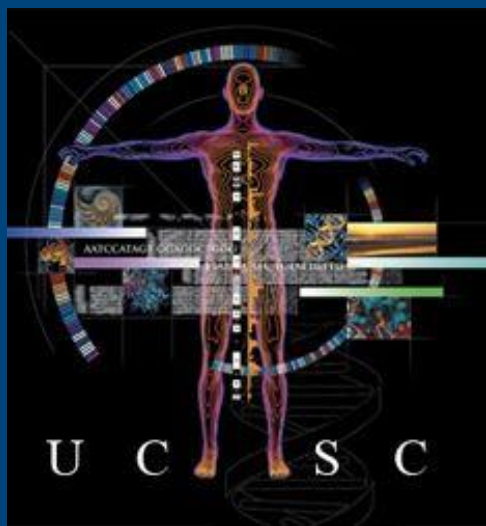


UCSC Genome Browser: HubSpace Track Storage



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Directly upload track hub data without needing web storage

- Track hub data can now be directly uploaded to UCSC, no longer do you need an institutional web server or DropBox, Github, etc accounts
- Each user gets 10Gb of storage, with more available upon request
- Files can be uploaded on the track hub connect page, or via the command line program hubtools
- Files are stored directly on UCSC servers, optimizing both speed and robustness

What are track hubs?

Track hubs are collections of remotely accessible data files like bigBed, bigWig, BAM, and VCF, that are described by a text file that defines how the track data is to be visualized in the Genome Browser. Traditionally, track hubs are hosted at your own institution or via Cloud Providers like DropBox and Github, and the Genome Browser only downloads the data needed to build the view for the particular genomic range being viewed. Over time, more visualization features exclusive to track hubs have been added, making them preferable to custom tracks. To facilitate ease of use, we are committed to providing dedicated storage for track hubs, up to 10Gb per user, perhaps even more in the future.

Using the HubSpace Interface

Click to start the upload process

Click on the folder icon or on a folder row to enter that data folder

Use the "back" icon or the breadcrumb to move back to the top level display.

Click on the checkbox or on the non-folder row to select the files

Public HubsConnected HubsHub DevelopmentHub Upload

Upload track hub files directly to UCSC from this page. You can then immediately view your bigBeds, bigWigs, BAMs (etc) without relying on third party hosting providers like DropBox or Google Drive or AWS. Users are limited to 10GB of total storage. Please keep a backup of your data. While we strive to maintain this service without interruption, we are unable to promise storage of your data indefinitely.

Selected file information

My Data

UploadUsing 19.7MB of 9.3GB

Search:

	File name	File size	File type	Genome	Hubs	File Last Modified	Upload Time
☐	defaultHub2	2.2MB	dir	hg38		6/15/2010, 6:42:42 AM	2025-04-17 15:16:38
☐	defaultHub	244.1KB	dir	hg38		2/05/2024, 1:00:09 AM	2025-04-16 14:14:42

Showing 1 to 2 of 2 entries (filtered from 7 total entries)

After file selection, you can delete the files or view them in the Genome Browser. You can also use the "View" buttons in the table to quickly view just that one track.

Public HubsConnected HubsHub DevelopmentHub Upload

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1 file selected. View selectedDelete selected

My Data > defaultHub

UploadUsing 19.7MB of 9.3GB

Search:

	File name	File size	File type	Genome	Hubs	File Last Modified	Upload Time	
☐	defaultHub	244.1KB	dir	hg38		2/05/2024, 1:00:09 AM	2025-04-16 14:14:42	
☐	hub.txt	0.2KB	hub.txt	hg38	defaultHub	4/16/2025, 9:14:42 PM	2025-04-16 14:14:42	
☒	View in Genome Browser	clinGenMaplo.bb	243.8KB	bigBed	hg38	defaultHub	2/04/2024, 5:00:09 PM	2025-04-16 14:14:42

Showing 1 to 2 of 3 entries (filtered from 6 total entries) 1 row selected

Example BAM file upload

Track Data Hubs

Public HubsConnected HubsHub DevelopmentHub Upload

Cancel

Editing bamExample.bam

Upload track hub files directly to UCSC from this page. You can then immediately view your bigBeds, bigWigs, BAMs (etc) without relying on third party hosting providers like DropBox or Google Drive or AWS. Users are limited to 10GB of total storage. Please keep a backup of your data. While we strive to maintain this service without interruption, we are unable to promise storage of your data indefinitely.

Selected file information

My Data

UploadUsing 19.7MB of 9.3GB

Search:

	File name	File size	File type	Genome	Hubs	File Last Modified	Upload Time
☐	defaultHub2	2.2MB	dir	hg38		6/15/2010, 6:42:42 AM	2025-04-17 15:16:38
☐	defaultHub	244.1KB	dir	hg38		2/05/2024, 1:00:09 AM	2025-04-16 14:14:42

Showing 1 to 2 of 2 entries (filtered from 7 total entries)

When uploading multiple files at once, a batch editor is available

Choose a popular genome from the dropdown list, or search from thousands of GenArk genomes available from NCBI/GenBank

UCSC TEST Genome Browser on Human Mar. 2006 (NCBI36/hg18)

Move <<< << < > >> >>> Zoom in 1.5x 3x 10x Base Zoom out 1.5x 3x 10x 100x

Multi-region chr21:33,020,574-33,060,722 40,149 bp. gene, chromosome range, search terms, help pages, see examples Search Examples

chr21 (q22.11) 21p13 21p12 21p11.2 q11.2 21q21.1 21q21.2 21q21.3 21q22.1 21q22.2 21q22.3

Scale chr21: 33,025,000| 33,030,000| 33,035,000| 33,040,000| 33,045,000| hg18 33,050,000| 33,055,000| 33,060,000|

bamExample.bam

Collapse all Track search Highlight Hide all Add custom tracks Configure Reverse Resize Expand all

Hub: defaultHub3

No Info Disconnect Refresh

bamExample.bam bamExample.bam.bai

dense hide

Mapping and Sequencing Refresh

Phenotype and Disease Associations Refresh

V2 Features: Edit trackDb configuration directly from user interface

Track type and genome are automatically inferred, but can be manually configured with the dropdowns or by changing the file name extension. A track hub name is automatically generated for you.

References

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tus: <https://tus.io/>
uppy: <https://uppy.io/>

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More Information

Have questions?
Send us a question on our public mailing list: genome@soe.ucsc.edu

Genome Browser tutorials and videos: <https://genome.ucsc.edu/training/index.html>

Digital copy of this poster available at: