Viewing ENCODE Composite Tracks At A Locus Of Interest

(Updated 30 September 2013, Mike Pazin)

ENCODE has produced composite tracks that summarize information from several key assays, across a variety of cell types; this is a good way to start viewing a locus of interest, such as a gene, or the genome surrounding a genetic variant. First, you will download a session file. Any time you want to see a locus in this view, first open the session file, then navigate to the locus of interest.

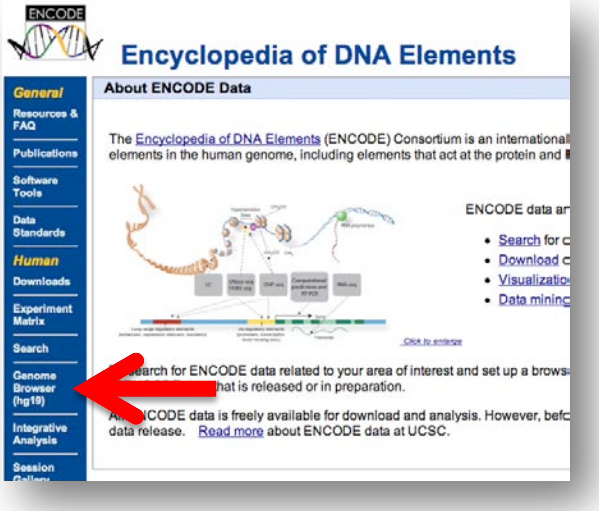
1) Download the session file:

From the NHGRI ENCODE tutorials, site (http://www.genome.gov/27553901), download the session file from at the link: [A standard session for viewing ENCODE data](#)

Depending on your browser, you may automatically download the file to your downloads folder, or open the file in your browser. If the the file opens instead of downloading, try right-clicking (PC) or control-clicking (Apple) on the link, and from the contextual menu that opens, chose Save linked file to Downloads. The file name is <ENCODE_GWAS_HG19_PazinV2.txt>

2) Opening the session:

1 Go to http://encodeproject.org/ or the UCSC browser



Encyclopedia of DNA Elements

About ENCODE Data

The Encyclopedia of DNA Elements (ENCODE) Consortium is an international
elements in the human genome, including elements that act at the protein and

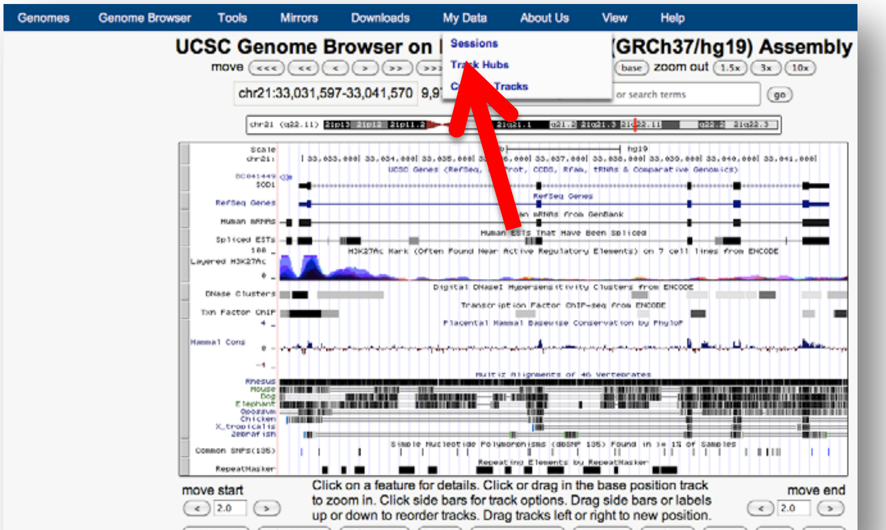
ENCODE data ar

earch for ENCODE data related to your area of interest and set up a brows
hat is released or in preparation.

ICODE data is freely available for download and analysis. However, befc
data release. Read more about ENCODE data at UCSC.

2 Select the human browser, 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:

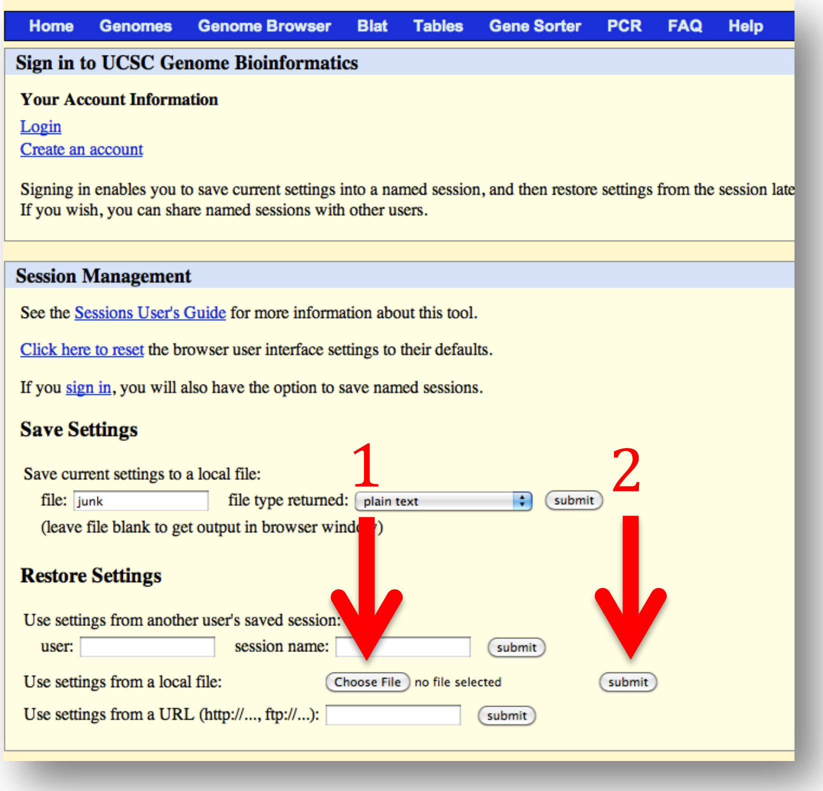


UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr21:33,031,597-33,041,570

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.

4 Click on the “Choose File” button (arrow 1), navigate to the session file you want to open, then click on the “submit” button (arrow 2):



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 the session late
If you wish, you can share named sessions with other users.

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

Save current settings to a local file:

file: junk file type returned: plain text submit

(leave file blank to get output in browser wind)

Restore Settings

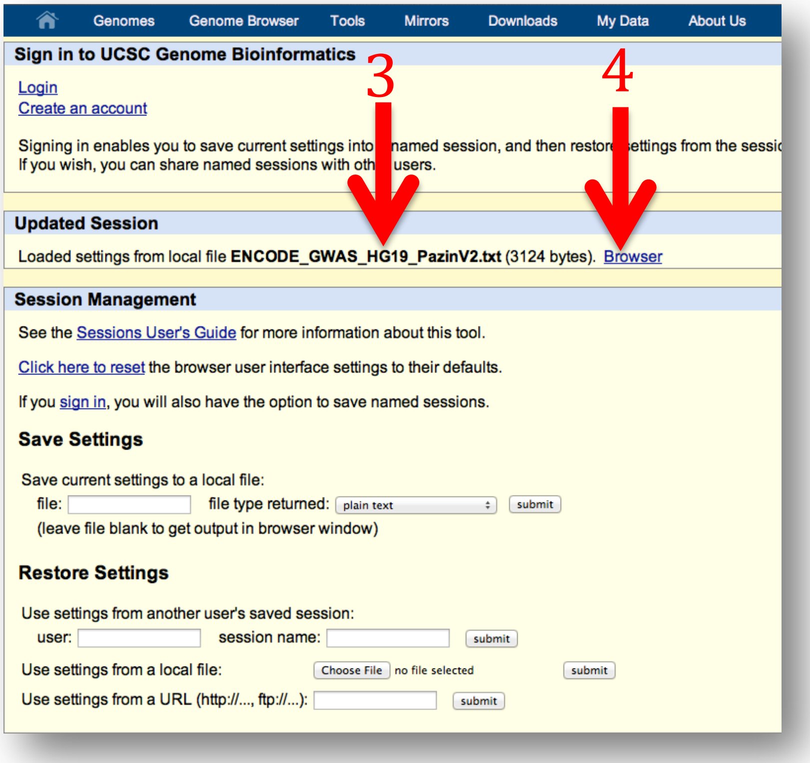
Use settings from another user's saved session:

user: session name: submit

Use settings from a local file: Choose File no file selected submit

Use settings from a URL (http://..., ftp://...): submit

5 The name of the session that is ready to load appears next to the browser link (arrow 3); click on the browser link to load the session (arrow 4):



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If you wish, you can share named sessions with other users.

Updated Session

Loaded settings from local file **ENCODE_GWAS_HG19_PazinV2.txt** (3124 bytes). Browser

Session Management

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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.

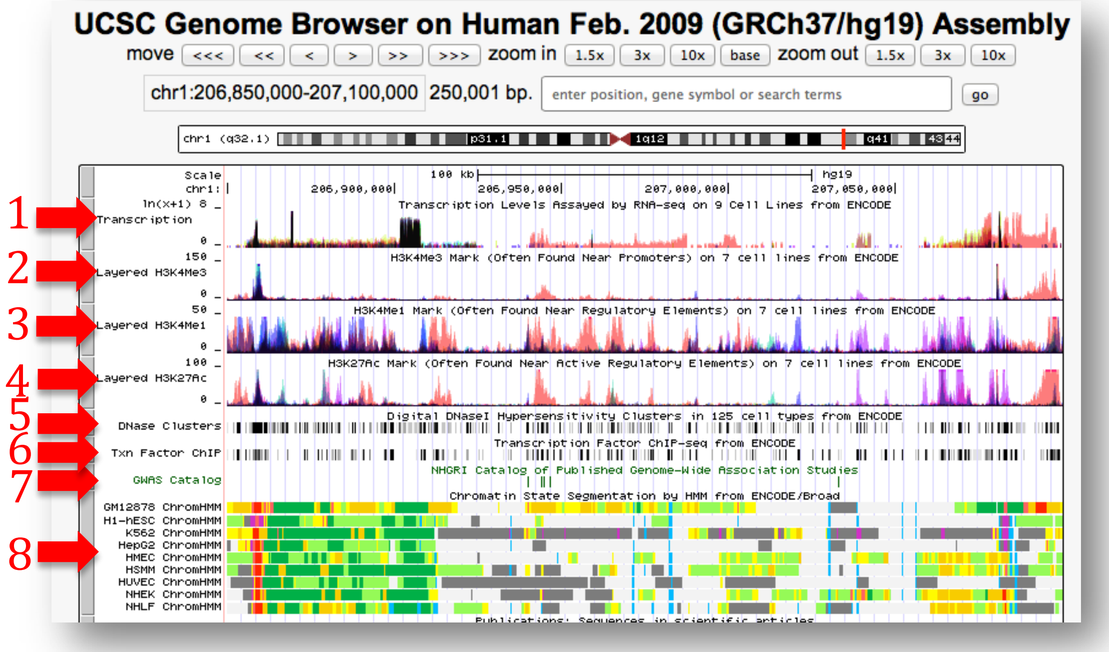
Save Settings

Save current settings to a local file:
file: file type returned: plain text submit
(leave file blank to get output in browser window)

Restore Settings

Use settings from another user's saved session:
user: session name: submit
Use settings from a local file: Choose File no file selected submit
Use settings from a URL (http://..., ftp://...): submit

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.


UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr1:206,850,000-207,100,000 250,001 bp.

The Transcription track (arrow 1) displays ENCODE RNA-seq data from 9 cell types, color-coded by cell type. The H3K4me3 Track (arrow 2) displays data for a histone modification frequently found at promoters. The H3K4me1 Track (arrow 3) displays a histone modification frequently found at enhancers. The H3K27ac Track (arrow 4) displays a histone modification frequently found at active enhancers and active promoters. The DNase Clusters track (arrow 5) displays DNase Hypersensitive sites, a marker of open or active chromatin, from 125 cell types. The Txn Factor ChIP track (arrow 6) displays regions of transcription factor binding. The GWAS catalog is displayed (arrow 7). ENOCDE chromatin states (arrow 8) are displayed one row for each cell type. Possible activity of a regions is color-coded; for example, active promoters are red, active gene bodies are dark green or light green, candidate regulatory regions are orange or yellow, and repressed regions are gray.