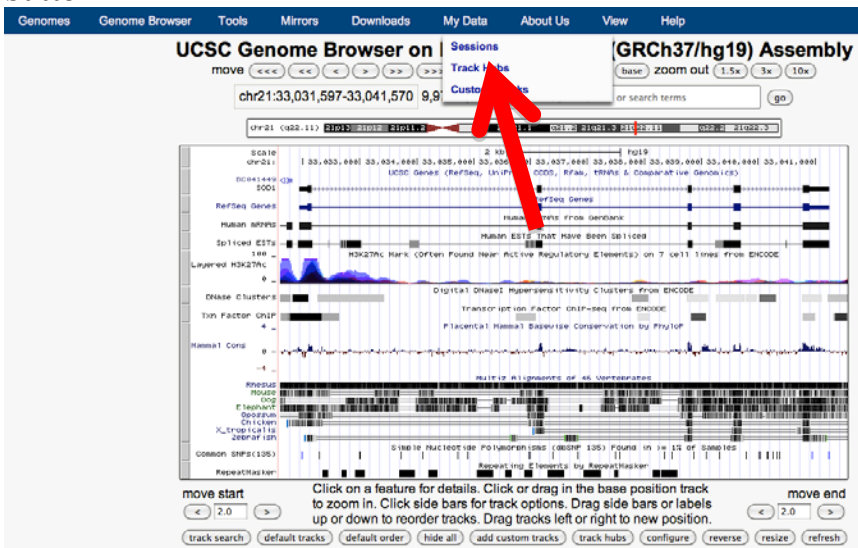


Using UCSC Genome Browser Sessions for ENCODE data analysis

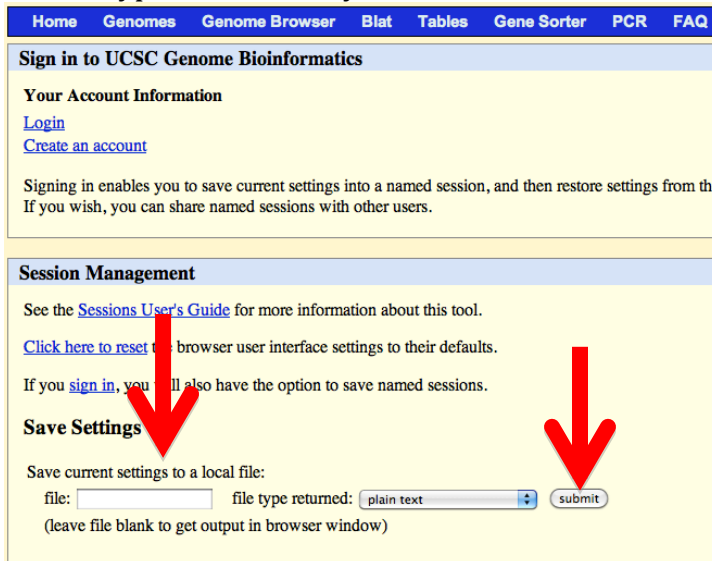
(Updated 18 September 2012, Mike Pazin)

Saving a session:

- 1 Go to <http://encodeproject.org/ENCODE/> or the UCSC browser
- 2 Select the human (or mouse) browser (or preview browser), as desired, from the buttons along the left hand side of the window.
- 3 Customize by turning on the desired tracks, and turning off tracks you don't want to visualize.
- 4 Mouse over the "My Data" button along the top, then click on the "Sessions" button:



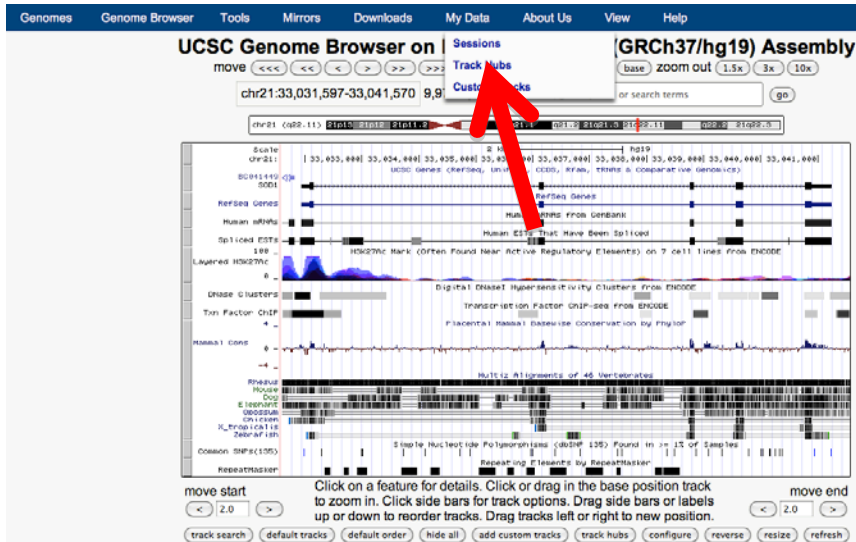
- 5 Type in the name you'd like to use for the session file, then click "submit":



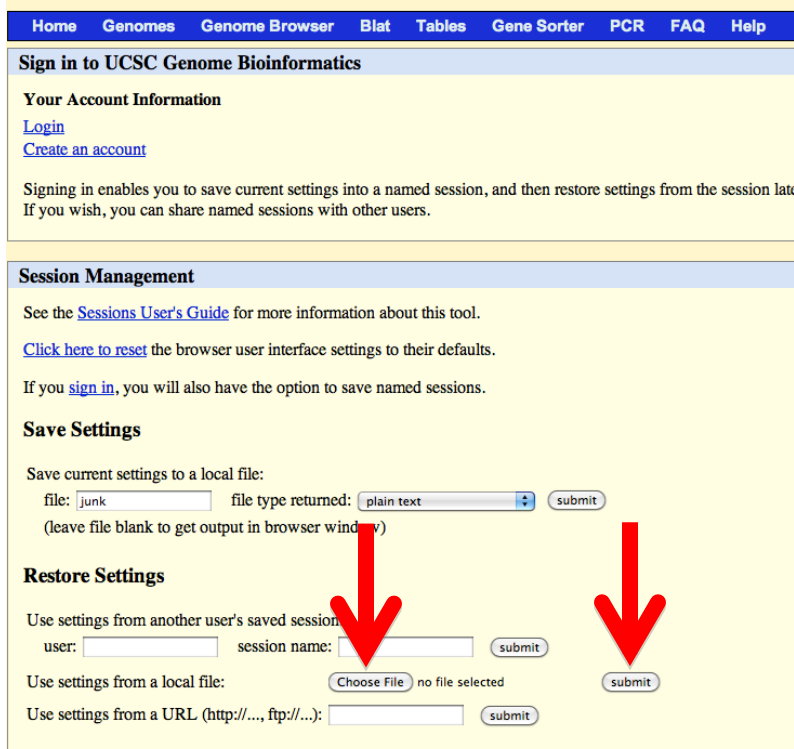
The session will be saved as a text file to your downloads folder.

Opening a session:

- 1 Go to <http://encodeproject.org/ENCODE/> or the UCSC browser
- 2 Select the human (or mouse) browser (or preview browser), as desired, from the buttons along the left hand side of the screen.
- 3 Mouse over the “My Data” button along the top, then click on the “Sessions” button:



- 4 Click on the “Choose File” button, navigate to the session file you want to open, then click on the “submit” button:



- 5 The name of the session that is ready to load appears next to the browser link; click on the browser link to load the session:

Home Genomes Genome Browser Blat Tables Gene Sorter PCR FA

Sign in to UCSC Genome Bioinformatics

Your Account Information
[Login](#)
[Create an account](#)

Signing in enables you to save current settings into a named session, and then restore settings from it. If you wish, you can share named sessions with other users.

Updated Session
 Loaded settings from local file **Pazin V6 Hg19 Standard** (3307 bytes). [Browser](#)

Session Management

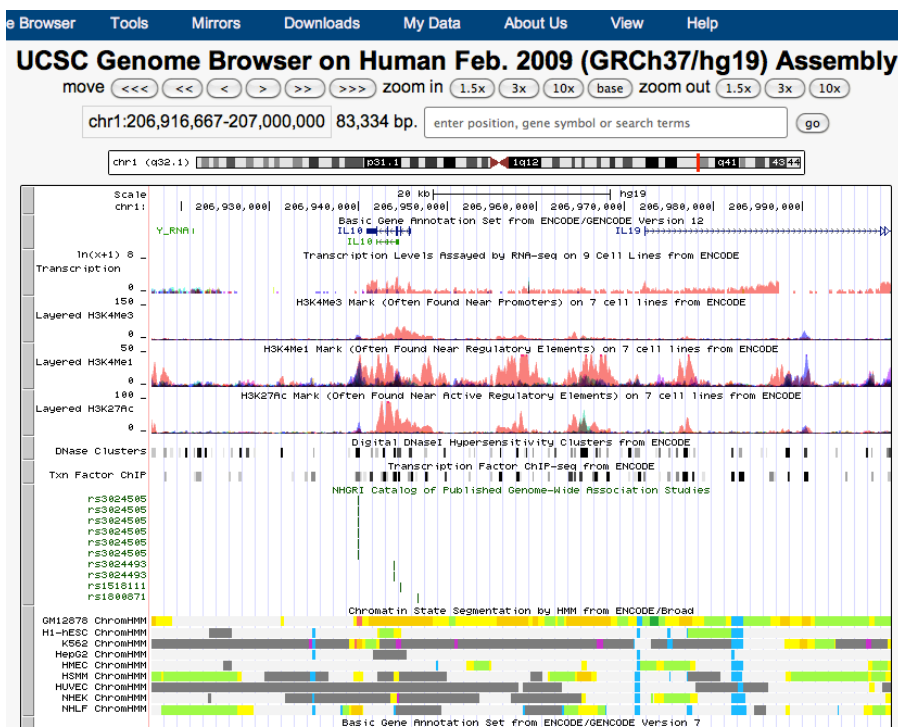
See the [Sessions User's Guide](#) for more information about this tool.

[Click here to reset](#) the browser user interface settings to their defaults.

If you [sign in](#), you will also have the option to save named sessions.

Save Settings

6 The selected tracks will be displayed, at the saved genomic region:



7 From here, you are free to move to another genomic coordinate, and save a new session, or change the displayed tracks, and save a new session.

Sharing a session:

One easy way to share a session is to create the session you want, save that as a text file, and e-mail the session file to a colleague that knows how to load the session.

UCSC has a guide to using sessions:

<http://encodeproject.org/goldenPath/help/hgSessionHelp.html>

To display Roadmap Epigenomics data:

- 1 Go to <http://encodeproject.org/ENCODE/> or the UCSC browser
- 2 Select the human browser (or preview browser), as desired, and customize as desired.
- 3 Mouse over the “My Data” button along the top, then click on the “Track Hubs” button:

The screenshot shows the UCSC Genome Browser interface for the GRCh37/hg19 assembly. The top navigation bar includes 'Genomes', 'Genome Browser', 'Tools', 'Mirrors', 'Downloads', 'My Data', 'About Us', 'View', and 'Help'. The 'My Data' menu is open, and the 'Track Hubs' option is highlighted with a red arrow. Below the navigation bar, the browser displays genomic tracks for chromosome 21:33,031,597-33,041,570. The tracks include RefSeq Genes, Human RefSeqs, Spliced ESTs, Layered H3K27me, DNase Clusters, Transcription Factor ChIP, RepeatMasker, and Common SNPs (CDS). The 'Track Hubs' button is located in the top right corner of the browser interface.

- 4 Check the box for “Roadmap Epigenomics data”, then click the “Load Selected Hubs” button:

The screenshot shows the 'Track Data Hubs' page in the UCSC Genome Browser. The page lists various public hubs that can be imported into the browser. The 'Roadmap Epigenomics Data Complete Collection at Wash U VizHub' is selected, indicated by a blue checkmark in the 'Display' column. A red arrow points to this checkmark. Another red arrow points to the 'Load Selected Hubs' button at the bottom of the page. The table below shows the details of the selected hub.

| Display | Hub Name | Description | Assemblies | URL |
|-------------------------------------|---|--|------------|---|
| <input type="checkbox"/> | ENCODE Integrative Analysis Hub | ENCODE Integrative Analysis Data Hub | hg19 | http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/hub.txt |
| <input type="checkbox"/> | miRcode microRNA target sites in GENCODE transcripts | Predicted microRNA target sites in GENCODE transcripts | hg19 | http://www.mircode.org/ucscHub/hub.txt |
| <input checked="" type="checkbox"/> | Roadmap Epigenomics Data Complete Collection at Wash U VizHub | Roadmap Epigenomics Data Complete Collection at Wash U VizHub | hg19 | http://vizhub.wustl.edu/VizHub/RoadmapReleaseAll.txt |
| <input type="checkbox"/> | UMassMed ZHub | UMassMed H3K4me3 ChIP-seq data for Autistic brains | hg19 | http://zlab.umassmed.edu/zlab/publications/UMassMedZHub/hub.txt |
| <input type="checkbox"/> | Cancer genome polyA site & usage | An in-depth map of polyadenylation sites in cancer (matched-pair tissues and cell lines) | hg19 | http://johnlab.org/xpad/Hub/UCSC.txt |

Load Selected Hubs Contact genome@soe.ucsc.edu to add a public hub.

5 Select desired tracks from the list, and customize as desired:

The screenshot displays the UCSC Genome Browser interface for the region chr1:206,928,010-206,952,700 (24,691 bp). The main visualization area contains several tracks:

- Scale:** 10 kb, hg19 assembly coordinates (206,935,000 to 206,950,000).
- Basic Gene Annotation Set:** from ENCODE/GENCODE Version 12, showing the IL10 gene structure.
- Transcription Levels:** Assayed by RNA-seq on 9 Cell Lines from ENCODE.
- Layered H3K4Me3 Mark:** (Often Found Near Promoters) on 7 cell lines from ENCODE.
- Layered H3K4Me1 Mark:** (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE.
- Layered H3K27Ac Mark:** (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE.
- DHase Clusters:** Digital DNaseI Hypersensitivity Clusters from ENCODE.
- Txn Factor ChIP:** Transcription Factor ChIP-seq from ENCODE.
- GNAS Catalog:** NHGRI Catalog of Published Genome-Wide Association Studies.
- Chromatin State Segmentation:** by HMM from ENCODE/Broad.
- Chromosomes:** A list of chromosomes with corresponding colored bars: GM12878, H1-hESC, K562, HepG2, H1hESC, H1hESC, HUVEC, H1hESC, NHLF.
- Basic Gene Annotation Set:** from ENCODE/GENCODE Version 7, showing the IL10 gene structure.

Below the tracks, there are controls for track search, default tracks, default order, hide all, add custom tracks, track hubs, configure, reverse, resize, refresh, collapse all, and expand all. A red arrow points to the 'collapse all' button.

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

Roadmap Epigenomics Data Complete Collection at Wash U VizHub refresh

| | | | | | |
|---|--------------------------------------|--------------------------------------|--|---|--|
| Broad Histone hide | UCSD Histone hide | UCSF Histone hide | DNase hide | Footprinting hide | RNA hide |
| DNA Methylation hide | By Assay... show | By Sample... show | Assay Summary... show | Sample Summary... show | Methylation Summary... show |