

UCSC Genomebrowser

04/10/2022

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WHAT IS IT?

- A graphical interface used to display biological information.
- Enables us to visualize entire genomes
- Compare our own samples against a genome through “trackhubs”
- <https://genome-euro.ucsc.edu/>

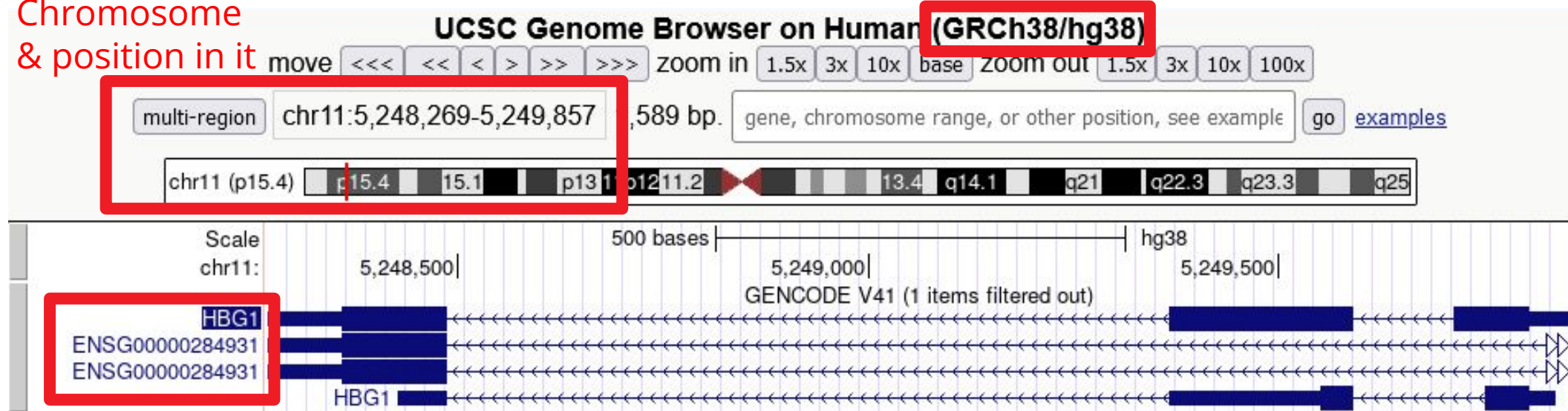
The screenshot shows the UCSC Genomics Institute website. The header includes the University of California Santa Cruz logo, the Genomics Institute name, and the UCSC logo. A navigation bar contains links for Home, Genomes, Genome Browser (highlighted with a red box), Tools, Mirrors, and Downloads. Below the navigation bar is a section titled 'Browse/Select Species' with a 'Find Position' link. Under 'POPULAR SPECIES', there are icons for Human, Mouse, Rat, Zebrafish, Fruitfly, Worm, and Yeast. A search bar prompts users to 'Search through thousands of genome browsers' and 'Enter species, common name or assembly ID'. A link 'Unable to find a genome? Send us a request.' is provided. The 'UCSC SPECIES TREE AND CONNECTED ASSEMBLY HUBS' section displays a phylogenetic tree with Human at the top, followed by Chimp, Bonobo, Gorilla, Orangutan, and Gibbon. On the right side, there are links for 'Human A' (Dec. 201), 'Position/' (Enter position, Current position), and 'Human' (UCSC Genome Browser hg38 Sequencing Genome Browser GRCh38.p1 Assembly).

THE BROWSER

- <https://genome-euro.ucsc.edu/>

Chromosome
& position in it

Aligned to hg38



Visualized hemoglobin 1

THE BROWSER

The screenshot displays a genomic browser interface with several tracks and data visualization options. The tracks are organized into sections: Mapping and Sequencing, Genes and Gene Predictions, and Phenotype and Literature. The Genes and Gene Predictions section is expanded, showing various tracks such as UCSC Genes, NCBI RefSeq, CCDS, CRISPR Targets, Ensembl Genes, and others. The UCSC Genes and NCBI RefSeq tracks are highlighted with a red box, and a red text box points to them with the text "Data visualized and the level of detail". The Phenotype and Literature section is also highlighted with a red box, and a red text box points to it with the text "Another basic track". The interface includes a "refresh" button for each track, which is also highlighted with a red box and a red text box pointing to it with the text "Any changes need to be refreshed".

Mapping and Sequencing

Genes and Gene Predictions

UCSC Genes full ▾ NCBI RefSeq full ▾

CCDS hide ▾ CRISPR Targets hide ▾ Updated Ensembl Genes hide ▾ 17 EvoFold hide ▾

Exoniphy hide ▾ GENCODE H-Inv 7.0 IKMC Genes Mapped lincRNAs LRG Transcripts

ORFeome Clones Other RefSeq Pfam in UCSC Gene New Prediction Archive

Retroposed Genes sno/miRNA hide ▾ TransMap V5 tRNA Genes UCSC Alt Events UniProt

Vega Genes Yale Pseudo60 hide ▾

Phenotype and Literature

COVID-19

mRNA and EST

Expression

Regulation

Comparative Genomics

Neandertal Assembly and Analysis

Denisova Assembly and Analysis

Variation

Repeats

Any changes
need to be
refreshed

DISPLAYING CUSTOM DATA

- UCSC requires genomic data in the bigwig format
 - Can be loaded by clicking on “my data” -> “custom tracks”
- To save time, it also accepts trackhubs
 - Which is basically a collection of bigwigs
- Previously mention pipeline seq2science creates trackhubs
- Find the current trackhub at:
https://mbdata.science.ru.nl/ghe_2022/day2/trackhub/RNA-seq_trackhub.hub.txt

DISPLAYING CUSTOM DATA



The screenshot shows the 'Track Data Hubs' page. The navigation bar at the top includes 'Genomes', 'Genome Browser', 'Tools', 'Mirrors', 'Downloads', 'My Data', 'Projects', and 'Help'. The 'My Data' menu is open, showing options: 'Custom Tracks', 'My Sessions', 'Track Hubs' (highlighted in blue), 'Track Collection Builder', and 'Public Sessions'. A red box highlights the 'Track Hubs' option, with a red arrow pointing to it from the text 'Click here to connect a custom hub'. Another red box highlights the 'Connected Hubs' tab in the main content area, with a red arrow pointing to it from the same text. Below the tabs, there is a text input field for a URL and an 'Add Hub' button. A red box highlights this input area, with a red arrow pointing to it from the text 'Insert the url and click "add hub"'. The URL entered in the box is 'https://mbdata.science.ru.nl/ghe_2022/day2/trackhub/RNA-seq_trackf'. Below the input field, there is a list of instructions for connecting to hubs.

Click here to connect a custom hub

Public Hubs Connected Hubs

Enter hub URLs below to connect hubs. Hubs connected this way are users by default.

If you wish to share your hub you can create a [session link](#). First, connect the hub and configure the tracks image as desired, then publish it. You can then share the link with others. Alternatively, you can create a public session, which will be visible to all users by default.

[Contact us](#) if you wish to submit a hub to the list of public hubs.

URL:

Insert the url and click "add hub"

- Enter its URL into the input box above and click 'Add Hub'.
- Alternatively, you can go to the 'Public Hubs' tab on this page and connect one of the hubs that were submitted to us.
- Another way to connect to hubs is via a direct connection link copied using the copy icon, shown on this page, when a hub is connected.
- You can also connect to hub by following a short link to a saved session, created through the menu 'My Data > My Sessions', if the Genome Browser had connected hubs when the session was saved.

DISPLAYING CUSTOM DATA

