Description

This track shows probable binding sites of the specified transcription factors (TFs) in the given cell types as determined by chromatin immunoprecipitation followed by high throughput sequencing (ChIP-seq). Included for each cell type is the input signal, which represents the control condition where no antibody targeting was performed. For each experiment (cell type vs. antibody) this track shows a graph of enrichment for TF binding (*Signal*), along with sites that have the greatest evidence of transcription factor binding (*Peaks*).

The sequence reads, quality scores, and alignment coordinates from these experiments are available for download.

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. ENCODE tracks typically contain one or more of the following views:

Peaks
: Regions of signal enrichment based on processed data (normalized data from pooled replicates). ENCODE Peaks tables contain fields for statistical significance, including the minimum false discovery rate (FDR) threshold at which the test may be called significant (qValue).

Signal
: Density graph (wiggle) of signal enrichment based on processed data.

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. Further preparations were similar to those previously published (Euskirchen *et al.*, 2007) with the exceptions that the cells were unstimulated and sodium orthovanadate was omitted from the buffers. For details on the chromatin immunoprecipitation protocol used, see (Euskirchen *et al.*, 2007) and (Rozowsky *et al.*, 2009).

DNA recovered from the precipitated chromatin was sequenced on the Illumina (Solexa) sequencing platform and mapped to the genome using the Eland alignment program. ChIP-seq data was scored based on sequence reads (length ~30 bp) that align uniquely to the human genome. From the mapped tags a signal map of ChIP DNA fragments (average fragment length ~ 200 bp) was constructed where the signal height is the number of overlapping fragments at each nucleotide position in the genome.

For each 1 Mb segment of each chromosome a peak height threshold was determined by requiring a false discovery rate less than or equal to 0.05 when comparing the number of peaks above threshold as compared the number obtained from multiple simulations of a random null background with the same number of mapped reads (also accounting for the fraction of mapable bases for sequence tags in that 1 Mb segment). The number of mapped tags in a putative binding region is compared to the normalized (normalized by correlating tag counts in genomic 10 kb windows) number of mapped tags in the same region from an input DNA control. Using a binomial test, only regions that have a p-value less than or equal to 0.05 are considered to be significantly enriched compared to the input DNA control.

Release Notes

This is Release 3 (August 2012). This release adds in 37 new experiments including 1 new cell line and 7 new antibodies.

Credits

These data were generated and analyzed by the labs of Michael Snyder at Stanford University; Mark Gerstein and Sherman Weissman at Yale University; Peggy Farnham at University of Southern California; and Kevin Struhl at Harvard.

Contact: Philip Cayting.

References

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Publications

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Linnemann AK, O'Geen H, Keles S, Farnham PJ, Bresnick EH. Genetic framework for GATA factor function in vascular biology. *Proc Natl Acad Sci U S A*. 2011 Aug 16;108(33):13641-6.

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 on the track configuration page and the download page. The full data release policy for ENCODE is available here.