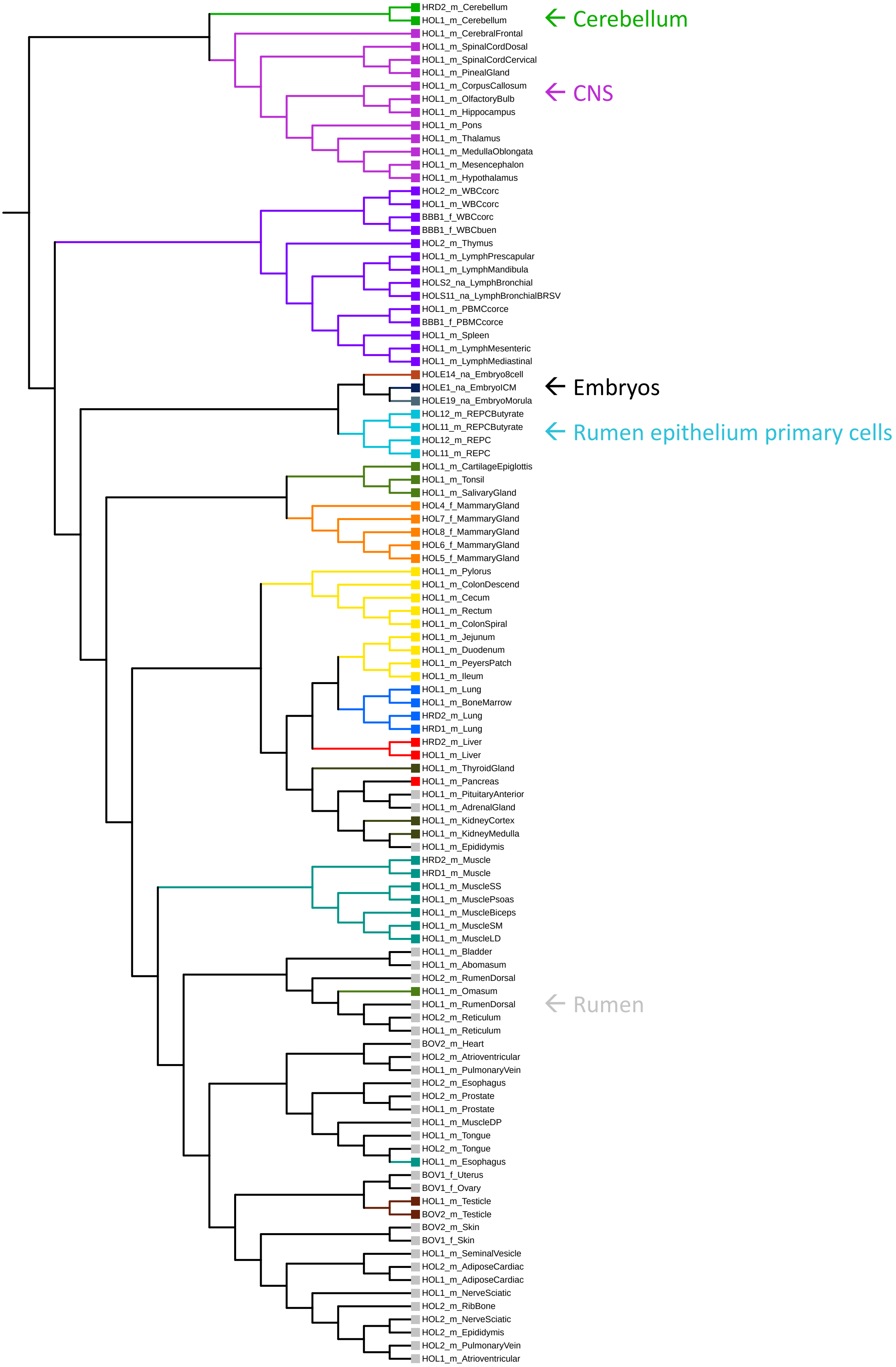

Supplemental Figure S7: Hierarchical clustering of the 104 samples using the Ward.D2 method implemented with the hclust R function, and the accessibility (measured as the fold-enrichment over genomic DNA background at the nucleotide position in the peak with the highest such value) of 934,972 distal (and hence more tissue specific) peaks. The samples are color-coded by their highest NMF component as in main Fig. 1A and F. Samples discussed in the main text are marked.