



Supplementary Figure 7

Chromatin accessibility is linked to differences in gene expression and DNA methylation.

a) Hexbin scatterplot visualizing the weak correlation (Pearson's $r = 0.33$) between gene expression levels and the chromatin accessibility at associated regulatory regions. Shown are averages across ten samples with matched ATAC-seq and RNA-seq data. The color gradient is on a logarithmic scale. b) Pearson correlation (top) and significance of the association (bottom) between gene expression levels and chromatin accessibility values at associated regulatory regions, plotted over the distance of the accessible region to the gene's transcription start site. c) Mean chromatin accessibility across CLL-accessible regions associated with genes that were upregulated in *IGHV*-mutated or in *IGHV*-unmutated CLL. d) Mean chromatin accessibility in CLL-accessible regions that overlap with regions described as hypermethylated in *IGHV*-mutated or in *IGHV*-unmutated CLL (Kulis et al. 2012 Nature Genetics).