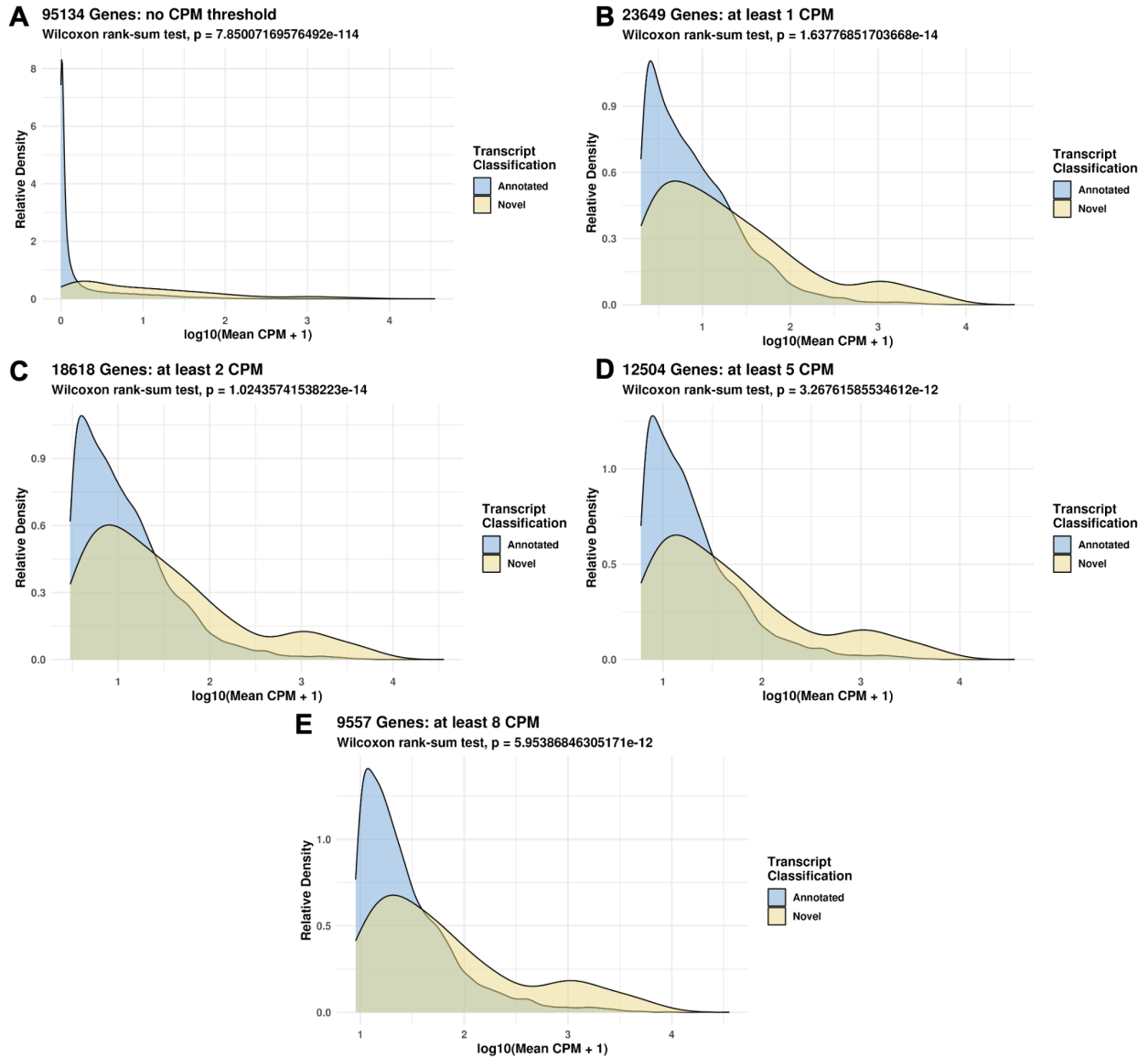
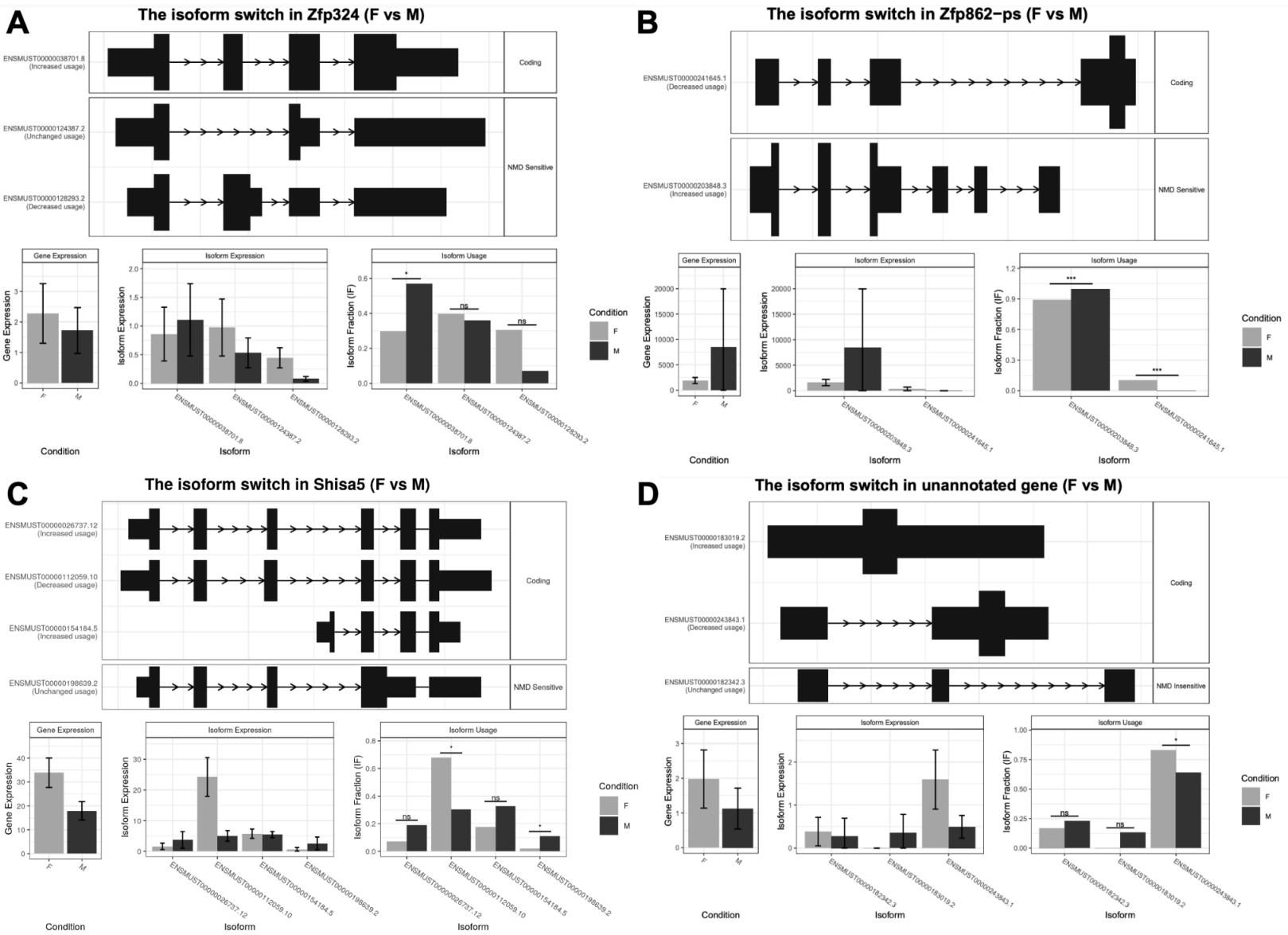


Supplementary Figure 1. Novel transcripts are expressed more highly than annotated transcripts. Density plot showing expression levels (measured in counts per million, CPM) between the novel (yellow) and annotated (blue) transcripts. Density is calculated by kernel density estimation. When we ran a one-sided Wilcoxon rank sum test at 5 mean CPM thresholds (**A** - 0 CPM, **B** - 1 CPM, **C** - 2 CPM, **D** - 5 CPM, and **E** - 8 CPM), the two distributions were significantly different at every level.



Supplementary Figure 2. Genes with DTU across sex for the whole brain. SwitchPlots showing transcript summary, gene expression, isoform expression, and isoform usage of the genes for all brain regions across males (M; dark gray) and females (F; light gray). Genes shown are *Zfp324* (A), *Zfp862-ps* (B), *Shisa5* (C), and unannotated gene or *Gm10605* (D).



Supplementary Figure 3. *Tsr2* has a non-significant presence or absence of female-specific transcripts in the hippocampus. SwitchPlot showing transcript summary, gene expression, isoform expression, and isoform usage of the genes for all brain regions across males (M; dark gray) and females (F; light gray).

