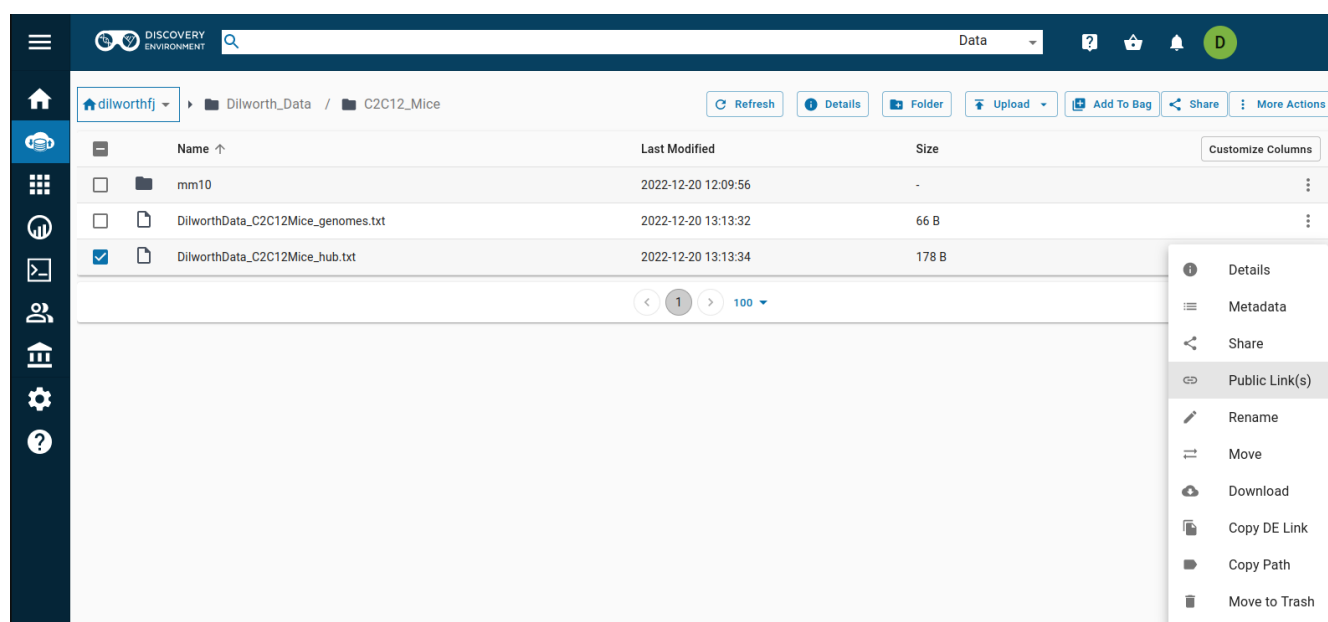


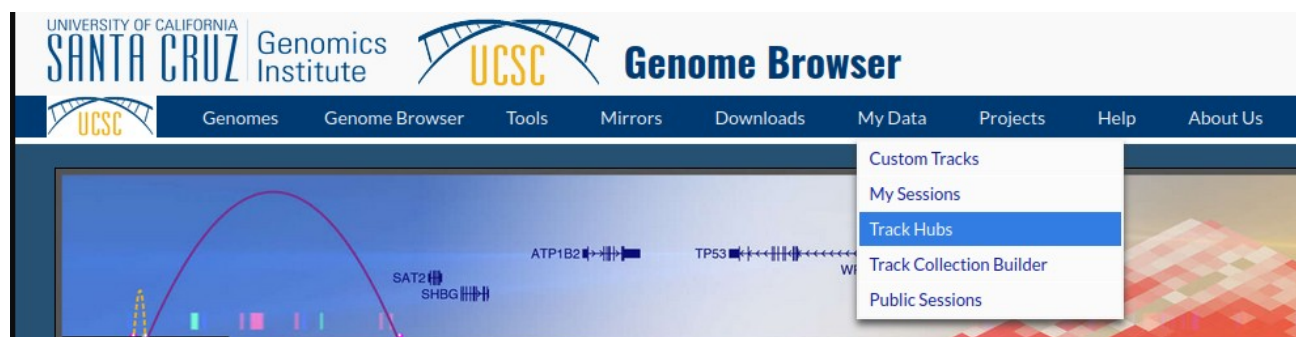
Viewing CyVerse Hubs in the UCSC Genome Browser

This guide assumes you have URL links to the hub.txt files hosted on CyVerse, where associated data is also stored. These links may have been shared between lab members.

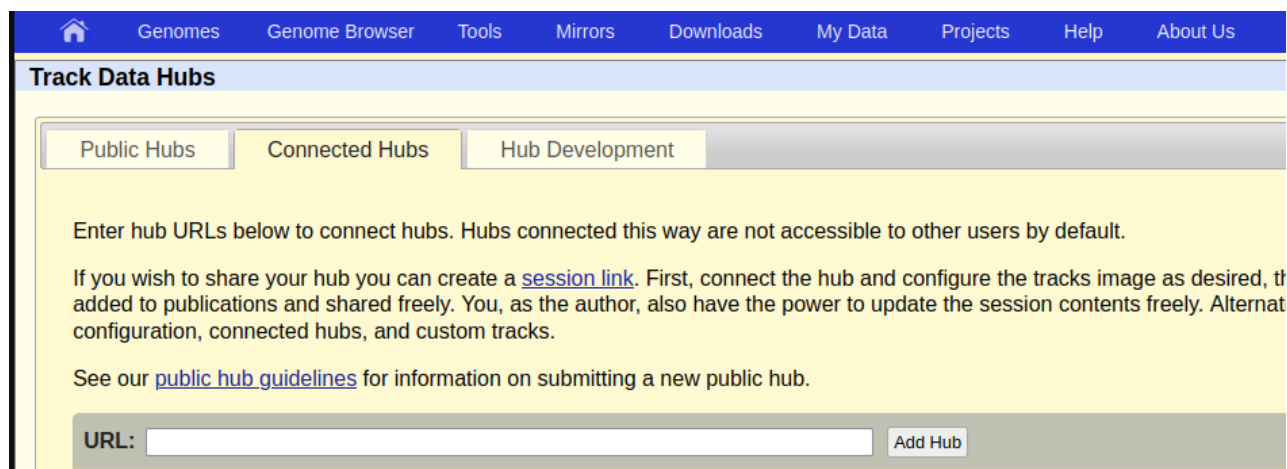
If not provided, hub links can be obtained from CyVerse (must have access to the account) by finding the desired hub.txt file and copy/pasting the Public Link into UCSC with the following steps.



Go to <https://genome.ucsc.edu/> -> **My Data** -> **Track Hubs**



Under **Connected Hubs** copy and paste the link URLs and click **Add Hub**

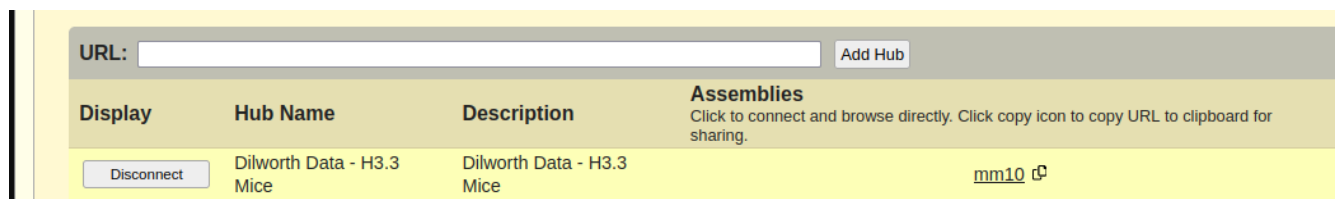


The screenshot shows the 'Track Data Hubs' interface. At the top is a navigation bar with links: Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below this is a section titled 'Track Data Hubs' with three tabs: 'Public Hubs', 'Connected Hubs', and 'Hub Development'. The 'Connected Hubs' tab is selected. The main content area contains instructions: 'Enter hub URLs below to connect hubs. Hubs connected this way are not accessible to other users by default.' It also explains that users can create a 'session link' to share their hub and that they can update session contents. A link to 'public hub guidelines' is provided. At the bottom, there is a form with a 'URL:' label, a text input field, and an 'Add Hub' button.

You will be redirected to the home page. Just go back to **My Data -> Track Hubs -> Connected Hubs**.

You should see the hub connected now.

Open it in the genome browser by selecting the genome assembly, e.g. click "mm10" below:

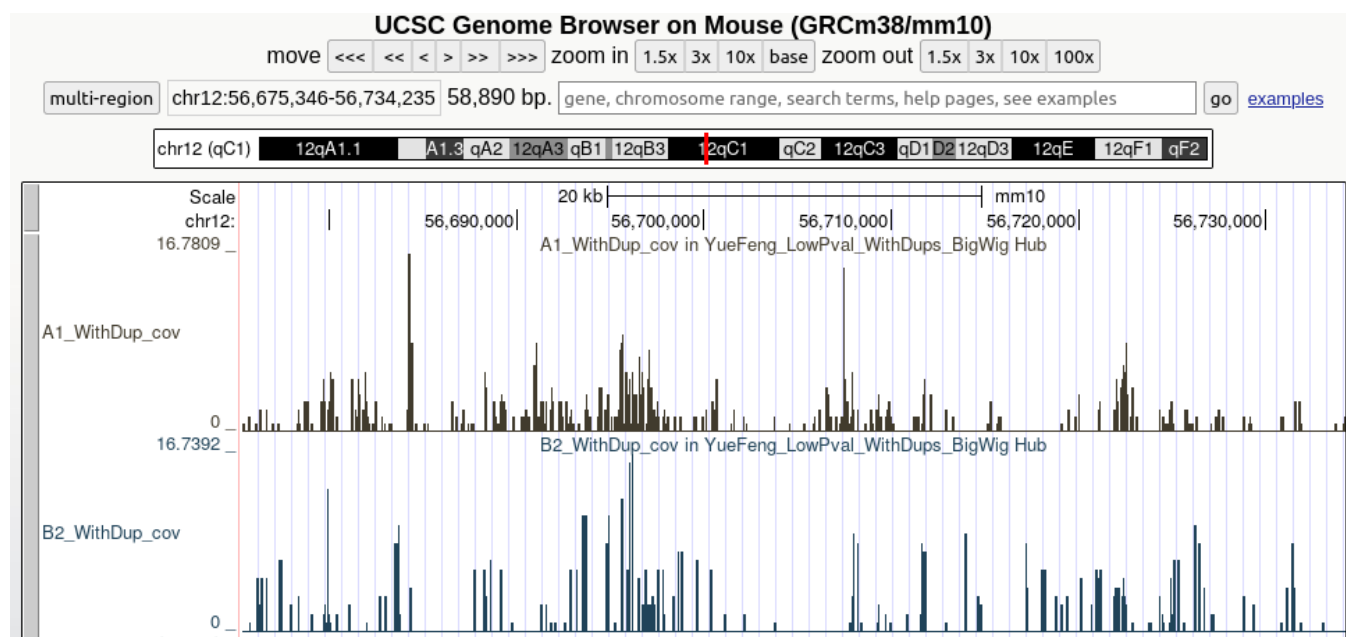


URL: <input type="text"/> <button>Add Hub</button>			
Display	Hub Name	Description	Assemblies
<button>Disconnect</button>	Dilworth Data - H3.3	Dilworth Data - H3.3	Click to connect and browse directly. Click copy icon to copy URL to clipboard for sharing.
	Mice	Mice	mm10

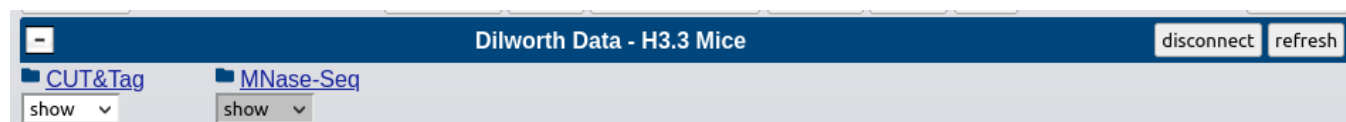
You will see **currently visible tracks** along with additional reference tracks available from UCSC and visible by default.

You can **search for genes** or genomic regions in the search bar and zoom in/out of the chromosome/regions.

Also note the **scale** when comparing tracks of bigwig files, this can be changed in settings.



If you **scroll to the bottom**, you can **hide/show supertracks** (collections of track groups), e.g. "CUT&Tag" and "MNase-Seq" below:



You can also click on the supertracks and **hide/show track groups**:

CUT&Tag Tracks

A super-track of H3.3 Mice CUT&Tag data tracks

Display mode:

All

<input type="checkbox"/>	hide	Gquad	YuefengLi-Gquad
<input type="checkbox"/>	hide	H3.1	YuefengLi-H3.1
<input type="checkbox"/>	hide	H3.3	YuefengLi-H3.3
<input type="checkbox"/>	hide	RNA_PolII_S5P	YuefengLi-RNA_PolII_S5P
<input checked="" type="checkbox"/>	full	YueFeng_LowPval_WithDups_BED	YueFengLi-LowPval_WithDups_BED Tracks supertrack
<input checked="" type="checkbox"/>	full	YueFeng_LowPval_WithDups_BigWig	YueFengLi-LowPval_WithDups_BigWig Tracks supertrack
<input checked="" type="checkbox"/>	full	YueFeng_LowPvalTracks_bigBed	YueFengLi-LowPvalTracks_bigBed Tracks supertrack
<input checked="" type="checkbox"/>	full	YueFeng_Tracks_bigBed	YueFengLi-Tracks_bigBed Tracks supertrack
<input checked="" type="checkbox"/>	full	YueFeng_Tracks_bigWig	YueFengLi-Tracks_bigWig Tracks supertrack

And go further into the individual tracks and change settings:

CUT&Tag YueFeng_LowPval_WithDups_BigWig Track Settings

YueFengLi-LowPval_WithDups_BigWig Tracks supertrack

Track collection: ▲ [A super-track of H3.3 Mice CUT&Tag data](#)

All tracks in this collection (9)

Display mode: [Reset to defaults](#)

Type of graph:

Track height: pixels (range: 11 to 128)

Data view scaling: Always include zero:

Vertical viewing range: min: max: (range: 0 to 127)

Transform function: Transform data points by:

Windowing function: Smoothing window: pixels

Negate values: ☐

Draw y indicator lines: at y = 0.0: at y =

[Graph configuration help](#)

List subtracks: ☐ only selected/visible ☒ all

<input checked="" type="checkbox"/>	full	Configure	A1_WithDup_cov	A1_WithDup_cov in YueFeng_LowPval_WithDups_BigWig Hub	Schema
<input checked="" type="checkbox"/>	full	Configure	B2_WithDup_cov	B2_WithDup_cov in YueFeng_LowPval_WithDups_BigWig Hub	Schema
<input checked="" type="checkbox"/>	full	Configure	C3_WithDup_cov	C3_WithDup_cov in YueFeng_LowPval_WithDups_BigWig Hub	Schema
<input checked="" type="checkbox"/>	full	Configure	D4_WithDup_cov	D4_WithDup_cov in YueFeng_LowPval_WithDups_BigWig Hub	Schema

Note:

Sometimes when opening a hub assembly, the tracks may show as an error/couldn't connect. In this case, try to refresh the page to let UCSC fetch the data again (hosted on [CyVerse](#)), or disconnect/reconnect the hub. Give it a minute or so.