

Description

This track was produced as part of the ENCODE Project. This track displays maps of genome-wide binding of the CTCF transcription factor in different [cell lines](#) using ChIP-seq high-throughput sequencing.

Display Conventions and Configuration

This track is a multi-view composite track that contains multiple data types (*views*). For each view, there are multiple subtracks that display individually on the browser. Instructions for configuring multi-view tracks are [here](#).

For each cell type, this track contains the following views:

HotSpots

ChIP-seq affinity zones identified using the HotSpot algorithm.

Peaks

ChIP-seq affinity sites identified as signal peaks within affinity zones (FDR 1.0%).

Raw Signal

The density of tags mapping within a 150 bp sliding window (at a 20 bp step across the genome).

Metadata for a particular subtrack can be found by clicking the down arrow in the list of subtracks.

Methods

Cells were grown according to the approved [ENCODE cell culture protocols](#). Cells were crosslinked with 1% formaldehyde, and the reaction was quenched by the addition of glycine. Fixed cells were rinsed with PBS, lysed in nuclei lysis buffer, and the chromatin was sheared to 200-500 bp fragments using Fisher Dismembrator (model 500). Sheared chromatin fragments were immunoprecipitated with specific polyclonal antibodies at 4 °C with gentle rotation. Antibody-chromatin complexes were washed and eluted. The cross linking in immunoprecipitated DNA was reversed and treated with RNase-A. Following proteinase K treatment, the DNA fragments were purified by phenol-chloroform-isoamyl alcohol extraction and ethanol precipitation. A quantity of 20-50 ng of ChIP DNA was end-repaired, adenine ligated to Illumina adapters was added, and a Solexa library was made for sequencing.

ChIP-seq affinity was directly measured through raw tag density (*Raw Signal*), which is shown in the track as density of tags mapping within a 150 bp sliding window (at a 20 bp step across the genome). ChIP-seq affinity zones (*HotSpots*) were identified using the HotSpot algorithm described in Sabo *et al.* (2004); 1.0% false discovery rate thresholds (FDR 0.01) were computed for each cell type by applying the HotSpot algorithm to an equivalent number of random uniquely mapping 36mers. ChIP-seq affinities (*Peaks*) were identified as signal peaks within affinity zones (FDR 1.0%) using a peak-finding algorithm.

All tracks have a False Discovery Rate of 1% (FDR 1.0%).

Verification

Data were verified by sequencing biological replicates displaying correlation coefficients > 0.9 .

Release Notes

Release 3 (February 2012) contains 3 new experiments.

Credits

These data were generated by the UW ENCODE group.

Contact: [Richard Sandstrom](#)

References

Sabo PJ, Hawrylycz M, Wallace JC, Humbert R, Yu M, Shafer A, Kawamoto J, Hall R, Mack J, Dorschner MO *et al.* [Discovery of functional noncoding elements by digital analysis of chromatin structure](#). *Proc Natl Acad Sci U S A*. 2004 Nov 30;101(48):16837-42.

Data Release Policy

Data users may freely use ENCODE data, but may not, without prior consent, submit publications that use an unpublished ENCODE dataset until nine months following the release of the dataset. This date is listed in the *Restricted Until* column, above. The full data release policy for ENCODE is available [here](#).