



Supplementary Figure 2

Observed ATAC-seq fragment length distributions indicate high data quality.

Distribution of ATAC-seq fragment lengths for published GM12878 data (Buenrostro et al. 2013 Nature Methods) and for four randomly selected CLL samples from this study. Fragment lengths were inferred based on paired-end sequencing data. The characteristic patterns of nucleosome-associated fragment length are observed in all samples.