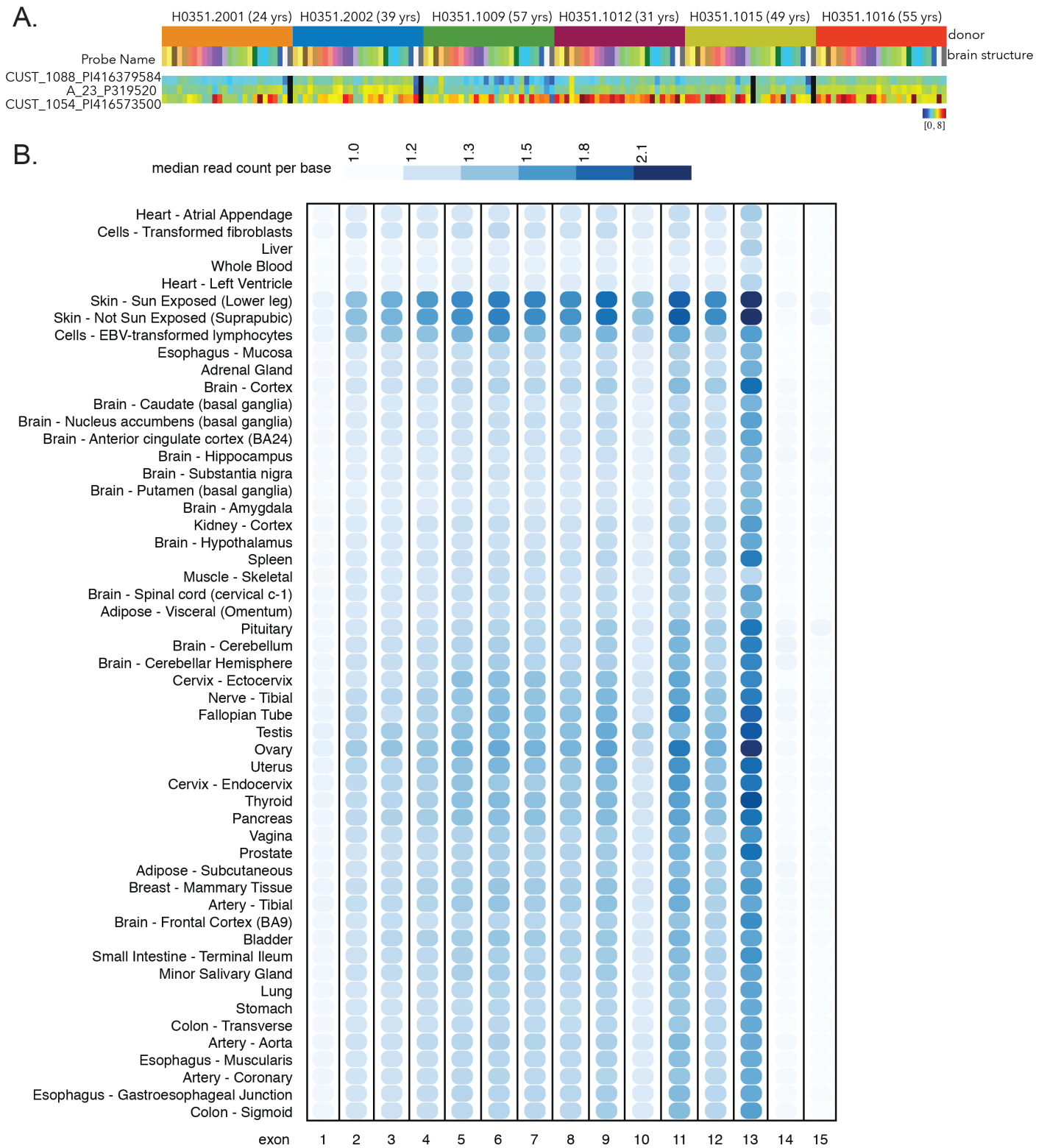
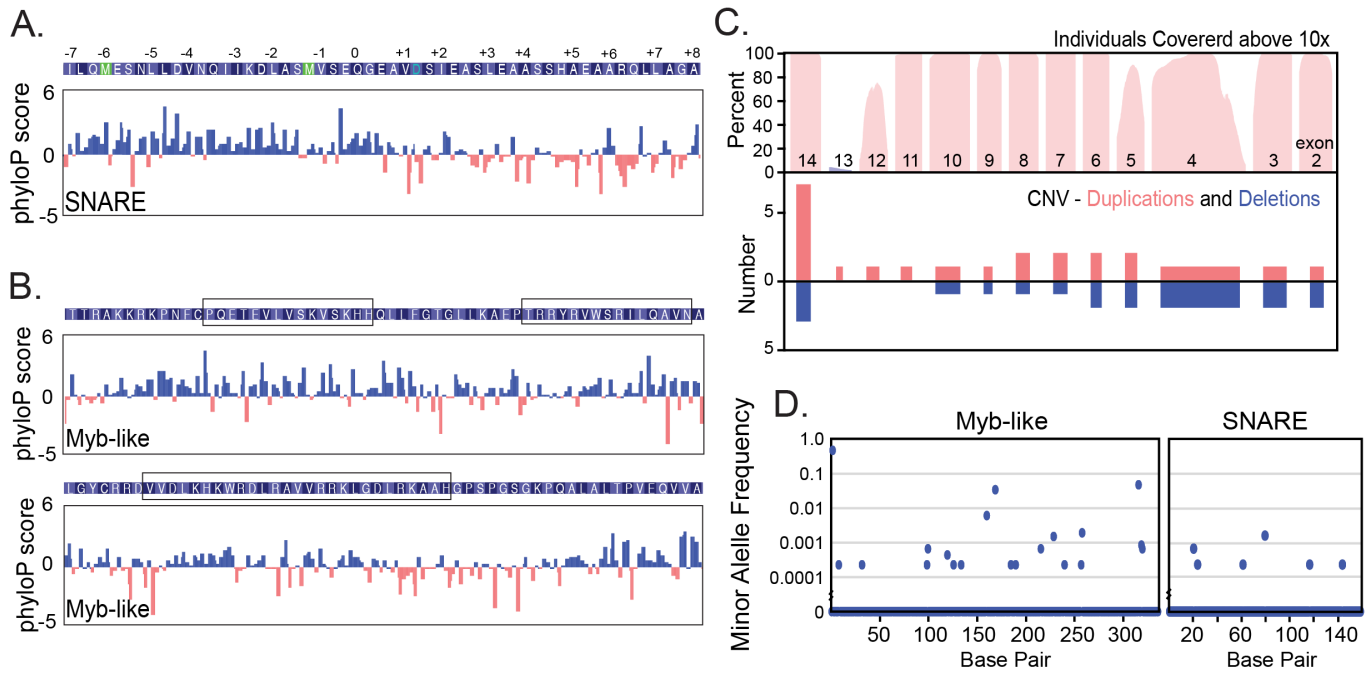


Supplementary Figure 1. *TSNARE1* gene expression by brain region. Brain microarray data displayed using the visualization tools on Allen Brain Atlas for *tSNARE1* enrichment in both (A) fetal and (B) adult brain.



Supplementary Figure 2. *TSNARE1* is alternatively spliced and the majority of transcripts lack a TM domain.

(A) Heat map of the log₂ intensity of the probe common to all *TSNARE1* isoforms (CUST_1054_P1416573500) and those probes that are contained within exon 14 (CUST_1088_P1416379584, A_23_P319520). (B) Heat map of the median read count per base from data adapted from GTEx.



Supplementary Figure 3. The SNARE and Myb-like domains of tSNARE1 are conserved. (A&B) phyloP scores computed from 100 vertebrate alignment per base of the (A) SNARE domain with the layers of interacting amino acids within the four-helical bundle marked and (B) the Myb-like domain with the predicted three helices boxed. (C) The percent of individuals with sequencing coverage above 10x at each base (top panel) and copy number variation (CNV) duplications and deletions (bottom) from the ExAC database. (D) The minor allele frequency (MAF) per base of each domain.