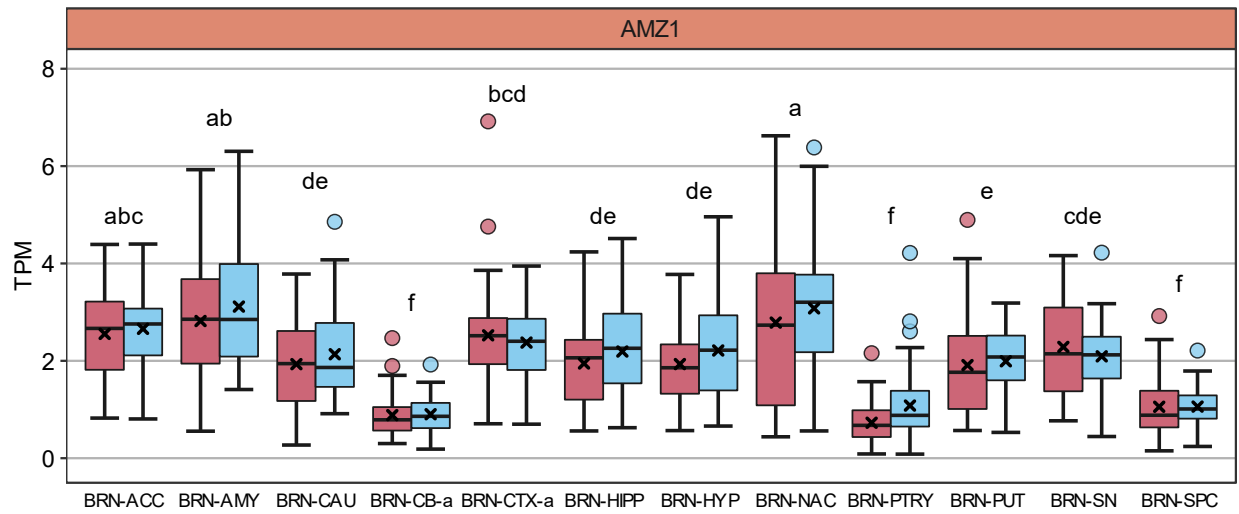
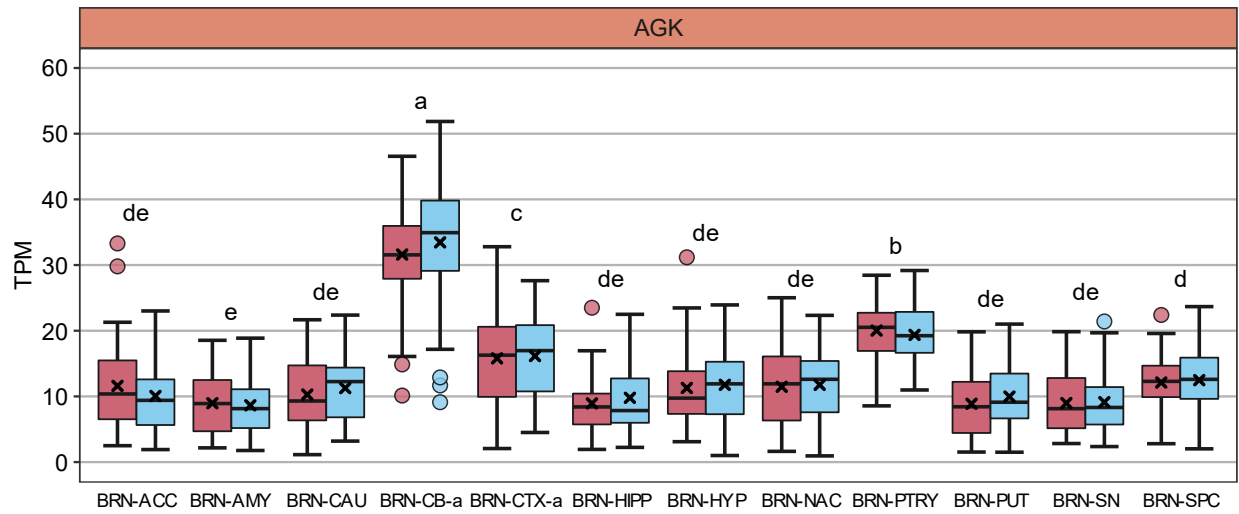
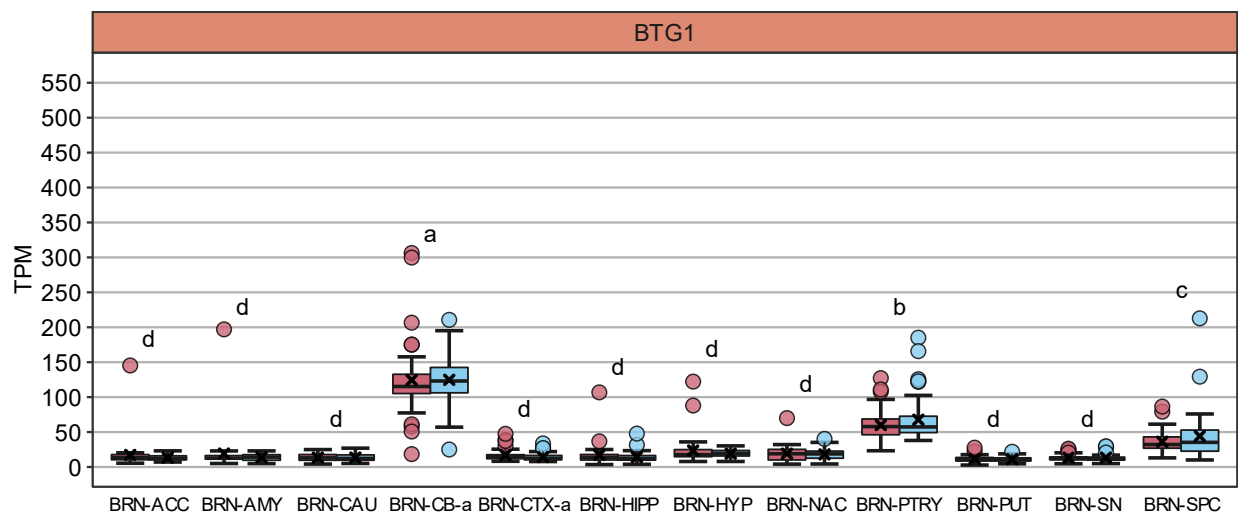
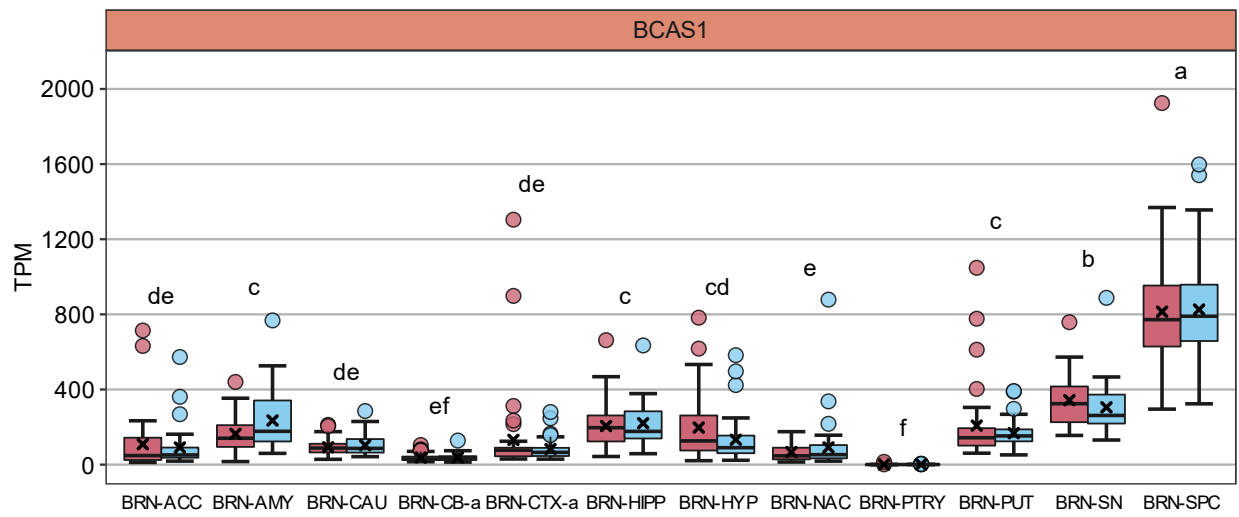
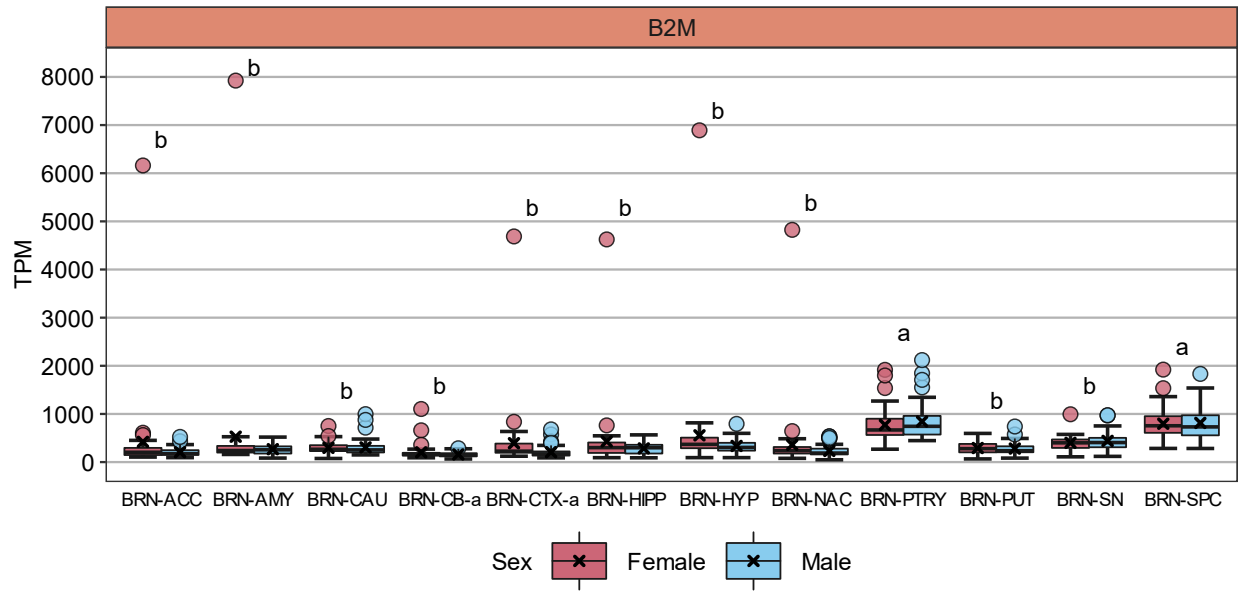
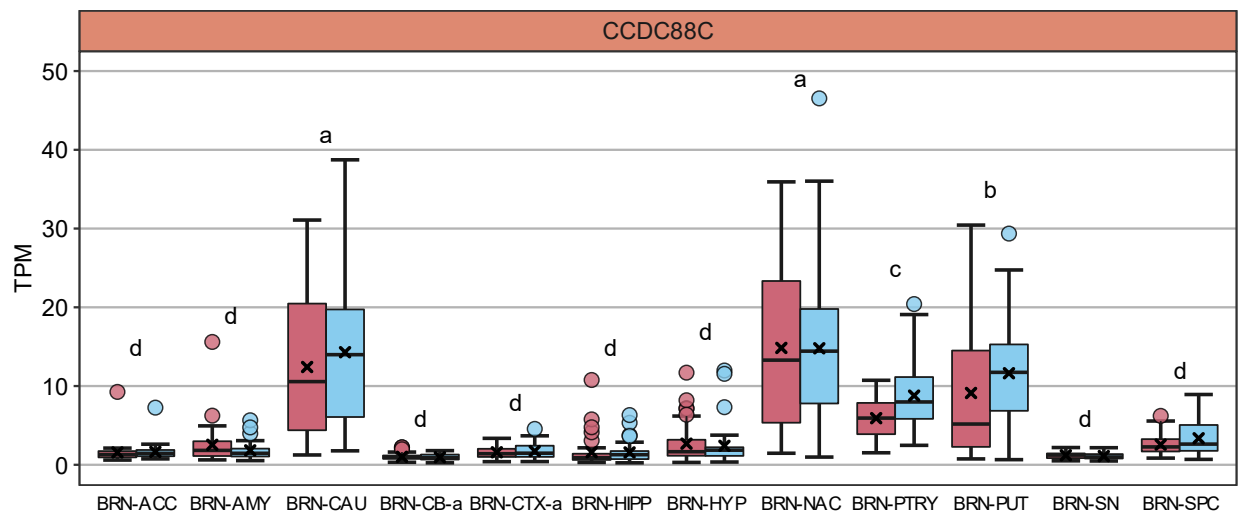
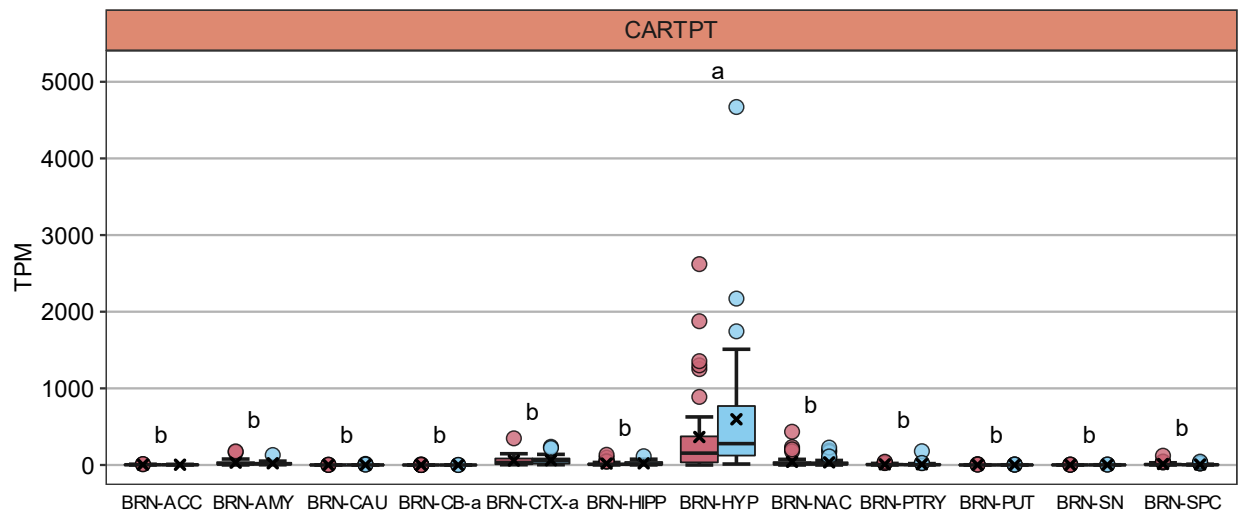
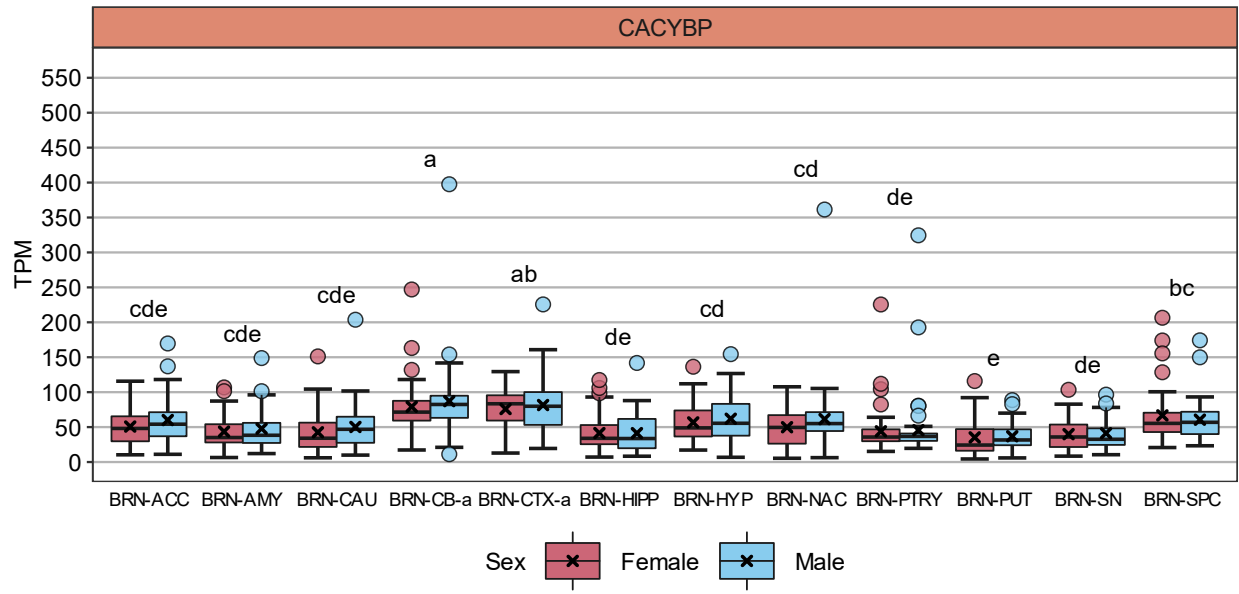
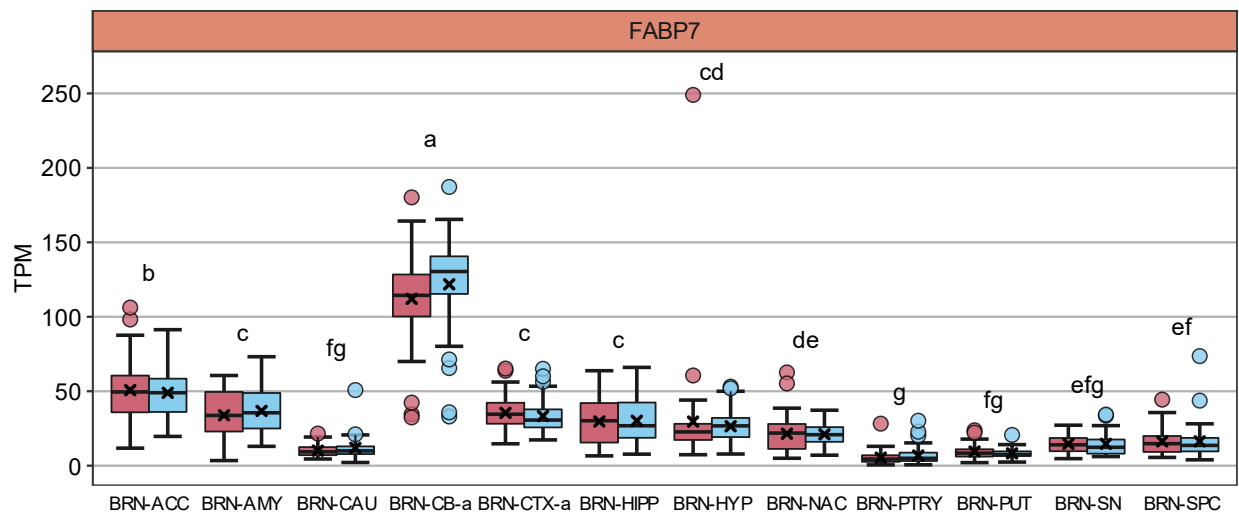
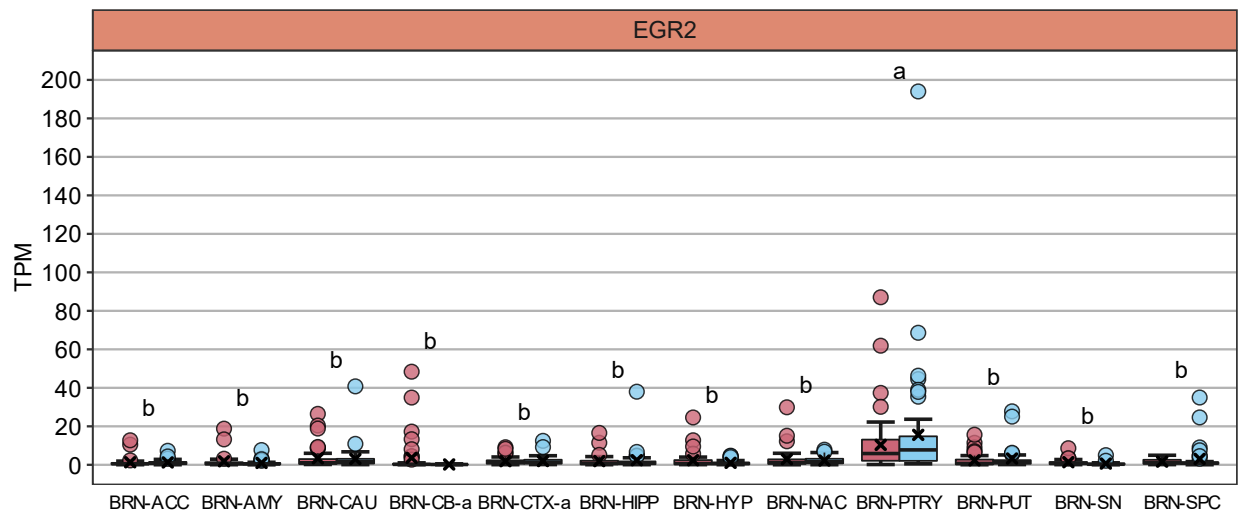
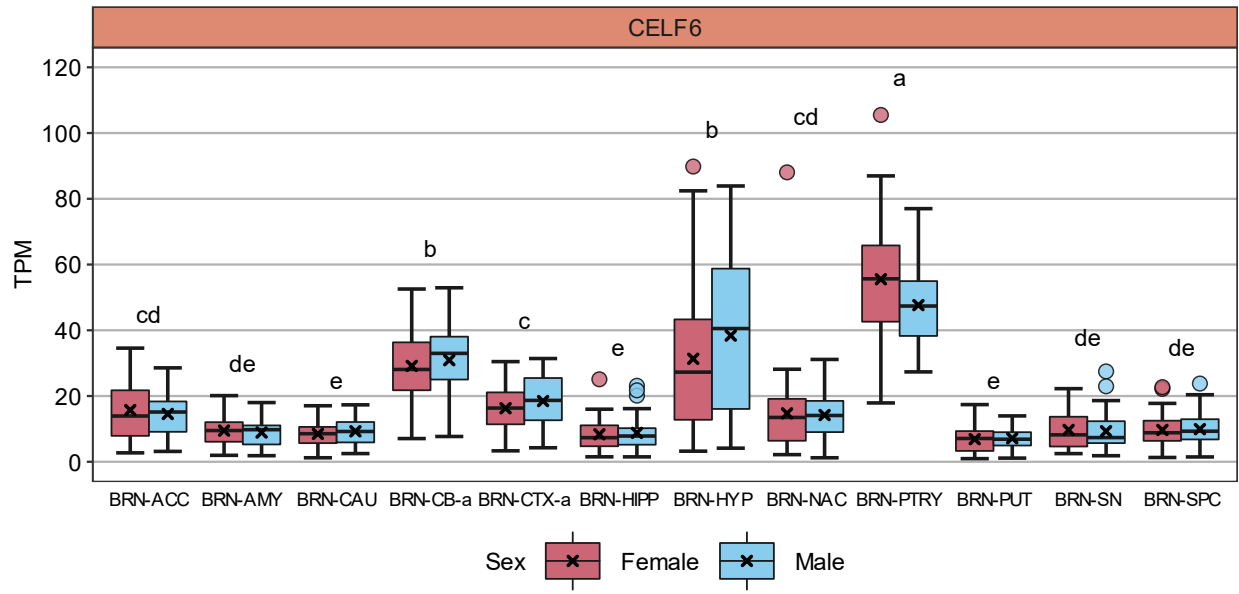


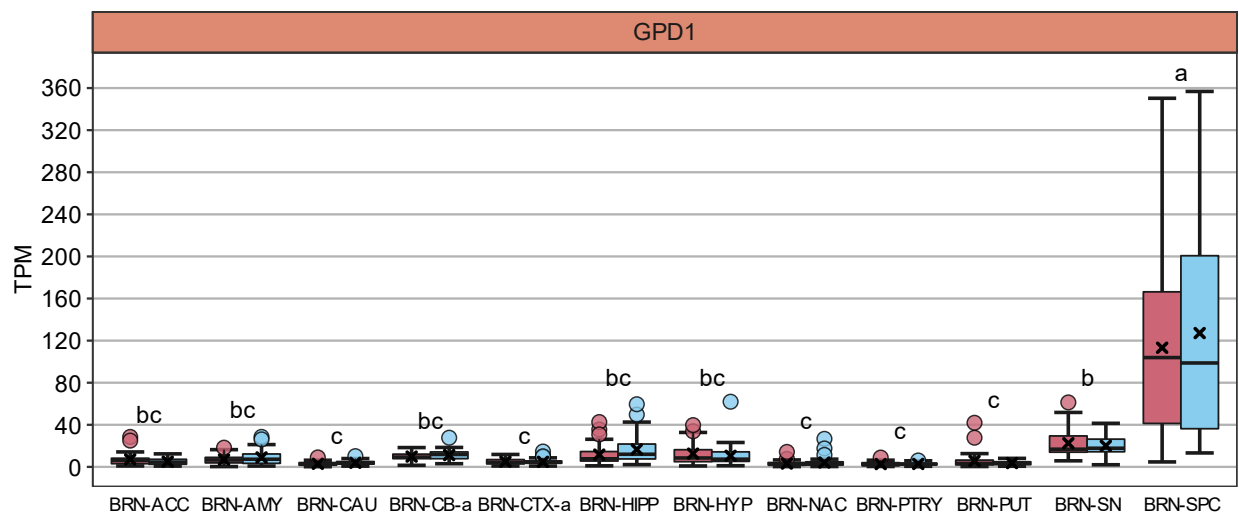
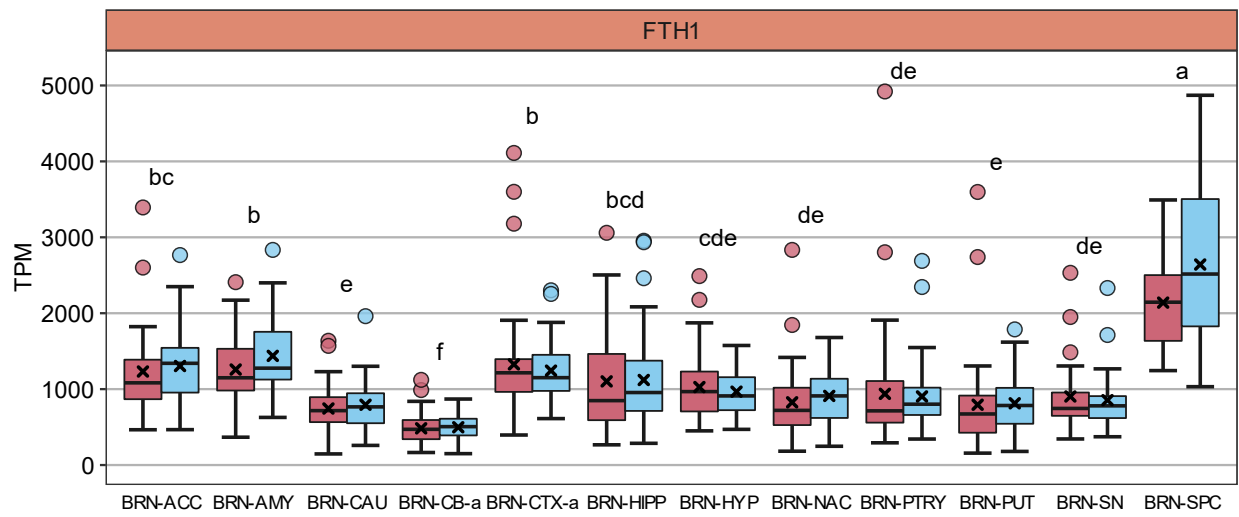
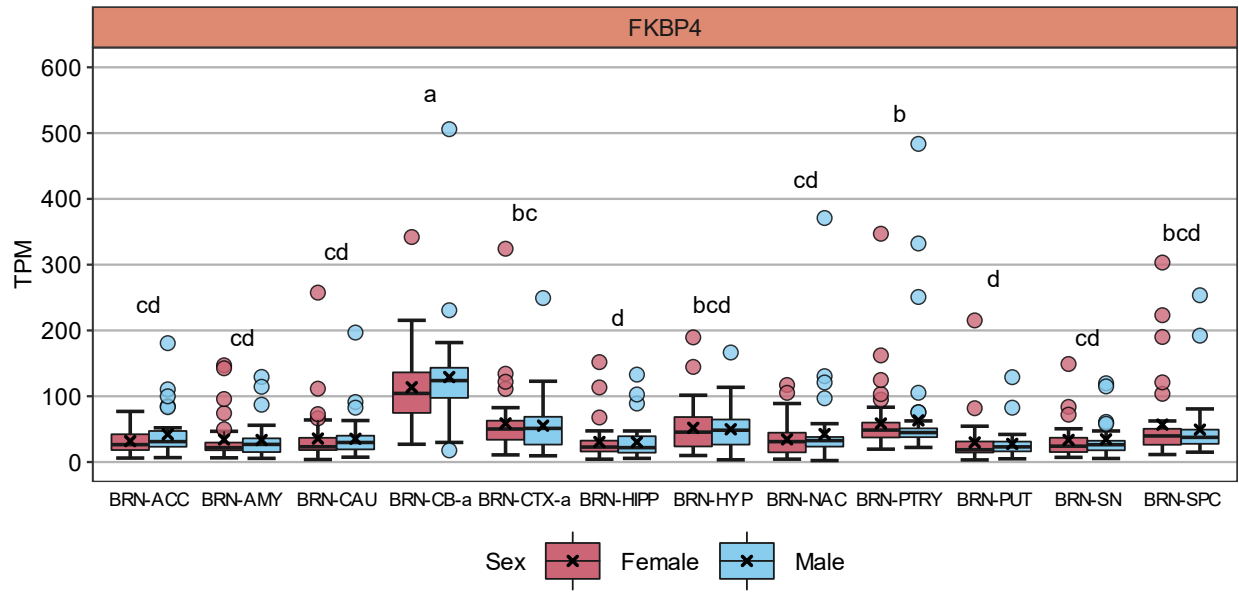
Chapter 4, Supplementary Figure 5

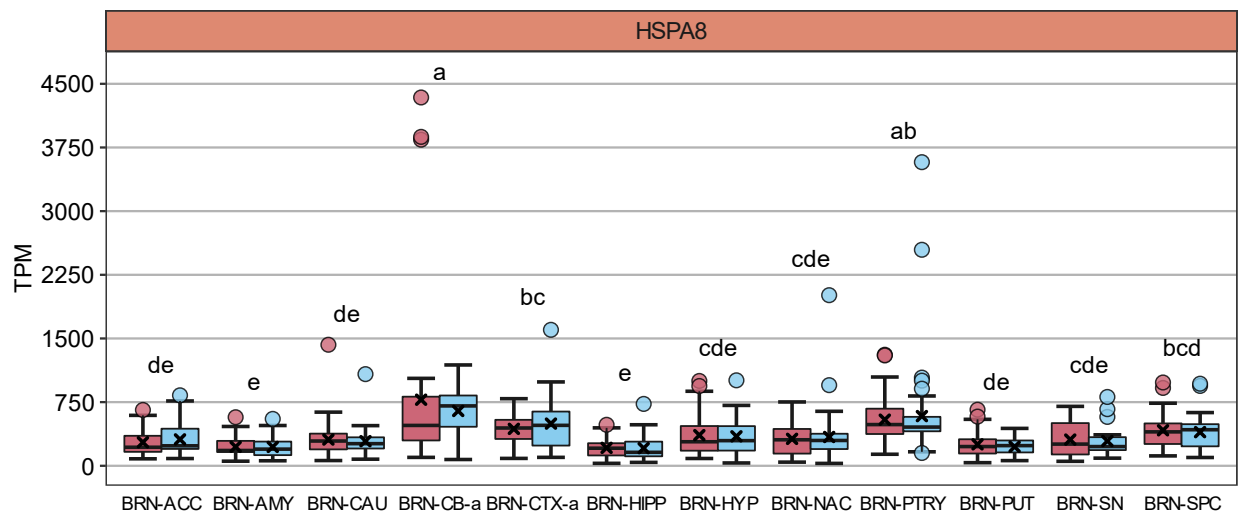
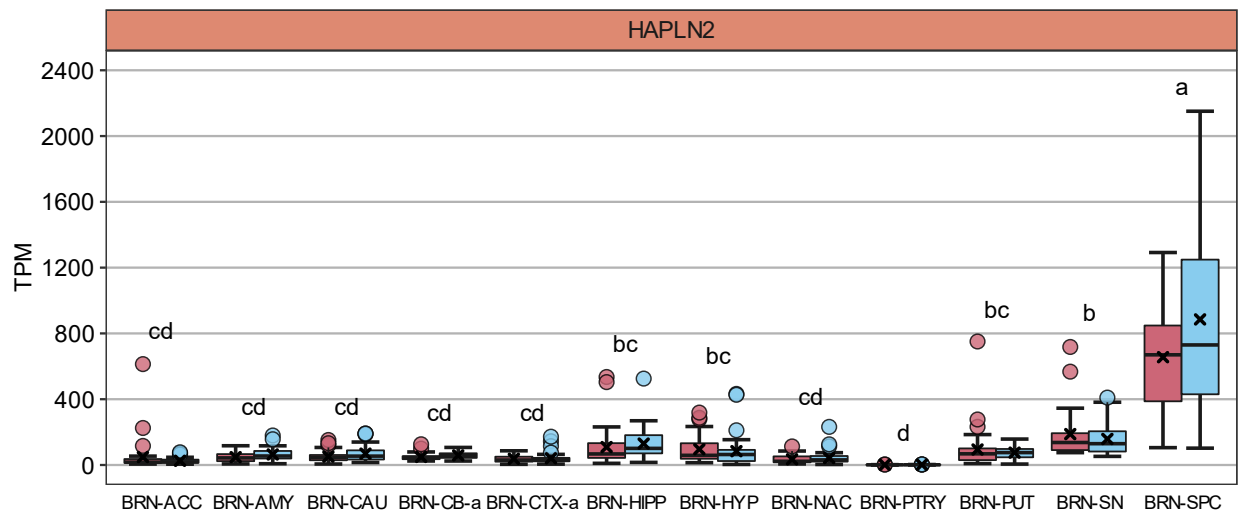
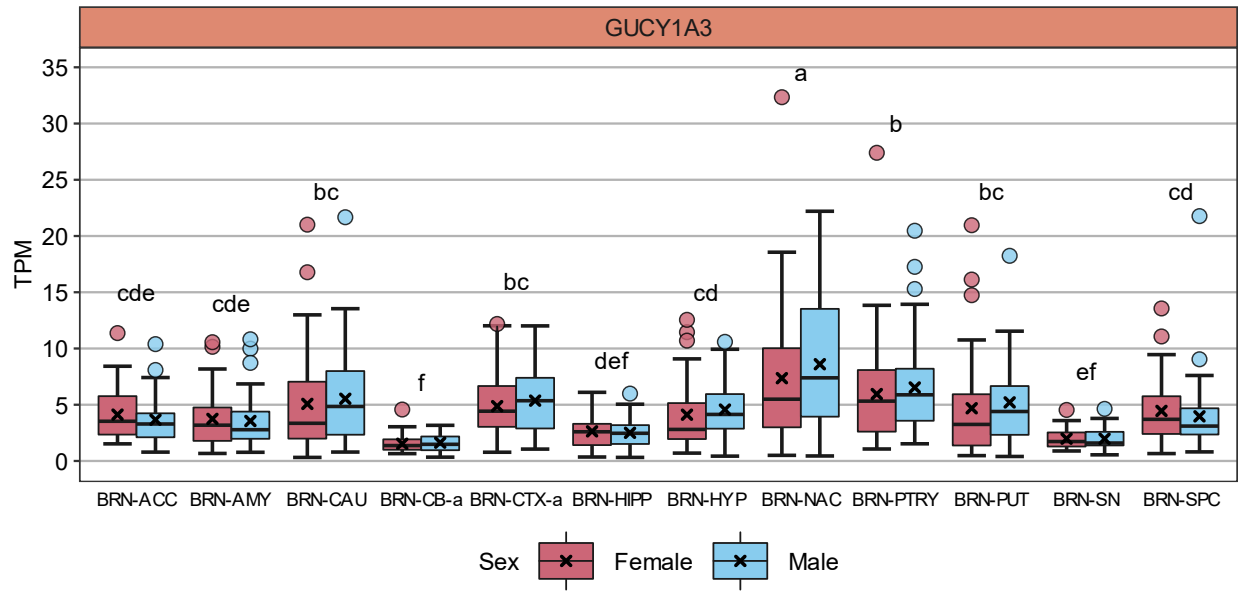


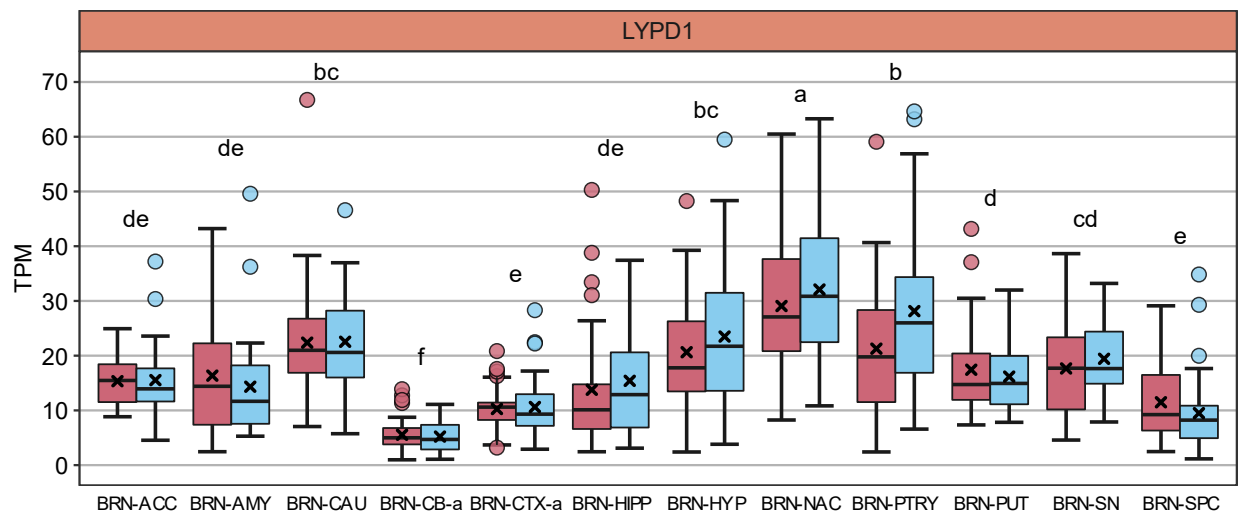
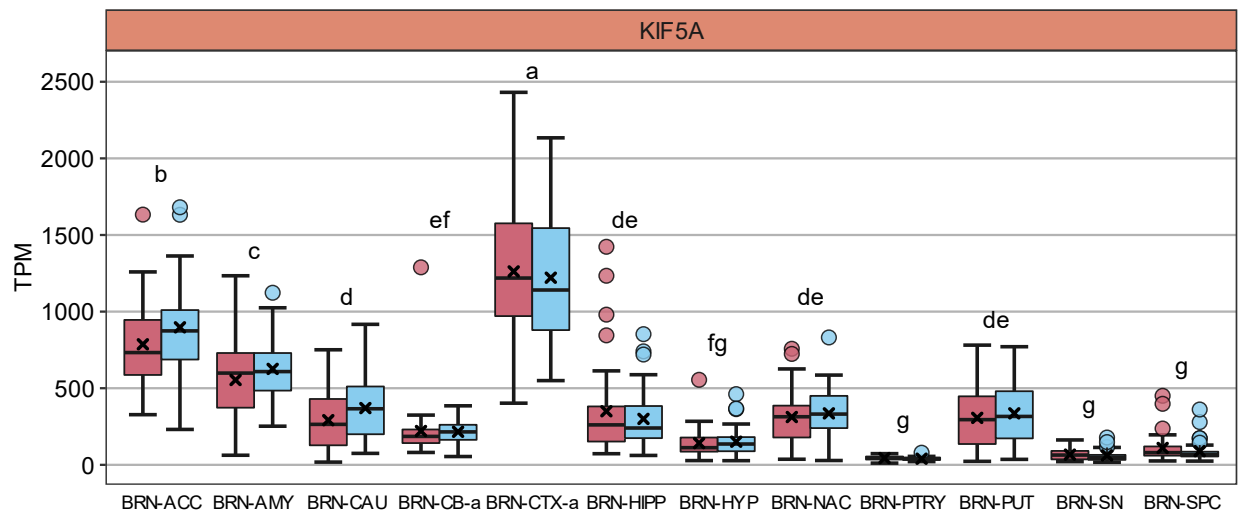
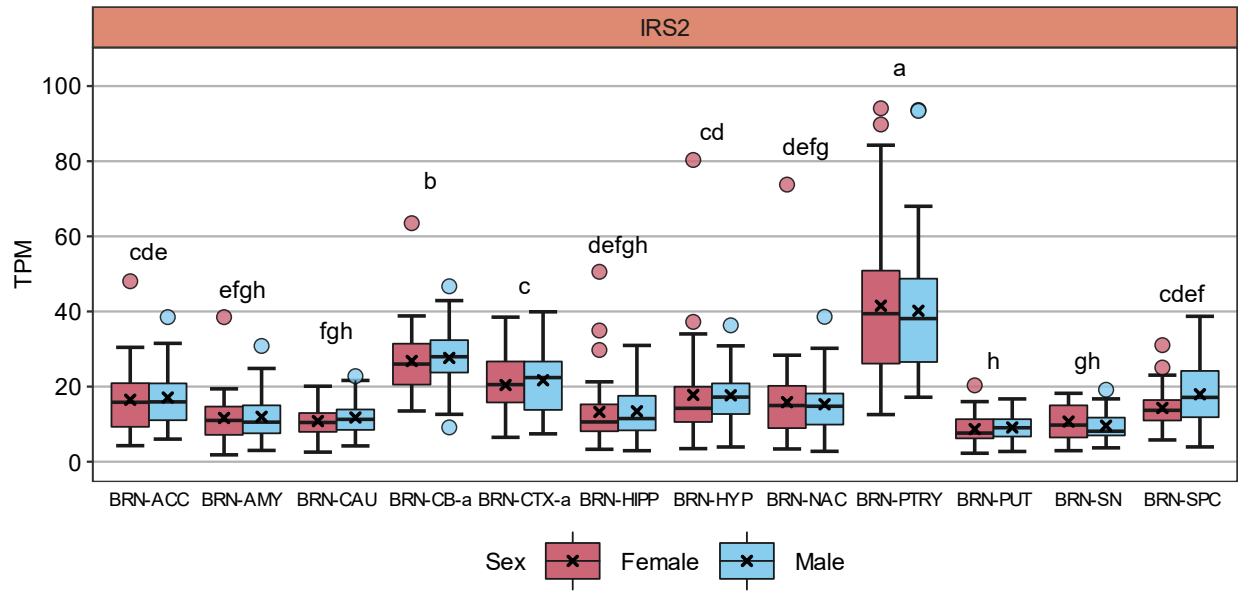


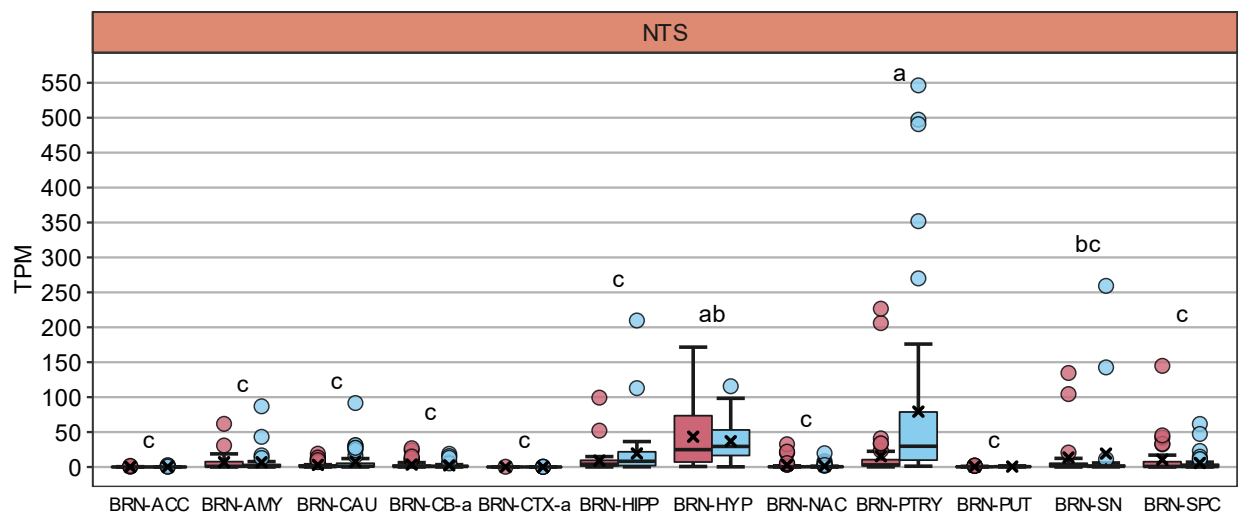
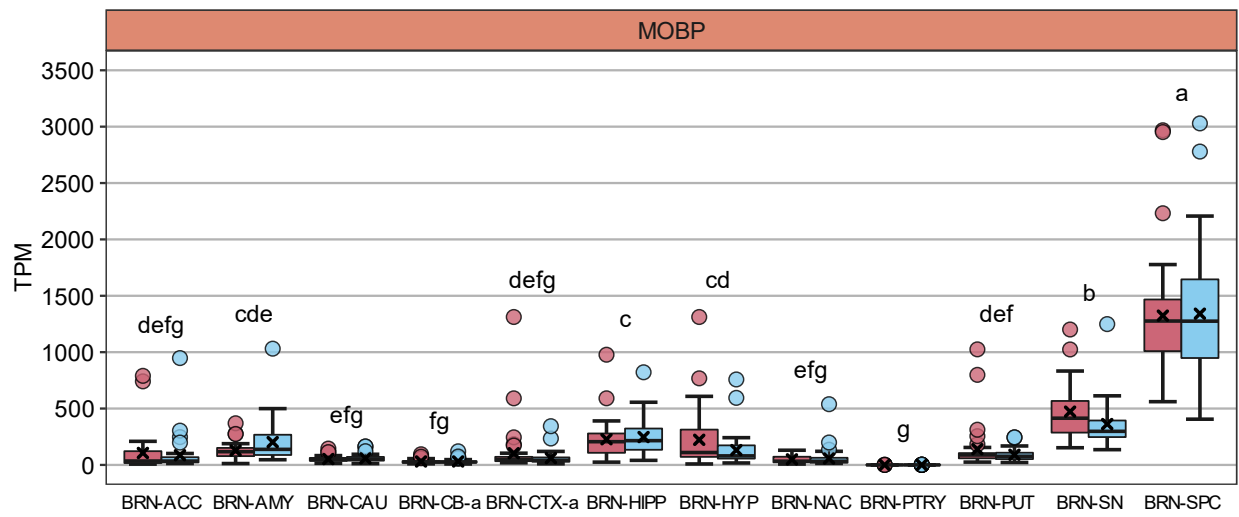
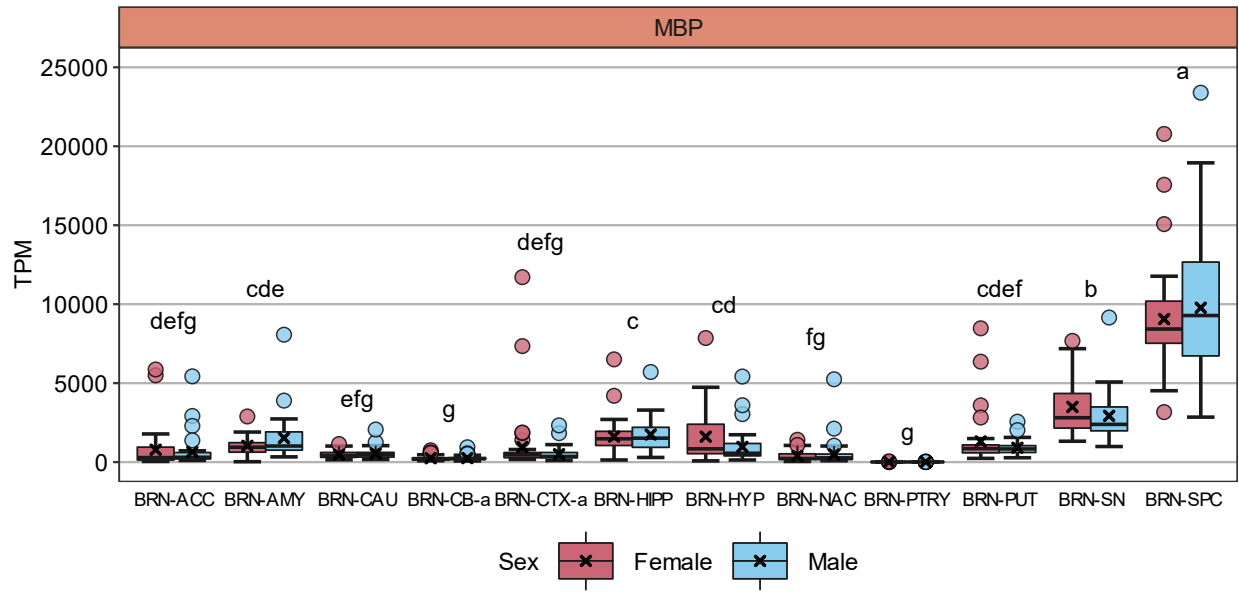


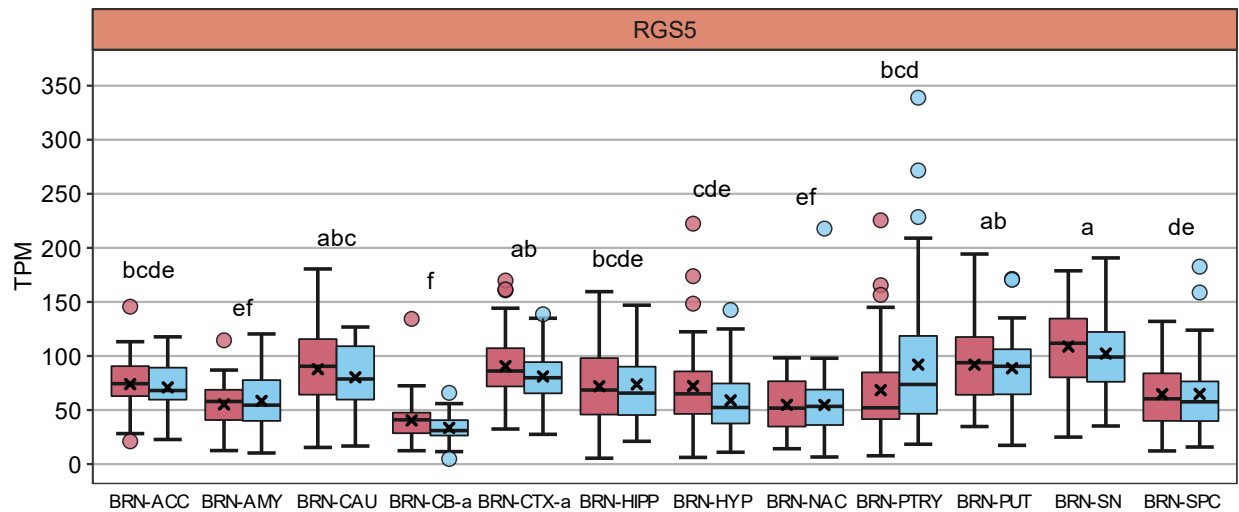
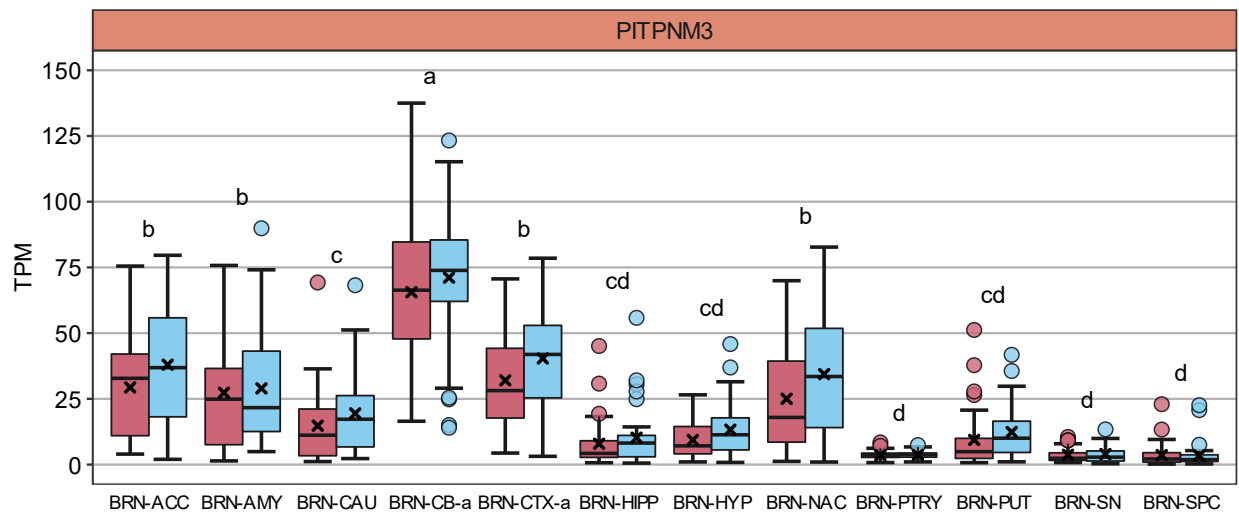
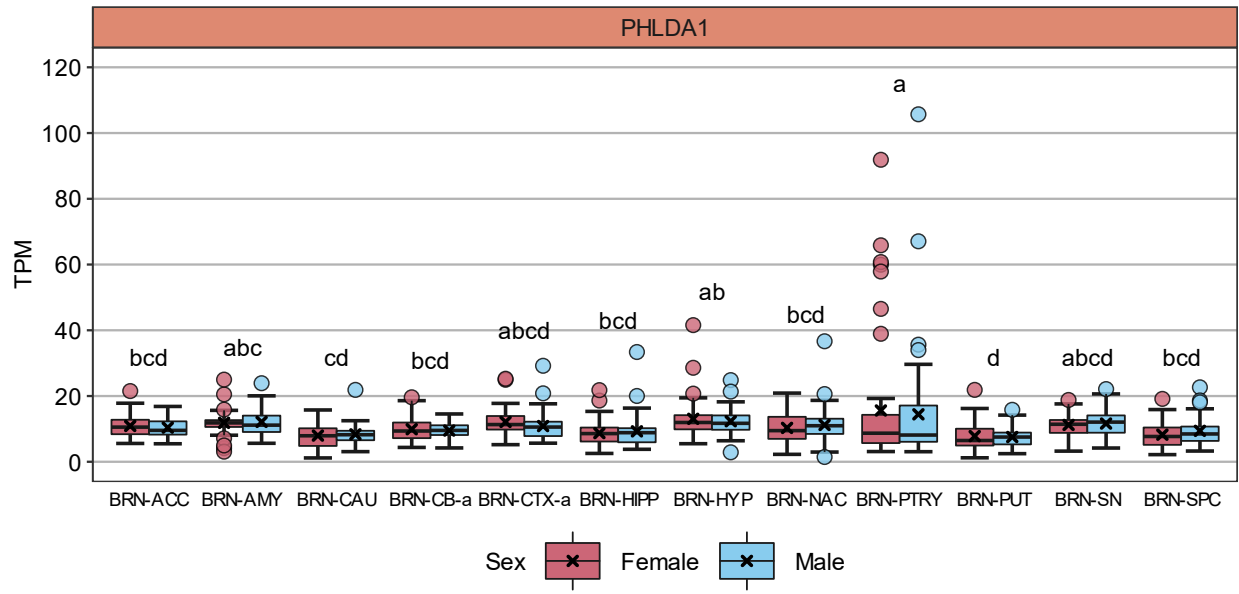


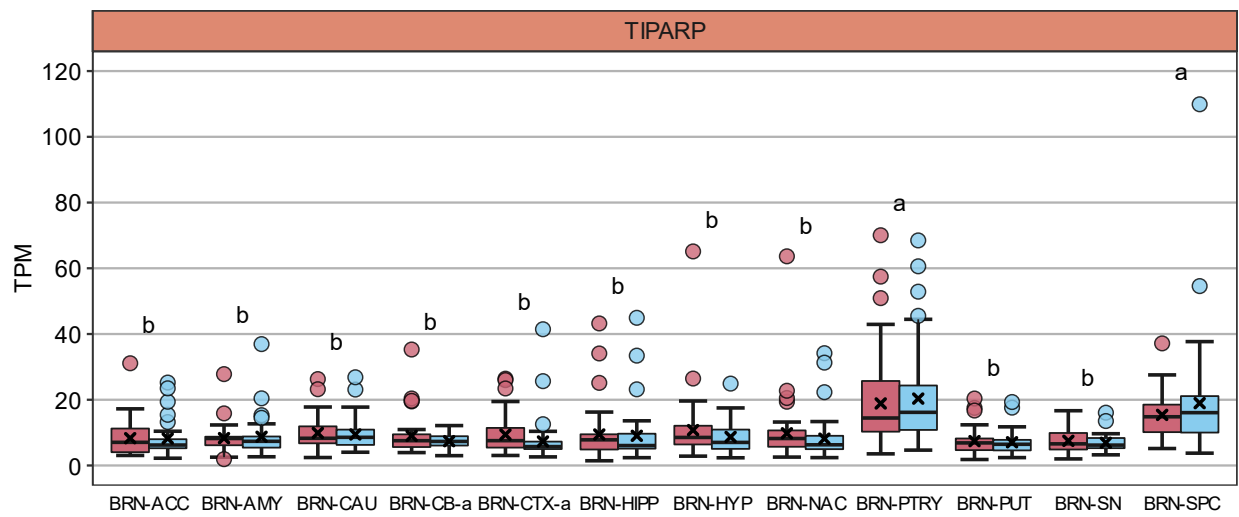
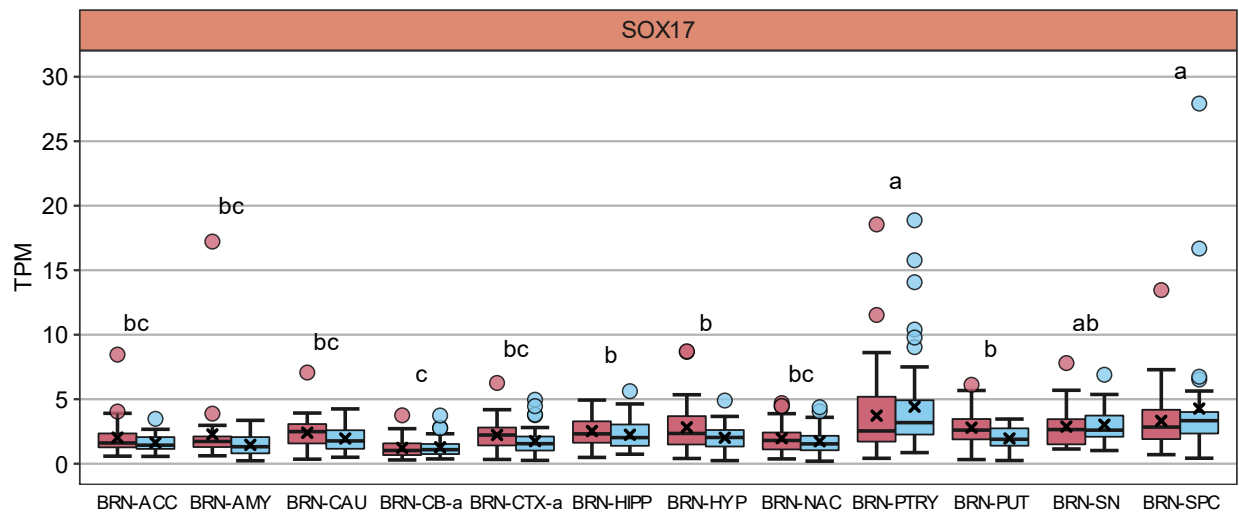
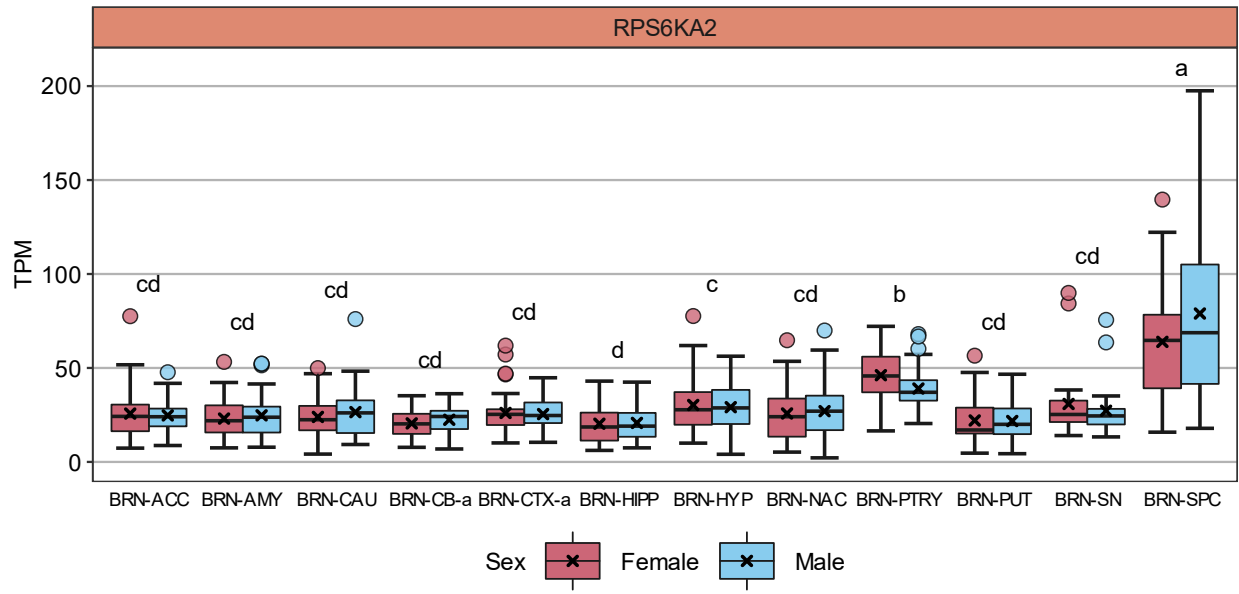


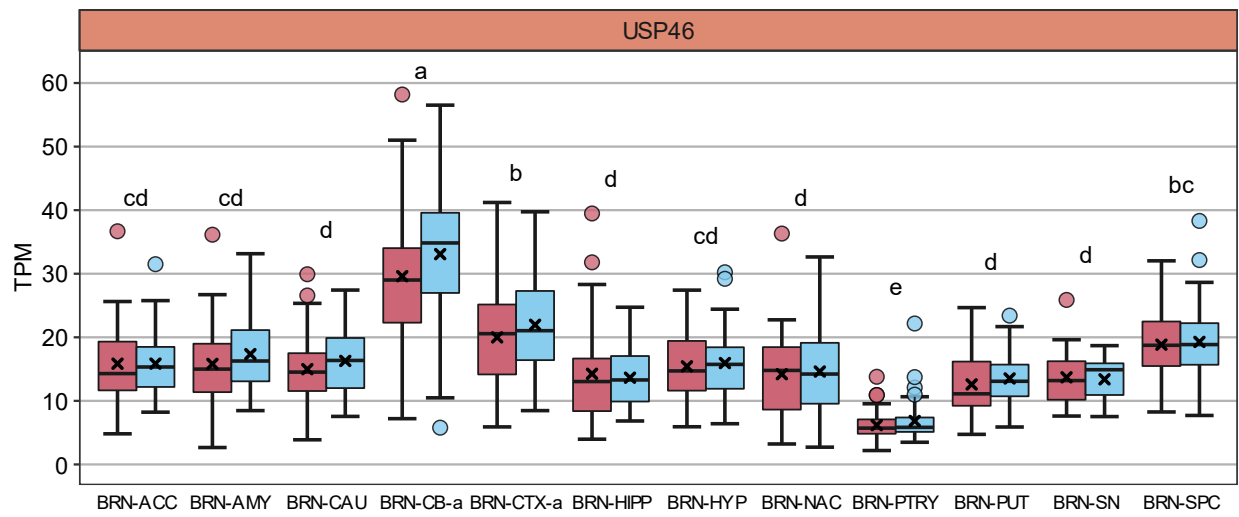
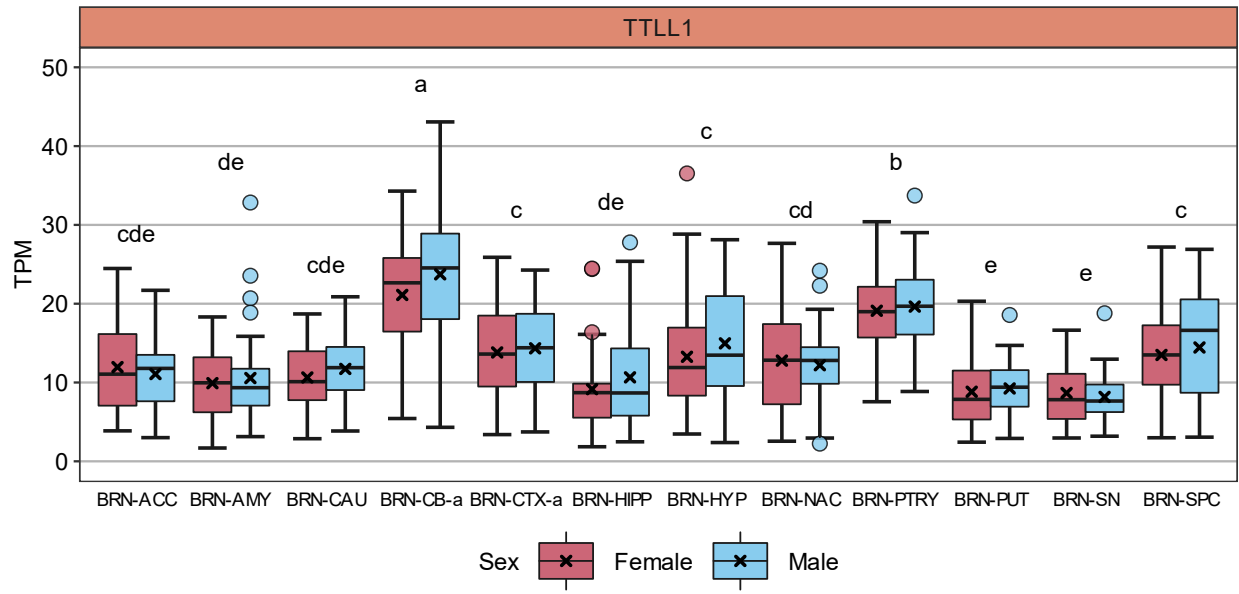


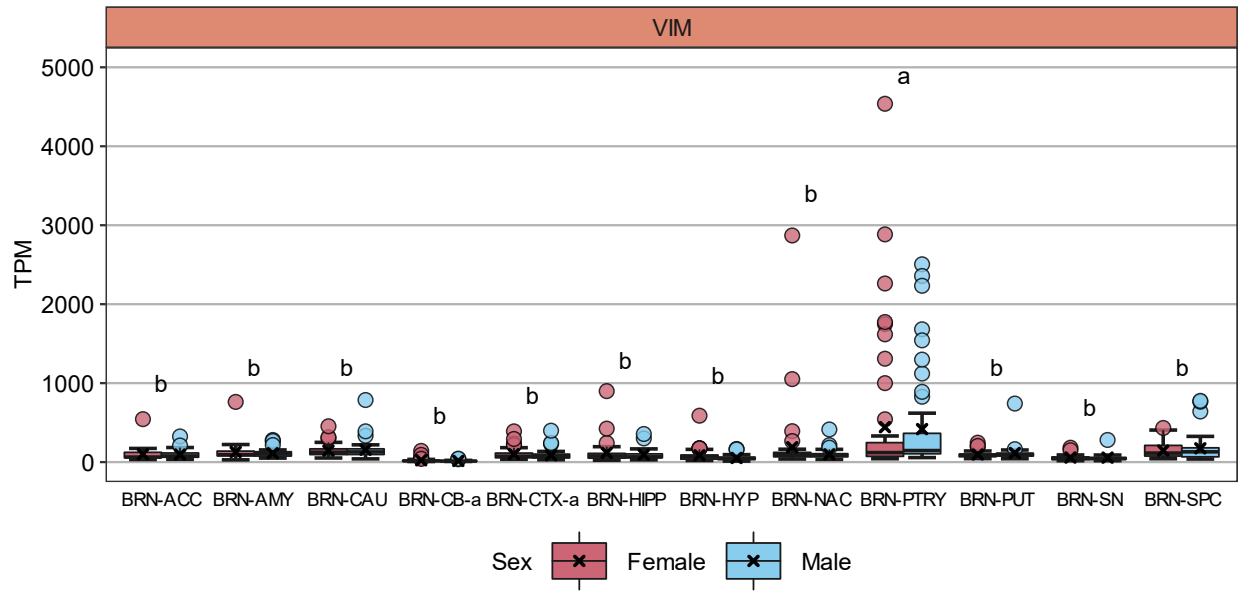












Chapter 3, Supplementary Figure 5. Expression by Sex and brain Tissue for age-matched males and females (≥ 55 years of age). Data were obtained from the GTEx database, which utilizes RNA-seq data from healthy human tissue. All genes showed significantly different expression across brain tissues. Letters indicate the categorical results of post-hoc Tukey's tests, and tissues with the same letter(s) show no difference in expression. The letter "a" indicates the brain tissue(s) with the highest expression, "b" indicates those with the second-highest expression, and so forth alphabetically. Tissues that are not significantly different from each other have the same letter(s). For example, if BRN-PTRY is "a", BRN-HYP is "ab", and BRN-SN is "bc" (see panel for *NTS*), the pituitary gland shows significantly higher expression compared to all other tissues except hypothalamus, and the hypothalamus shows significantly higher expression compared to all tissues except pituitary gland and substantia nigra. All 32 Craving genes are graphed in alphabetical order.