Viewing Human ENCODE ChIP-seq Data

(Updated October 2013)

ENCODE has a wide variety of ChIP-seq data available for a wide assortment of cell types. The ChIP-seq Matrix provides access to, and a quick visual summary of, what is available.

1) Navigate to the Human Experiment Matrix from the ENCODE portal:

Go to http://encodeproject.org/ or the UCSC browser. Directly select the Human Experiment Matrix link (bottom arrow).
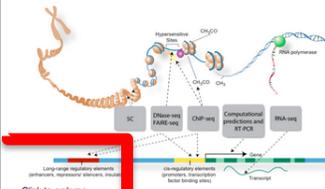
Alternatively visit the Resources & FAQ page link (top arrow) first. Notice other useful links (such as to Tutorials, Cell Types, Antibodies, Publications, and Track and File Search). Click the link to the Human Experiment Matrix.

2) From the Experiment Matrix click one of the links to the ChIP-seq Matrix.

3) Choose the corresponding Antibody Target and Cell Type of interest, such as ATF3 in K562 cells (select tracks to view data, or files to download).

4) Alternatively Click the Experiment Summary link to select a ChIP factor across cell types.

5) From the resulting ChIP-seq Matrix click through to the Track Search page, change the visibility of the desired tracks from hide to pack (left arrow).

Alternatively, modify or add new Track Search parameters (right arrow).

6) Click the "View in Browser" button to see track displayed. Then click the left bar to click through to the related ChIP-seq Track Setting page.

7) From the Track Setting page, you can see other subtracks and options (such as setting a score range) as well as read the Track Description at the bottom.

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Description

This track represents a comprehensive set of human transcription factor binding sites based on ChIP-seq experiments generated by production groups in the ENCODE Consortium from the inception of the project in September 2007, through the March 2012 internal data freeze. The track represents peak calls (regions of enrichment) that were generated by the ENCODE Analysis Working Group (AWG) based on a uniform processing pipeline developed for the ENCODE Integrative Analysis effort and published in a set of coordinated papers in September 2012. Peak calls from that effort, based on datasets from the January 2011 ENCODE data freeze) are available at the ENCODE Analysis Data Hub. This track is an update that includes newer data, and slightly modified methods for the peak calling.

This track contains 690 ChIP-seq datasets representing 161 unique regulatory factors (generic and sequence-specific factors). The datasets span 91 human cell types and some are in various treatment conditions. These datasets were generated by the five ENCODE TFBS ChIP-seq production groups: Broad, Stanford/Yale/UC-Davis/Harvard, HudsonAlpha Institute, University of Texas-Austin and University of Washington, and University of Chicago. The University of Chicago ChIP-seq were performed with an alternative epitope-tagged ChIP-seq methodology. The primary and lab-processed data (along with methods descriptions, credits and references) on which this track is based are available in the following ENCODE tracks: HAIB TFBS, SYDH TFBS, UChicago TFBS, UTA TFBS, UW CTCF Binding. These tracks are accessible from the ENC TF Binding Super-track.