

## SUPPLEMENTARY TABLE

[Supplementary Table 1.xlsx]

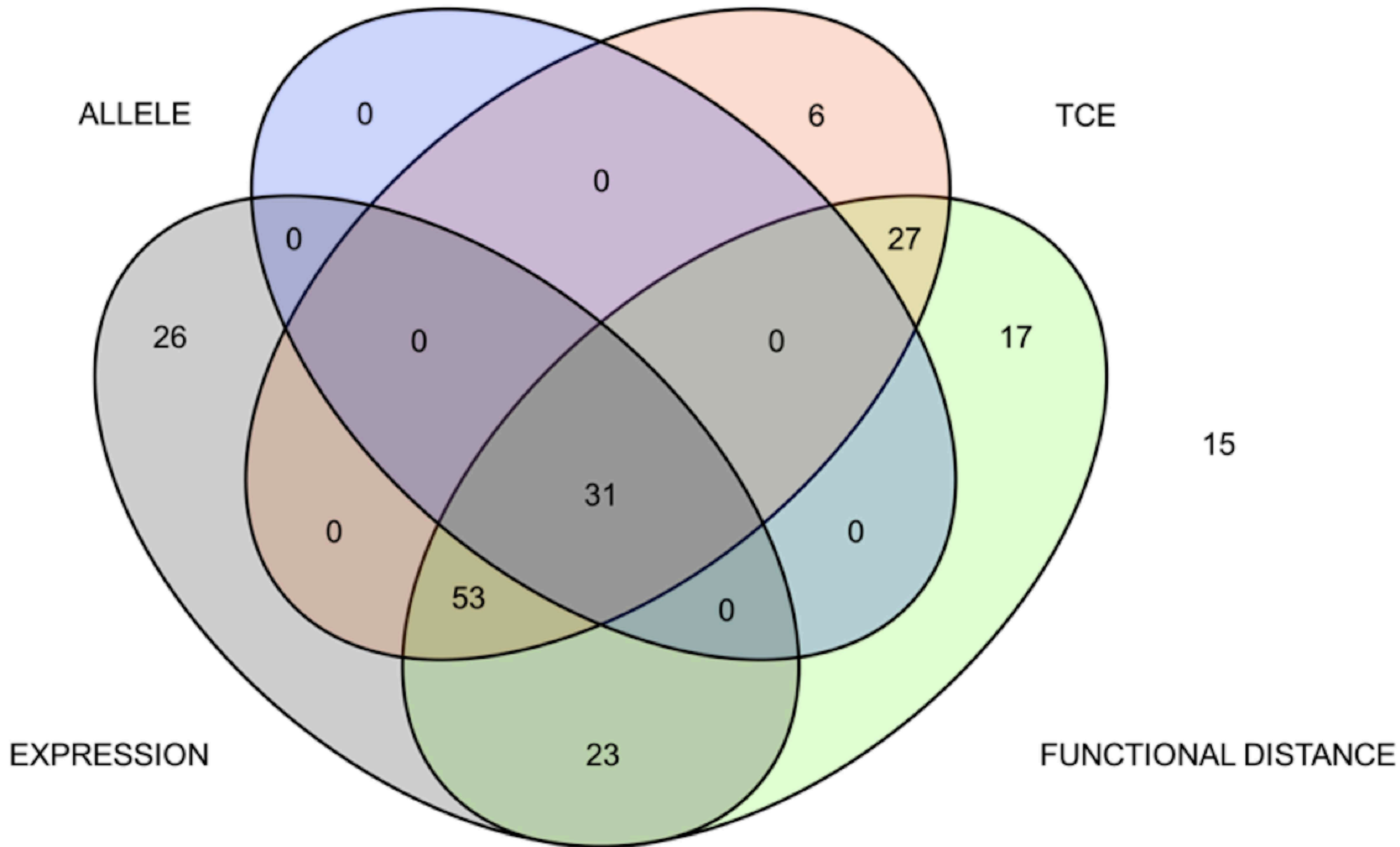
*Autosomal MiHAs do not associate with acute GVHD. Each row represents a single MiHA present in the whole genome sequencing (WGS) or microarray cohort (or both) with characterized restricted HLA allele, encoding single nucleotide polymorphism (SNP), gene, and counts in acute GVHD and non-GVHD groups. P-values were calculated, and multiple hypotheses corrected for, as described in Methods. MAF – minor allele frequency.*

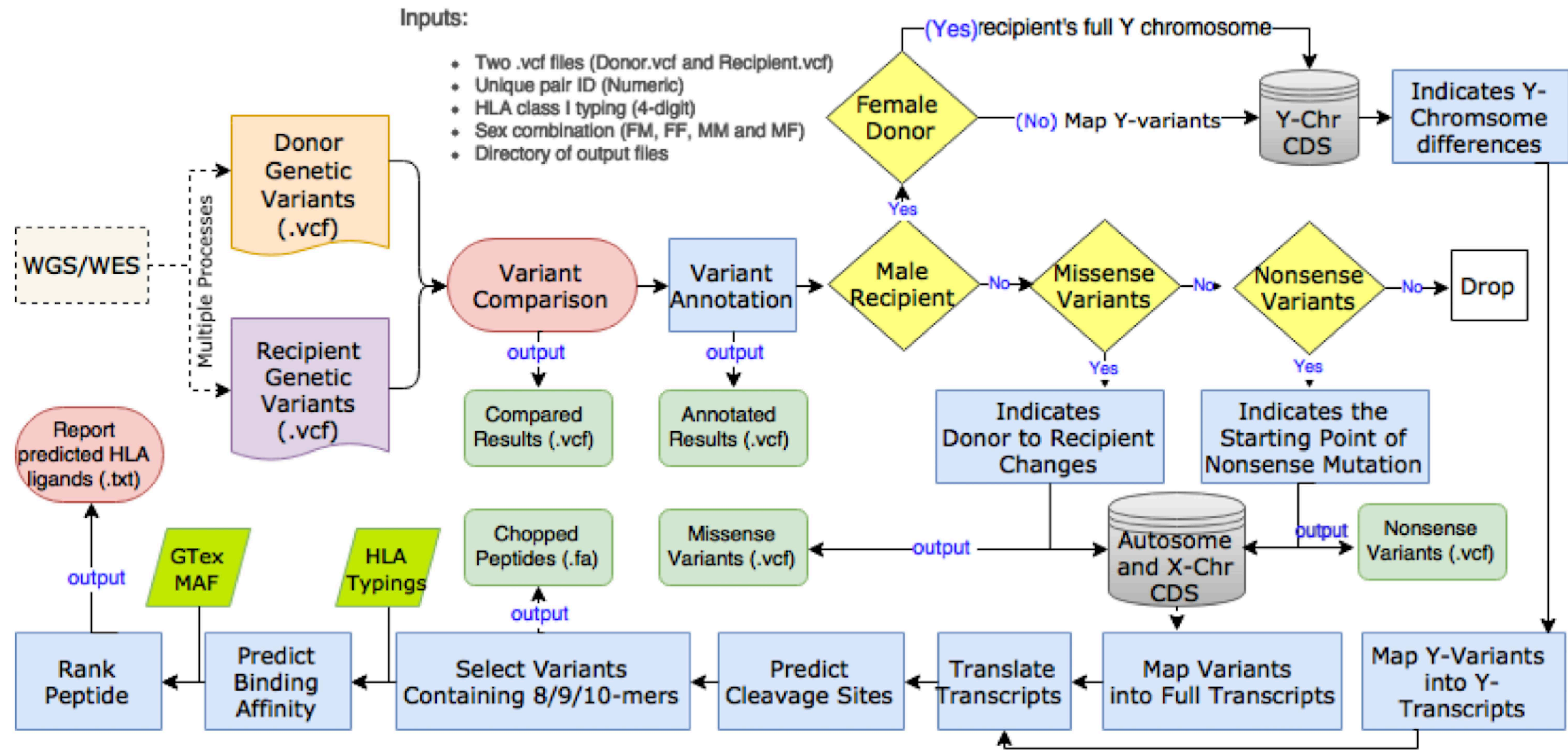
## SUPPLEMENTARY FIGURES

*Supplementary Figure 1: A Venn diagram shows individual counts in overlapping categories for donor-recipient pairs that were retrospectively matched at HLA-DPB1 by allele, T-cell epitope permissibility (TCE), expression, and functional distance.*

*Supplementary Figure 2: A genomic annotation workflow to identify known and novel outcomes-associated variants. Raw sequence data were processed as described (Methods) to generate a single binary alignment (BAM) and variant call format (VCF) file per sample. Comparative analysis of donor-recipient pairs resulted in a single VCF file containing patient-specific variants, which were annotated further. Male recipients with female donors were treated separately to analyze variants on the Y chromosome.*

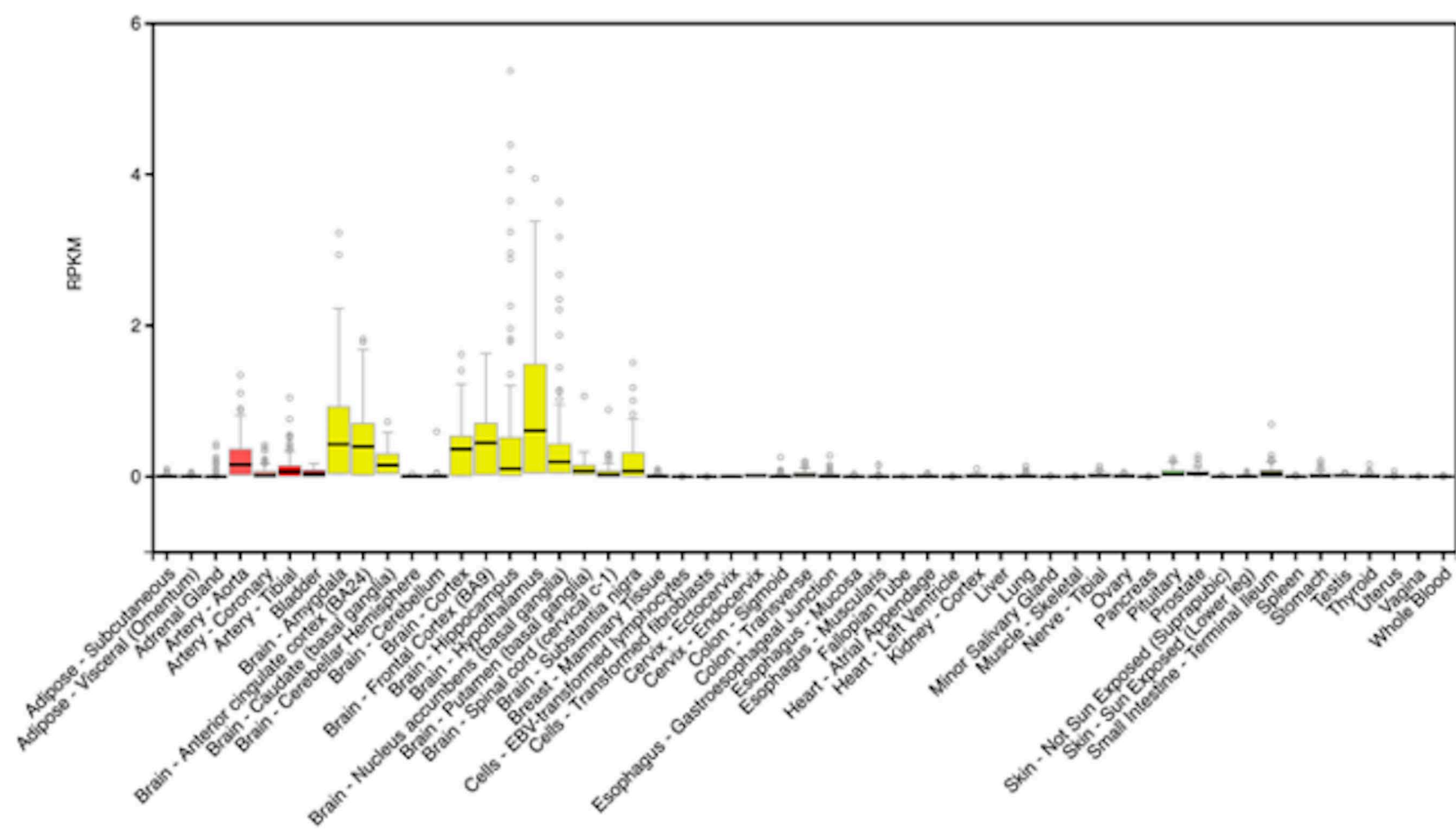
*Supplementary Figure 3: Tissue-specific gene expression for PCDH11Y (A), USP9Y (B), UTY (C), and NLGN4Y (D).*



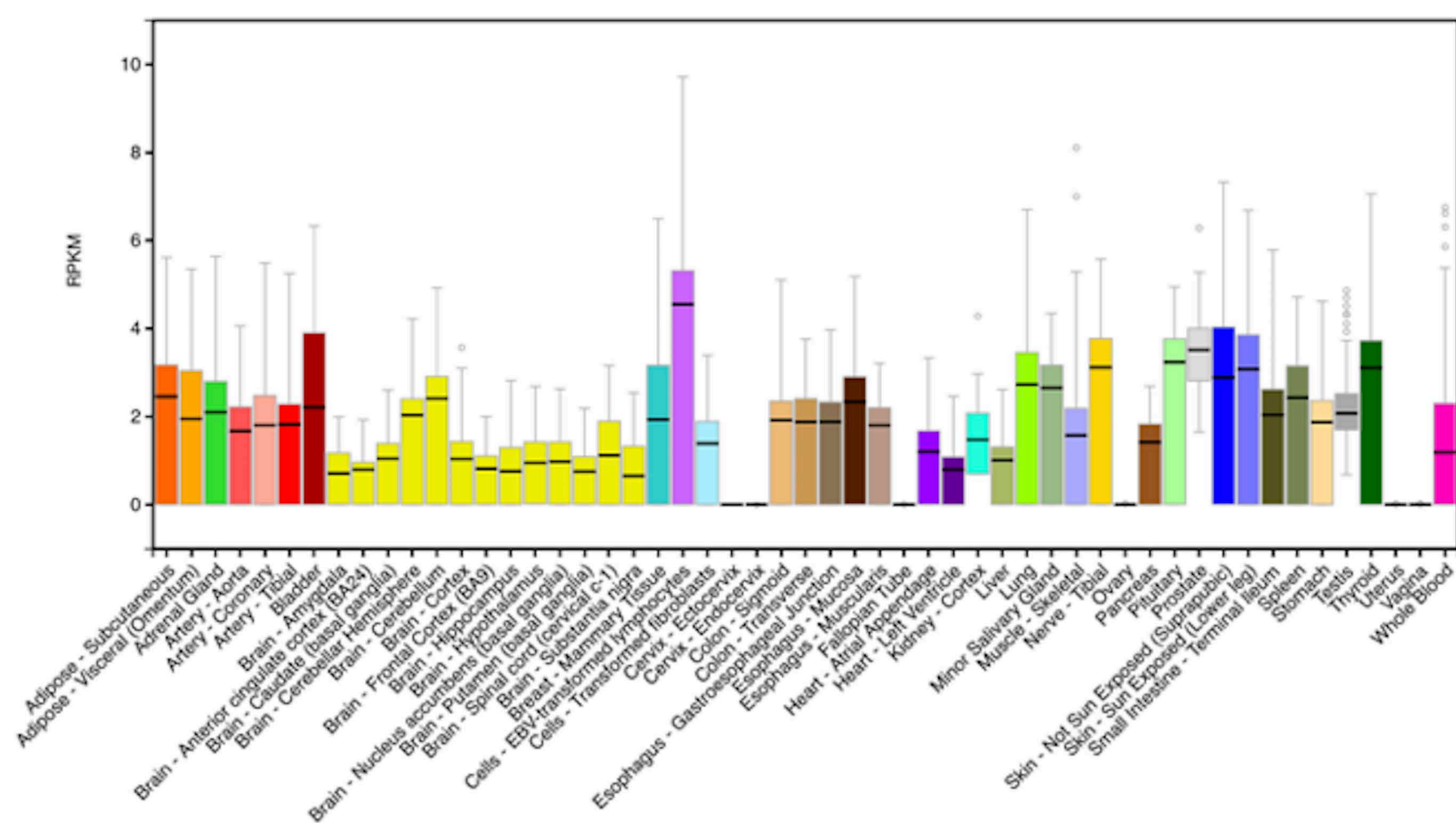




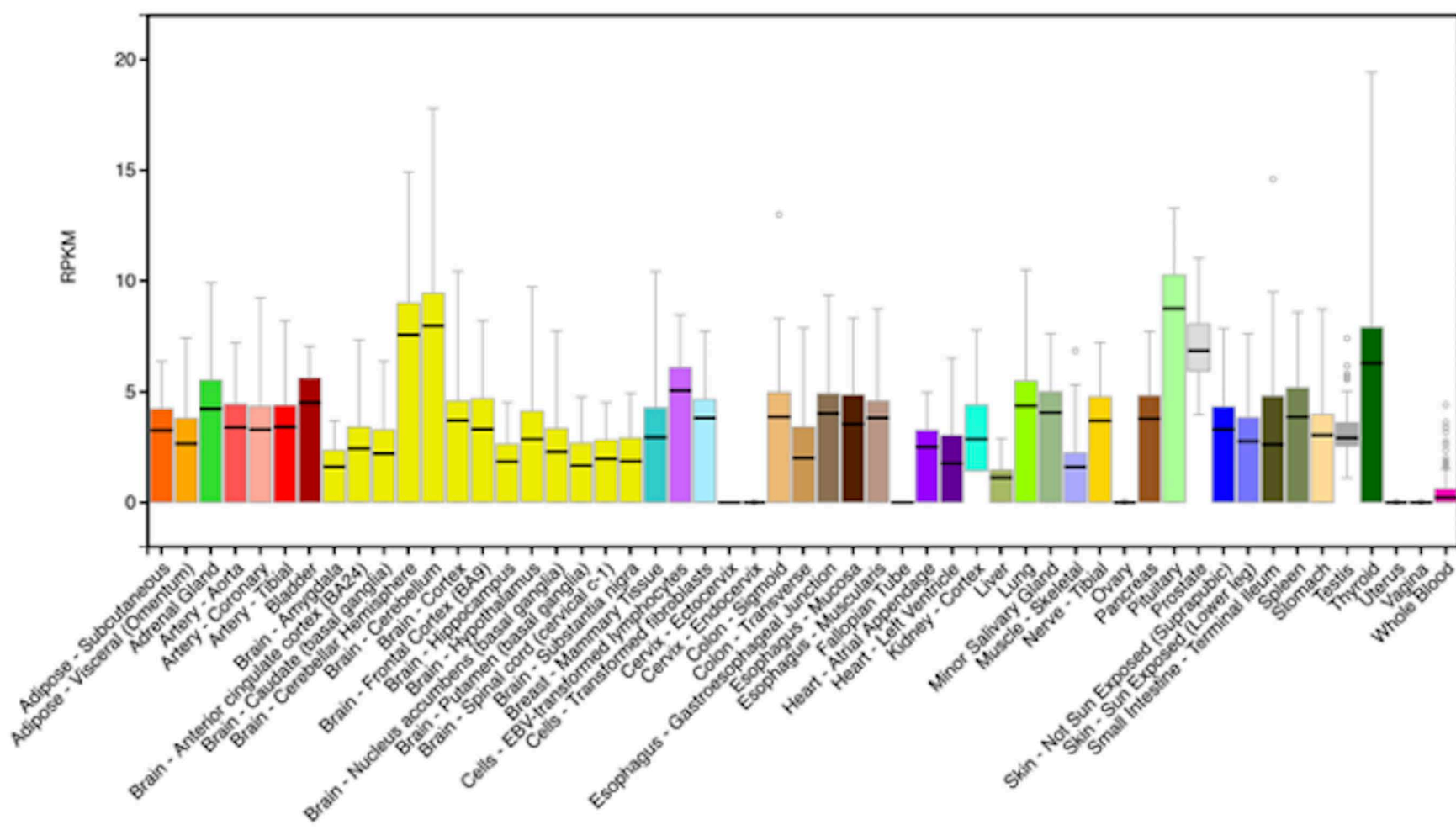
A



C



B



D

