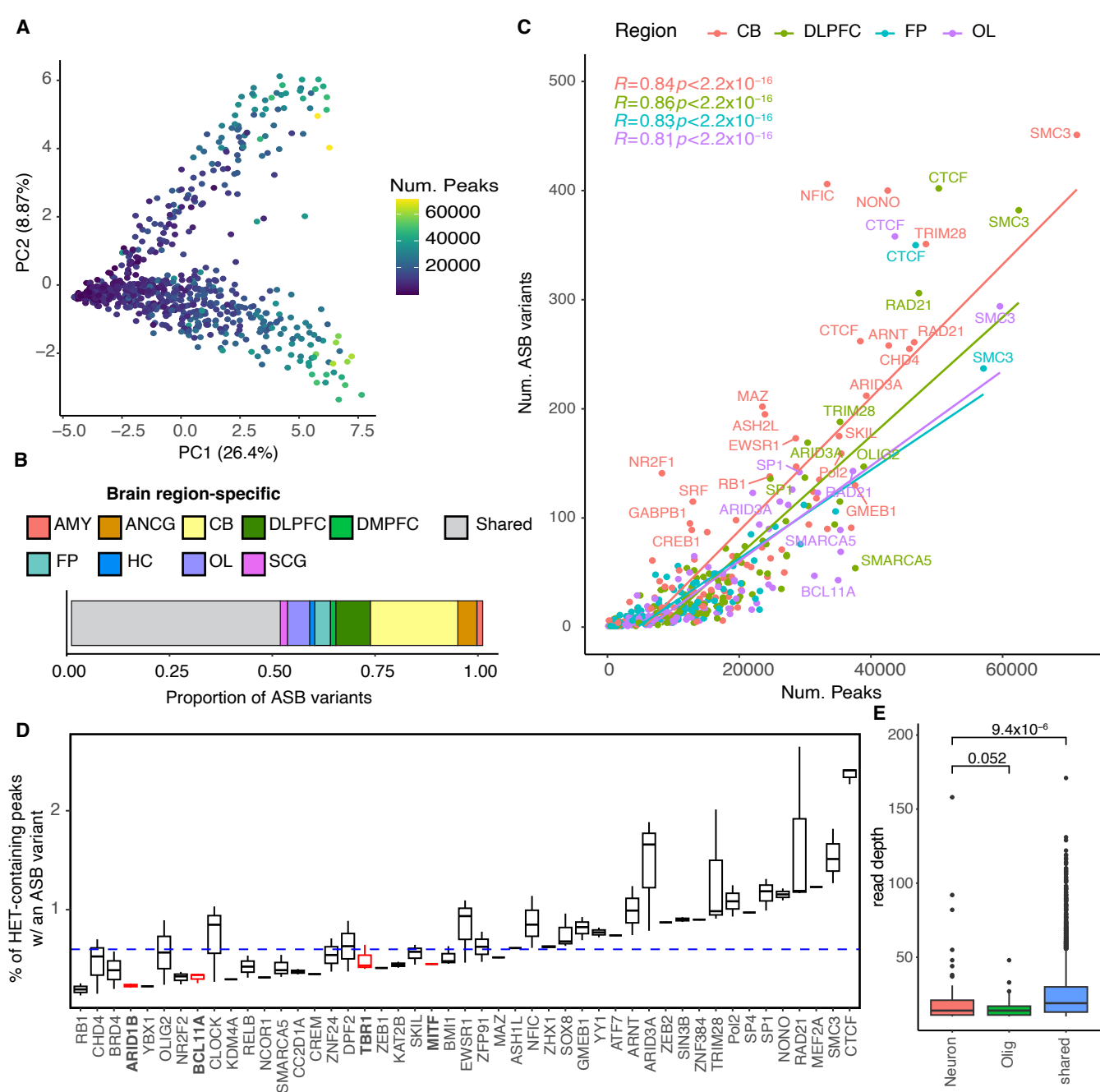




Supplemental Figure 4. Supplemental to Figure 3. A. PC1 and PC2 from a PCA analysis of $-\log_{10}(p\text{-values})$ of all ASB variant. Points (TF-brain region pairs) are colored by the number of peaks called for that dataset. **B.** The proportion of ASB variants that are shared across brain regions or specific to a particular brain region. **C.** The number of peaks called versus the number of ASB variants per ChIP-seq dataset for the 4 large brain regions. Line indicates the best fit line for each brain region. Pearson correlations are reported for each brain region. **D.** Distribution of the percentage of HET-containing peaks with an ASB by TF. Dashed line indicates the average percentage. Only TFs with at least 6,000 peaks are shown. **E.** Read depth at ASB variants overlapping snATAC-seq peaks