

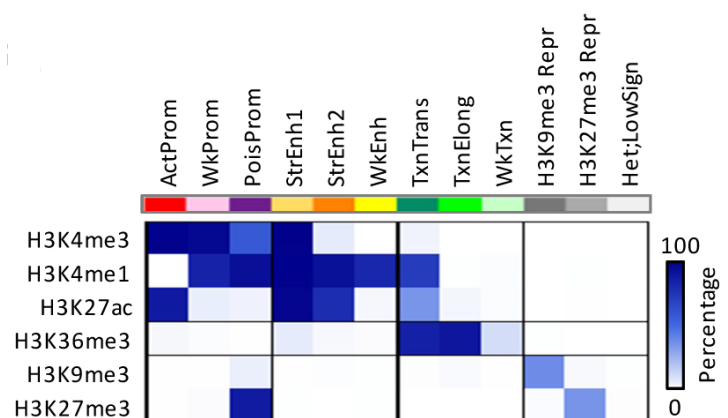
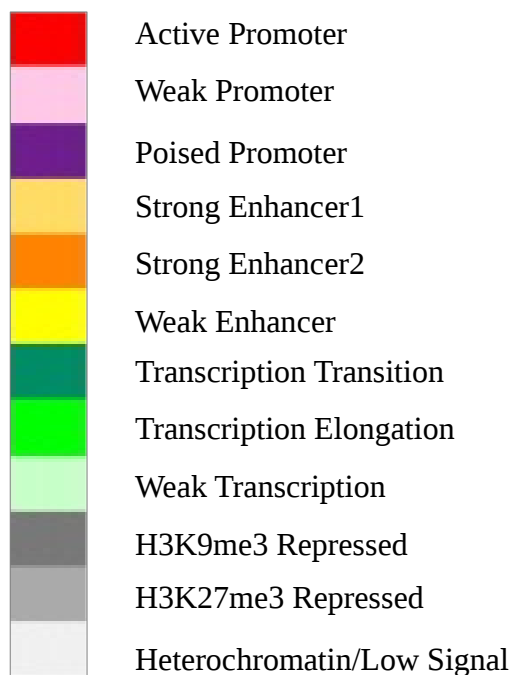
The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia

UCSC Genome Browser Tracks Description

Individual tracks

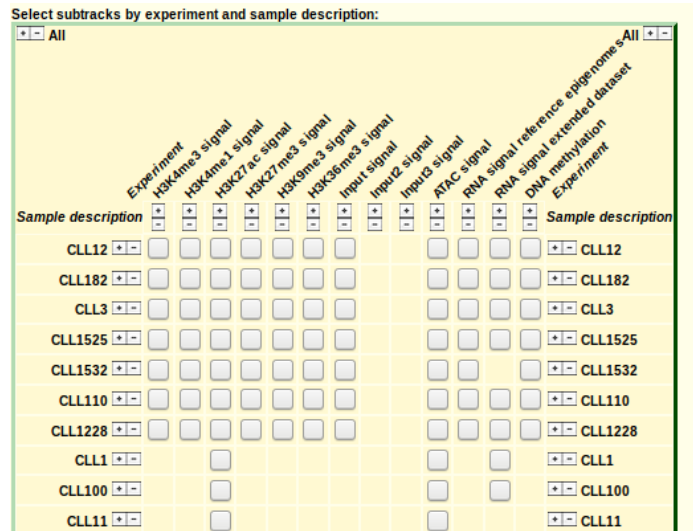
ChromHMM

The ChromHMM track shows the chromatin states for the 7 CLL and 15 normal B-cell samples from the reference epigenome. Colors codes are described below:



Epigenome CLL

Individual sample signals of H3K4me3, H3K4me1, H3K27ac, H3K27me3, H3K9me3, H3K36me3, input, ATAC-seq, RNA-seq and DNA methylation can be shown in the browser. In order to configure this track, click on “Epigenome_CLL” and select the desired subtracks.



Summary tracks

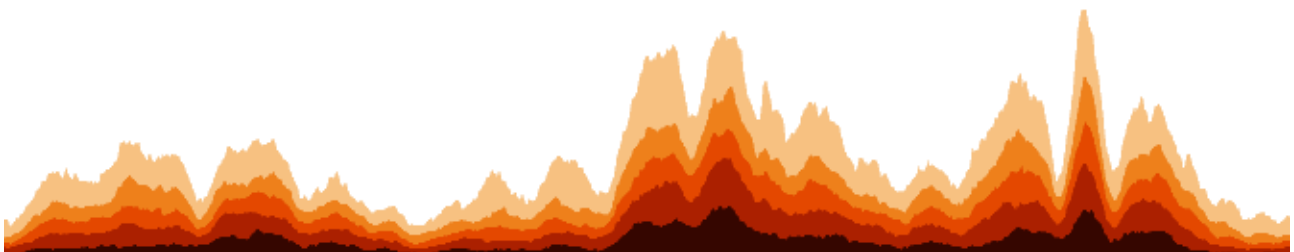
This section includes the median signal intensity from different populations of samples for different experiments:

Reference epigenomes. It shows separately the median signal of the 7 CLLs and the 15 normal B cells. For H3K27ac and ATAC-seq it also includes the median signal of the different subpopulations of B cells analyzed, that is, naive B cells from blood, naive B cells from tonsil, germinal center B cells, plasma cells and memory B cells.

Extended dataset: The extended set of CLLs analyzed for H3K27ac, ATAC-seq and RNA-seq. They are presented for all the CLL samples as well as for the subgroups of U-CLL and M-CLL, respectively CLLs with unmutated and mutated IGHV.

Overlay tracks

This section includes overlay tracks with the 5th, 25th, 50th, 75th and 95th percentiles of signal intensity for different sample populations and experiment groups. The darker color in the track corresponds to the 5th percentile whereas the lighter color represents the 95th percentile.



It is possible to select which percentiles are displayed by configuring the tracks.