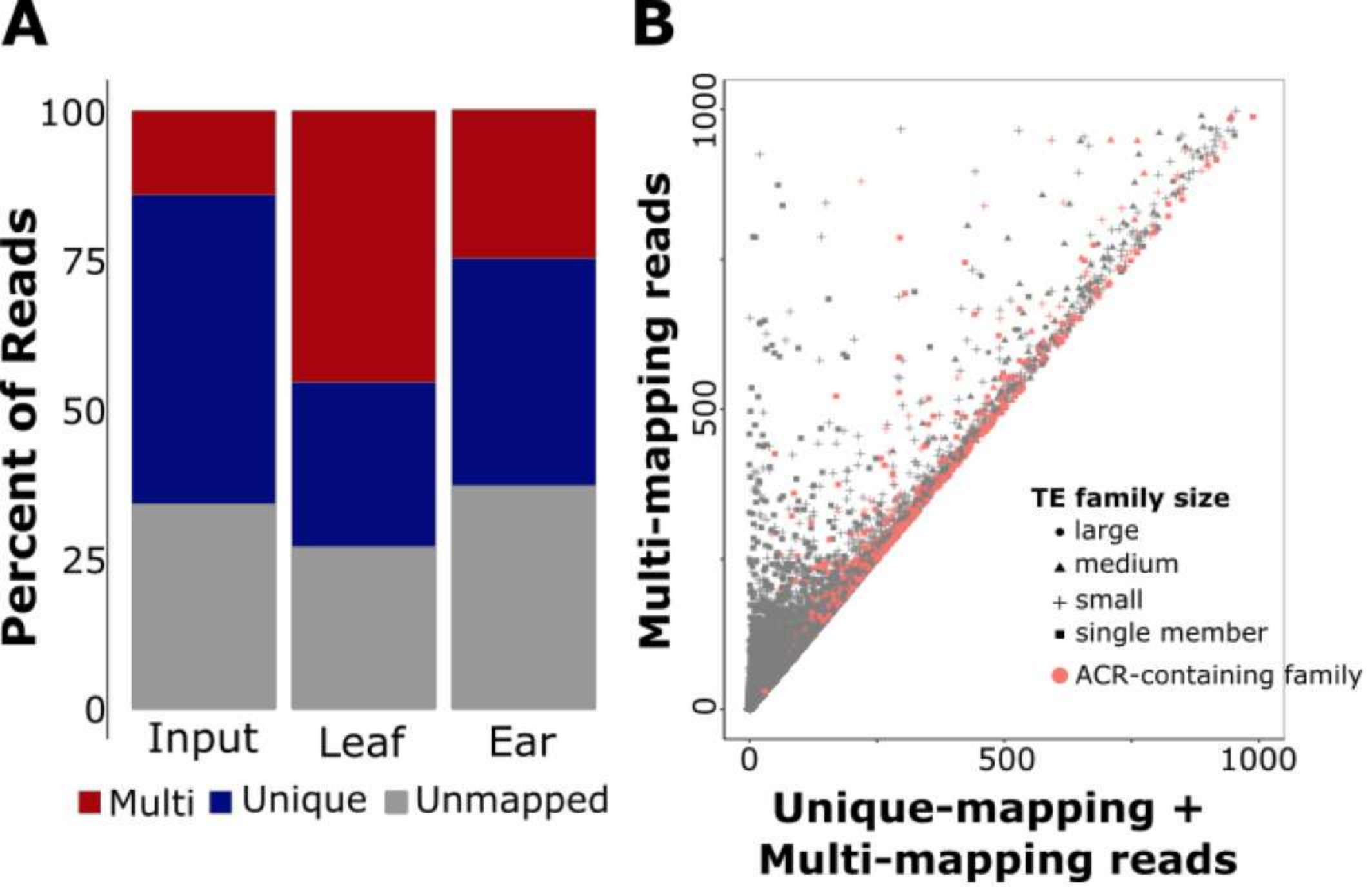

Figure S5: ATAC-seq unique and multi-mapping. A) Proportion of reads uniquely mapped, multi-mapped, or unmapped to the B73v4 genome for an input WGS dataset, ATAC-seq leaf dataset, and ATAC-seq ear dataset. B) Per family unique vs. multi-mapped read counts. Families defined by an ACR (based on unique mapping peak calling) are indicated in red.