



Supplementary Figure 6

Unsupervised analysis identifies IGHV mutation status as a key source of variation.

Principal component analysis based on the chromatin accessibility for all 88 samples at each of the 112,298 chromatin-accessible regions in the CLL cohort. The first five principal components are plotted, and samples are colored according to clinical annotations and molecular diagnostics data (top four rows) as well as the sample processing batch for the ATAC-seq experiments (bottom row).