

Supplementary Figure 9

Subtype-specific signature regions overlap with differential ATAC-seq peaks.

a) Venn diagrams showing the overlap between CLL subtype-specific regions identified by the machine learning analysis (left) compared to those identified by differential peak analysis between mCLL and uCLL using DESeq2. b) Scatterplot (left), volcano plot (center) and MA plot (right) comparing the two analytical approaches across all chromatin-accessible regions.