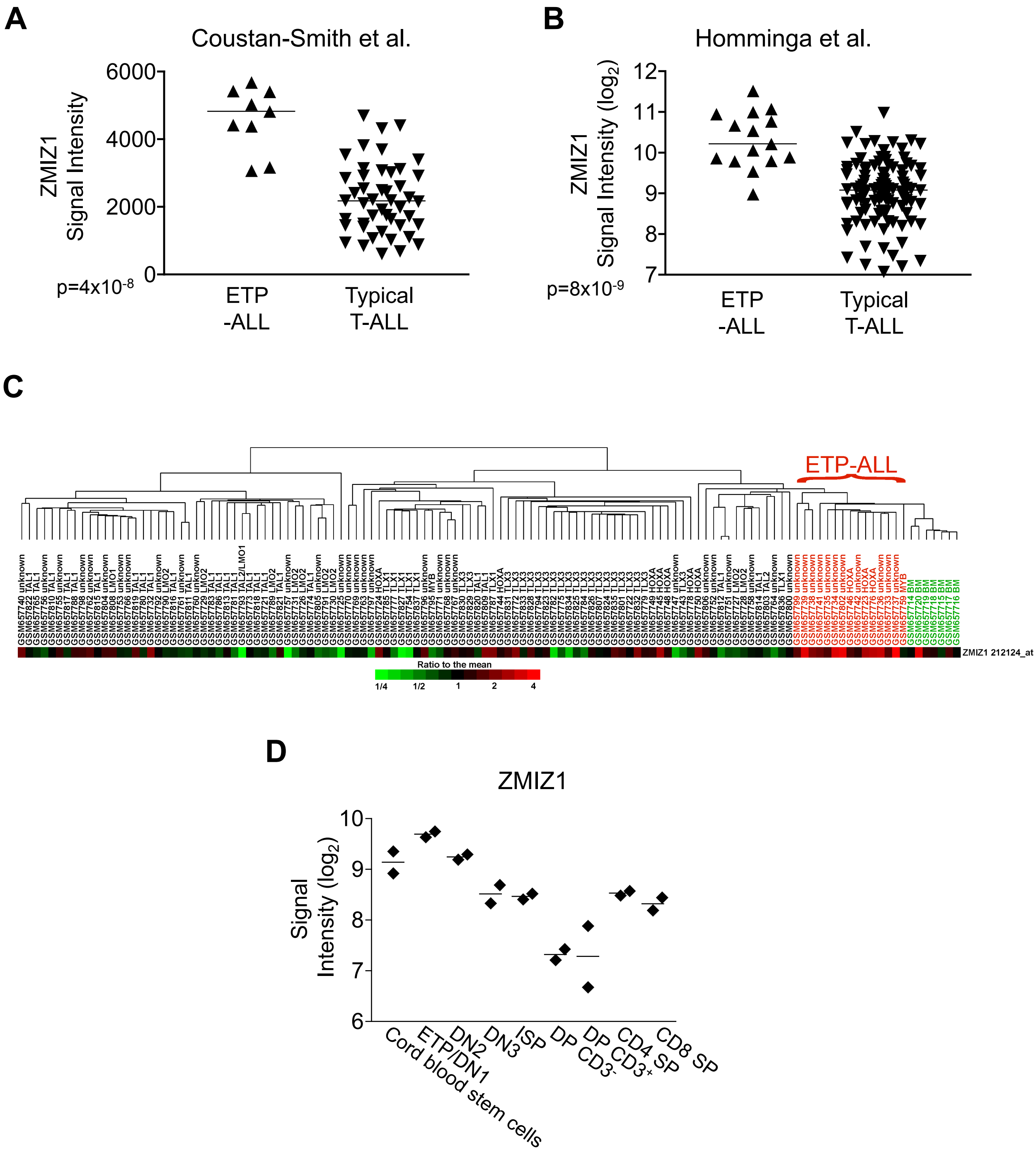

Figure S2. Gene expression profiling showing expression of ZMIZ1 in human T-ALL and normal thymopoiesis. (A) Gene expression of ZMIZ1 (212124_at) in the GSE8879 data set generated by Coustan-Smith et al.(28). GSE8879 contains data from 9 pediatric human primary ETP-ALL samples and 46 pediatric human primary typical T-ALL samples. (B) Gene expression of ZMIZ1 (212124_at) in the GSE26713 data set generated by Homminga et al.(29), which contains data from U133A_plus_2 GeneChips for 117 T-ALLs and 7 normal bone marrow samples from GEO series GSE26713. We performed a clustering analysis similar to (29) using Eisen "average" clustering based on Pearson correlation and the same 435 probe-set used by Homminga et al.(29). The resulting dendrogram and ZMIZ1 expression are shown in (C). 15 samples clustered as “immature” or “ETP-ALL.” (D) Gene expression of ZMIZ1 (212124_at) in GSE22601 generated by Dik and colleagues(30). GSE22601 contains data using U133A GeneChips on duplicate samples of sorted normal human thymic subsets and human CD34$^+$ cord blood cells.