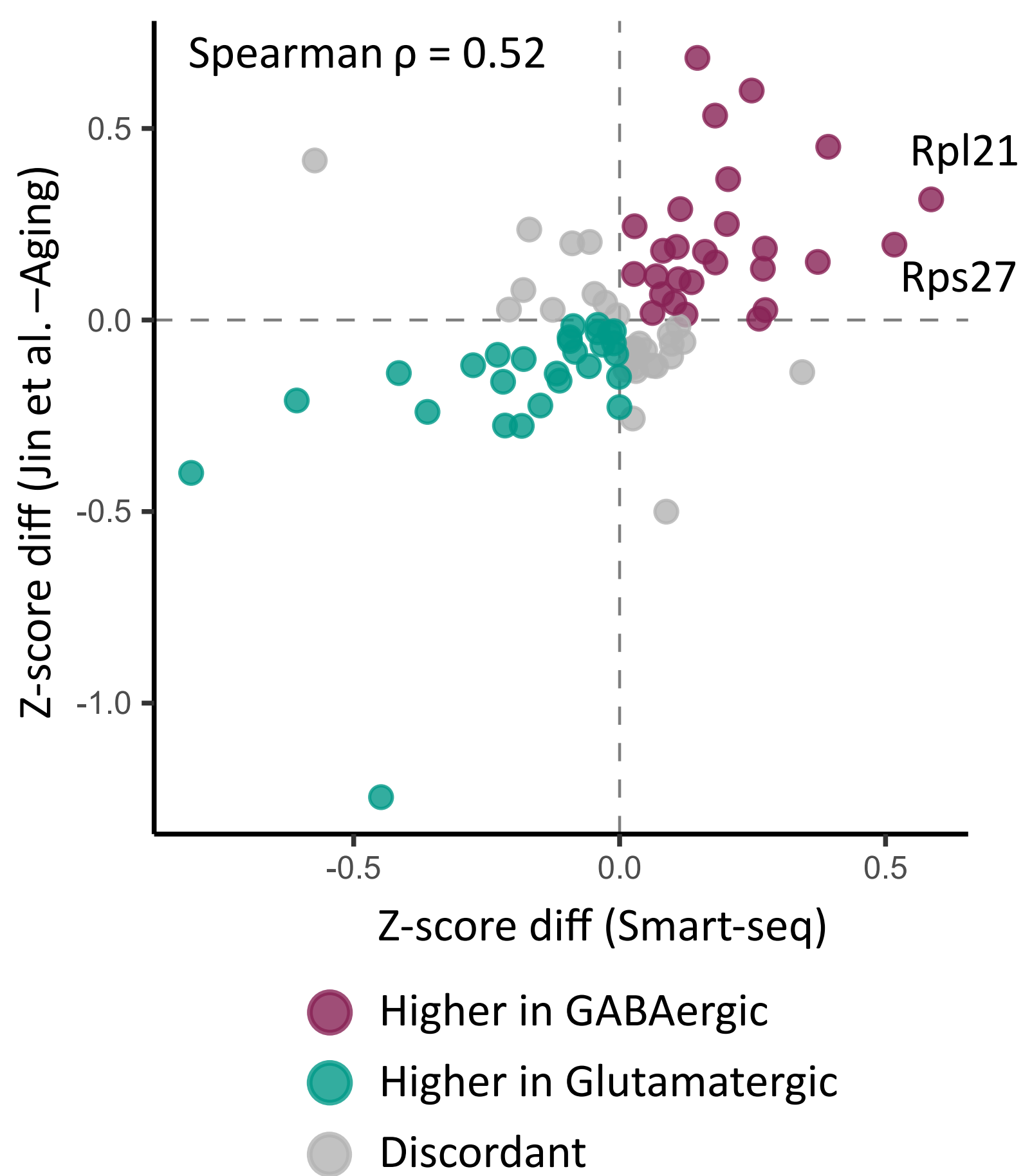


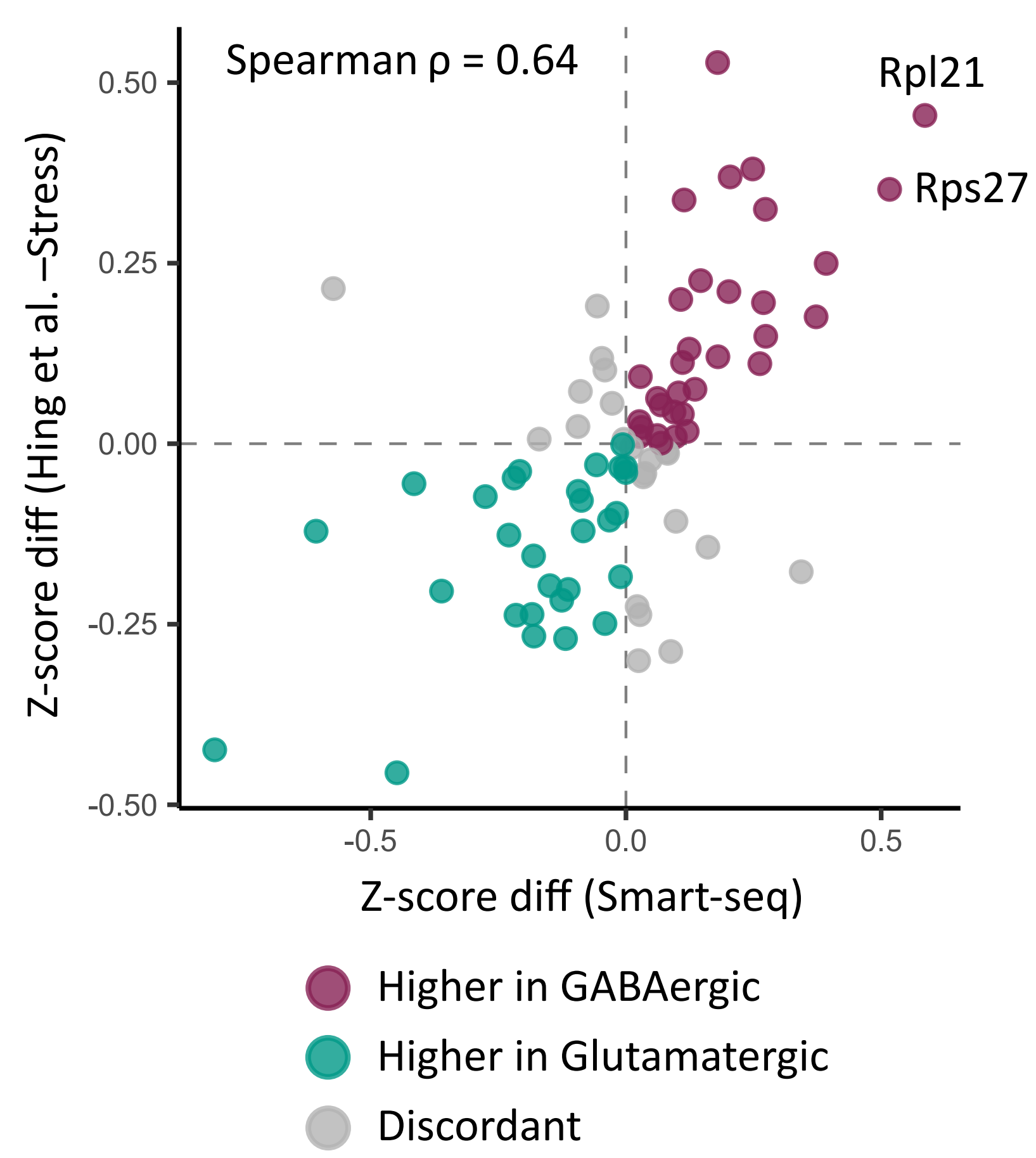
A

RP clustering drivers (GABA - Glut)



B

RP clustering drivers (GABA – Glut)



C

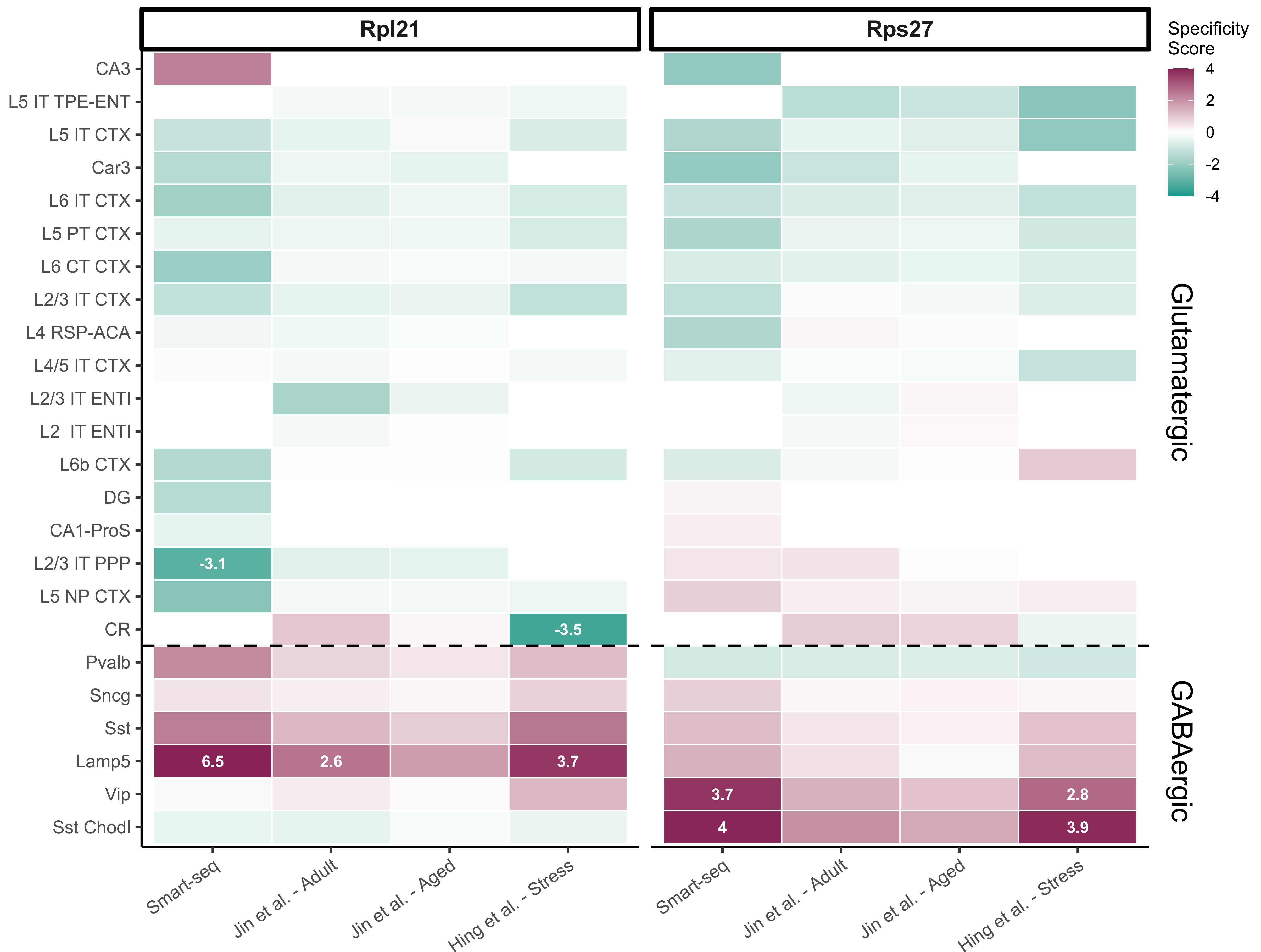


Figure S8. Cross-dataset concordance of RP gene expression differences between GABAergic and glutamatergic neurons. (A-B) Scatter plots showing the Z-score difference (GABAergic minus glutamatergic) for each RP gene in Smart-seq versus Jin et al. - Aging (A) and Smart-seq versus Hing et al. - Stress (B). Each dot represents one RP gene, colored according to the direction of expression difference in both datasets: higher in GABAergic neurons in both datasets (purple), higher in glutamatergic neurons in both datasets (teal), or discordant between datasets (grey). Spearman correlation coefficients are indicated. (C) Heatmap showing specificity scores for Rpl21 and Rps27 across neuronal subclasses in all four datasets. Specificity scores were calculated as standardized residuals from a linear model of subclass mean expression versus global mean expression, following the same approach as Figure 3B. Values exceeding the ± 2.5 threshold are shown in white text. The dashed line separates GABAergic (below) from Glutamatergic (above) neuronal subclasses.