Description

This track was produced as part of the ENCODE Project. This track displays genome-wide maps of histone modifications 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 FDR 1.0% affinity zones.

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 cross-linked 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 a 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 the 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, followed by addition of adenine, ligation to Illumina adapters, and creation of a Solexa library for sequencing.

ChIP-seq affinity was directly measured through the 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). One percent false discovery rate thresholds (FDR 1.0%) were computed for each cell type by applying the HotSpot algorithm to an equivalent number of random uniquely mapping 36-mers. ChIP-Seq affinities (*Peaks*) were identified as signal peaks within FDR 1.0% hypersensitive zones 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 a correlation coefficient greater than 0.9.

Release Notes

Release 5 (July 2012) of this track removes experiments with K562/Zinc finger knockouts and adds in some missing inputs.

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.