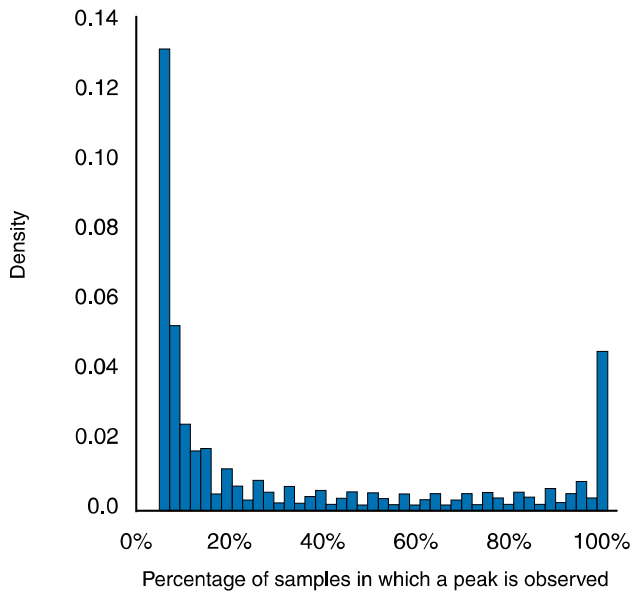
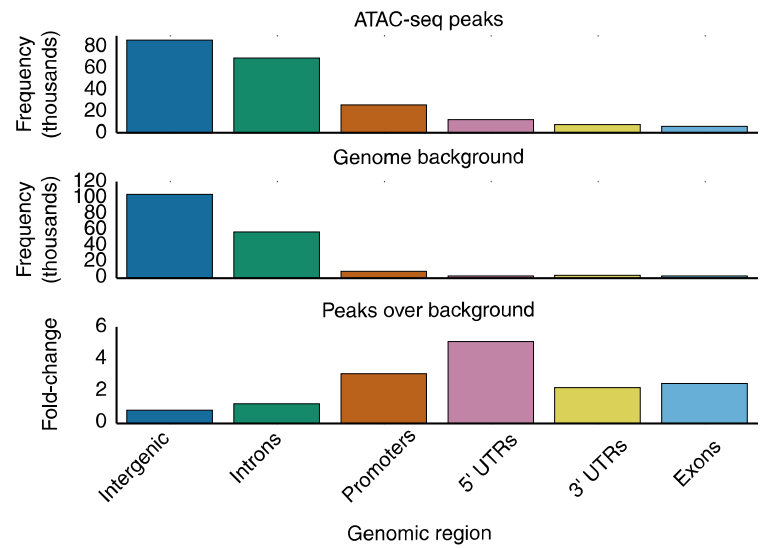


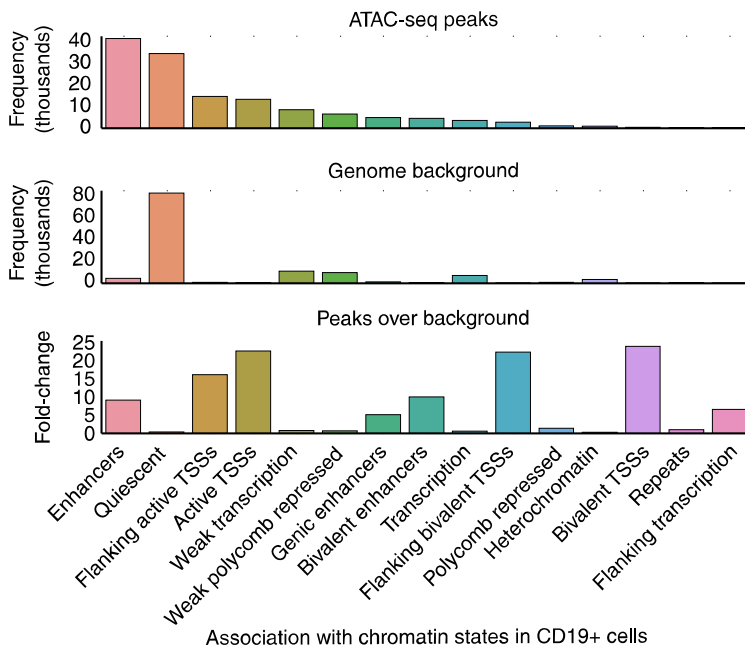
a



b



c



Supplementary Figure 4

Chromatin-accessible regions in CLL are enriched for promoters and enhancers.

a) Histogram showing the number of samples in which a given chromatin-accessible region from the CLL consensus map was detected as a significant ATAC-seq peak. b) Frequency of overlap and enrichment of Ensembl gene annotation for regions in the CLL consensus map, compared to region sets of identical size and lengths that were randomized 1,000 times across the genome. c) Frequency of overlap and enrichment of chromatin state segmentations for CD19+ B cells (data from the Roadmap Epigenomics project), compared to region sets of identical size and lengths that were randomized 1,000 times across the genome.