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 (<u>http://www.genome.gov/27553901</u>), download the session file from at the link: <u>A standard session for viewing ENCODE</u> <u>data</u>

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 <u>http://encodeproject.org/</u> or the UCSC browser



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:



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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):

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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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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.



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.