



Supplementary Figure 20

Disease subtype-specific networks detect differentially regulated genes and genomic regions.

a) Violin plots showing the distribution of ChIPmentation levels for each histone mark in regulatory regions associated with genes that are differentially connected between the subtype-specific networks. b) Violin plots showing the ratio between the ChIPmentation signal for histone marks associated with active (H3K4me1, H3K27ac) over repressed (H3K27me3) chromatin. c) Subnetworks with the neighbors of PAX9 and CD22, shown separately for the mCLL and uCLL networks. Edge width indicates the strength of the connection as measured by the calculated interaction score. d) ATAC-seq and ChIPmentation signal for three histone marks at representative differentially connected genes between the mCLL and uCLL networks. In panel a and b, significance was assessed using the Mann-Whitney U test, and comparisons with p -values above 0.05 were labeled as not significant (n.s.).