

# How to have your sequencing data in the UCSC browser

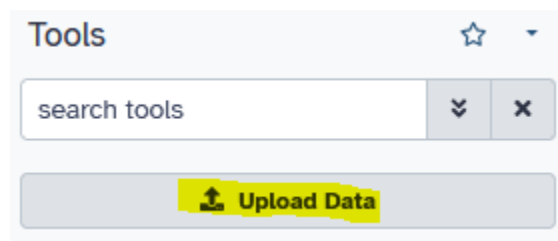
By M. Clara Hernández Cañas

What do you need??

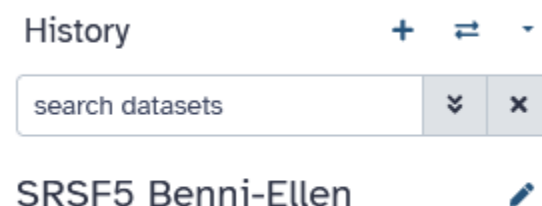
- You need an account in Galaxy
- You need an account in the UCSC
- Your files in (bigBed, bigBarChart, bigChain, bigGenePred, bigInteract, bigLolly, bigMaf, bigPsl, bigWig, BAM, barChart, VCF, BED, BED detail, bedGraph, broadPeak, CRAM, GFF, GTF, hic, interact, MAF, narrowPeak, Personal Genome SNP, PSL, or WIG)

How to do it:

1. The first step is to upload the data in the galaxy. On the right you can name the experiment

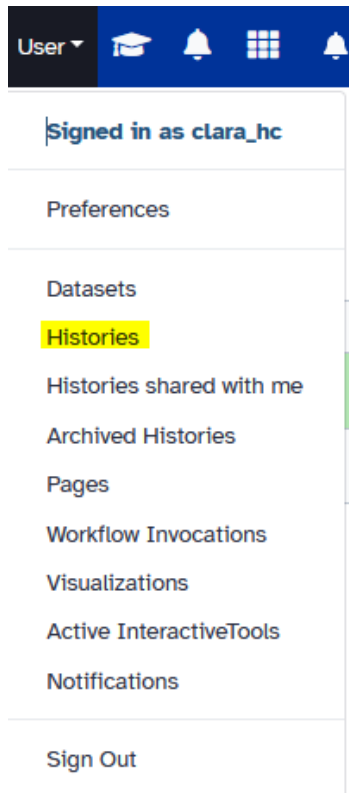


Where to upload the data in the galaxy page.



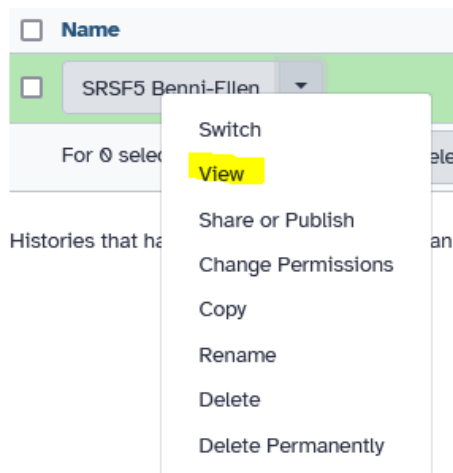
Name the experiment.

2. Once all data is uploaded you go to User > Histories.



Where the data is.

3. Go to view in your experiment tab



Finding your files

4. In this tab you have all your uploaded samples:

77: HeLa\_WT\_merged.rev.RPKM.coverage.bigWig

76: HeLa\_WT\_merged.fwd.RPKM.coverage.bigWig

75: HeLa\_SR5\_KO\_merged.rev.RPKM.coverage.bigWig

74: HeLa\_SR5\_KO\_merged.fwd.RPKM.coverage.bigWig

### Samples

5. This step should be done for ALL samples.
- First select view



77: HeLa\_WT\_merged.rev.RPKM.coverage.bigWig

Add Tags 

392.4 MB

format **bigwig**, database **hg38**

uploaded bigwig file

Binary UCSC Bigwig file

- A new window will open. Click the first option “display at UCSC ( main )”. A new window in the UCSC browser will open

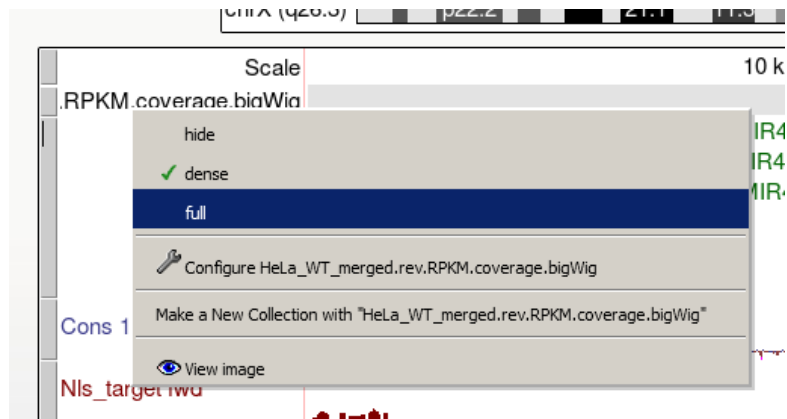
You can display your dataset with the following links:

1. **display at UCSC ( main )**
2. **display in IGB ( View )**
3. **display with IGV ( web current , local )**

or select a visualization from below.

*TIPP: You should wait between each sample so that all of them get loaded to the same session. It will open one page for each sample in the UCSC browser. So keep the last one.*

6. Once all samples are for each of them you have to go to the configuration of each one. In the same pop window you can go to configuration of the sample and select how to view it (eg. scale)



### HeLa\_WT\_merged.rev.RPKM.coverage.bigWig Track Settings ✕

#### HeLa\_WT\_merged.rev.RPKM.coverage.bigWig

Display mode: dense ▾ Remove custom track Update custom track

Type of graph: bar ▾

Track height: 128 pixels (range: 11 to 128)

Data view scaling: auto-scale to data view ▾ Always include zero: OFF ▾

Vertical viewing range: min: 0 max: 2095850 (range: 0 to 2.09585e+06)

Transform data points by: NONE ▾

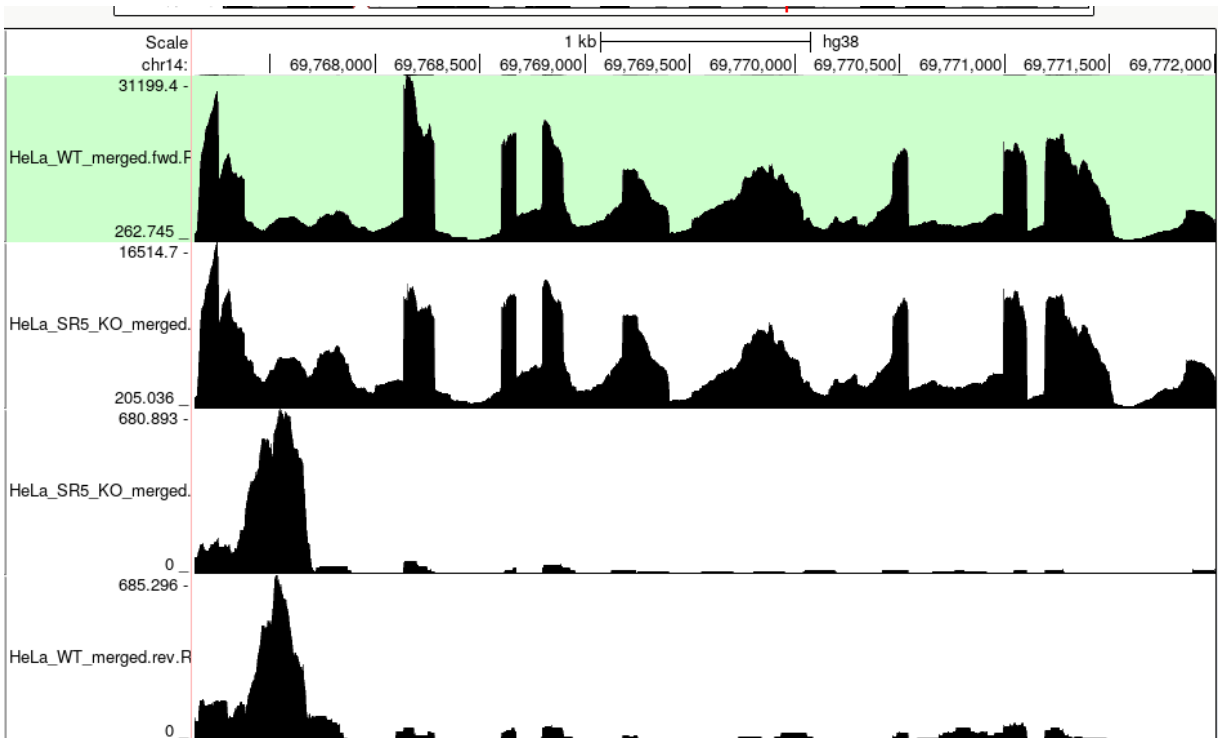
Windowing function: mean+whiskers ▾ Smoothing window: OFF ▾ pixels

Negate values: ☐

Draw y indicator lines: at y = 0.0: OFF ▾ at y = 0 OFF ▾

[Graph configuration help](#)

Apply OK

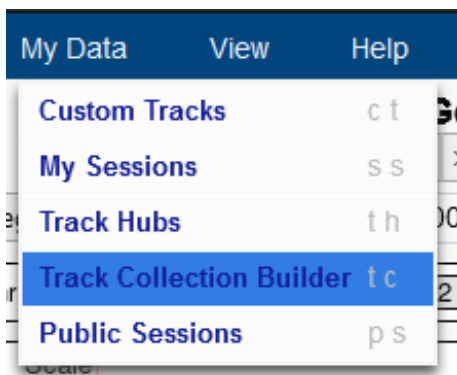


Here is how it looks when you view the full

- At this point, you have your samples in the browser.
- The next steps are to make them too look better like this:




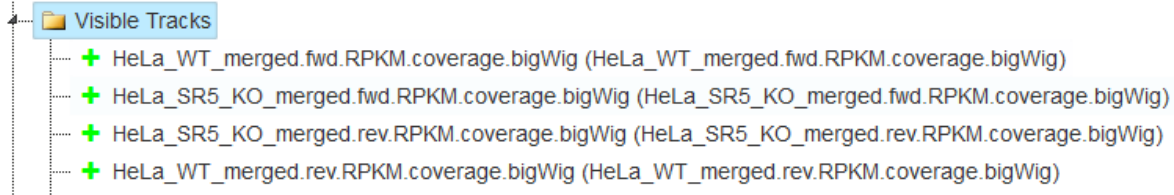
7. Go to My data> Track Collection Builder



8. On the left you have the available

#### Available Tracks


Below are all available graphing tracks that can be added to any collection. Click the arrow to the left of each folder below to s  
Click the green "plus"  symbol to add a track to any *selected* collection in the right window. See "Getting Started" below for tip



9. On the left side you can add a collection

#### Collected Tracks

Add Collection

To make a new collection of tracks, click the 'Add Collection' button above. Once saved, double-click the new collection to edit the name, description, and graph color. To remove a track from a collection, click the red "minus"  symbol to the left of each track. Click "GO" (upper right) to see collections in the browser.

**Note:** You must [save your session](#) to preserve collections long-term.

10. A pop window will appear: where you can add some info, like the name and color

Create New Collection close

Enter the name and description of the collection.

Name:


Description:

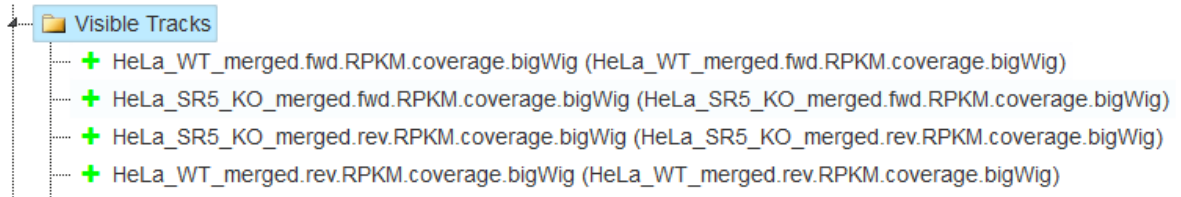
Color:



11. Click the green "plus" symbol to add a track to any *selected* collection in the right window.

#### Available Tracks

Below are all available graphing tracks that can be added to any collection. Click the arrow to the left of each folder below to s  
Click the green "plus"  symbol to add a track to any *selected* collection in the right window. See "Getting Started" below for tip




12. Once you added all the samples you can rename them

Edit Track close

Enter the name and description of the copied track.

**Name:**

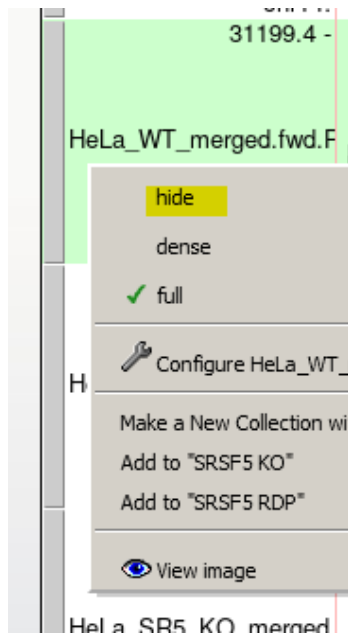
**Description:**

**Color:**  

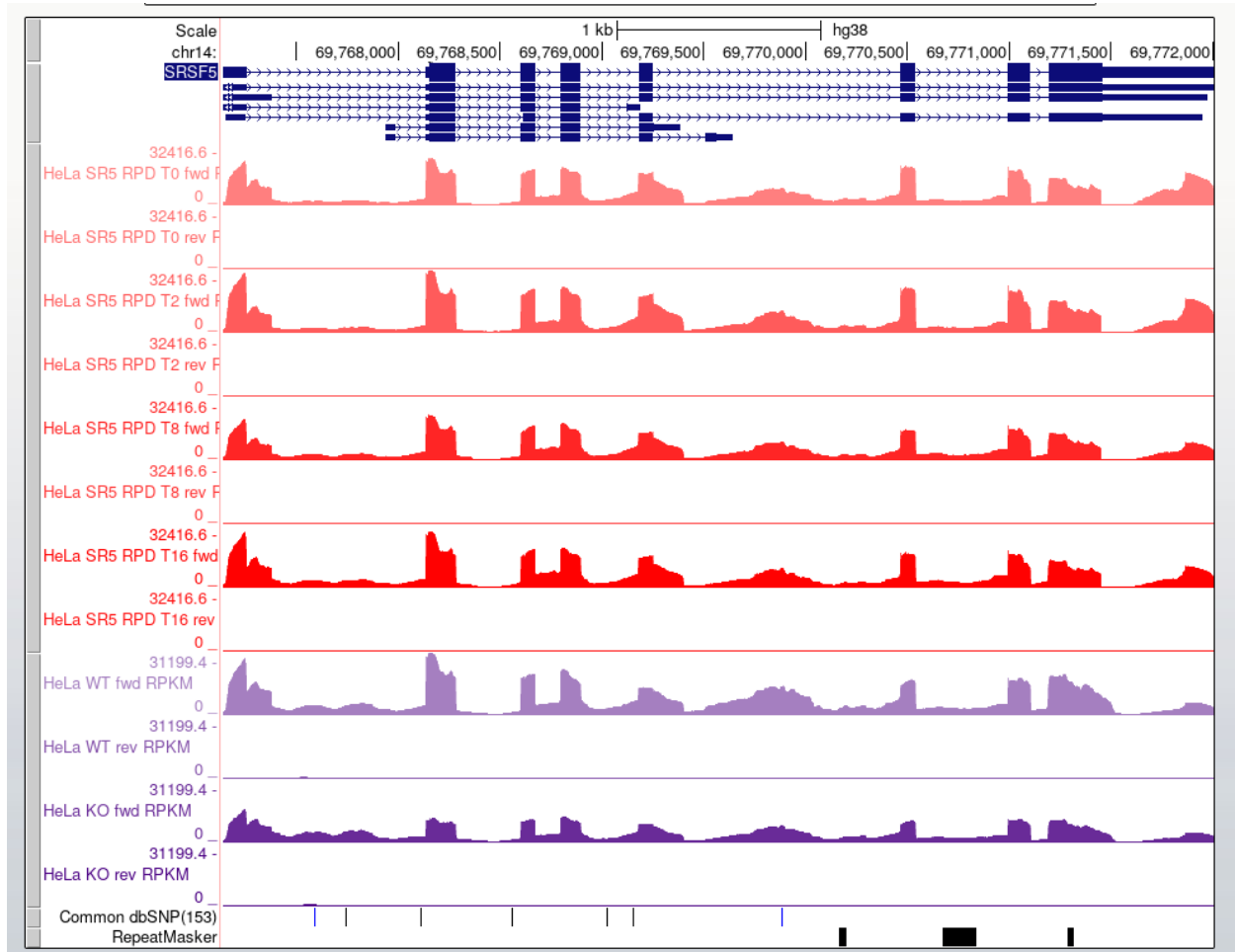
- 📁 SRSF5 KO (New Collection description)
- ☒ HeLa WT fwd RPKM (HeLa\_WT\_merged.fwd.RPKM.coverage.bigWig)
  - ☒ HeLa WT rev RPKM (HeLa\_WT\_merged.rev.RPKM.coverage.bigWig)
  - ☒ HeLa KO fwd RPKM (HeLa\_SR5\_KO\_merged.fwd.RPKM.coverage.bigWig)
  - ☒ HeLa KO rev RPKM (HeLa\_SR5\_KO\_merged.rev.RPKM.coverage.bigWig)

13. Once you are done you go to the tracks. Go to Go

14. Here I would hide the track that are outside the collection

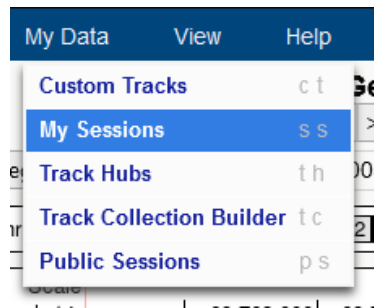


15. Here is how it looks at the end. But we are not done





16. Now we have to save it so you can access it again later. Data > My Sessions



17. You can name it and then you click on submit

### Save Settings

Save current settings as named session:

name:  ☒ allow this session to be loaded by others

Save current settings to a local file:

file:  file type returned: ☒ plain text ☐ gzip compressed (ignored if output file is blank)

Save Custom Tracks:

back up custom tracks to archive .tar.gz

18. In the same place you will have your session.

### My Sessions

Show  entries

Search:

session name (click to load)	created on	assembly	view/edit details	delete this session	share with others?	post in public listing?	send to mail
<a href="#">SRSF5 RDP-KO HeLa</a>	2023-09-08	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>

- You can have several and click them to load them to the browser

### My Sessions

Show  entries

Search:

session name (click to load)	created on	assembly	view/edit details	delete this session	share with others?	post in public listing?	send to mail
<a href="#">SRSF5 RDP-KO HeLa</a>	2023-09-08	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>
<a href="#">HUVEC_SE_HELA_SE_CAGE_APEX_STRIGTIE</a>	2023-07-17	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>
<a href="#">Listeria infection majiq comparisons</a>	2023-07-10	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>
<a href="#">HUVEC_SE_HELA_SE_CAGE_APEX</a>	2022-12-08	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>
<a href="#">SE_HUVEC_HeLa</a>	2022-12-08	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>
<a href="#">Listeria infection hg38</a>	2022-07-07	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>
<a href="#">USP 39 KD hg38</a>	2022-05-24	hg38	<input type="button" value="view/edit"/>	<input type="button" value="delete"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<a href="#">Email</a>

Showing 1 to 7 of 7 entries

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