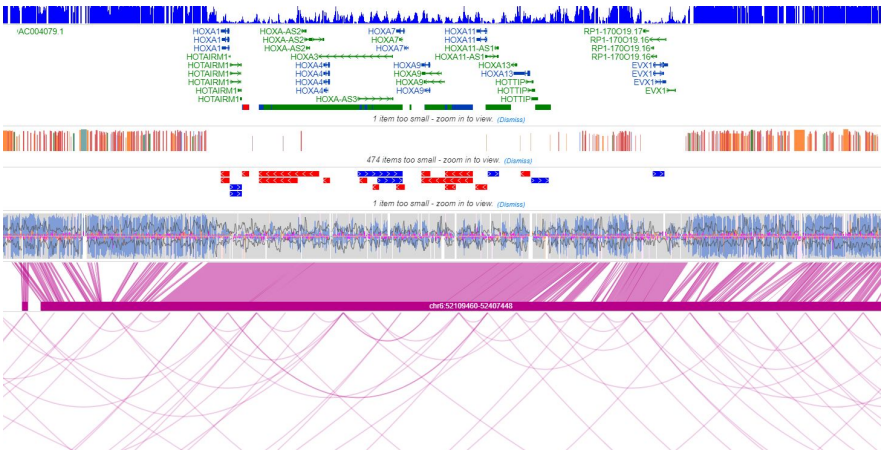
Everything can be found at

epigenomegateway.wustl.edu



REFERENCES

1. Zhou X, et al., Nature Methods 8, 989-990 (2011)
2. Zhou X & Wang T, Current Protocols in Bioinformatics Unit 10.10 (2012)
3. Zhou X, et al., Nature Methods 10, 375-376 (2013)
4. Zhou X, et al., Bioinformatics 30, 2206-2207 (2014)
5. Zhou X, et al., Nature Biotechnology 33, 345-346 (2015)

FUNDING

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LATEST DEVELOPMENT

Documentation: eg.rtfd.io
Google groups: http://bit.ly/egGroup
Facebook: http://bit.ly/2SZpvpz
Slack channel: https://bit.ly/2T1OKmP
Twitter: @wuepgg

SUPPORT

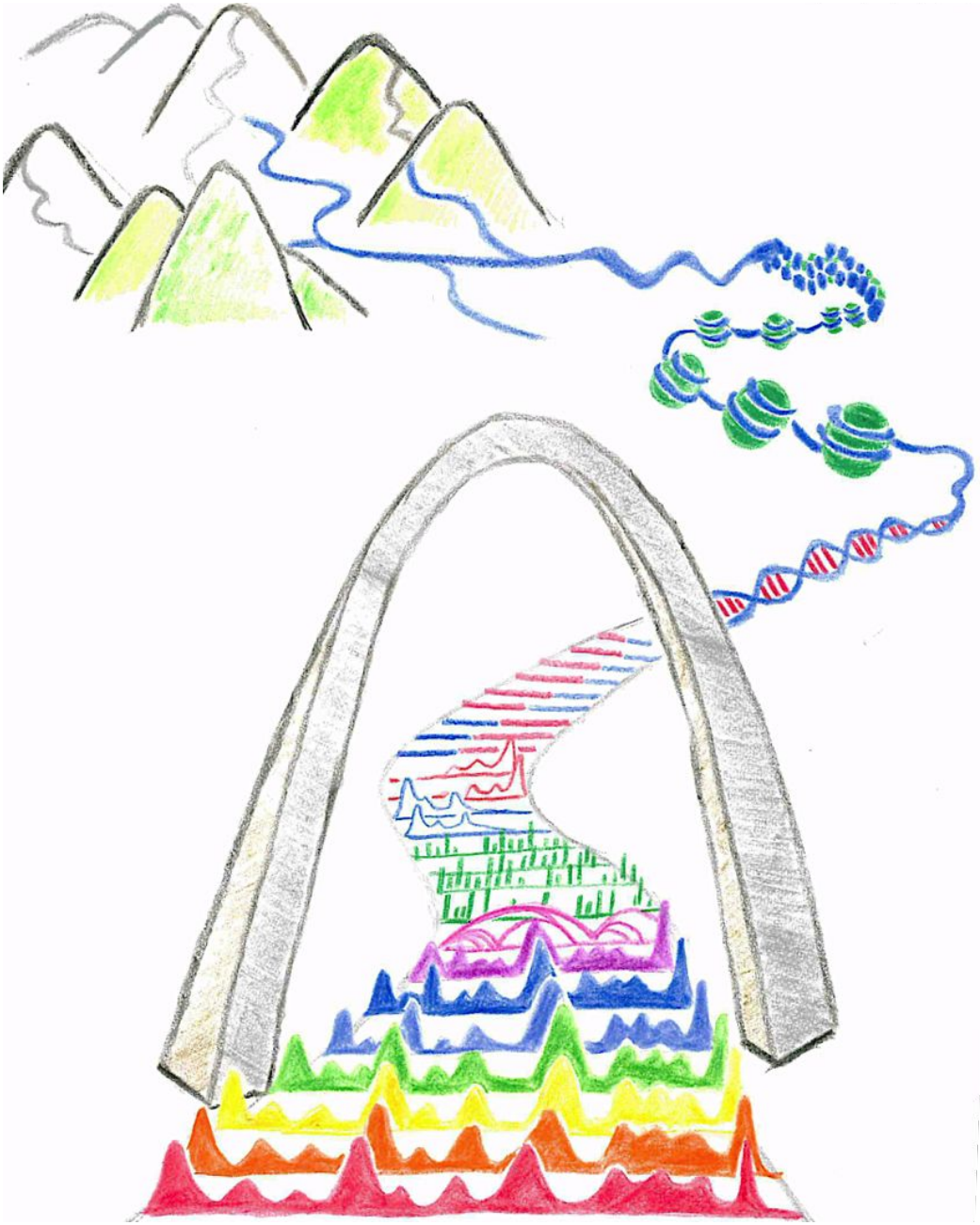
epigenomegateway.wustl.edu/support/

CONTACT US

Lab: wang.wustl.edu

Authors: Daofeng Li, Renee Sears, Deepak Purushotham, Ting Wang
Cover art: Ting Wang

V: 3/2019

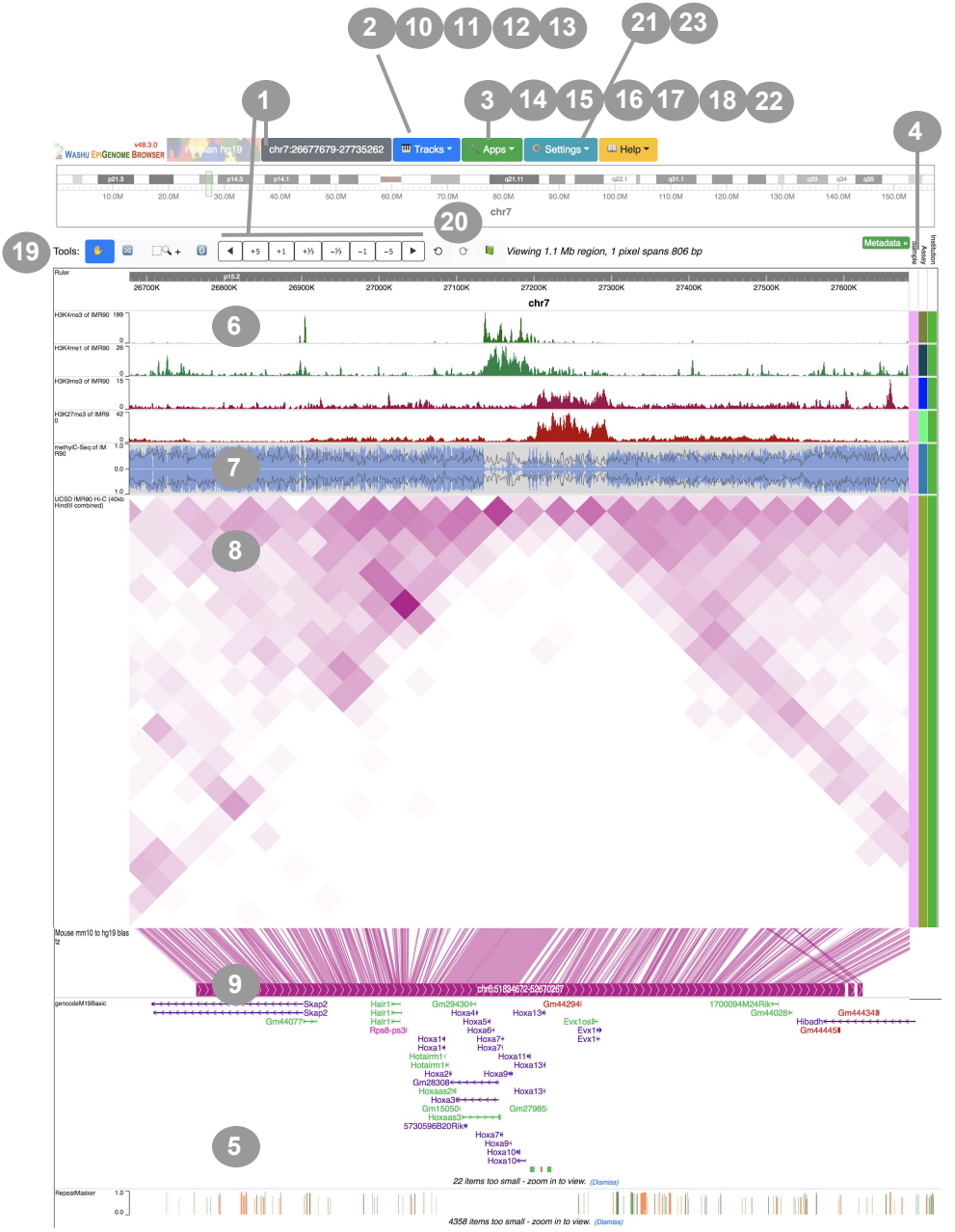


WASHU EPIGENOME BROWSER

2019

epigenomegateway.wustl.edu

BROWSER MAP

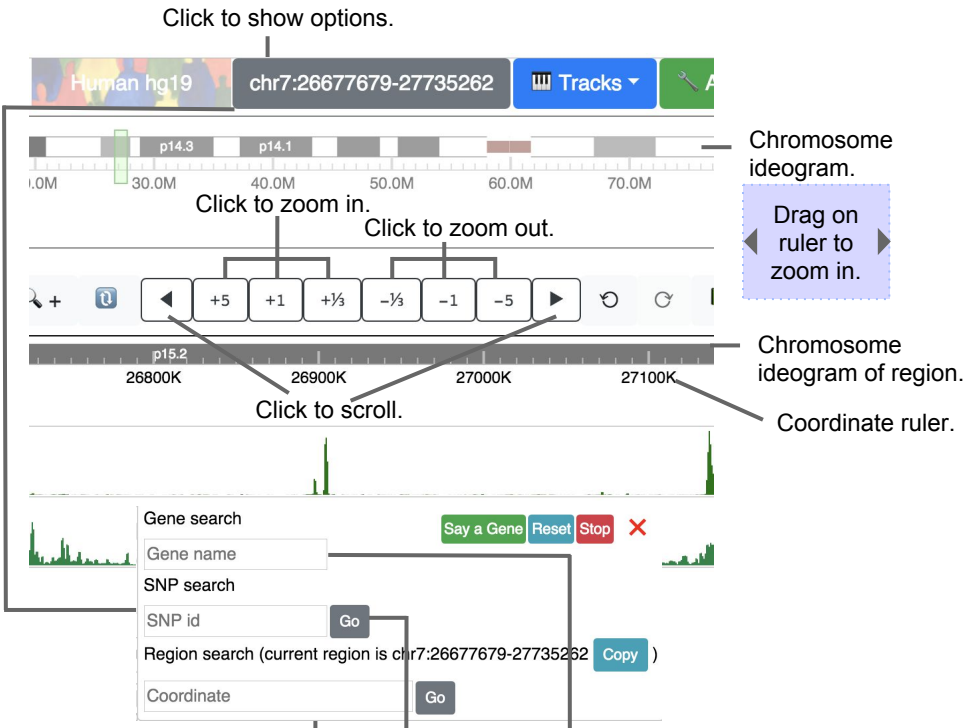


Key

1 = Go to this page number to learn about the browser feature

TABLE OF CONTENTS

Browser Features: Navigation



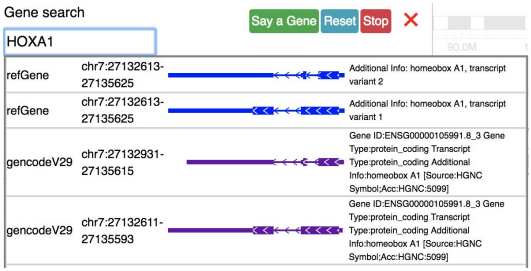
Enter coordinates to jump to a region.

In the form of "chr1:345-678", fields can be joined by space/tab/colon/hyphen

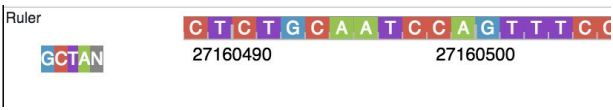
Enter the reference SNP cluster ID (rsID) to jump to a specific SNP.

Enter a gene name to jump to a gene.

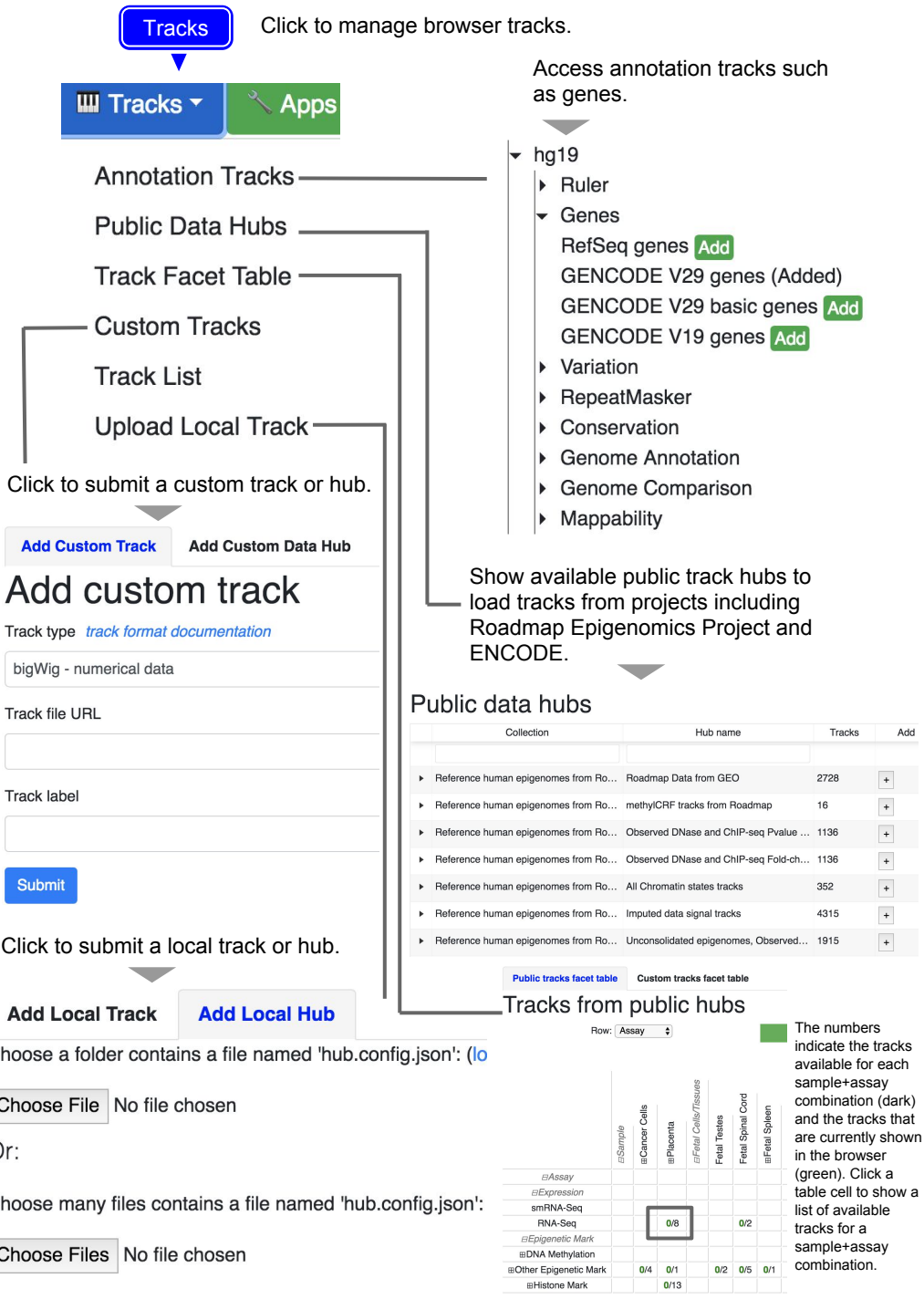
Multiple gene models may be shown for a gene. Choose one gene model to jump to its location.



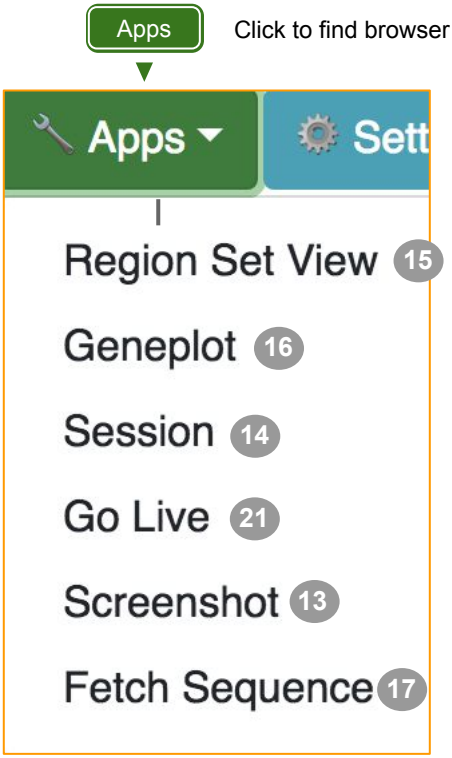
At fine resolution, the chromosome ideogram is replaced by the DNA sequence.



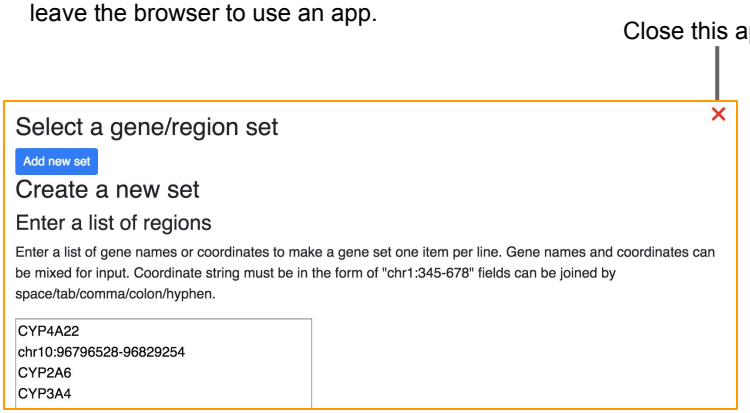
A browser **track** is a visualization of a dataset along a genome. Examples of browser tracks include gene annotation tracks and RNA-seq expression tracks.

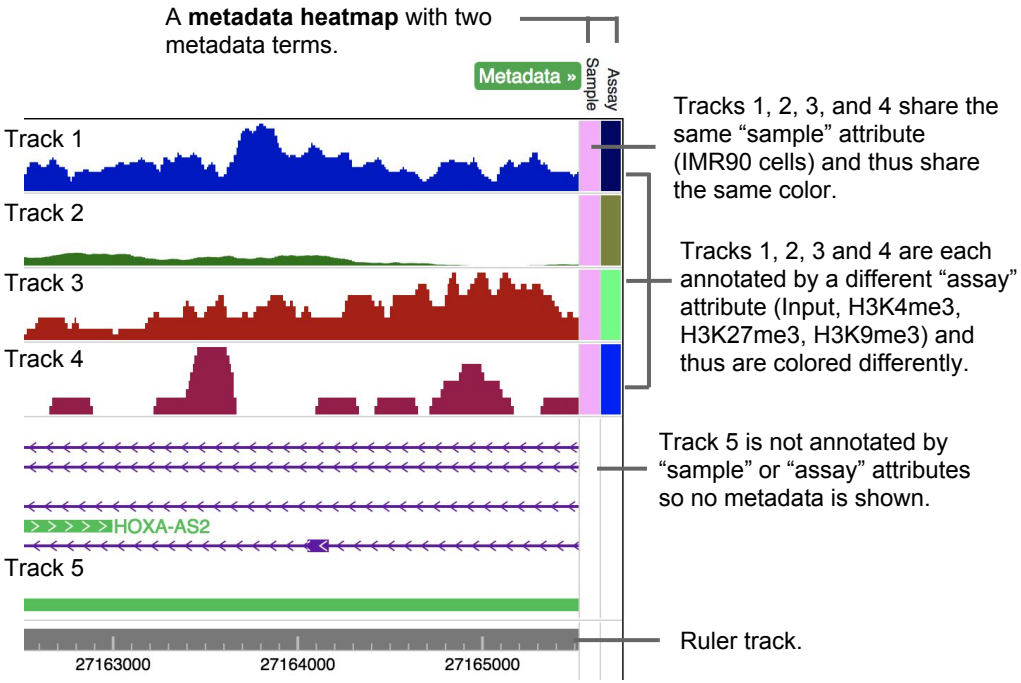


A browser **app** is a self-contained program for executing a specific task. Examples of browser apps include uploading files and taking screenshots.

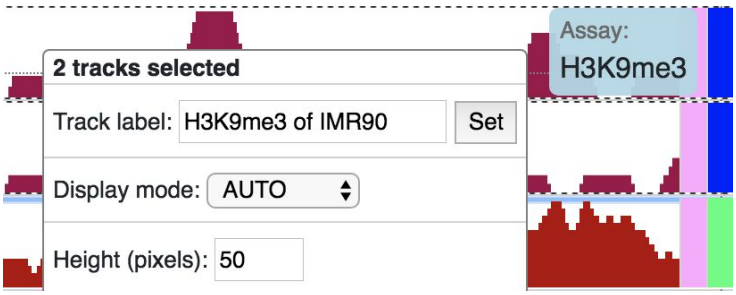


Apps usually appear as new panels on top of the browser and are used in the context of browser visualization. You never have to leave the browser to use an app.

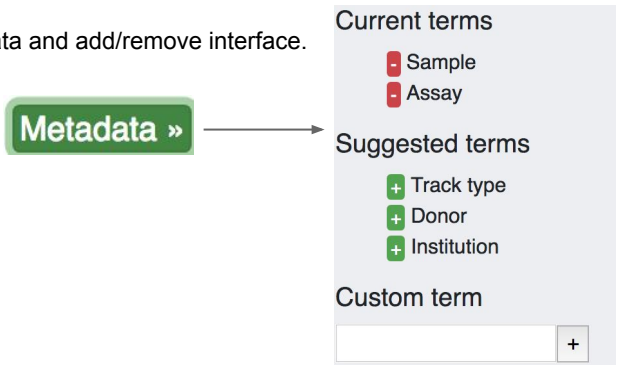


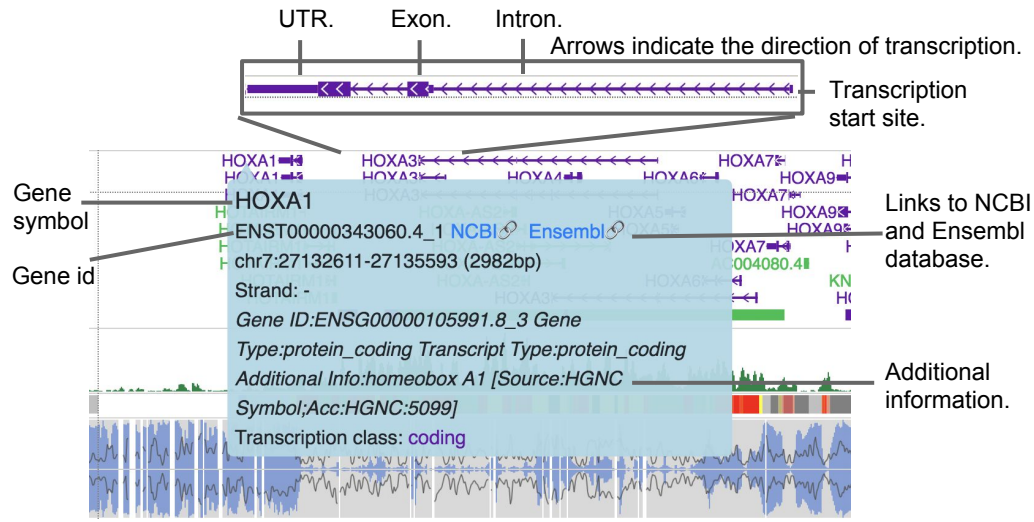


Click the metadata bar to quickly select tracks annotated with the same metadata term.



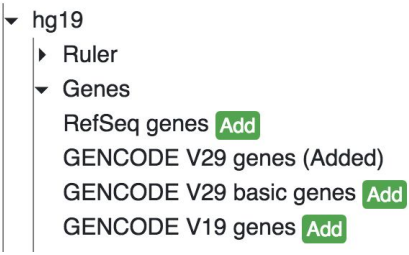
Switch Metadata and add/remove interface.

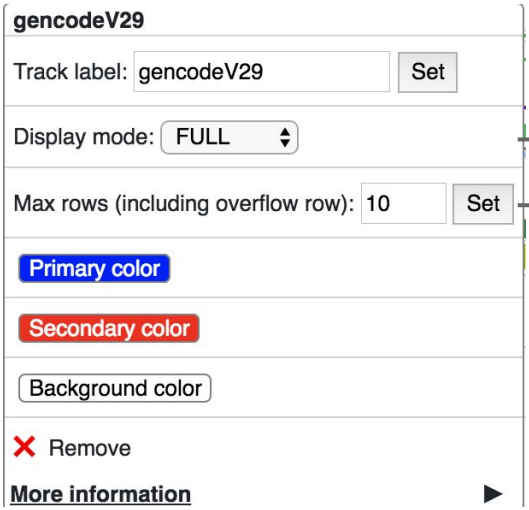




The human **Gencode V29 gene track** for *HOXA3* is shown above. The tooltip bubble displays information on the *HOXA3* gene.

Multiple gene tracks are usually available for a genome. To find other gene tracks, go to “Tracks” > “Annotation tracks” >“Genes”.





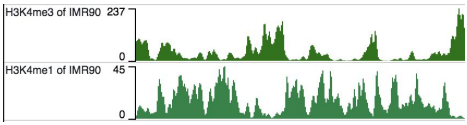
Right-click on the gene track (and any other tracks) for the **configuration menu**.

Display modes.

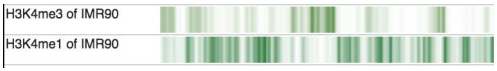
Configure the number of rows for displaying genes

A **numerical track** displays a series of quantitative values along the genome as a highly customizable graph. When the track height is small, the track is shown as a heatmap, otherwise it is shown as a bar plot.

Bar plot (track height ≥ 20 pixels)

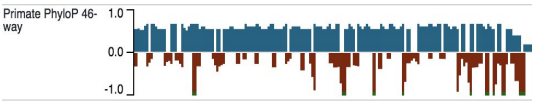


Heatmap (track height < 20 pixels)

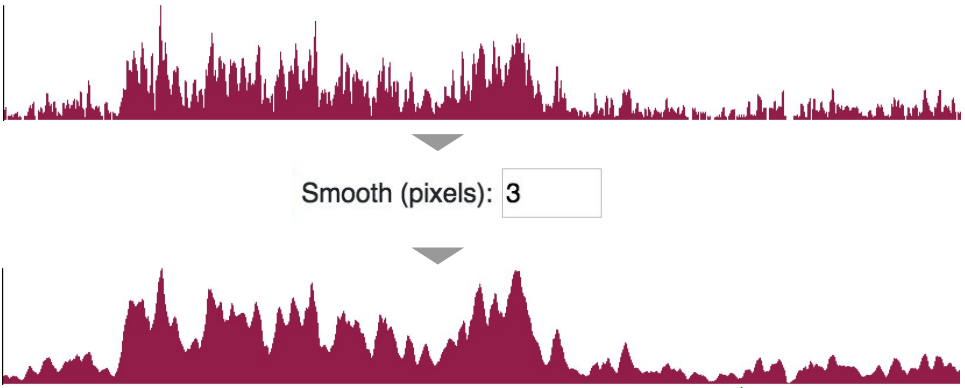


Positive and negative values are rendered using different colors.

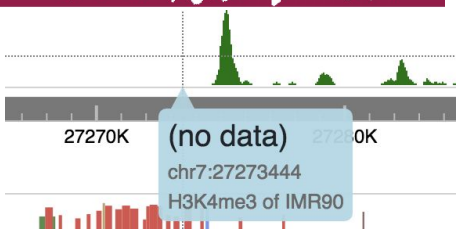
The default y-axis scale is an automatic scale which can be changed into a fixed scale using the configuration menu. Bars with values beyond a set threshold are indicated with a different color on their peaks.



Bar plot shape can be smoothed using the configuration menu.



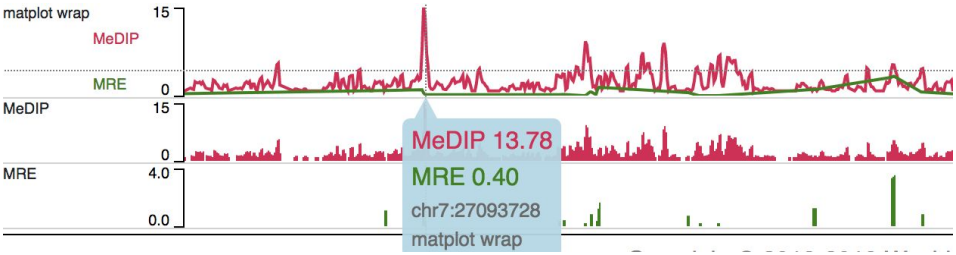
Missing values are labelled as “No data” on the tooltip for bedGraph format tracks (not applicable for bigWig format tracks).



Docs

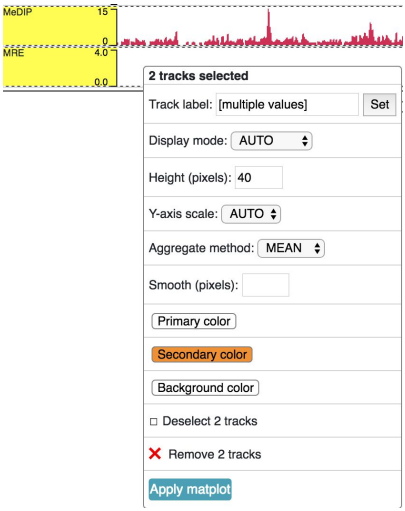
Learn more about the supported numerical track formats bedGraph and bigWig at https://eg.readthedocs.io/en/latest/tracks.html#numerical-tracks.

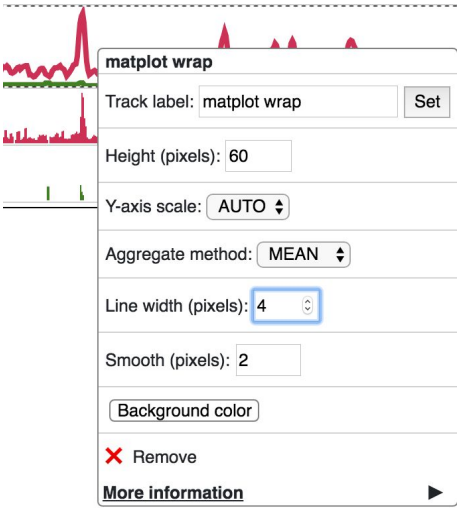
A **matplot** (also called a line plot) displays multiple numerical tracks on the same X and Y axes to easily compare datasets. Data is plotted as curves instead of bar plots.



Matplots can be created while browsing:

1. Hold shift and click on track names to select multiple numerical tracks. (Track names will be highlighted in yellow.)
2. Right-click on the selected tracks and select “Apply matplot."



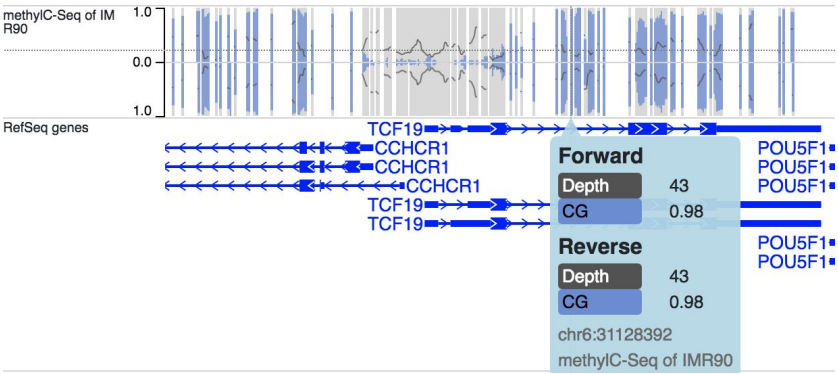


Matplot track can be treated as regular tracks. Right Click for the configuration menu.

Docs

Matplots can be defined in datahub. Learn more at https://eg.readthedocs.io/en/latest/datahub.html#example-matplot-track.

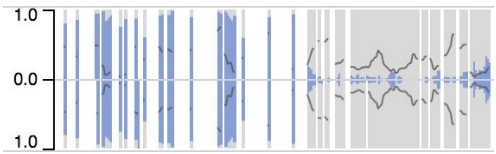
The **methylC track**[1] is designed to display DNA methylation data from whole-genome bisulfite sequencing experiments. It distinguishes cytosine methylation levels (as bar plots) on separate strands and in different sequence contexts and integrates sequencing read depth (as curves) as a measure of confidence.



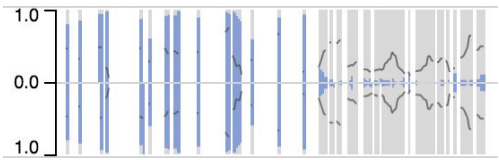
The color legend for a methylC track can be viewed using its configuration menu. All colors are configurable by clicking on the color boxes.

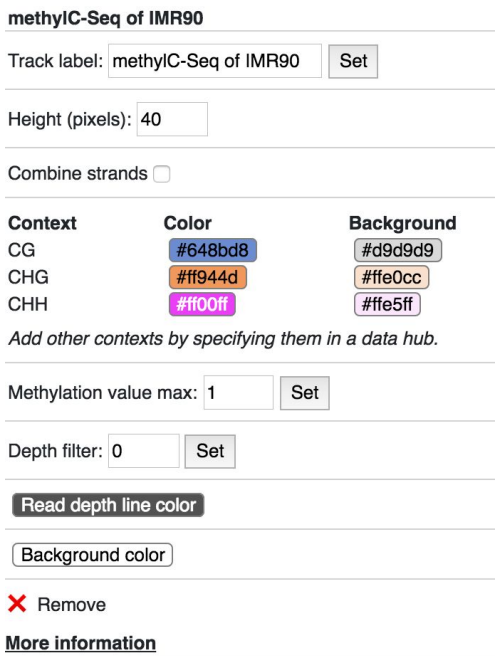
To filter methylation data by read depth select the configuration menu, click “Filter by read depth," enter a threshold, and click “Apply."

No filtering

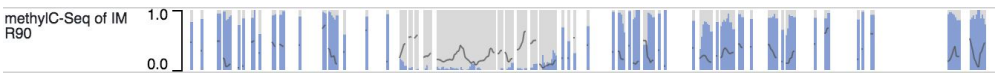


Filtered by read depth value 15





To combine the forward and reverse strands, in the configuration menu, select “Combine strands."

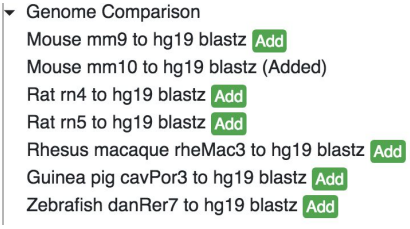


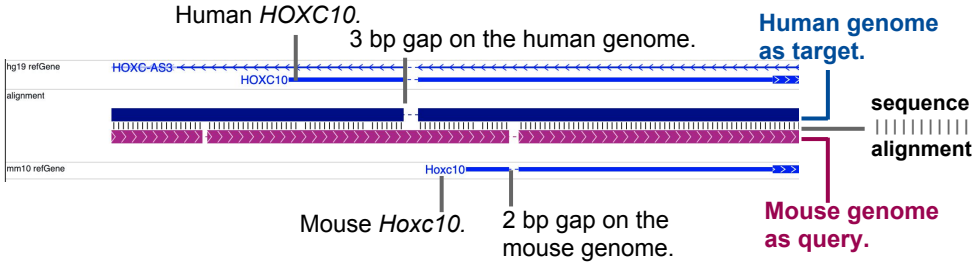
[1]Zhou X, et al., Bioinformatics 30, 2206-2207 (2014)

The **genome comparison track** visualizes pairwise alignments of two genomes allowing for comparison at fine (base pair) or large (megabase) scale. Alignment is unbiased with gaps in both the query and target genomes.

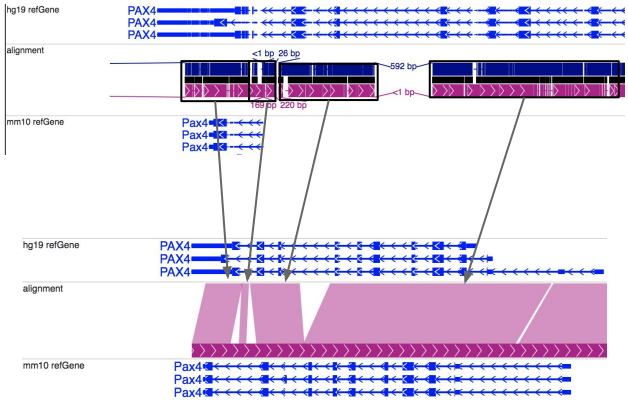
To add the genome comparison track, go to “Tracks” > “Annotation tracks” > “Genome Comparison."

Many pre-built genome comparison tracks are available.





At 10 bp/pixel resolution, the browser will transition from individual alignment blocks to a joined alignment block.



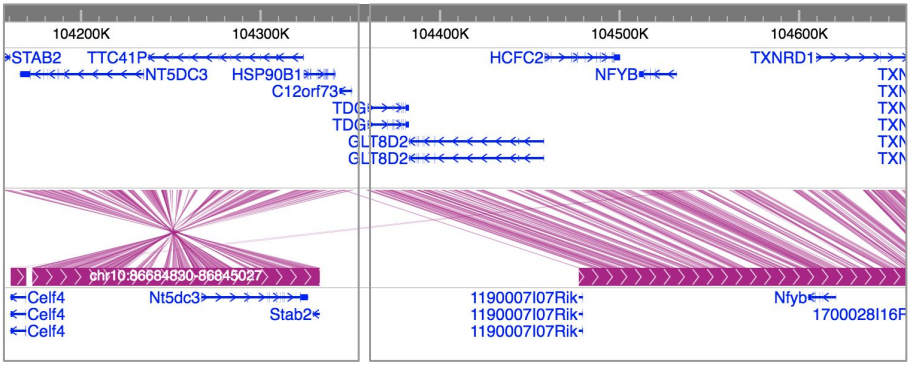
Individual alignment blocks.

8 bp/pixel

Joined alignment block.

17 bp/pixel

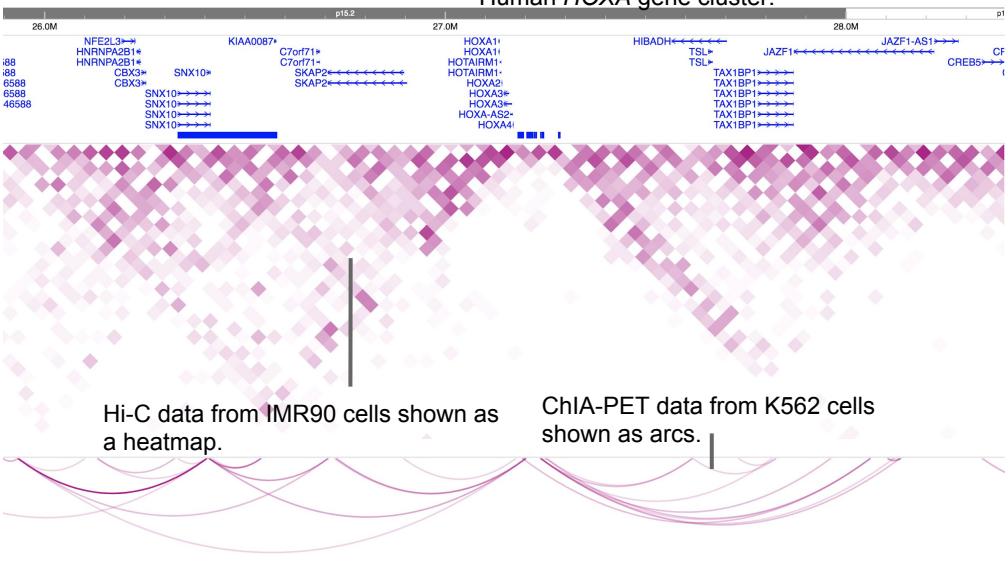
Complex genome rearrangements can be visualized by observing synteny blocks.



Long-range chromatin interaction experiments can be accessed through public track hubs[1].

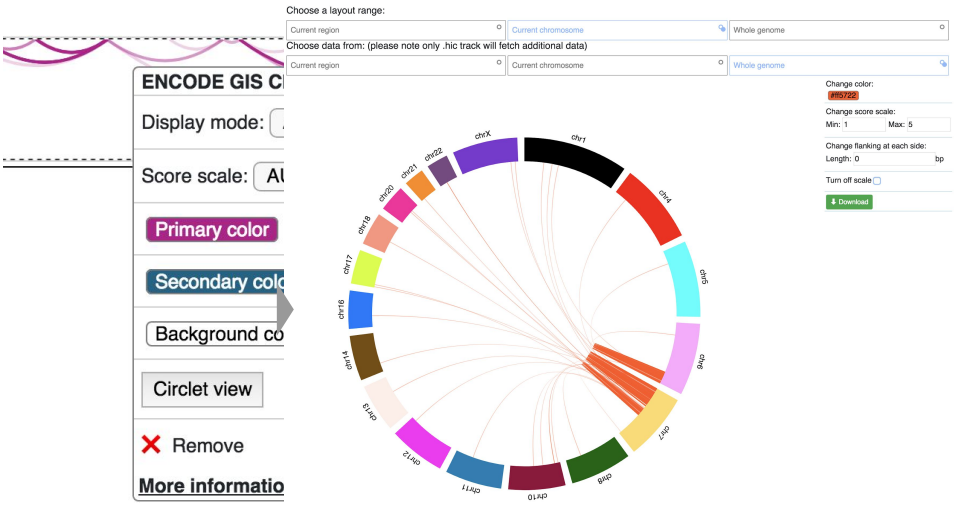
▸ Long-range chromatin interaction experiments	Long-range chromatin interaction experiments	203	+
▸ HiC interaction from Juicebox	HiC interaction from Juicebox	193	+
▸ HiC interaction from HiGlass	HiC interaction from HiGlass	41	+

Human *HOXA* gene cluster.



Highlights:

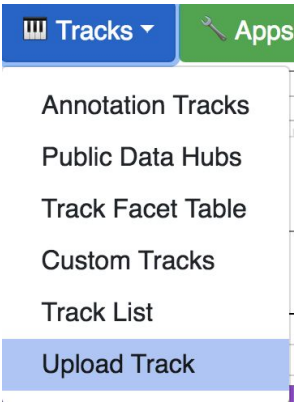
1. Supports pairwise chromatin interaction results from Hi-C, 5C, and ChIA-PET.
2. Multiple display modes: heatmaps and arcs.
3. Visualizes interactions from distant regions and different chromosomes.
4. The **Circlet view** visualizes global interactions.

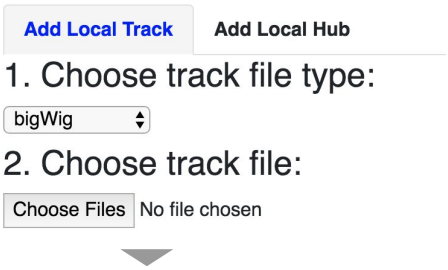


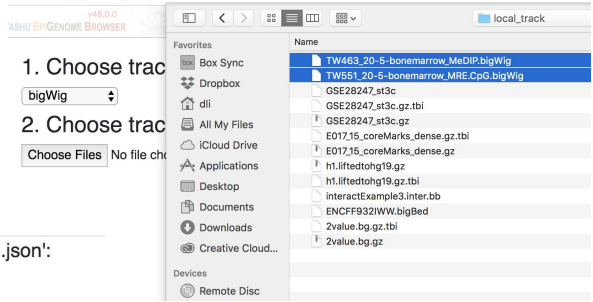
[1]Zhou X, et al., Nature Methods 10, 375-376 (2013)

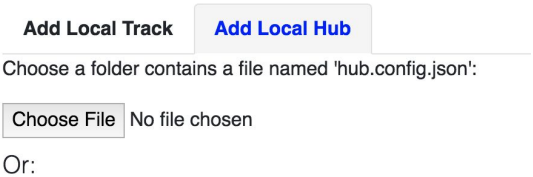
Data Management: Local tracks and datahub

Track files from your local hard drive can be displayed directly on the browser and they can be organized into a local datahub too. Local tracks and datahubs are usually loaded faster than URL hosted tracks since network transfer is avoided.

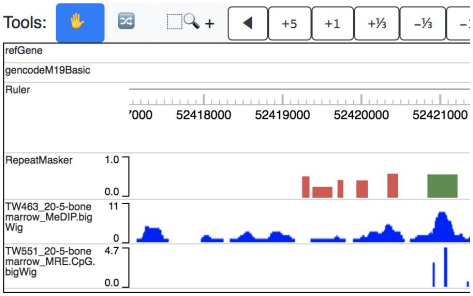


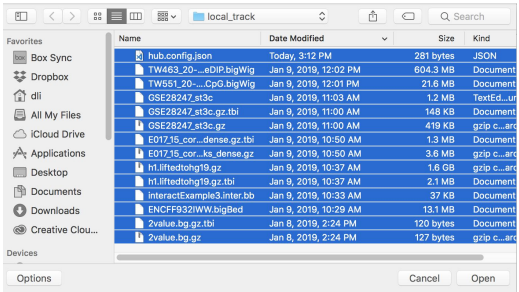




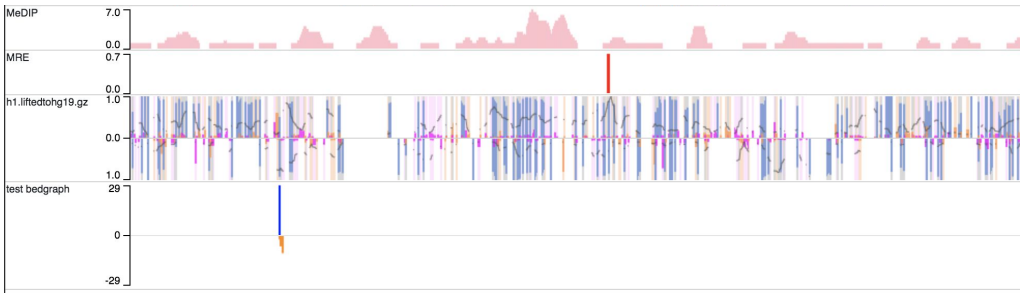


Example upload of 2 local bigWig files





Example upload of local datahub



A **datahub** is a collection of data from multiple sources.

An example datahub.

```
[
{
    "type": "bedgraph",
    "url": "http://vizhub.wustl.edu/hubSample/hg19/GSM432686.gz",
    "name": "my track",
    "showOnHubLoad": true,
    "options": {
        "color": "#ff33cc",
        "height": 50
     }
}
]
```

Highlights:

1. Batch uploading of many tracks at the same time.
2. Custom track information is preserved in a datahub.
3. Tracks in a datahub can come from different servers.
4. Track rendering style can be customized.
5. Tracks can be annotated with metadata.

A datahub is written in JSON text.

Use the Tracks -> Custom Tracks menu to upload a datahub to the browser.

A datahub file can be either hosted on the Web or saved locally.

If the datahub is hosted on the Web, it can be referenced by the browser through the URL parameter. In this way you can bookmark the parameterized browser link for quick reference or sharing.

http://epigenomegateway.wustl.edu/browser/?genome=hg19&hub=https://vizhub.wustl.edu/hg19/hubsample.json

Dissecting the browser URL parameters.

browser URL	?genome=	genome identifier	&hub=	datahub URL

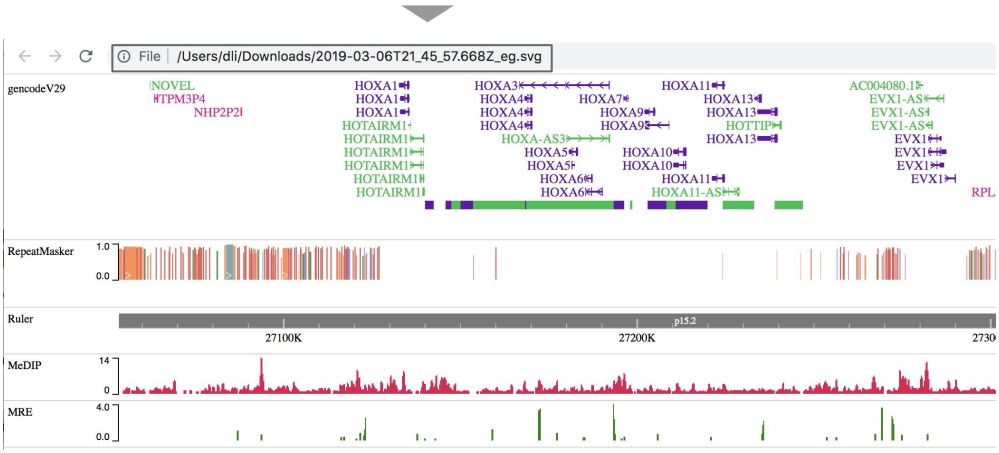
Docs

Learn more about datahubs (https://eg.readthedocs.io/en/latest/datahub.html) and URL parameters (https://eg.readthedocs.io/en/latest/url.html).

Use the **Screenshot** app in the Apps menu to save images of the current genomic view.

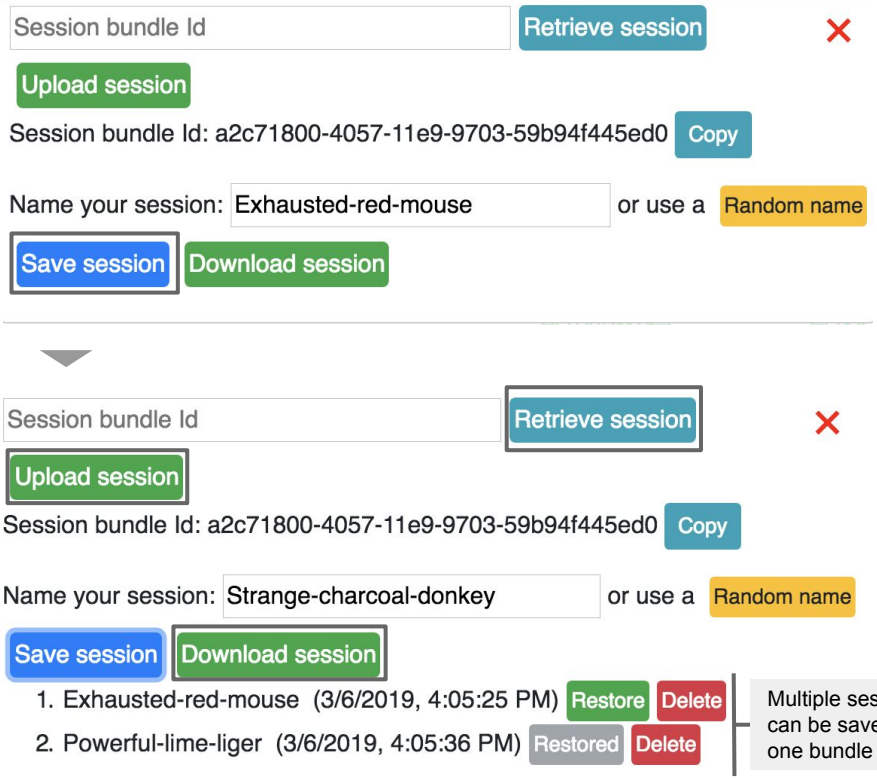
Click the green Download button to save the screenshot as an SVG file to your computer.

The “Screenshot” app will convert the browser contents to an SVG file. The SVG file is a high-quality vector-based graphics file.



Use the **Session** app in the Apps menu to save the current browser status including tracks, view range, and customization, for later viewing.

To save a session, click the “Save” button. Enter a name for this session (optional). The user can download their session as a JSON file.



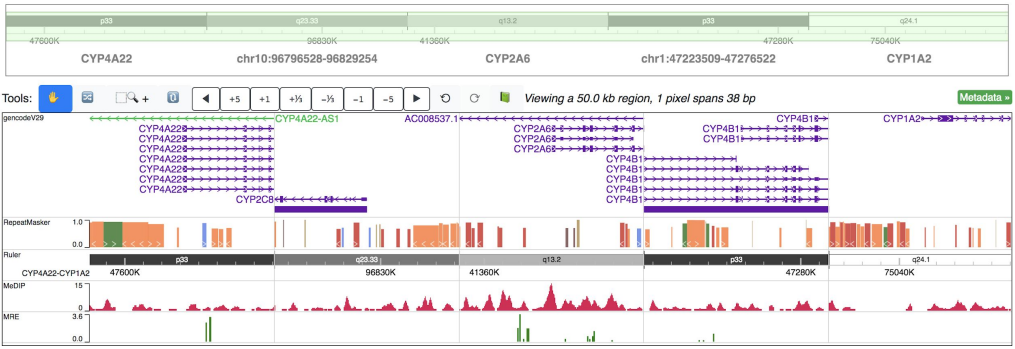
A session can be recovered in three ways:

1. Use the “?bundle=session_bundle_id” URL parameter to reload the session.
2. Upload a saved JSON file by clicking the “Upload” button in the “Sessions” app.
3. Copy the session ID and paste this into the “Retrieve” box in the “Sessions” app.

Sessions and datahubs only record information about tracks; they do not save actual track data. If the track file has been moved, the browser won’t be able to recover that track from the session or datahub.

Apps: Region Set View

Use the **Region Set View** app to show track data over a set of genes or regions. The "Region Set View" app enables track data to be displayed over regions that are not adjacent on a chromosome or even on different chromosomes.



Select a gene/region set

Add new set

Create a new set

The user can create many sets of genes or regions of interest by clicking the "Add new set" button.

Enter a list of regions

Enter a list of gene names or coordinates to make a gene set
678" fields can be joined by space/tab/comma/colon/hyphen.

```
CYP4A22
chr10:96796528-96829254
CYP2A6
CYP3A4
chr1:47223509-47276522
CYP1A2
```

Gene and region sets can be submitted by pasting a list of gene names or genomic coordinates. Gene names and coordinates can be mixed for input. Coordinate string must be in the form of "chr1:345-678" and fields can be joined by space/tab/comma/colon/hyphen.

Add | Clear

1. Rename this set: New set

2. Add one region or delete region(s) from the table below

New region name: | New region locus: | Add new region

Name	Locus	Strand	Coordinates to view	
CYP4A22	chr1:47603096-47614526	+	chr1:47603096-47614526	Delete
chr10:96796528-96829254	chr10:96796528-96829254	-	chr10:96796528-96829254	Delete
CYP2A6	chr19:41349442-41356352	-	chr19:41349442-41356352	Delete
chr1:47223509-47276522	chr1:47223509-47276522	-	chr1:47223509-47276522	Delete
CYP1A2	chr15:75041185-75048948	+	chr15:75041185-75048948	Delete

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

3. Set flanking region

Upstream bases: 5000 | Downstream bases: 5000 | Surrounding: Transcription start

Select a gene/region set

New set (5 regions) | Enter region set view | DELETE

"Region set view" can be applied to see all regions in one browser view. To quit the gene set view, click the yellow button:

Exit region set view

Use the **Gene plot** app to explore the data variation and distribution of a numerical track with respect to a group of genes or regions of interest. The gene set needs to be loaded using the “Region View Set” app before using the “Gene plot" app.

1. Choose a region set

Choose a gene set.

Pick your set: New set

2. Choose a numerial track:

Select the data to be plotted.

Pick your track: MeDIP

Three plots (box plot, line plot, and heatmap) are available, and each is fully customizable.

3. Choose a plot type:

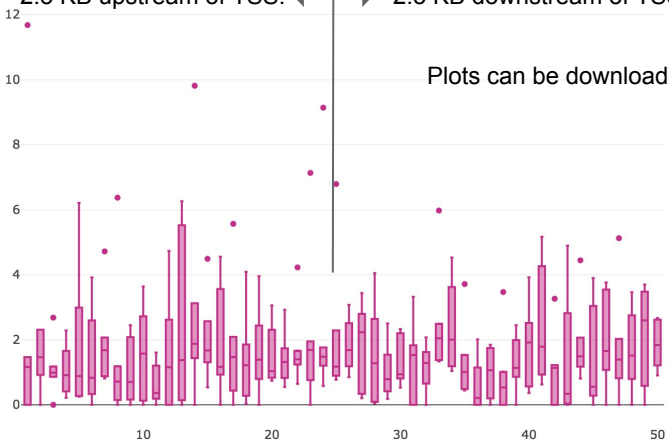
Pick your plot type: box data points: 50

All genes and genomic intervals are tiled together, genes are plotted.

Plot

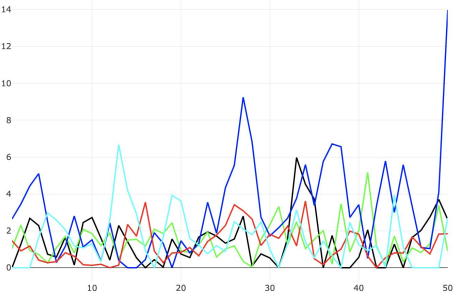
Gene transcription start sites.

2.5 KB upstream of TSS. 2.5 KB downstream of TSS.

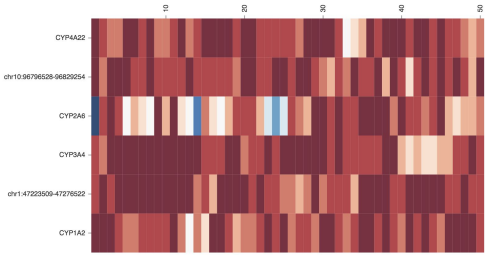


Plots can be downloaded in SVG format.

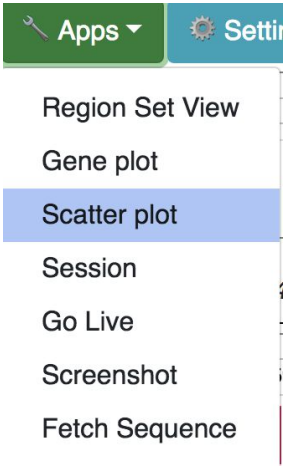
The above boxplot shows the bone marrow MeDIP signal distribution over 5 KB regions centered on the transcription start site of 5 human genes. Data from each region is evenly summarized into 50 data points and a boxplot is shown over each summary point to indicate the data distribution.



Individual curves for each item



Heatmap



This App allows the user to compare different datasets, across multiple genomic regions.

1. Choose a region set

Pick your set: 20TEs-ext2.5Kb

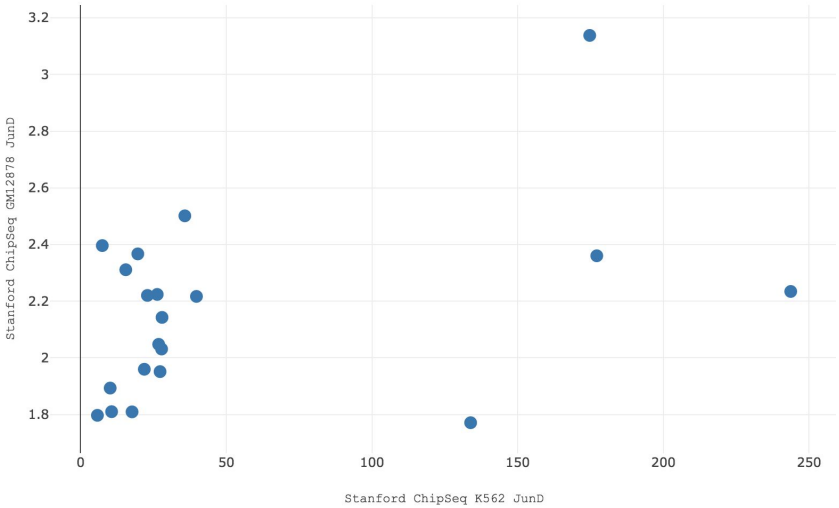
2. Choose a numerial track for X-axis:

Pick your track: Stanford ChipSeq K562 JunD

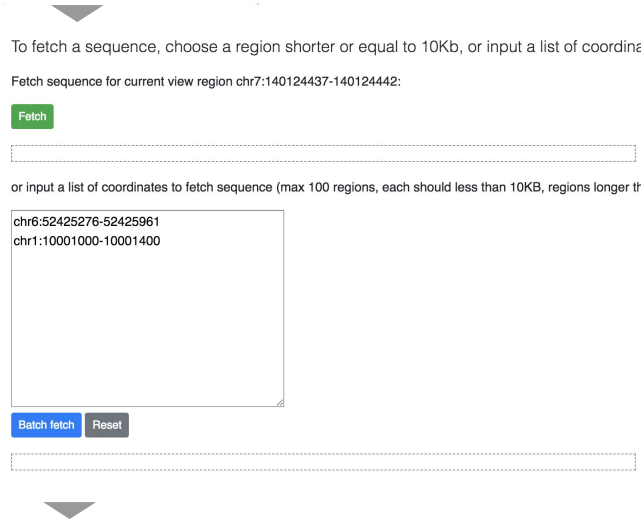
3. Choose a numerial track for Y-axis:

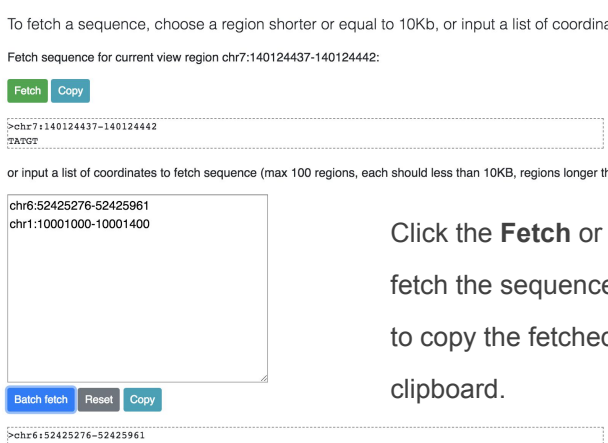
Pick your track: Stanford ChipSeq GM12878 JunD

Plot

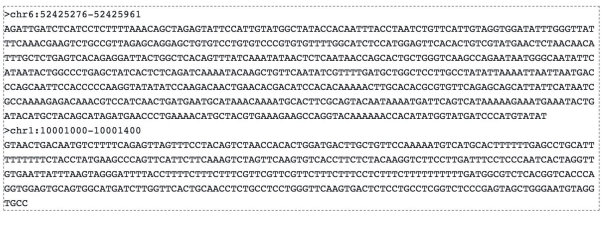


This App allows the user to retrieve the genomic sequence of the current view region. Users can also specify a list of regions from which to fetch sequences from. Each region should be no longer than 10KB.

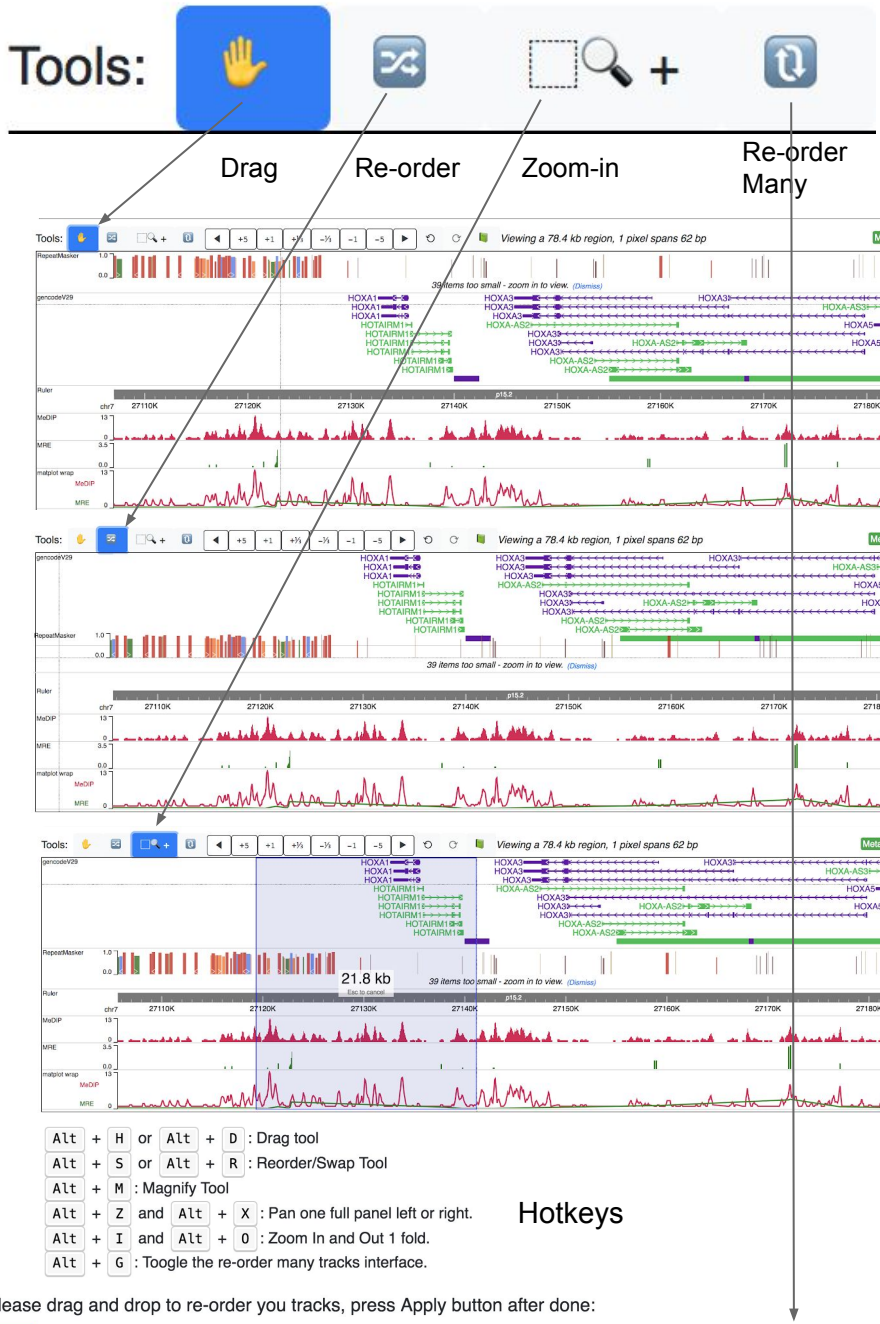




Click the **Fetch** or **Batch fetch** button to fetch the sequence. Click the **Copy** button to copy the fetched sequence to your clipboard.



Track Operation Tools



Hotkeys

- `Alt` + `H` or `Alt` + `D` : Drag tool
- `Alt` + `S` or `Alt` + `R` : Reorder/Swap Tool
- `Alt` + `M` : Magnify Tool
- `Alt` + `Z` and `Alt` + `X` : Pan one full panel left or right.
- `Alt` + `I` and `Alt` + `0` : Zoom In and Out 1 fold.
- `Alt` + `G` : Toogle the re-order many tracks interface.

Please drag and drop to re-order you tracks, press Apply button after done:

Apply

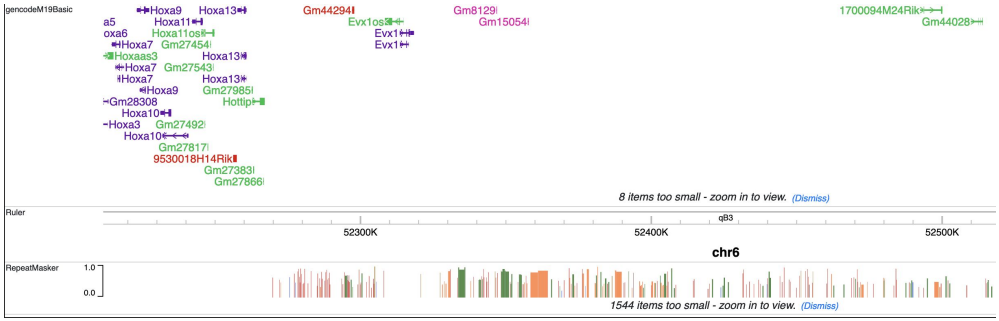
You can adjust column numbers using the slider below:

3

gencodeV29 (geneannotation)	RepeatMasker (repeatmasker)	Ruler (ruler)
MeDIP (bigwig)	MRE (bigwig)	matplot wrap (matplot)

The figure on the left shows how to remove the refGene track from the current view.

The view below is after the refGene track has been removed.



When we click the Undo button, the refGene track is added back. Click the History button to see a history of operations.

Operation history

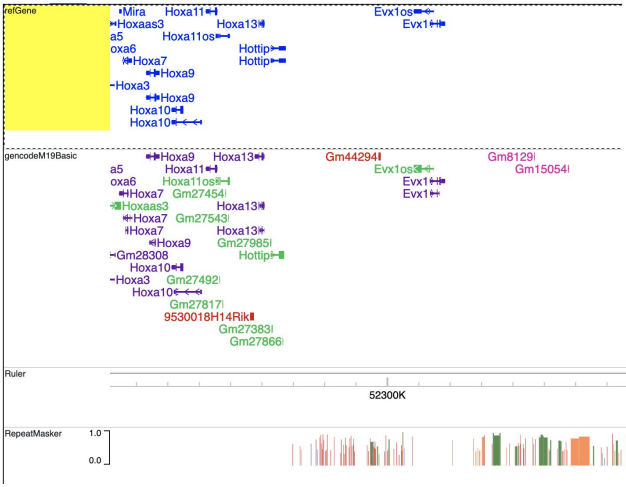
Close | Clear History

Go back:

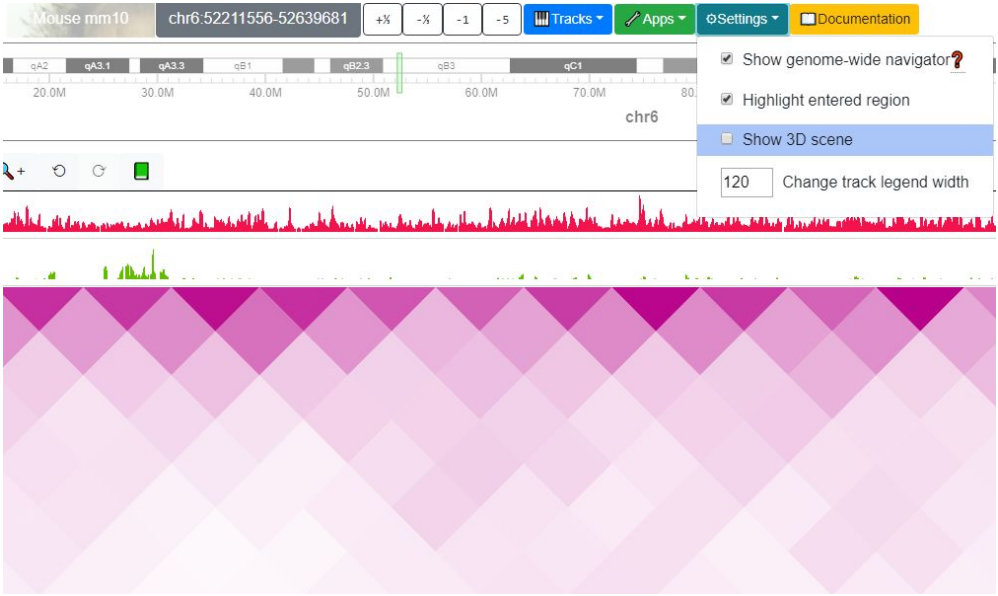
1. Region: (none), # of tracks: 0
2. Region: chr6:52425276-52425961, # of tracks: 4
3. Region: chr6:52423906-52427331, # of tracks: 4
4. Region: chr6:52417056-52434181, # of tracks: 4
5. Region: chr6:52382806-52468431, # of tracks: 4
6. Region: chr6:52211556-52639681, # of tracks: 4

Go forward:

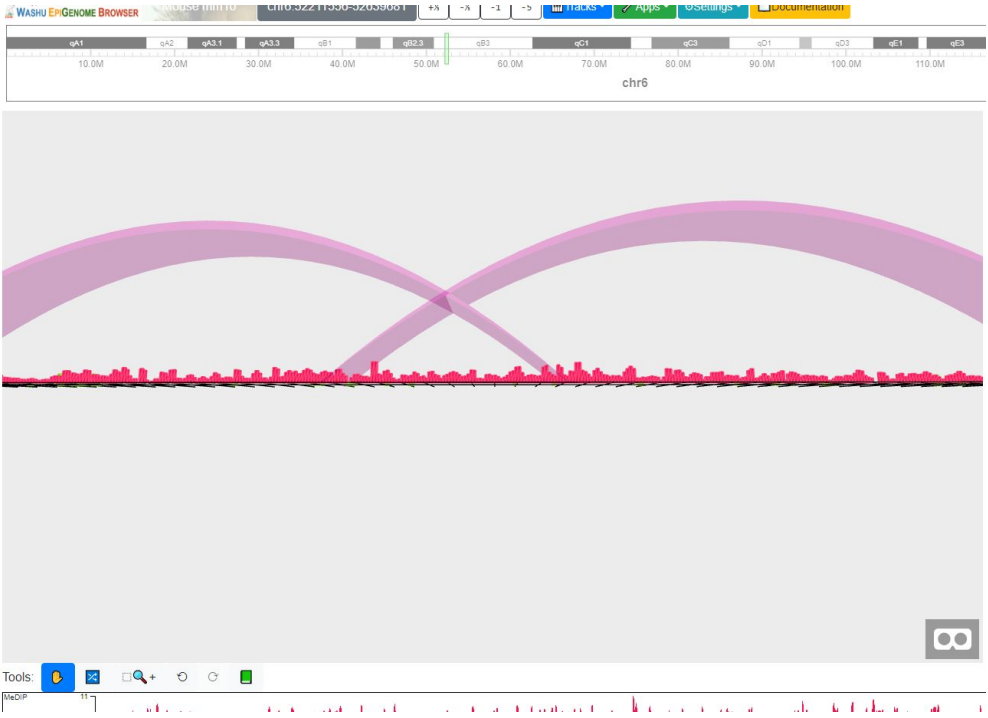
1. Region: chr6:52211556-52639681, # of tracks: 3

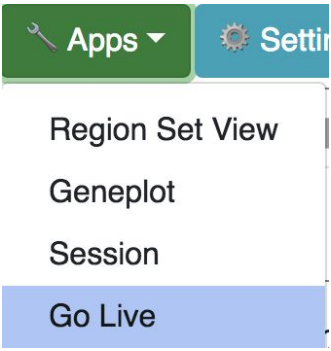


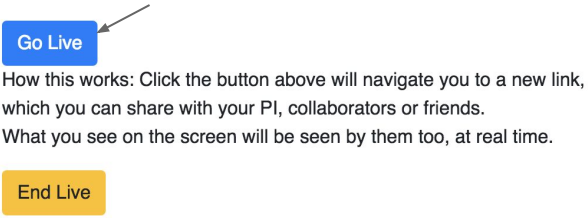
VR Display Mode



The user can choose to toggle the VR display mode of tracks. After choose the **Show 3D scene** submenu, a new container with VR view of the tracks will appear.

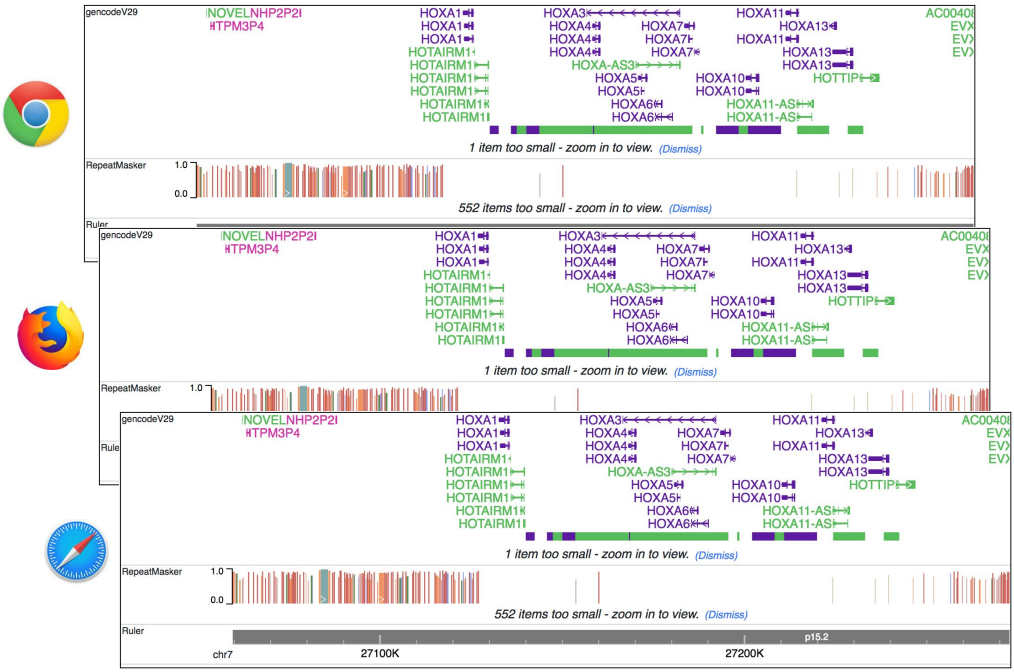




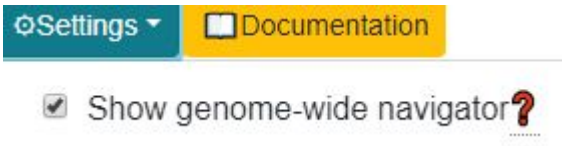


http://epigenomegateway.wustl.edu/browser/live/DMEryQEVe

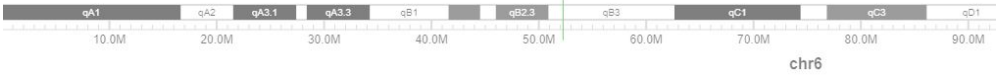
The browser view will be synchronized to the users who is visiting this Live URL.



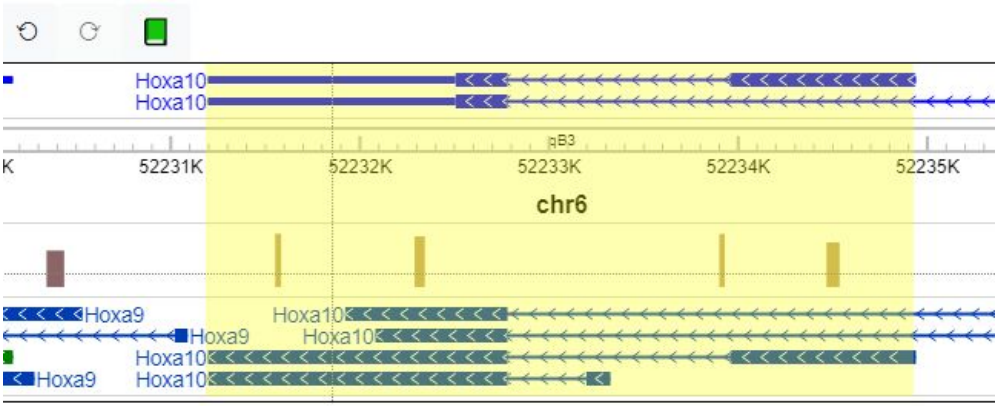
Toggle display of the Genome Navigator

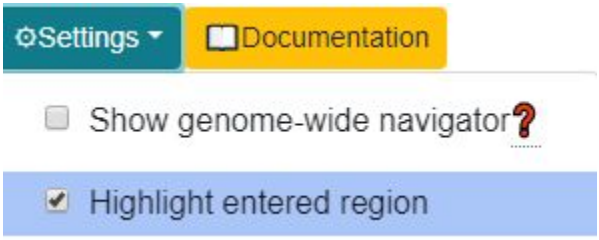


- Left mouse drag: select
- Right mouse drag: pan
- Mousewheel: zoom



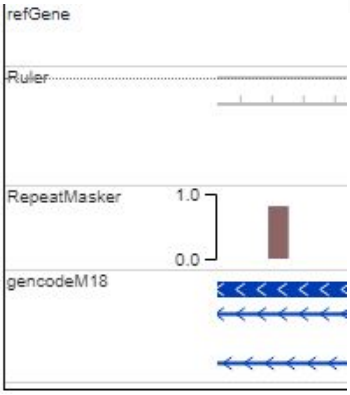
Toggle highlighting of enter region





When a user jumps to a region or gene using the Genomic Region Locator, that region or gene is highlighted with a light yellow box by default.

Change track label width



The default width of track label is 120 pixels.