



Supplementary Figure 14

Clustering based on CLL subtype-specific signature regions reflects IGHV mutation status.

Hierarchical clustering of all CLL samples based on sample-wise correlation of chromatin accessibility for the most discriminatory regions that were identified between the *IGHV*-mutated and the *IGHV*-unmutated disease subtype. The clustering tree is annotated with clinical data, and samples from the same patient are connected by curved black lines.