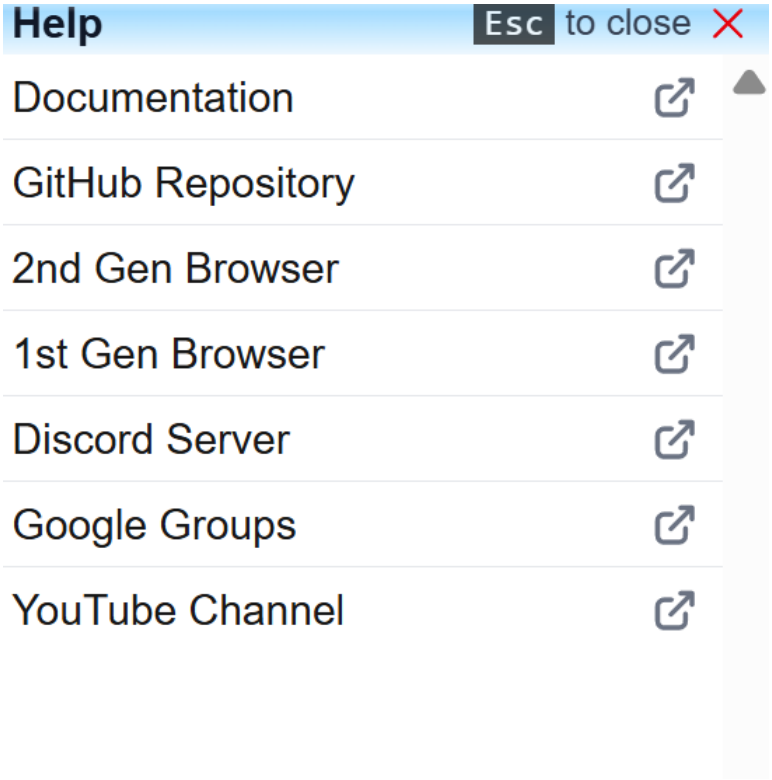
3.2.3. Tooltip

- The controls enable moving across the genome, using the zoom-in and zoom-out.
- Use the Left arrow to jump to lower adjacent regions and right arrow to jump to higher adjacent regions.
- Use magnifier tool to zoom in on the selected area on the track. Click the tool and click + hold on the track and select the region.


Opens Nav Search
+ Zoom in
- Zoom Out
< Scroll Left
Scroll Right >
Drag on ruler to zoom in
Chromosome ideogram
Tracks
Apps
Help
10.1 Mb
Esc to cancel
chr7
320.4 Kb in 855px, 1px equals 375 bp
Metadata
Ruler
refGene
Coordinate ruler
Chromosome ideogram of region
Highlight search
GENE SEARCH
Gene symbol
SNP SEARCH
SNP id
Go
REGION SEARCH
chr7:27053396-27373765
e.g. chr1:1000-2000
Go
Enter coordinates to jump to a region.
In the form of "chr1:345-678", fields can be joined by space/tab/colon/hyphen
Enter a gene name to jump to a gene.
Multiple gene models may be shown for a gene. Choose one gene model to jump to its location.
Enter the reference SNP cluster ID (rsID) to jump to a specific SNP.
Gene search
HOXA1
At fine resolution, the chromosome ideogram is replaced by the DNA sequence.
27160490
27160500

3.2.4. Help

- This menu contains links to: (i) hotkeys information, (ii) the documentation on the browser, (iii) link to the ‘old’ browser and (iv) discussion forums (on Google groups, Slack channel, Google+ and Facebook, as well as source code repository) for the browser.



4. Sessions: saving and retrieving browsing sessions

4.1. Saving sessions

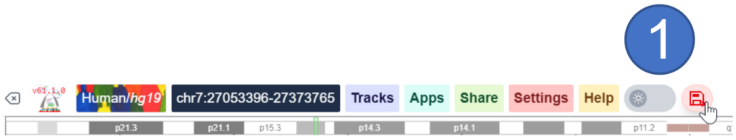
4.1.1. Saving Locally/Sessionfile

- Click Download current session
- Store json file after completion for later upload

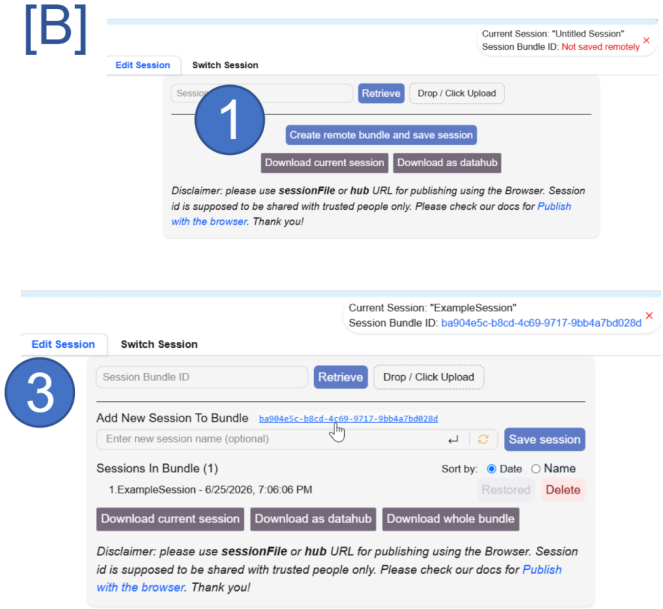
4.1.2. Saving Remotely

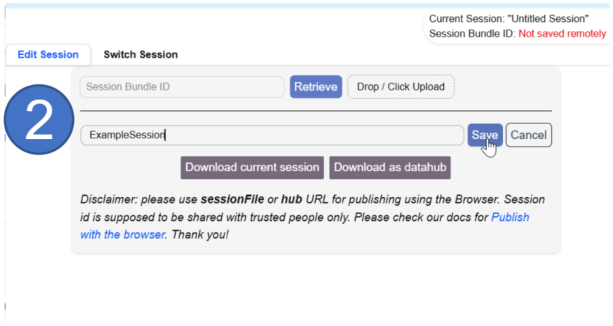
- [A] Click on the Apps menu, and then select Session.
- [B] Click the Save session button.

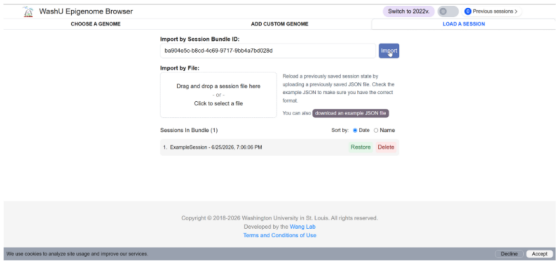
[A]



[B]







4.2. Retrieving sessions

4.2.1. Using session bundle id

- Paste the session bundle id to the input box and click the Retrieve session button.
- To Share a link for collaboration copy the session bundle id, and the session can be accessed using link:

https://epigenomegateway.wustl.edu/browser/ ? bundle=session_bundle_id

4.2.2. Upload a session file

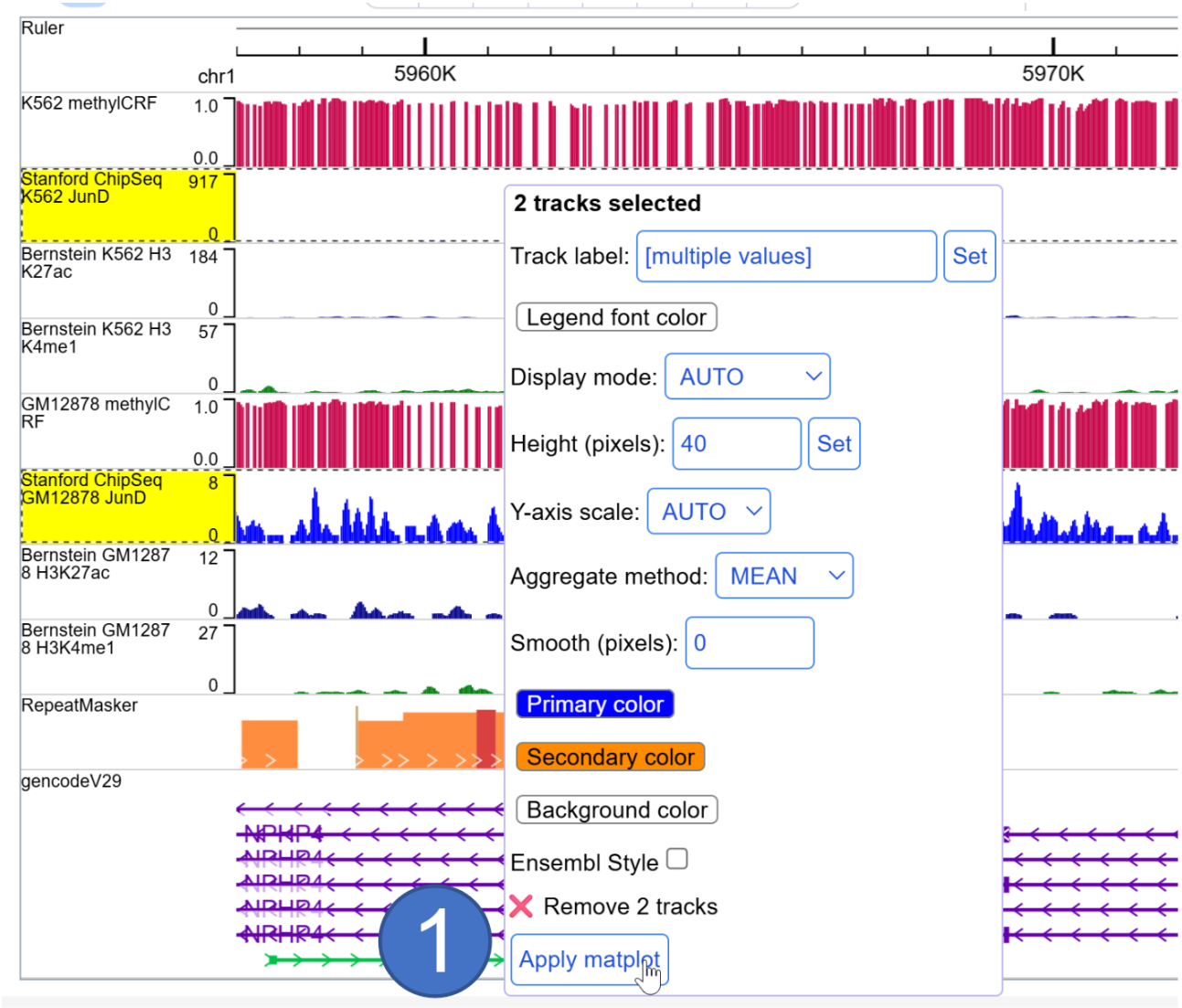
- Launch a new instance of the Epigenome browser in a new window (URL: https://epigenomegateway.wustl.edu/browser).
- [A] Click the Upload session button.
- [B] Choose the MLT1.json file provided on the workshop website.
- The browser will load this session as shown in [C].
- In this session, we will be using ENCODE datasets to analyze the cell-type specificity of JunD binding on transposable elements.
- The MLT1 session shows the specific binding of JunD to a transposable element, MLT1 in K562, specifically. This is corroborated by K562-specific hypomethylation of MLT1, and GM12878-specific hypermethylation.



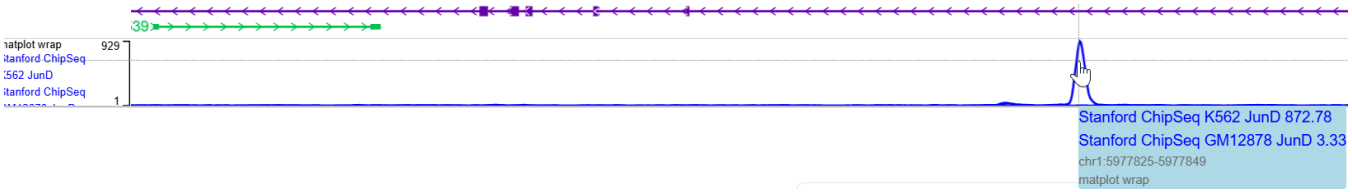
5. Using Apps and Functions on the Epigenome Browser

5.1. Matplot: Compare two or more data tracks by plotting datasets to one y-axis scale.

- Select the two JunD ChipSeq tracks and right-click on any of the tracks' names. Click on Apply matplot.



- This results in a track where the ChipSeq data for JunD binding in K562 and GM12878 share the same y-axis, and can be easily compared. It is evident from this view, that there is much more JunD binding in K562 compared with GM12878, on this MLT1 element.



- To exit from the matplot view, right-click on the matplot track name and click on Remove.

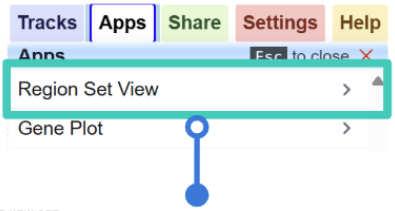
5.2. Region-set: Visualizing multiple genomic regions in parallel.

- [A] To view data on multiple genomic loci at a time, click on the Apps menu and then select Region Set View.
- [B] Clear the placeholder list, and input following 20 regions.

```
chr1:1045099-1045732
chr1:1253756-1254042
chr1:1545345-1545429
chr1:1617801-1617888
chr1:1790105-1790455
chr1:1814987-1815095
chr1:1828629-1828773
chr1:1927723-1927931
chr1:2107510-2107829
chr1:3398974-3399081
chr1:3492059-3492417
chr1:3577197-3577986
chr1:3691608-3691772
chr1:3709956-3710478
chr1:3724332-3724667
chr1:3786598-3786703
chr1:4068006-4068170
chr1:5916634-5917048
chr1:5953222-5954230
chr1:5977802-5978150
```

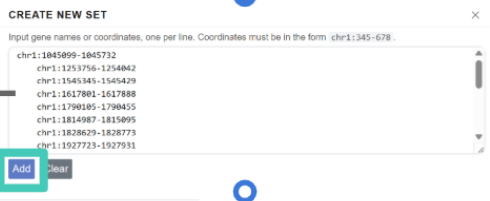
- [C] Rename this set to 20TEs-ext2.5Kb, set flanking region to upstream 2500bp and downstream 2500bp, click the Add set & Save changes button.
- [D] To view this region set, click the button Enter region set view.

[A]

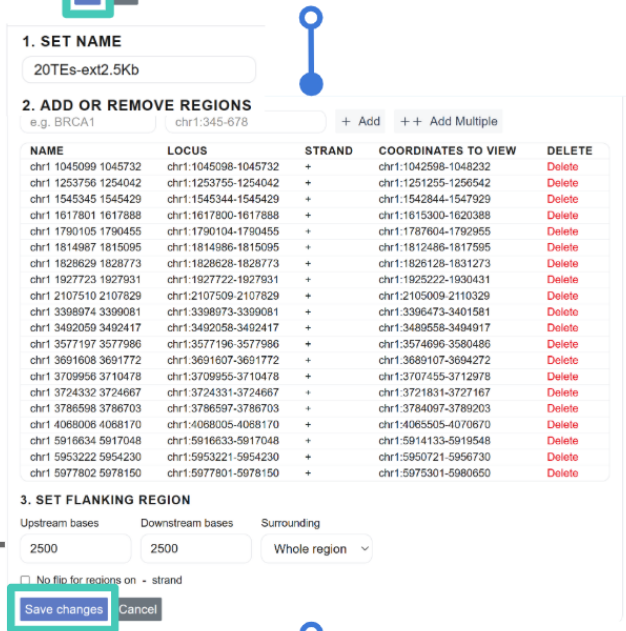


[B]

Enter a set of intervals, or gene name

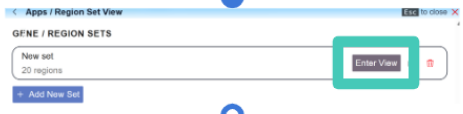


[C]



The user can specify custom flanking regions surrounding the gene transcriptional start sites to focus on the gene promoters.

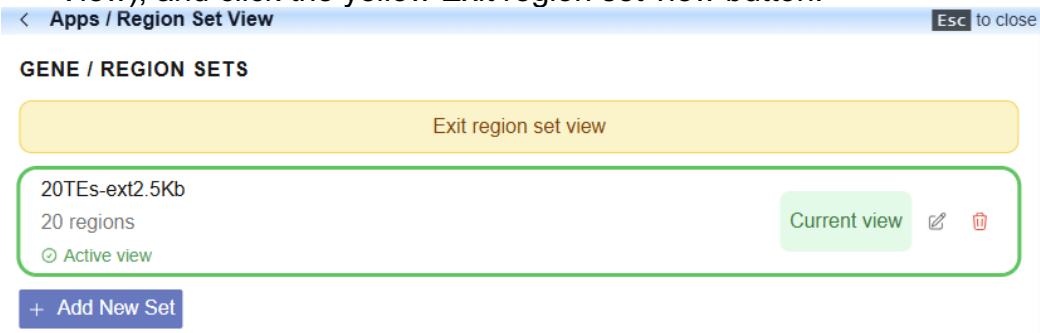
[D]





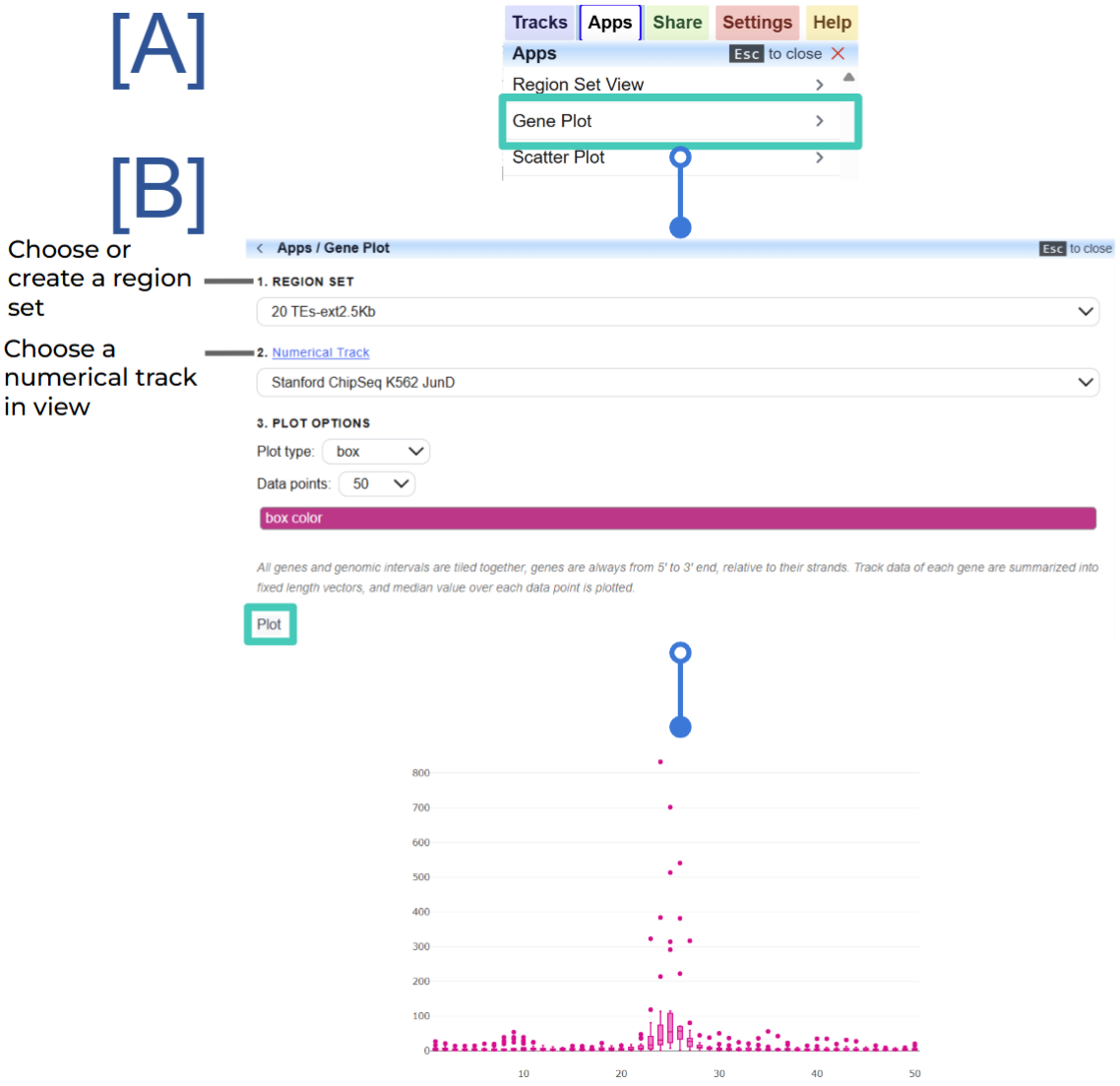
- This results in a tiled-view of all the TEs arranged beside each other. By setting the same y-axis scale for the two JunD ChipSeq tracks, the K562-specificity of JunD binding on these TEs is evident.

  - To exit the region set view, go back the region set interface (Apps -> Region Set View), and click the yellow Exit region set view button.

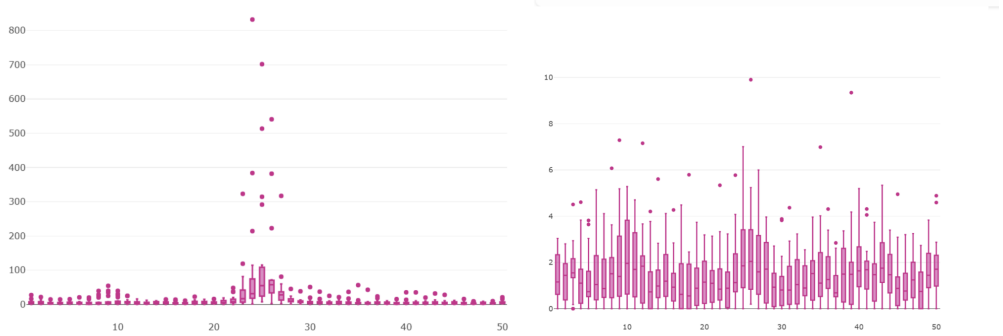


5.3. Gene plot: Summarize the data distribution across multiple regions, by splitting the regions into bins.

- [A] Click on the Apps menu. choose Geneplot app.
- [B] To make a gene plot, follow these steps:
  - Click on the Choose a region set dropdown menu. Select the 20 TEs-ext2.5Kb list of TEs for this analysis.
  - Click on the Choose a numerical track dropdown menu, and then select Stanford ChipSeq K562 JunD.
  - Click the Plot button.
  - The same process can be repeated for the Stanford ChipSeq GM12878 JunD.



- Comparing the two gene-plots reveals that the highest ChIP-seq signal for JunD binding in K562 is on the TEs (data points 23-29 on the x-axis). The ChIP-seq signal for JunD binding in GM12878 on TEs is comparable to the flanking region (data points 1-23 and 29-50).



K562 GM12878

Click the top and bottom number of y-axis can change/edit the y-axis scale. When mouse over the figure, click Autoscale 

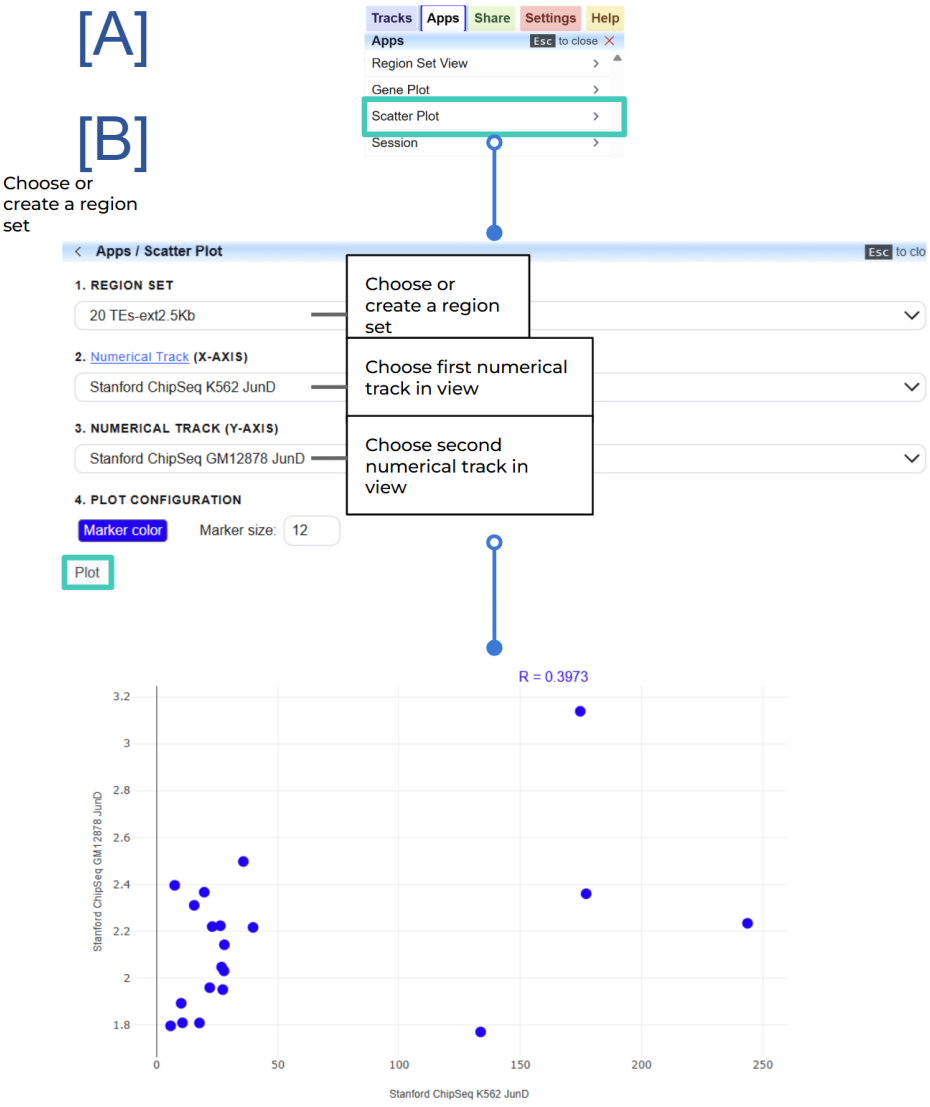
button to reset the scale.

5.4. Scatter plot: Correlate different datasets, across multiple genomic regions.

[A] Click on Apps -> Scatter plot

[B] Choose a region set, 2 tracks for X- and Y-axis, respectively.

[C] Click the Plot button.



5.5. Undo/Redo

The browser now enables the undo/redo function. Launch a new session with hg19 genome loaded.

- [A] Right click the gencodeV47 track, choose Remove
- [B] Click the Undo button.

- [C] The Removed gencode track is added back.

5.6. History

- Click History icon in Tooltip -> find session you want to restore

[A]

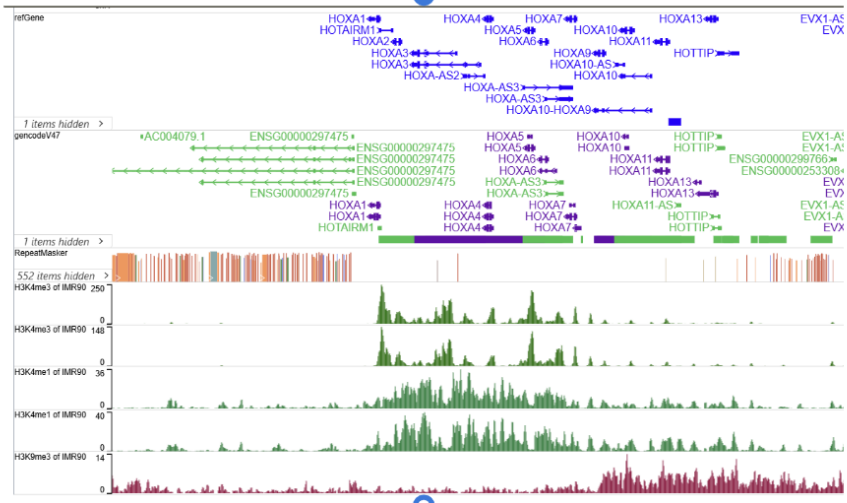
Shift left click tracks to select them

[B]

Right click a selected track and remove

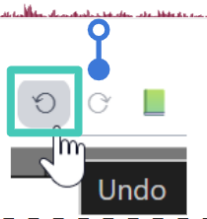


View after removing the 5 selected tracks



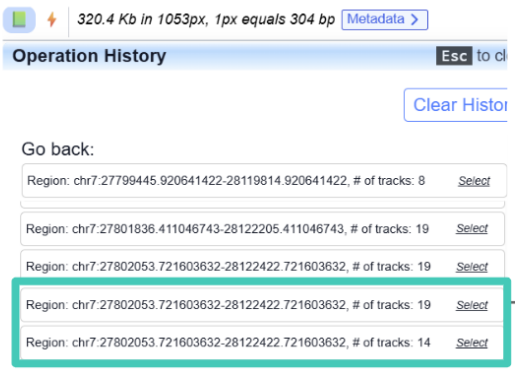
[C]

Click undo to reverse the deletion



➢ Utilizing History

Open History tool to see the previous 20 actions and jump to them



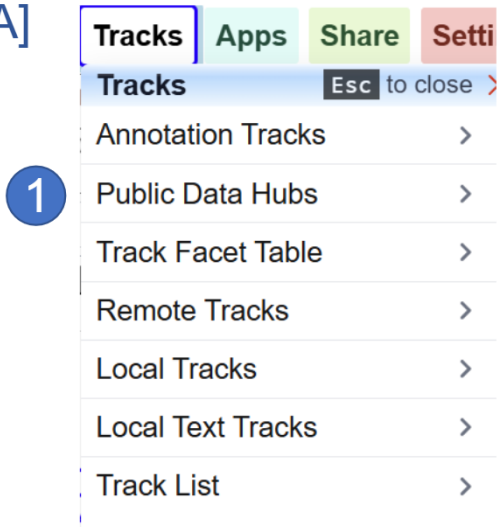
Here we see the differences in number of tracks. This is when the deletion occurred.

6. Exploring chromatin interaction data using the Epigenome Browser

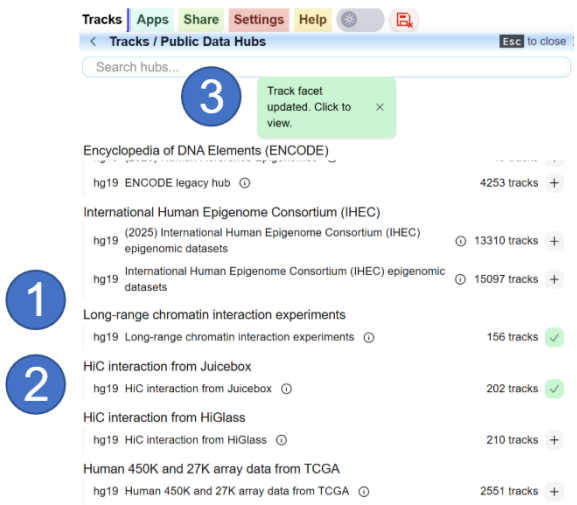
Let's load some chromatin interaction data to the browser.

- [A] Click Tracks -> Public Data Hubs.
- [B] Go to 2nd page of data hub list, load Long-range chromatin interaction experiments and HiC interaction from Juicebox hub.
- Click on the X at the top-right of the window to get back to the browser.

[A]

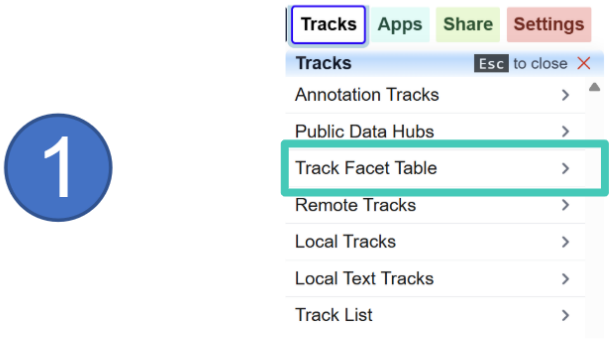


[B]

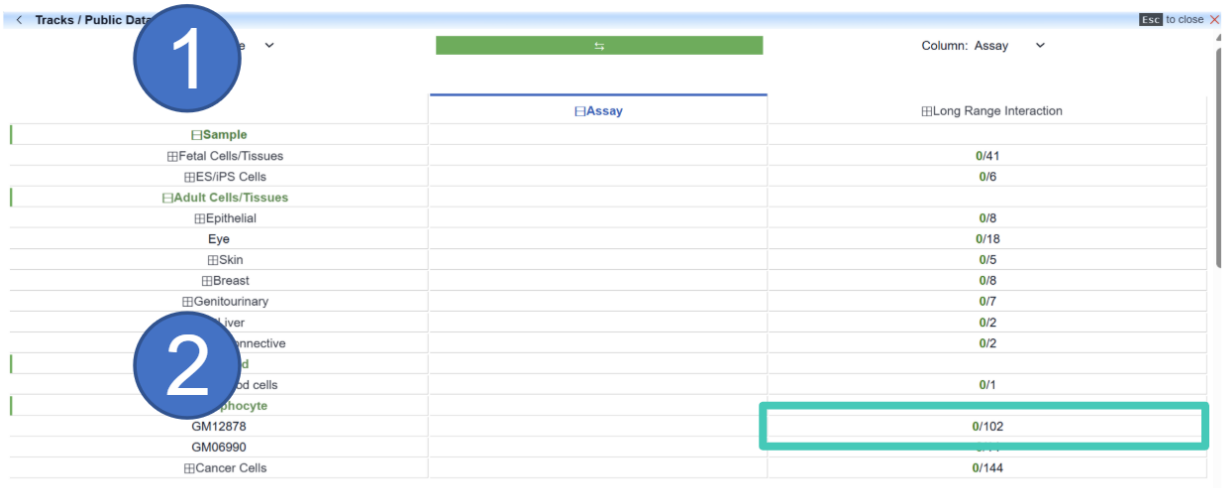


- [A] Click Tracks -> Track Facet Table.
- [B] Expand Sample by clicking the Sample term, Find GM12878 Under Adult Cells/Tissues -> Blood -> Lymphocyte, expand the Assay column as well.

[A]



[B]



- In the search bar, type “GM12878”, load the track named HiC.GM12878 and load the track named GM12878_1in_situ_1combined.
- Click on the X at the top-right of the window to get back to the browser.

GM12878 Free text search over track labels and metadata. Add all in page

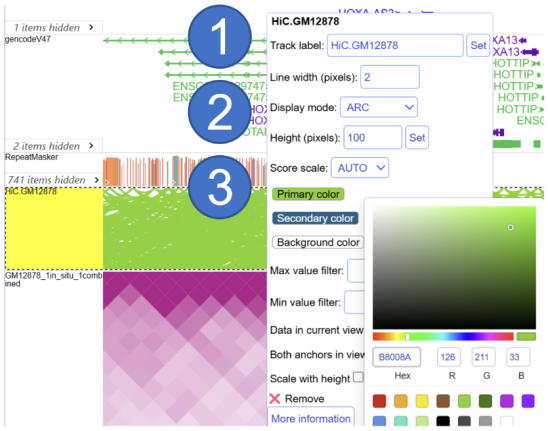
First ‹ › Last 1 10 per page 1 / 11

Genome	Name	Data hub	Sample	Assay	Format	Add
hg19	HiC.GM12878	Long-range chromatin interaction experiments	Adult Cells/Tissues > Blood > Lymphocyte > GM12878	Long Range Interaction > Hi-C	longrange	✓
hg19	GM12878_1in_situ_1combined	HiC interaction from Juicebox	Adult Cells/Tissues > Blood > Lymphocyte > GM12878	Long Range Interaction > Hi-C	hic	✓

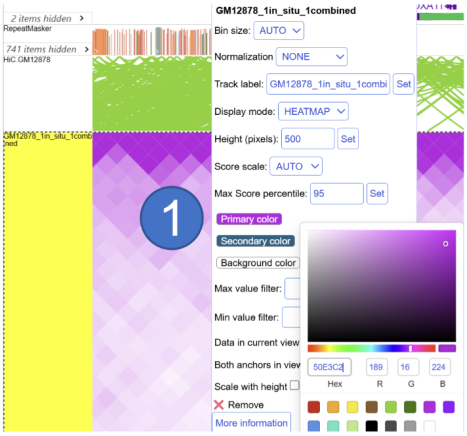
- [A] Right click the ChIA-PET track, change Display mode to ARC, change the height to 100, and Click the Primary color button to change color.
- [B] Right click the hic track, click the Primary color button to change color.

Now the browser view should look like this:

[A]



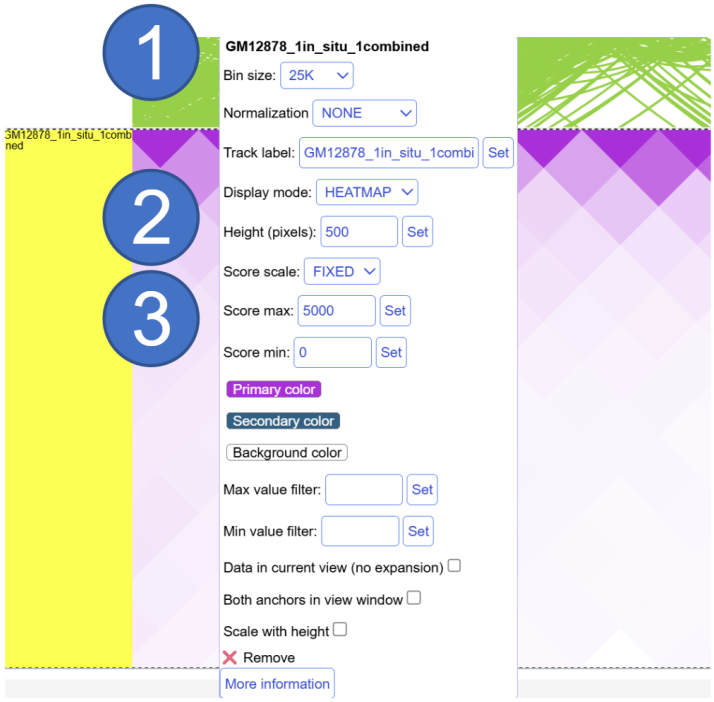
[B]



Click the -5 button to zoom out the view region.
[A] Right click on the hic track, change Bin size to 25K, and Score Scale to FIXED, and enter Score max to 5000, click the Set button.

[B] The updated hic track view after change bin size and scale.

[A]



[B]



7. Genome Comparison

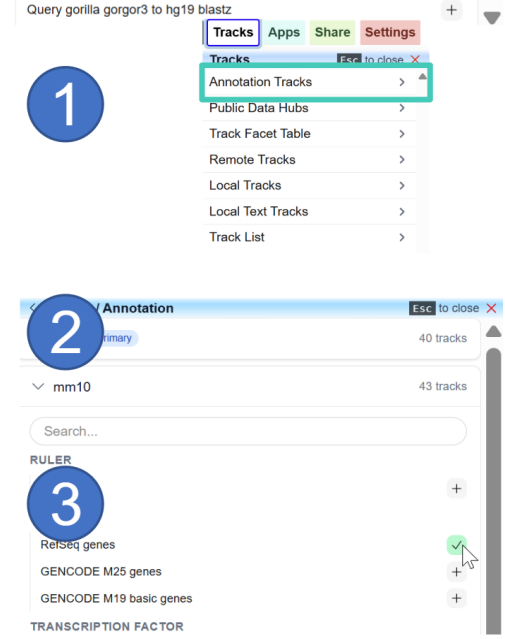
7.1. Adding Genome Align Track and Refgene Aligned to Query Genome:

- [A] Click Track in navbar -> Click Annotation Tracks -> select hg19 from the panel -> Use the search bar, type “Genome Comparison” or scroll down and click the plus icon to add Query mouse mm10 to hg19 blastz
- [B] Click Track in navbar -> Click Annotation Tracks -> select mm10 from the panel -> Add RefSeq genes

[A]



[B]

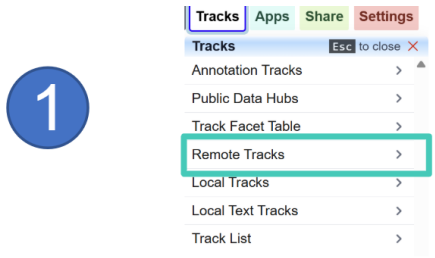


8. G3d

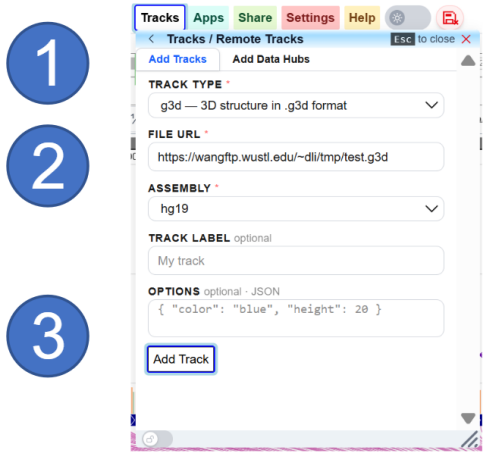
8.1. Adding G3d

- [A] Click Track in navbar -> Click Remote Tracks
- [B] For “Track Type”, select g3d - 3D structure in .g3d format. -> For “File Url”, copy and paste https://wangftp.wustl.edu/~dli/tmp/test.g3d -> Click Add Track
- [C] In Toolbar, click -5 to zoom out

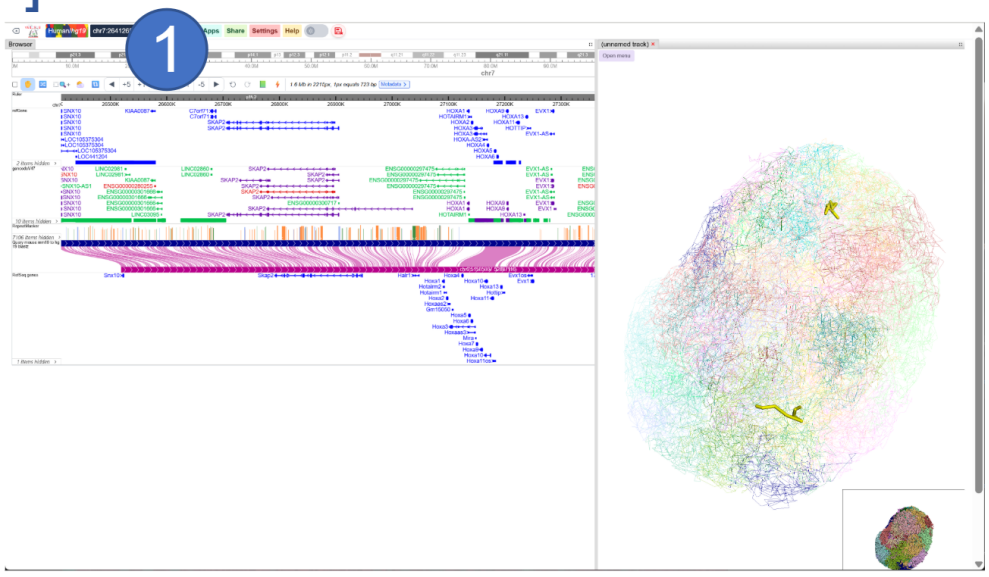
[A]



[B]



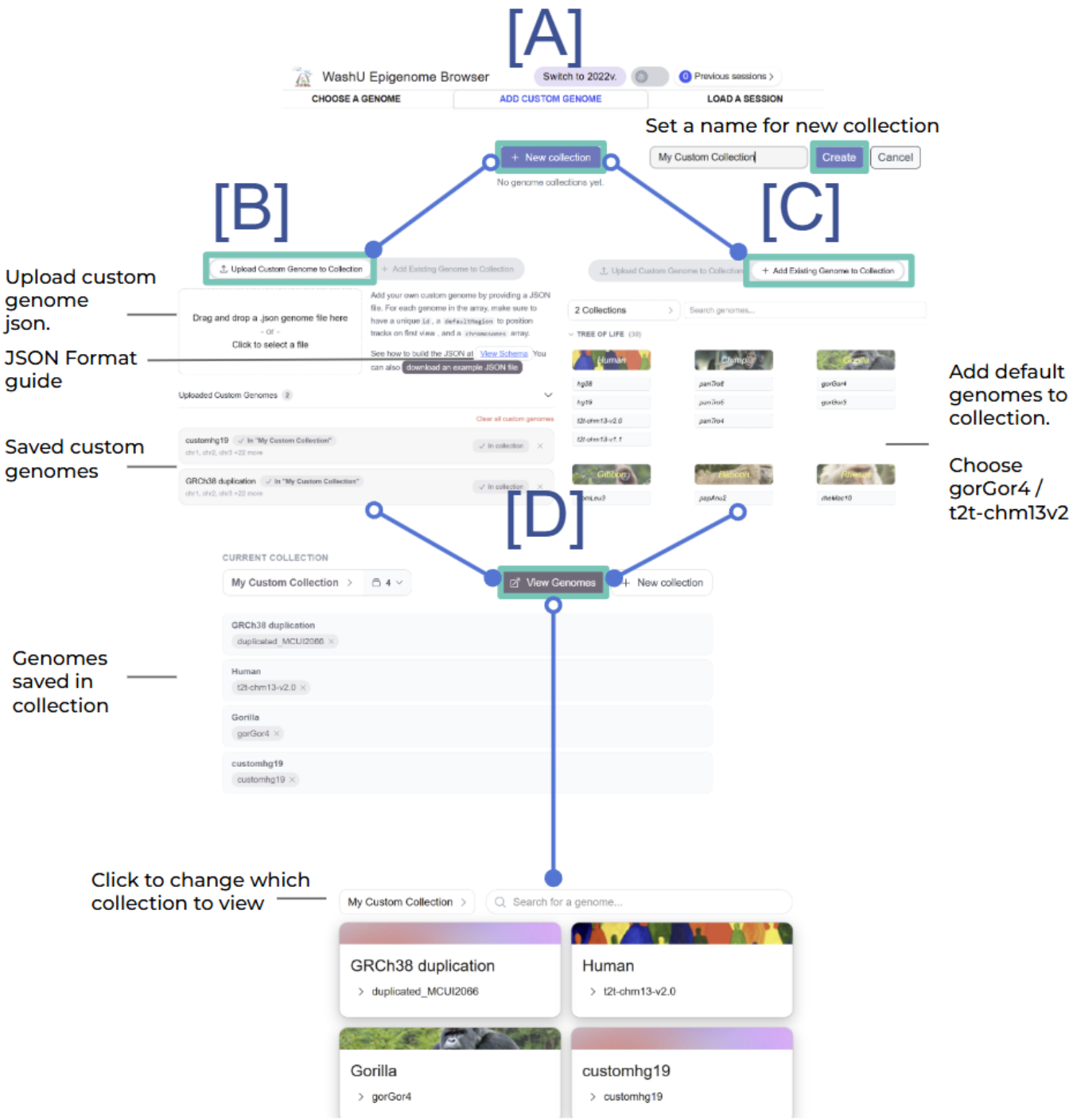
[C]



9. Create Collections

9.1. Create Collection

- [A] In the home screen, Click ADD CUSTOM GENOME tab -> create a name for your collection
- [B] To Add a Custom Genome, Click Upload Custom Genome to Collection tab -> “download an example JSON file” -> drop file in box or choose json.
- [C] To Add a genome already in the browser, Click Add Existing Genome to Collection tab -> click collection tab -> tree of life -> click gorGor4 and panTro4
- [D] Click View Genomes


[A]
WashU Epigenome Browser
Switch to 2022v.
Previous sessions
CHOOSE A GENOME
ADD CUSTOM GENOME
LOAD A SESSION
Set a name for new collection
[B]
[C]
+ New collection
No genome collections yet.
My Custom Collection
Create
Cancel
Upload Custom Genome to Collection
Add Existing Genome to Collection
Upload custom genome json.
Drag and drop a .json genome file here
- or -
Click to select a file
JSON Format guide
Add your own custom genome by providing a JSON file. For each genome in the array, make sure to have a unique id, a defaultRegion to position tracks on first view, and a chromSizes array.
See how to build the JSON at View Schema. You can also download an example JSON file
2 Collections
Search genomes...
TREE OF LIFE
Human
Chimp
Gorilla
Uploaded Custom Genomes
Clear all custom genomes
Saved custom genomes
customhg19
In "My Custom Collection"
GRCh38 duplication
In "My Custom Collection"
Add default genomes to collection.
Choose gorGor4 / t2t-chm13v2
[D]
CURRENT COLLECTION
My Custom Collection
View Genomes
New collection
Genomes saved in collection
GRCh38 duplication
duplicated_MCUI2066
Human
t2t-chm13-v2.0
Gorilla
gorGor4
customhg19
customhg19
Click to change which collection to view
My Custom Collection
Search for a genome...
GRCh38 duplication
duplicated_MCUI2066
Human
t2t-chm13-v2.0
Gorilla
gorGor4
customhg19
customhg19

10. Wuepgg package, embed the browser

WashU Epigenome Browser has been redesigned as a npm library. It can be directly installed from npm.js and be directly embedded in your React app. Create your genome portal and visualize your genome data offline or hosted in in your own website. Plans to integrate this libraries into future projects, such as the Pangenome Browser.

npm create vite@latest
npm install wuepgg
"wuepgg": "^61.9.5"

➢ Installation -

```bash
$ npm create vite@latest
```

```
npm install wuepgg
```

➢ Implementation -

Import GenomeHub component and its stylesheet, and render it in your app:

```
import { GenomeHub } from "wuepgg";
import "wuepgg/style.css";

const viewRegion = { genomeCoordinate: "chr7:27053397-27373765" };
const genomeName = "hg19";
const storeConfig = { storeId: "genome-1" };

export default function App() {
  return (
    <GenomeHub
      storeConfig={storeConfig}
      viewRegion={viewRegion}
      genomeName={genomeName}
    />
  );
}
```



➢ Support - - - - - - - - - - - - - - - - - - -

Get Node.js (version 20 above recommended) and yarn package management tool, clone the code.

Installation

```
yarn add wuepgg
```
or

```
npm install --save wuepgg
```

Basic Example

Render some tracks with URLs

```
import { GenomeViewer } from "wuepgg";
<GenomeViewer
  viewRegion="chr7:27181545-27245617"
  tracks={[
    {
      url: "https://hicfiles.s3.amazonaws.com/hiseq/gm12878/in-situ/combined.hic",
      name: "hictest",
      type: "hic",
    },
    {
      url: "https://vizhub.wustl.edu/hubSample/hg19/bam1.bam",
      name: "bamtest",
      type: "bam",
    },
    {
      name: "gencodeV47",
      type: "geneannotation",
    },
  ]}
  genomeName="hg19"
/>
```
See below for the full list of supported parameters.

Render the entire browser as a react component

```
import { GenomeHub } from "wuepgg";
<GenomeHub />
```
Render the browser's landing page where user can choose a genome to view

API Reference

GenomeViewer

A React component for visualizing genomes

Props:

- genomeName (string, required)
  Name of the genome to display (e.g., "hg38", "mm10").
  Example: "hg38"
- tracks (TracksProps[], required)
  An array of track configuration objects. Each object describes a data track to display in the viewer.

  TypeScript interface:

```
interface TracksProps {
  url?: string; // Optional: Data file URL, (track types such as geneannotation, ruler do not need a URL)
  name?: string; // Optional: Legend display name
  options?: { [key: string]: any }; // Optional: Track-specific options (e.g., color)
  type: string; // Required: Track type (e.g., "ruler", "bam", "hic", "geneannotation", "bigwig", "longrange"...)
}
```

  Example:

```
[
  {
    "type": "track_type1",
    "name": "track_name1",
    "url": "track_url1",
    "options": {}
  },
  {
    "type": "track_type2",
    "name": "track_name2",
    "url": "track_url2",
    "options": {}
  }
]
```

  For more details on track formatting, see the Epigenome Gateway Datahub documentation.

- viewRegion (string, optional)
  Genomic region to display, as a string.

  Template:

```
"chr<chromosome>:<start>-<end>"
```

  Example:

```
"chr7:27053397-27373765"
```

  Default: Uses the genomeConfig's default region if not provided.

- windowWidth (number, optional)
  Width of the genome viewer in pixels.
  Default: 1200

- customGenome (any, optional)
  Optional custom genome object if the user created their own genome matching the current formatting.

GenomeHub

A React component that renders the full genome browser interface.
No props are required.
Future updates will add options for customizing the appearance and behavior of the browser.