

# Genome Data Viewer (GDV)

NCBI's genome browser supporting the exploration and analysis of more than 600 eukaryotic assemblies

[ncbi.nlm.nih.gov/genome/gdv/](http://ncbi.nlm.nih.gov/genome/gdv/)

## See your data in context!

### Connect to a track hub

Track Hubs<sup>1</sup> have arrived in GDV, giving you a new option for analyzing externally-provided data alongside NCBI-provided tracks. You can connect and configure track hubs via a new configuration interface that is accessed from both the “User Data and Track Hubs” widget options or the “Tracks” menu.

Here's a quick tutorial to get started [bit.ly/track-hubs-tutorial](http://bit.ly/track-hubs-tutorial).

Supported file formats  
BAM,  
bigWig/Wig,  
bigBED/BED, VCF,  
HGVS, GFF3, GTF,  
GVF and more  
coming soon!

[1] Raney BJ, Dreszer TR, Barber GP, Clawson H, Fujita PA, Wang T, Nguyen N, Paten B, Zweig AS, Karolchik D, et al. 2014. Track data hubs enable visualization of user-defined genome-wide annotations on the UCSC Genome Browser. *Bioinformatics* 30: 1003–1005.

The screenshot displays the Genome Data Viewer interface for Homo sapiens, GRCh38.p12 (GCF\_000001405.38) on Chromosome 17 (NC\_000017.11). The main view shows a genomic track with various annotations, including genes (RPL27, RPL27-IT1) and transcripts (NM\_000968.4). A 'User Data and Track Hubs' configuration window is open on the left, showing details for the 'gencodecaptureSeq' hub, including its name, labels, and contact information. A 'Configure Track Hubs' button is highlighted in the 'Tools' menu on the right. The interface includes a search bar, navigation controls, and a detailed track view with coordinates and zoom options.

### BLAST widget

The **BLAST widget**, a new browser feature, provides direct access within GDV to execute and manage BLAST queries (blastn, tblastn) aligned to the specific assembly.

- Seamlessly connect from or to BLAST within GDV
- Run a search in BLAST and view track in GDV
- Video tutorial at [bit.ly/2CRobZ6](http://bit.ly/2CRobZ6)

### Other options to view your data in GDV

- Connect to a track hub
- Stream a remotely hosted file
- Upload your file!



Watch GDV in action!

Video tutorials here: [bit.ly/GDV-tutorials](http://bit.ly/GDV-tutorials)

# Other genome tools

## Genome Remapping Service

NCBI Genome Remapping Service

\* indicates required fields.

Assembly-Assembly Clinical Remap Alt loci remap

**Genome Information**

Source Organism \*  
Homo sapiens  
Start typing to get a list of available organisms

Source Assembly \*

Assem Name	Assem SeqID	Date
GRCh38.p11 :: Primary Assembly	GCF_000001305.14	2013/12/20
GRCh37.p13 :: Primary Assembly	GCF_000001305.13	2009/02/27
GRCh38.p12	GCF_000001405.38	2017/12/21
GRCh38.p11	GCF_000001405.37	2017/06/14
GRCh38.p10	GCF_000001405.36	2017/01/06

Target Assembly \*

Assem Name	Assem SeqID	Date
GRCh38.p12	GCF_000001405.38	2017/12/21
GRCh38.p9	GCF_000001405.35	2016/09/26
GRCh38.p8	GCF_000001405.34	2016/06/30
GRCh38.p7	GCF_000001405.33	2016/03/21
GRCh38.p6	GCF_000001405.32	2015/12/21

Alignments performed: March 21, 2017, software version: 1.8

Alignments	Source Assembly Coverage (GRCh38.p10, GCF_000001405.36)	Target Assembly Coverage (GRCh38.p7, GCF_000001405.33)	Percent Identity
First Pass (Reciprocal Best Hits)	99.539	99.844	100
Total	99.995	99.997	99.999

*Keep your annotations current!*

**NCBI Remap** is a tool that allows users to project annotation data from one coordinate system to another. This remapping (sometimes called 'liftover') uses genomic alignments to project features from one sequence to the other. For each feature on the source sequence, we perform a base-by-base analysis of each feature on the source sequence in order to project the feature through the alignment to the new sequence.

 [ncbi.nlm.nih.gov/genome/tools/remap](http://ncbi.nlm.nih.gov/genome/tools/remap)

Beta version of stand-alone remap is available to Mac and Windows users!

**New!**

## Genome Decoration Page

*Place your annotations on the genome!*

The **Genome Decoration Page** (GDP) is a service that allows users to upload their own annotation data and create a figure showing that annotation distributed on the genome. Annotation can be shown as a track, or set of tracks, drawn next to the chromosome. One annotation track can be selected to be drawn as an 'Overlay', such that the annotation information is drawn on top of the chromosome representation.

 [ncbi.nlm.nih.gov/genome/tools/gdp](http://ncbi.nlm.nih.gov/genome/tools/gdp)

