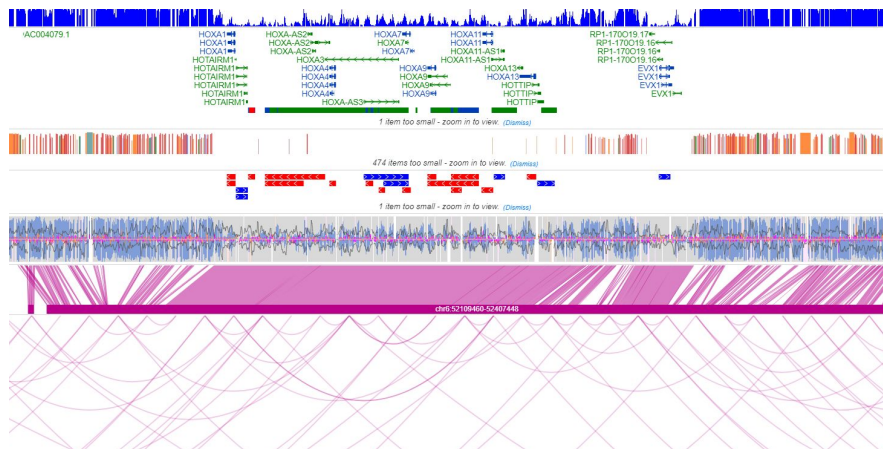


# Everything can be found at epigenomegateway.wustl.edu



## 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](http://eg.rtfd.io)

Google groups: <http://bit.ly/egGroup>

Facebook: <http://bit.ly/2SZpvpz>

Slack channel: <https://bit.ly/2T1OKmP>

Twitter: @wuepgg

## SUPPORT

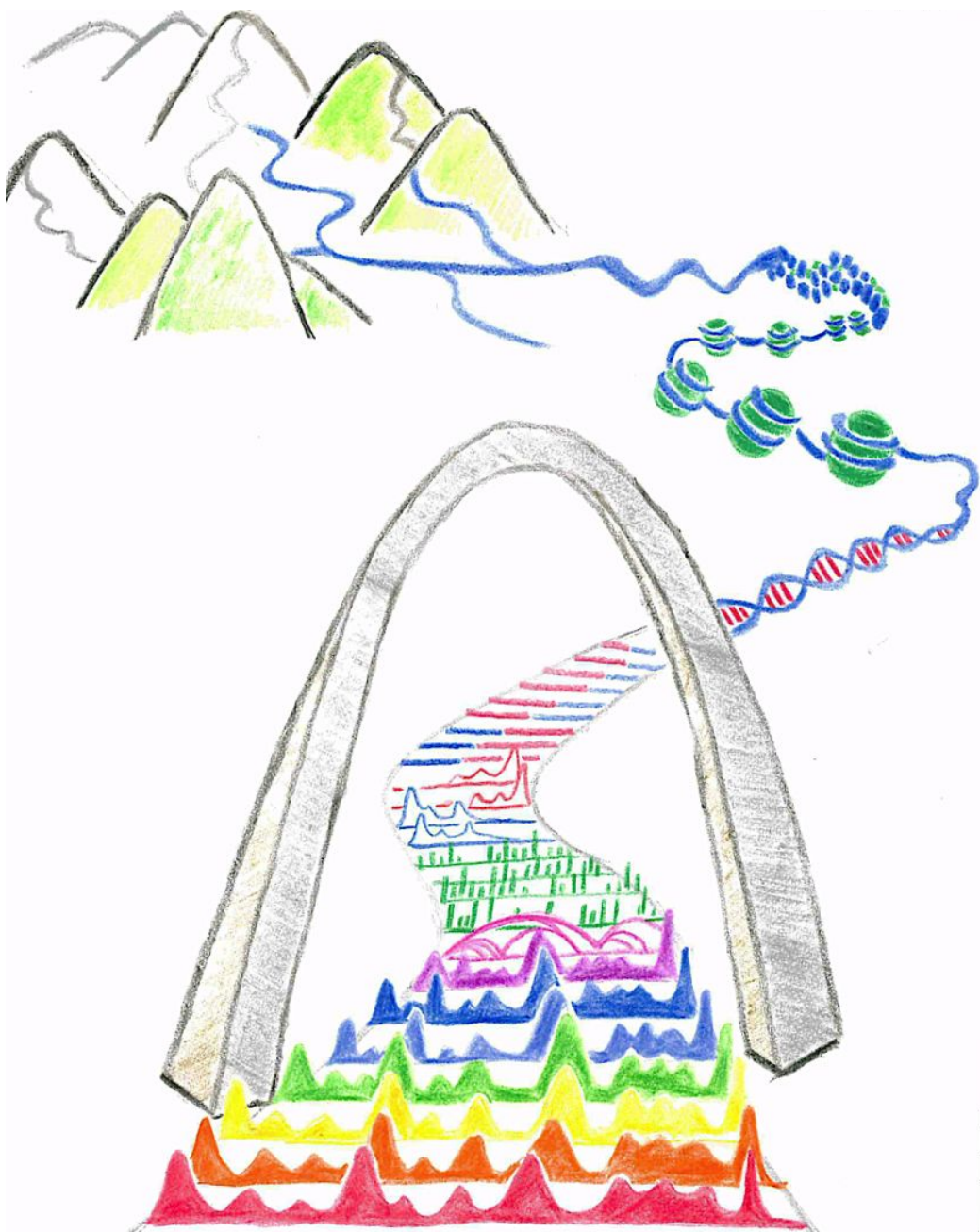
[epigenomegateway.wustl.edu/support/](http://epigenomegateway.wustl.edu/support/)

**CONTACT US** Lab: [wang.wustl.edu](http://wang.wustl.edu)

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Cover art: Ting Wang

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**WASHU EPIGENOME BROWSER**  
2019

[epigenomegateway.wustl.edu](http://epigenomegateway.wustl.edu)



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

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Click to show options.

Human hg19 chr7:26677679-27735262 Tracks

Chromosome ideogram.

Click to zoom in. Click to zoom out.

Drag on ruler to zoom in.

Chromosome ideogram of region.

Coordinate ruler.

Click to scroll.

Gene search

Gene name

SNP search

SNP id

Go

Region search (current region is chr7:26677679-27735262) Copy

Coordinate

Go

Say a Gene Reset Stop

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.

Gene search

HOXA1

Say a Gene Reset Stop

refGene	chr7:27132613-27135625	Additional info: homebox A1, transcript variant 2
refGene	chr7:27132613-27135625	Additional info: homebox A1, transcript variant 1
gencodeV29	chr7:27132931-27135615	Gene ID: ENSG00000105991.8_3 Gene Type: protein_coding Transcript Info: homebox A1 [Source: HGNC Symbol; Acc: HGNC:5099]
gencodeV29	chr7:27132611-27135593	Gene ID: ENSG00000105991.8_3 Gene Type: protein_coding Transcript Info: homebox A1 [Source: HGNC Symbol; Acc: HGNC:5099]

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

Ruler

GCTAN

CTCTGCAATCCAGTTTCC

27160490 27160500

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.

Tracks

Click to manage browser tracks.



Tracks ▾

Apps

Access annotation tracks such as genes.

Annotation Tracks

Public Data Hubs

Track Facet Table

Custom Tracks

Track List

Upload Local Track

Click to submit a custom track or hub.

Add Custom Track

Add Custom Data Hub

## Add custom track

Track type [track format documentation](#)

bigWig - numerical data

Track file URL

Track label

Submit

Click to submit a local track or hub.

Add Local Track

Add Local Hub

Choose a folder contains a file named 'hub.config.json': (io)

Choose File No file chosen

Or:

Choose many files contains a file named 'hub.config.json':

Choose Files No file chosen

hg19

▸ Ruler

▾ Genes

RefSeq genes **Add**

GENCODE V29 genes (Added)

GENCODE V29 basic genes **Add**

GENCODE V19 genes **Add**

▸ Variation

▸ RepeatMasker

▸ Conservation

▸ Genome Annotation

▸ Genome Comparison

▸ Mappability

Show available public track hubs to load tracks from projects including Roadmap Epigenomics Project and ENCODE.

## Public data hubs

Collection	Hub name	Tracks	Add
▸ Reference human epigenomes from Ro...	Roadmap Data from GEO	2728	<b>+</b>
▸ Reference human epigenomes from Ro...	methylation tracks from Roadmap	16	<b>+</b>
▸ Reference human epigenomes from Ro...	Observed DNase and ChIP-seq Pvalue ...	1136	<b>+</b>
▸ Reference human epigenomes from Ro...	Observed DNase and ChIP-seq Fold-ch...	1136	<b>+</b>
▸ Reference human epigenomes from Ro...	All Chromatin states tracks	352	<b>+</b>
▸ Reference human epigenomes from Ro...	Imputed data signal tracks	4315	<b>+</b>
▸ Reference human epigenomes from Ro...	Unconsolidated epigenomes, Observed...	1915	<b>+</b>

Public tracks facet table

Custom tracks facet table

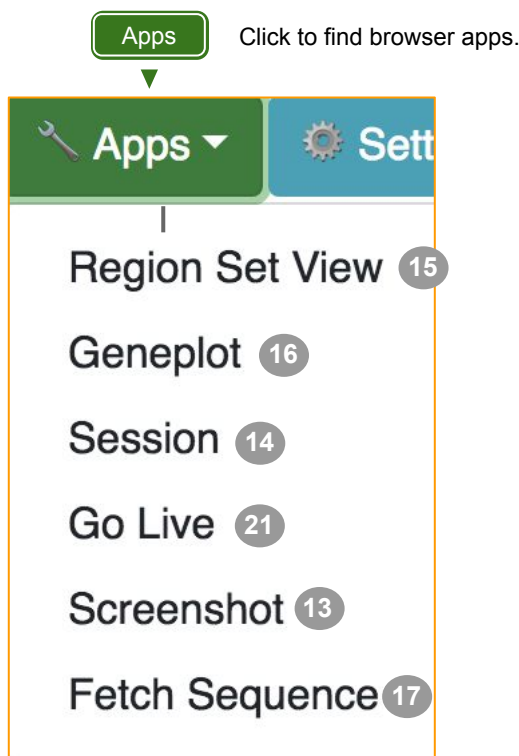
## Tracks from public hubs

Row: Assay ▾

	Assay	Sample	Cancer Cells	Placenta	Fetal Cells/Tissues	Fetal Testes	Fetal Spinal Cord	Fetal System
Assay								
Expression								
smRNA-Seq								
RNA-Seq								
Epigenetic Mark								
DNA Methylation								
Other Epigenetic Mark								
Histone Mark								

The numbers indicate the tracks available for each sample+assay combination (dark green) and the tracks that are currently shown in the browser (light green). Click a table cell to show a list of available tracks for a sample+assay combination.

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.

Close this app.

×

Select a gene/region set

Add new set

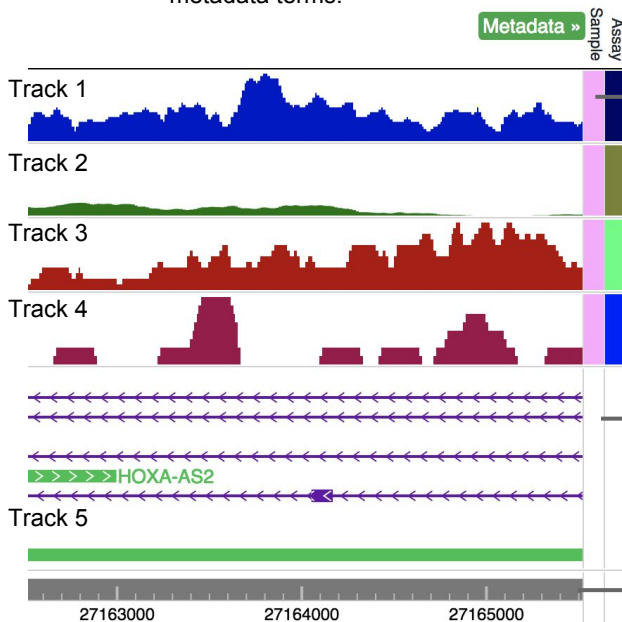
Create a new set

Enter a list of regions

Enter a list of gene names or coordinates to make a gene set one item per line. Gene names and coordinates can be mixed for input. Coordinate string must be in the form of "chr1:345-678" fields can be joined by space/tab/comma/colon/hyphen.

CYP4A22  
chr10:96796528-96829254  
CYP2A6  
CYP3A4

A **metadata heatmap** with two metadata terms.



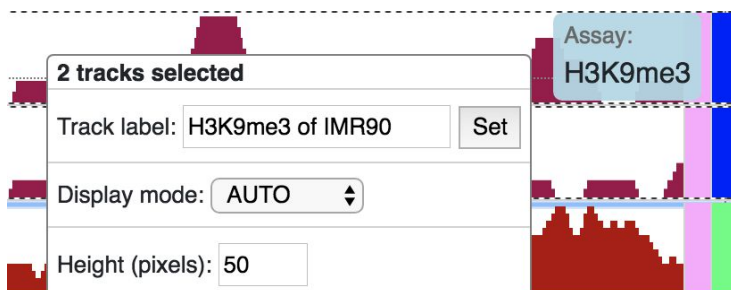
Tracks 1, 2, 3, and 4 share the same “sample” attribute (IMR90 cells) and thus share the same color.

Tracks 1, 2, 3 and 4 are each annotated by a different “assay” attribute (Input, H3K4me3, H3K27me3, H3K9me3) and thus are colored differently.

Track 5 is not annotated by “sample” or “assay” attributes so no metadata is shown.

Ruler track.

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



Switch Metadata and add/remove interface.

Metadata »

Current terms

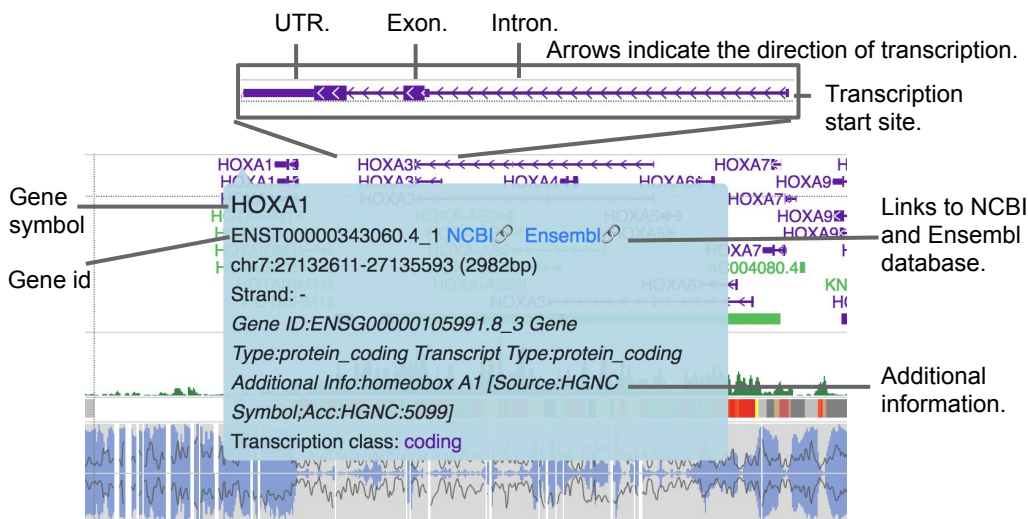
- Sample
- Assay

Suggested terms

- + Track type
- + Donor
- + Institution

Custom term

+



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”.

- ▼ hg19
  - ▶ Ruler
  - ▼ Genes
    - RefSeq genes [Add](#)
    - GENCODE V29 genes (Added)
    - GENCODE V29 basic genes [Add](#)
    - GENCODE V19 genes [Add](#)

**gencodeV29**

Track label:  [Set](#)

Display mode:  ▼

Max rows (including overflow row):  [Set](#)

[Primary color](#)

[Secondary color](#)

[Background color](#)

[Remove](#)

[More information](#)

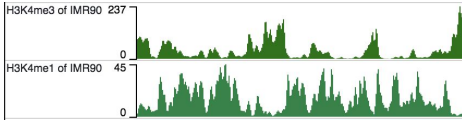
Right-click on the gene track (and any other tracks) for the **configuration menu**.

Display modes.

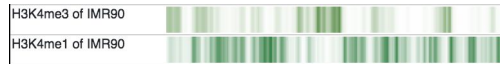
Configure the number of rows for displaying genes

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  $\geq 20$  pixels)



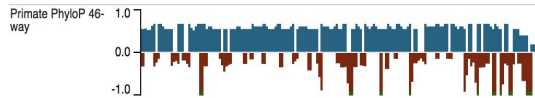
Heatmap (track height  $< 20$  pixels)



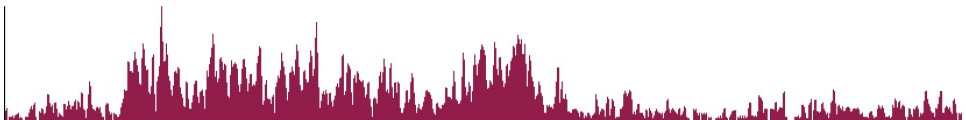
Positive and negative values are rendered using different colors.



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.



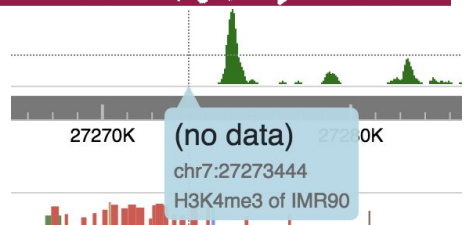
Bar plot shape can be smoothed using the configuration menu.



Smooth (pixels): 3

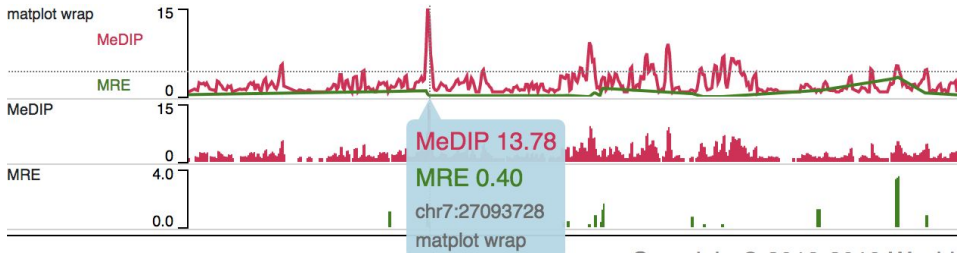


Missing values are labelled as “No data” on the tooltip for bedGraph format tracks (not applicable for bigWig format tracks).



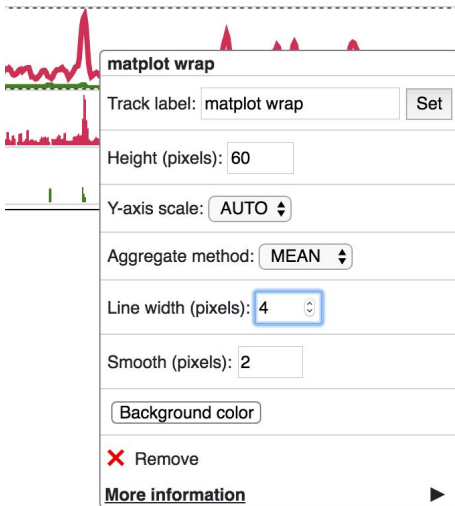
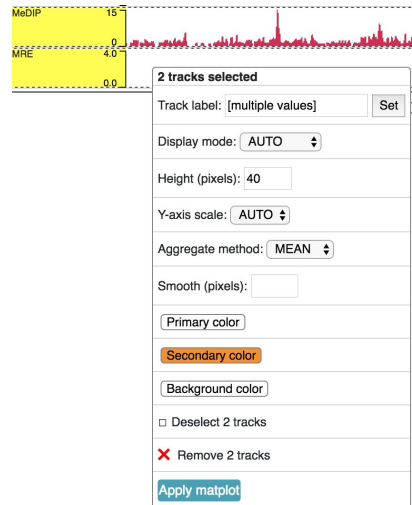


A **matplot** (also called a line plot) displays multiple numerical tracks on the same X and Y axes to easily compare datasets. Data is plotted as curves instead of bar plots.



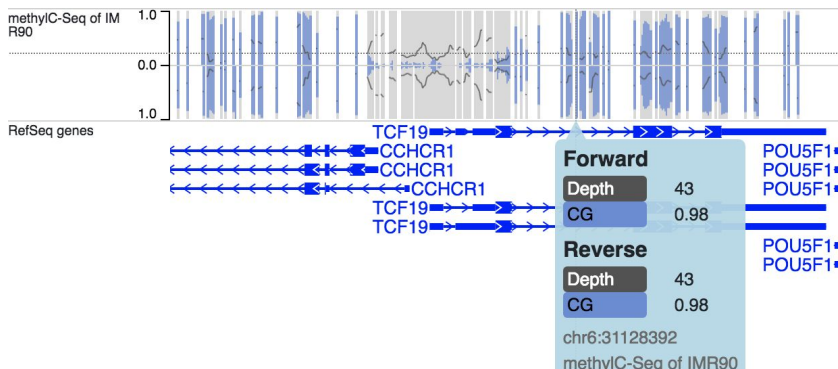
Matplots can be created while browsing:

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.

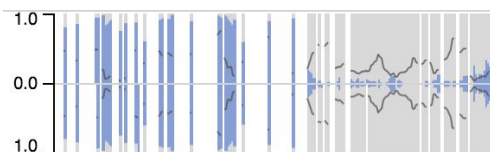
The **methylC track**<sup>1</sup> is designed to display DNA methylation data from whole-genome bisulfite sequencing experiments. It distinguishes cytosine methylation levels (as bar plots) on separate strands and in different sequence contexts and integrates sequencing read depth (as curves) as a measure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



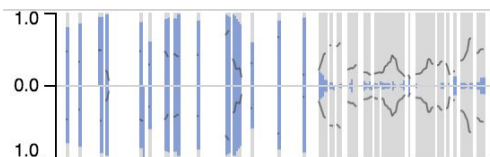
The color legend for a methylC track can be viewed using its configuration menu. All colors are configurable by clicking on the color boxes.

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



## methylC-Seq of IMR90

Track label: methylC-Seq of IMR90 Set

Height (pixels): 40

Combine strands ☐

Context	Color	Background
CG	#648bd8	#d9d9d9
CHG	#ff944d	#ffe0cc
CHH	#ff00ff	#ffe5ff

Add other contexts by specifying them in a data hub.

Methylation value max: 1 Set

Depth filter: 0 Set

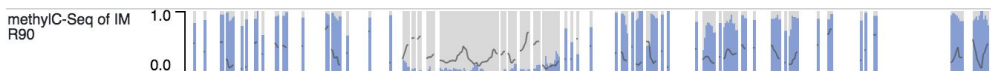
Read depth line color

Background color

Remove

More information

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



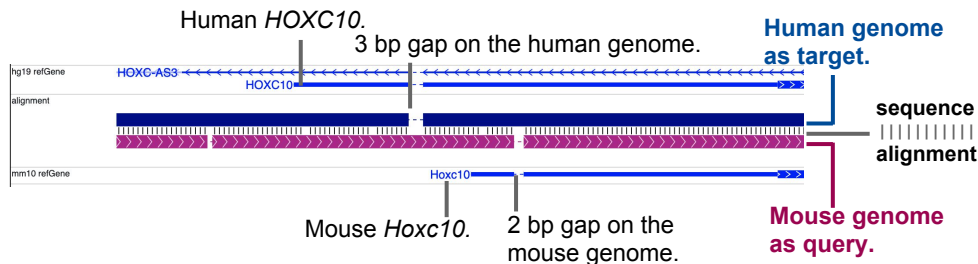
The **genome comparison track** visualizes pairwise alignments of two genomes allowing for comparison at fine (base pair) or large (megabase) scale. Alignment is unbiased with gaps in both the query and target genomes.

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

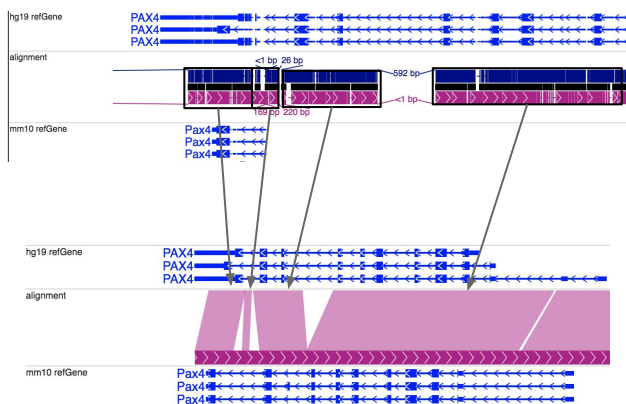
Many pre-built genome comparison tracks are available.

#### Genome Comparison

- Mouse mm9 to hg19 blastz [Add](#)
- Mouse mm10 to hg19 blastz (Added)
- Rat rn4 to hg19 blastz [Add](#)
- Rat rn5 to hg19 blastz [Add](#)
- Rhesus macaque rheMac3 to hg19 blastz [Add](#)
- Guinea pig cavPor3 to hg19 blastz [Add](#)
- Zebrafish danRer7 to hg19 blastz [Add](#)



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



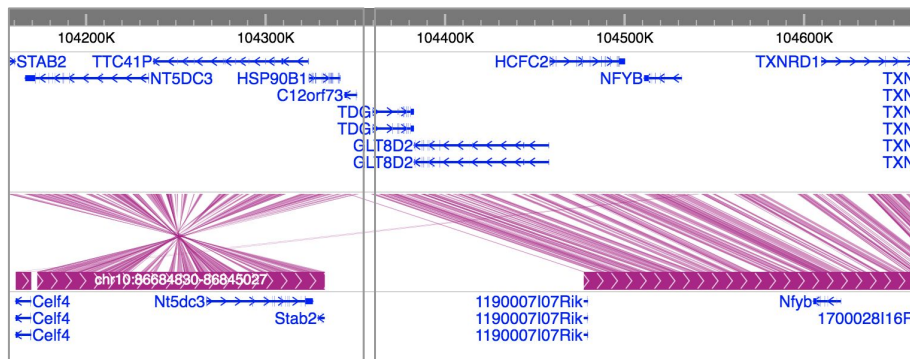
Individual alignment blocks.

8 bp/pixel

Joined alignment block.

17 bp/pixel

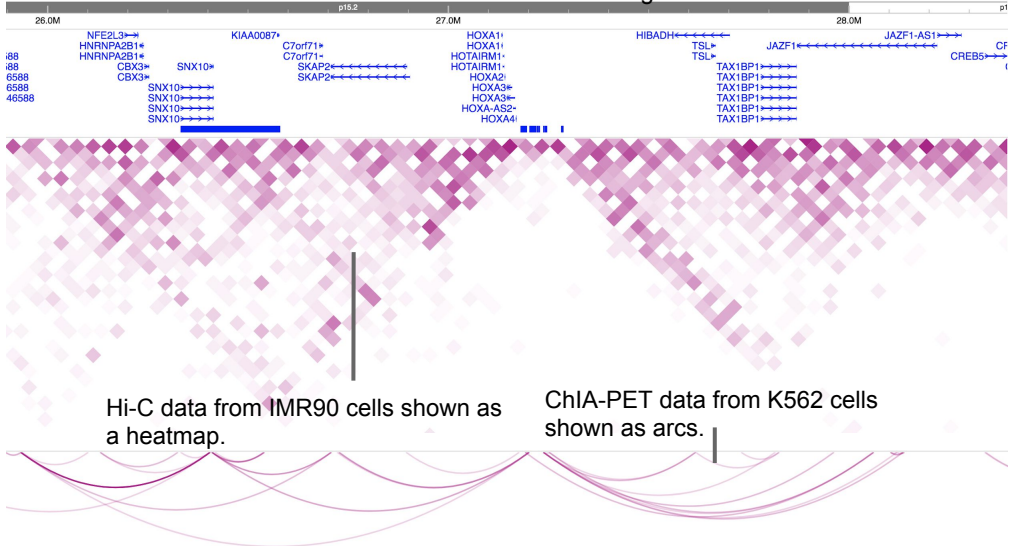
Complex genome rearrangements can be visualized by observing synteny blocks.



Long-range chromatin interaction experiments can be accessed through public track hubs<sup>1</sup>.

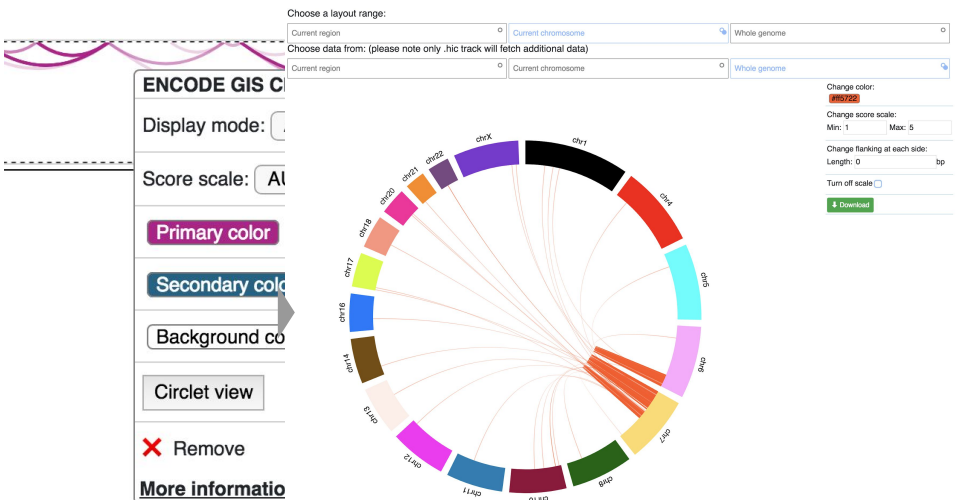
▶ Long-range chromatin interaction experiments	Long-range chromatin interaction experiments	203	+
▶ HiC interaction from Juicebox	HiC interaction from Juicebox	193	+
▶ HiC interaction from HiGlass	HiC interaction from HiGlass	41	+

## 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 **Circllet view** visualizes global interactions.



<sup>1</sup>Zhou X, et al., Nature Methods 10, 375-376 (2013)

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.



Annotation Tracks

Public Data Hubs

Track Facet Table

Custom Tracks

Track List

Upload Track

Add Local Track

Add Local Hub

1. Choose track file type:

bigWig

2. Choose track file:

Choose Files

No file chosen

1. Choose track

bigWig

2. Choose track

Choose Files

No file chosen

Add Local Track

Add Local Hub

Choose a folder contains a file named 'hub.config.json':

Choose File

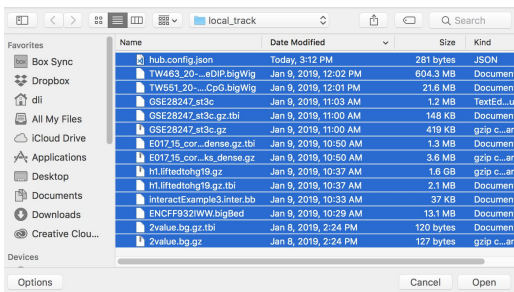
No file chosen

Or:

Choose many files contains a file named 'hub.config.json':

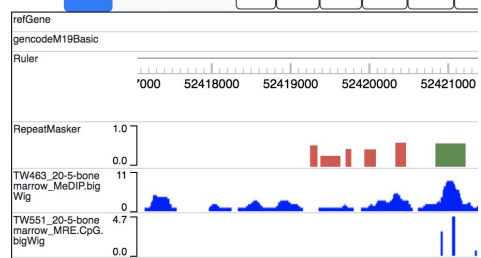
Choose Files

No file chosen

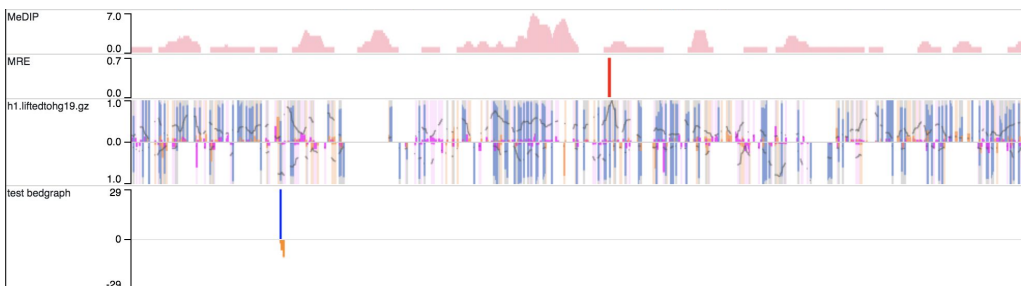


Example upload of 2 local bigWig files

Tools:



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=hq19&hub=https://vizhub.wustl.edu/hq19/hubsample.json>

Dissecting the browser URL parameters.

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







Region Set View

Geneplot

Session

Go Live

Screenshot

Fetch Sequence

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.

✗

Session bundle Id: a2c71800-4057-11e9-9703-59b94f445ed0

Name your session:  or use a

✗

Session bundle Id: a2c71800-4057-11e9-9703-59b94f445ed0

Name your session:  or use a

1. Exhausted-red-mouse (3/6/2019, 4:05:25 PM)
2. Powerful-lime-liger (3/6/2019, 4:05:36 PM)

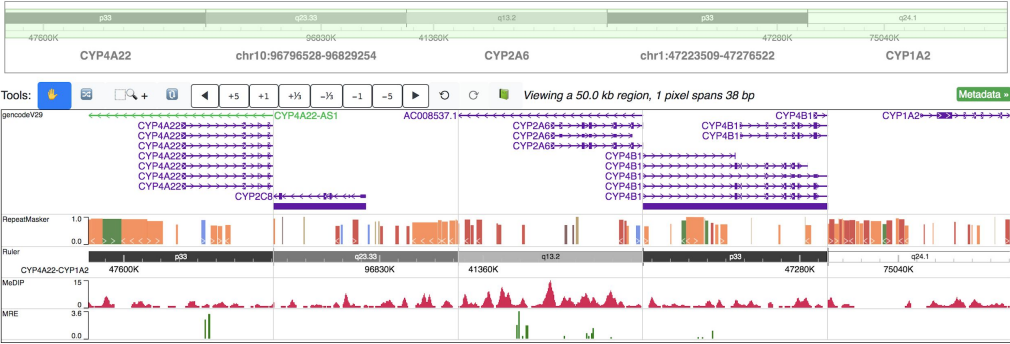
Multiple sessions can be saved under one bundle ID.

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.

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

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.

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

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.

AddClear

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

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

New set (5 regions)

Enter region set view

DELETE

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** ▾

Select the data to be plotted.

2. Choose a **numerical track**:

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

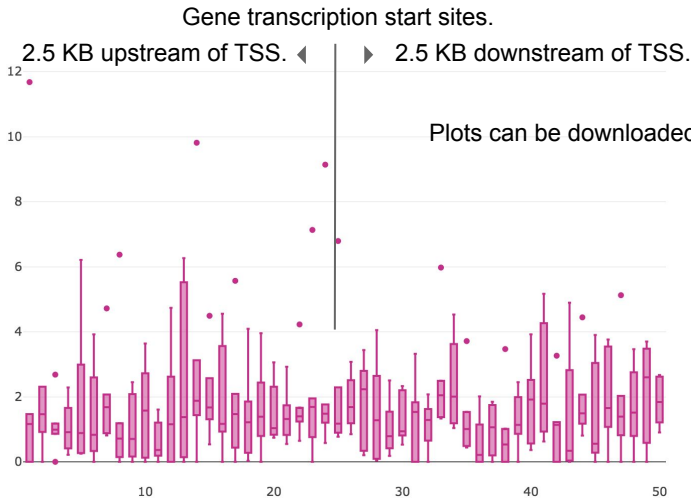
Pick your track: **MeDIP** ▾

3. Choose a plot type:

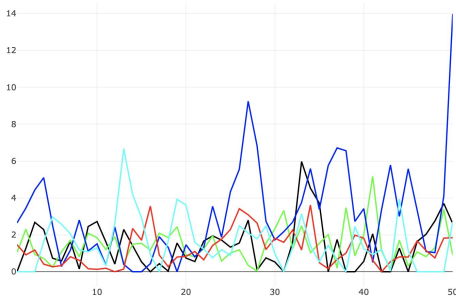
Pick your plot type: **box** ▾ data points: **50** ▾

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

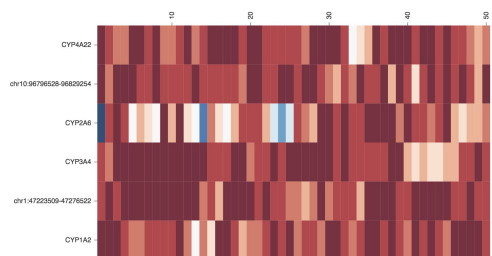
**Plot**



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

Apps ▾

Settings

Region Set View  
Gene plot  
Scatter plot  
Session  
Go Live  
Screenshot  
Fetch Sequence

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

1. Choose a region set

Pick your set: 20TEs-ext2.5Kb ▾

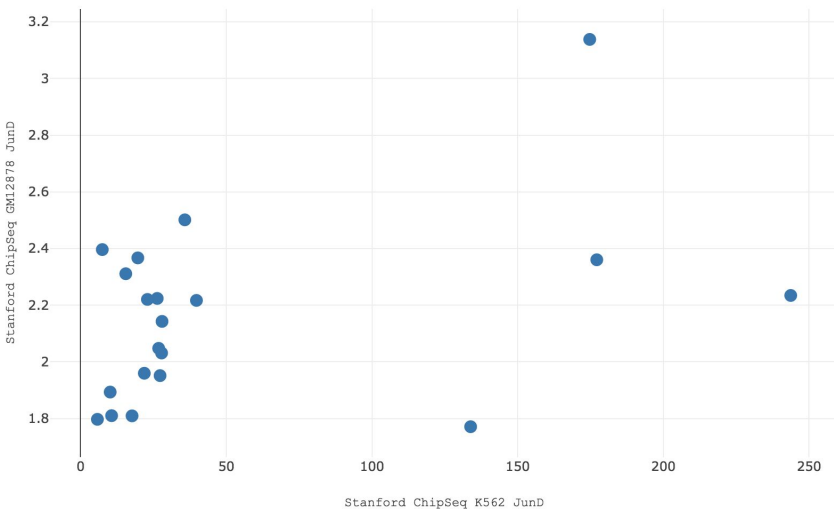
2. Choose a **numerical track** for X-axis:

Pick your track: Stanford ChipSeq K562 JunD ▾

3. Choose a numerical track for Y-axis:

Pick your track: Stanford ChipSeq GM12878 JunD ▾

Plot







Tools:



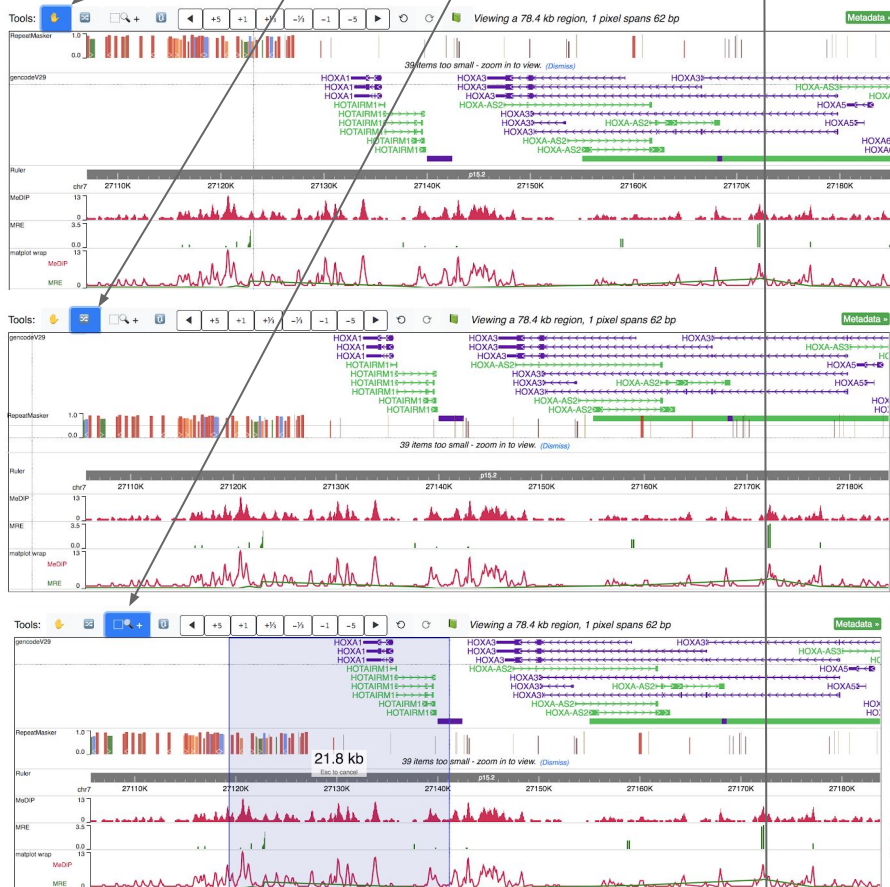
Drag



Re-order



Zoom-in

Re-order  
Many

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 + O : Zoom In and Out 1 fold.  
 Alt + G : Toggle the re-order many tracks interface.

Hotkeys

Please drag and drop to re-order your 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 view below is after the  
refGene track has been removed.

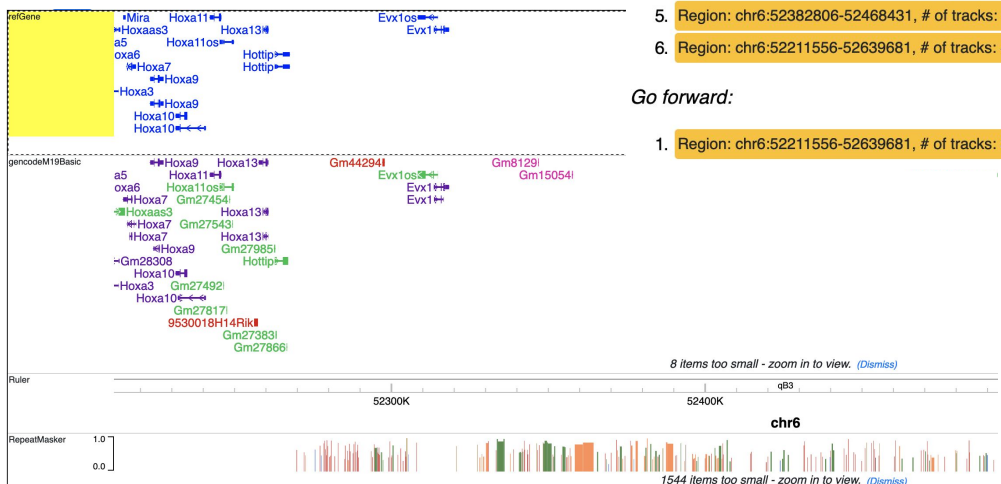


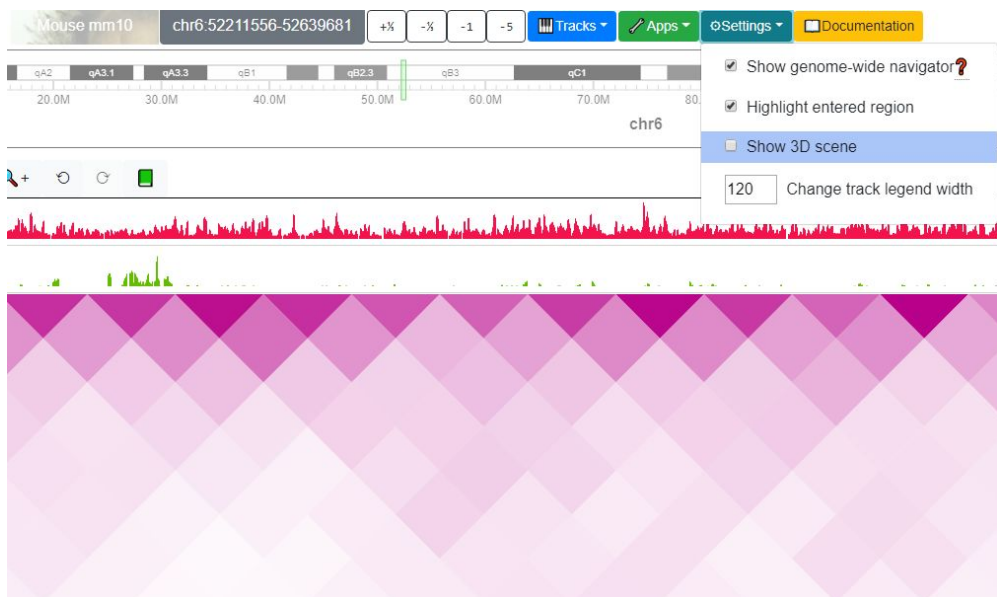
*Go back:*

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

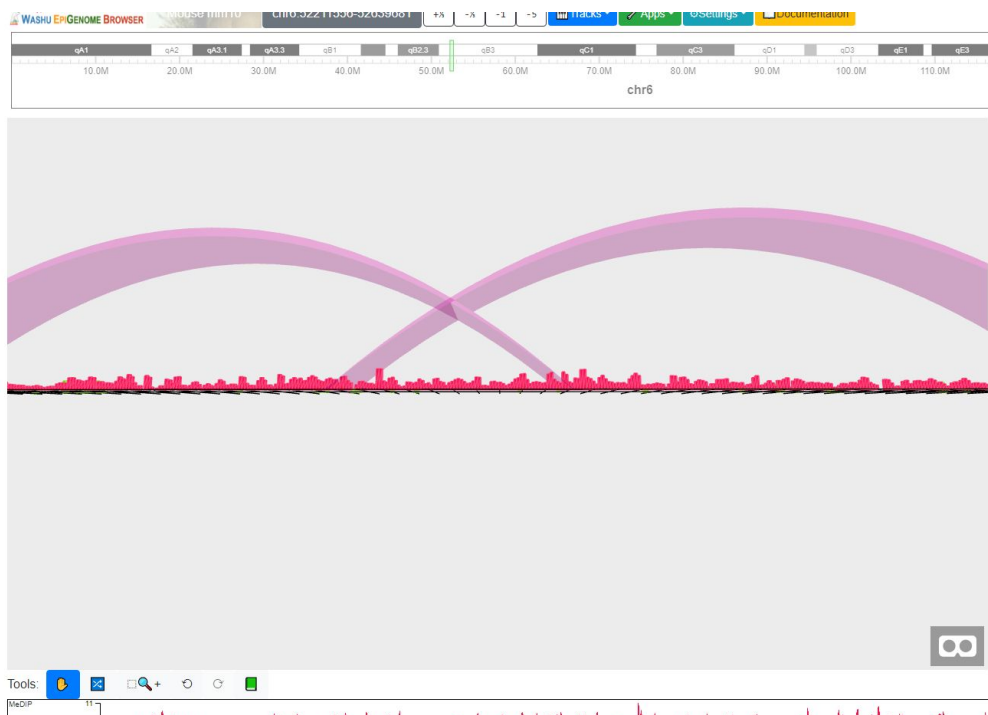
*Go forward:*

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



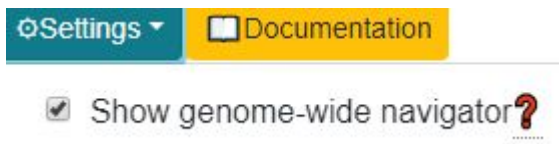


The user can choose to toggle the VR display mode of tracks. After choose the **Show 3D scene** submenu, a new container with VR view of the tracks will appear.





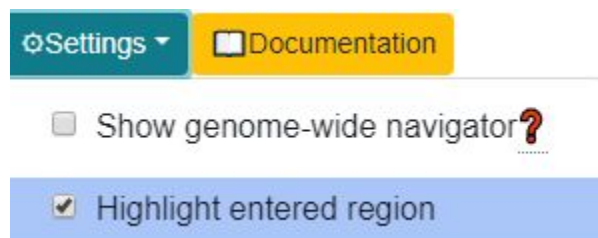
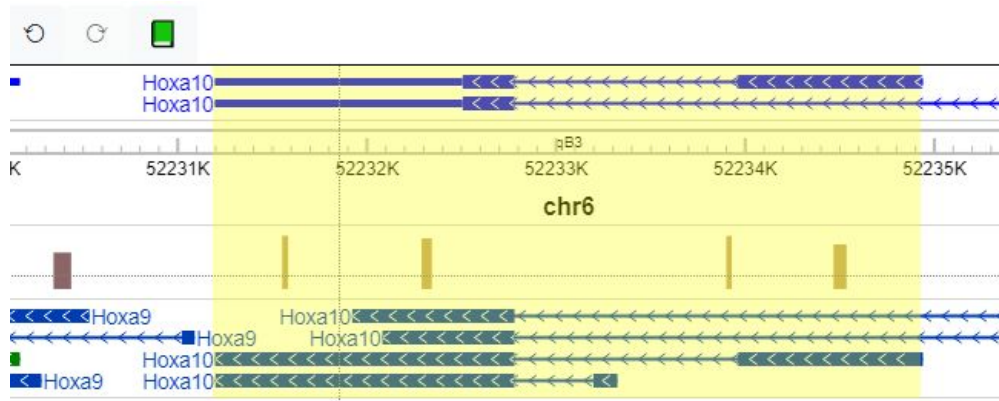
## Toggle display of the Genome Navigator



- 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.

