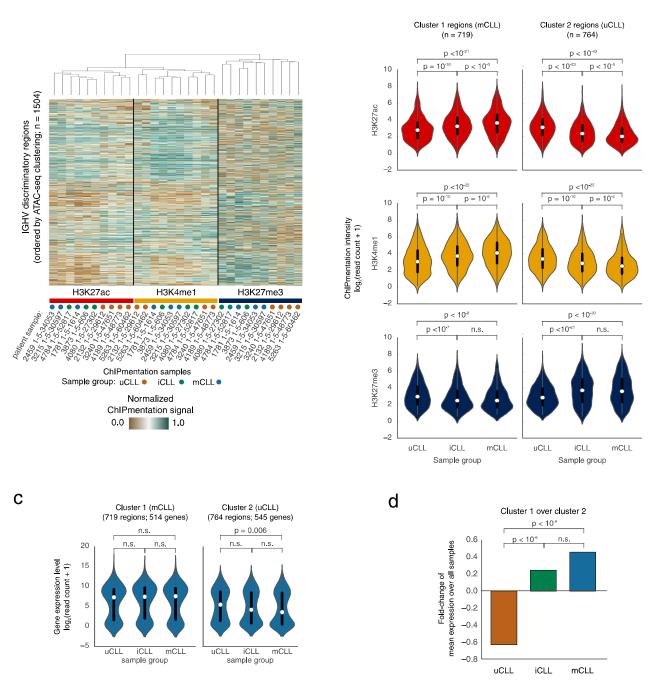**Supplementary Figure 15**

Histone marks and gene expression confirm the intermediate character of the iCLL sample cluster.

a) Hierarchical clustering and heatmap visualizing the ChIPmentation signal for three histone marks (H3K4me1, H3K27ac, H3K27me3) in ten CLL samples comprising three disease subtypes (mCLL, iCLL, uCLL). Regulatory regions were selected and sorted in the same way as in Figure 3c. b) Violin plots showing the distribution of ChIPmentation levels for each histone mark in the same regulatory regions as in panel a, grouped by disease subtype. In all panels, significance was assessed using the Mann-Whitney U test, and comparisons with p-values above 0.05 were labeled as not significant (n.s.). c) Mean gene expression values for genes associated with the regulatory regions from panel a, grouped by disease subtype. d) Barplot showing the mean fold change of genes associated with regulatory elements in cluster 1 (mCLL regions) over genes associated with cluster 2 (uCLL regions) across all genes, grouped by disease subtypes. Significance was assessed using the Mann-Whitney U test, and comparisons with p-values above 0.05 were labeled as not significant (n.s.).