



**Supplementary Figure 5**

*Heterogeneity in chromatin accessibility affects genes related to B cells and CLL.*

a) Histogram showing the percentage of chromatin-accessible regions that are shared between any two CLL samples. b) Distribution of variance in chromatin accessibility for promoter regions and putative distal regulatory regions across all genes (grey) and for a set of genes with a known role in B cell biology and/or CLL pathogenesis (blue/green). Chromatin accessibility scores were averaged across all regulatory regions assigned to a given gene. c) Violin plots of normalized chromatin accessibility values for gene promoters (regions located within 2,500 basepairs of the transcription start site) and distal regulatory elements (regions located at least 2,500 basepairs away from the nearest transcription start site) for the same genes as in panel b.