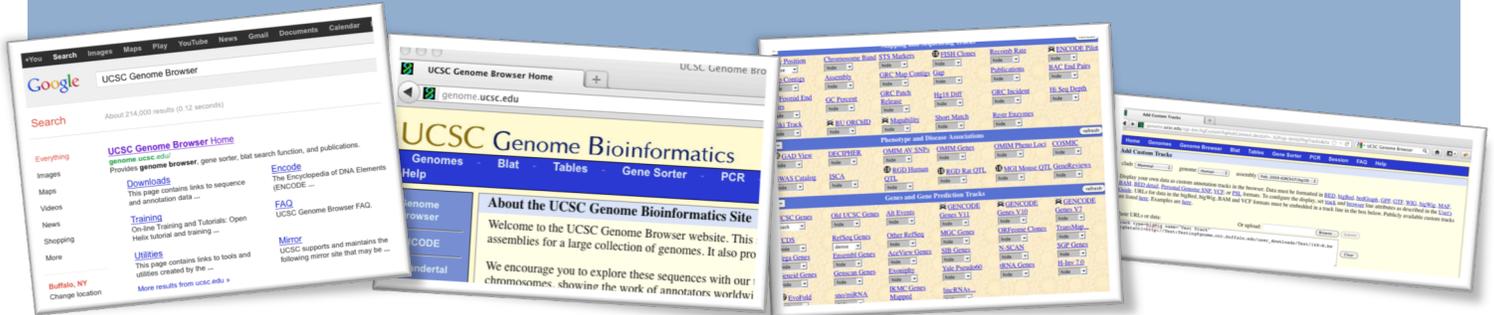


Viewing Data with UCSC

UB Next-Generation Sequencing and Expression Analysis Core

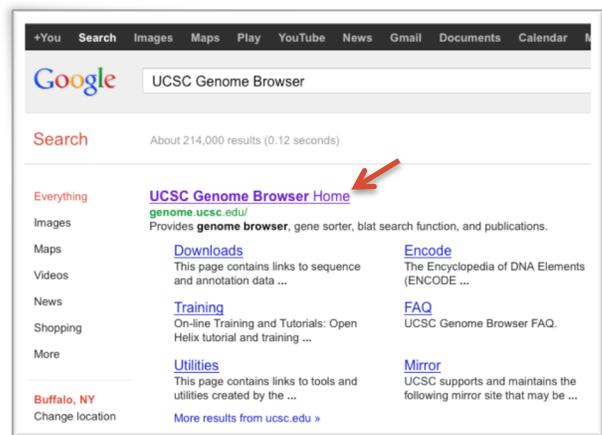


Getting Started with UCSC

Viewing data in the UCSC genome browser is a quick and easy, yet powerful way to delve deeper into the biology behind your recently sequenced samples. Below is a step-by-step guide that will get you browsing quickly.

Step 1

Navigate your favorite browser to the UCSC Genome Browser page. Click on the UCSC Genome Browser Home Link.



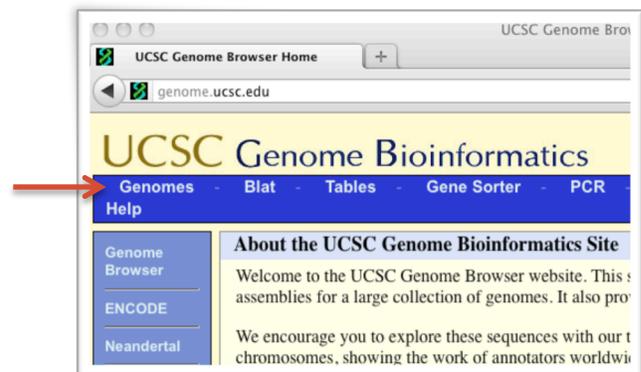
Step 1: Google Search for UCSC Genome Browser, and click on their home link.

Step 2

Once on the UCSC Home Page, Click on the Genomes menu item at the top left-hand corner of your screen

Step 3

After selecting the Genomes menu item, you will arrive at the Genome Selection Tool. Select your genome of choice, and then proceed to the “add custom tracks option”. Please make sure to verify the genome and the assembly, or build that you are utilizing.



Step 2: Click on the Genomes link at the top left-hand corner of the home page.



Step 3: Select the proper genome, and assembly for your project, and click on the add custom tracks



Step 4: Make sure the genome and assembly information is correct! Then paste your custom track information.

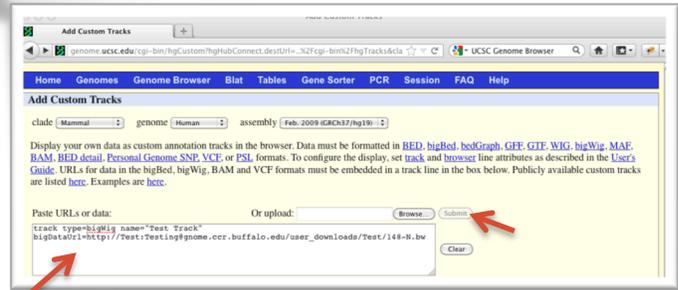
Step 5

Verify that the information has been copied correctly. A common error results from an extra space or new line inserted into the track information. When everything is ready, click submit.

Adding Custom Tracks

Step 4

After clicking on the add custom tracks button, you will land on an upload page. Make sure your genome and assembly are still the correct options, and then proceed to copy and paste the provided custom track information for your samples.

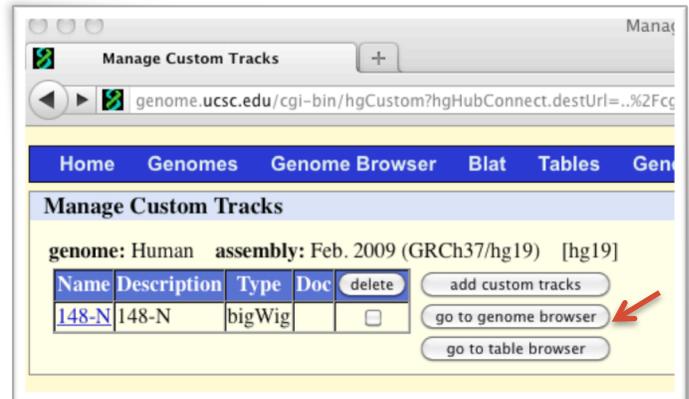


Step 5: When all information has been entered, press submit!

Managing Custom Tracks

Step 6

Once your tracks have been properly submitted, you will be taken to a page to manage the tracks that have been uploaded. Here you have the ability to rename, and change display attributes. This is more advanced and beyond the scope of this quick guide. For more information please review UCSC's helpful documentation. When ready to view your data, click on the "go to genome browser" option

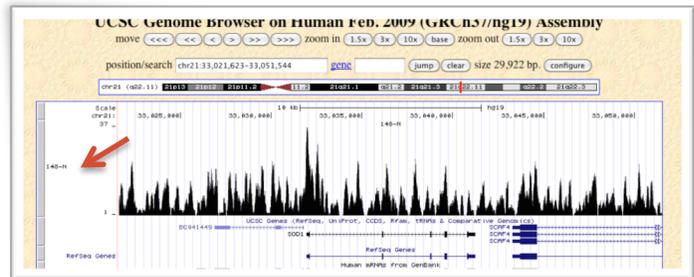


Step 6: Click on "go to genome browser."

Viewing Your Data

Step 7

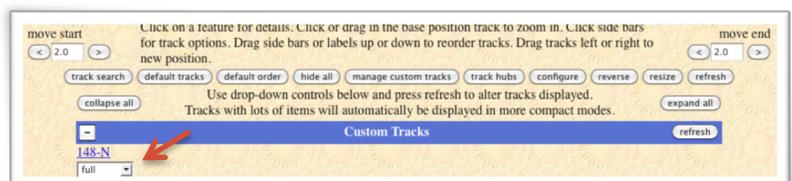
Once you have navigated to the genome browser, you can locate your custom tracks by their custom names. They will typically be found at the top of the genome browser.



Step 7: View your Data!

Step 8

Scrolling down in your browser will show you a Custom Tracks section, where you can adjust the visibility of your custom tracks, as well as numerous other reference tracks to compare your data against. Happy Browsing!

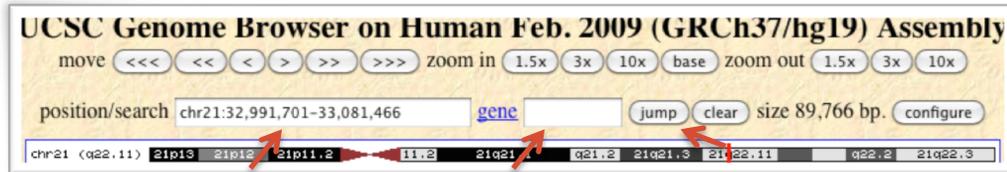


Step 7: Adjust the other tracks and how they display.

Adjusting Settings

Jumping to Specific Locations

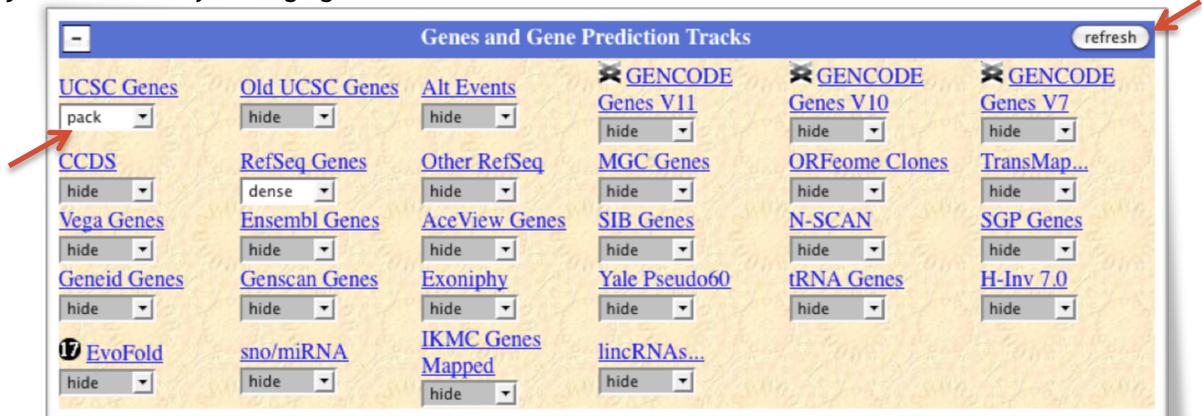
Now that all of your data has been successfully loaded into the browser, we can begin to look deeper into the biology behind your samples. The first step is to navigate to the regions of the genome you are interested in. At the top of the UCSC Browser, there is a navigation toolbar. This allows you to specify numerical coordinates in the chromosome:start-stop format, as well as a quick search for genes that you are interested in.



Jumping: Search by position, or by Gene name and “Jump” to the location.

Hiding Unused Tracks

Often the default browser has quite a lot of information that although is interesting, may not pertain to your study. It is helpful in this case to “hide” unnecessary information, which will make the browser less confusing. To do this, scroll your web browser down until you find the reference track that you do not need. Using the dropdown listing, toggle it to “hide” and then hit “refresh.” This will hide the track. If you want to undo this you can adjust the visibility setting again and click “refresh.”



Hiding Tracks: Scroll down and toggle “hide” and then “refresh!”

More Information

This guide covered the basics of using the UCSC Genome Browser. It covered loading the browser, adding custom data, adjusting the display settings as well as navigating around the genome. For more information please refer to the UCSC documentation found at:

<http://genome.ucsc.edu/goldenPath/help/hgTracksHelp.html>

<http://genome.ucsc.edu/FAQ/>