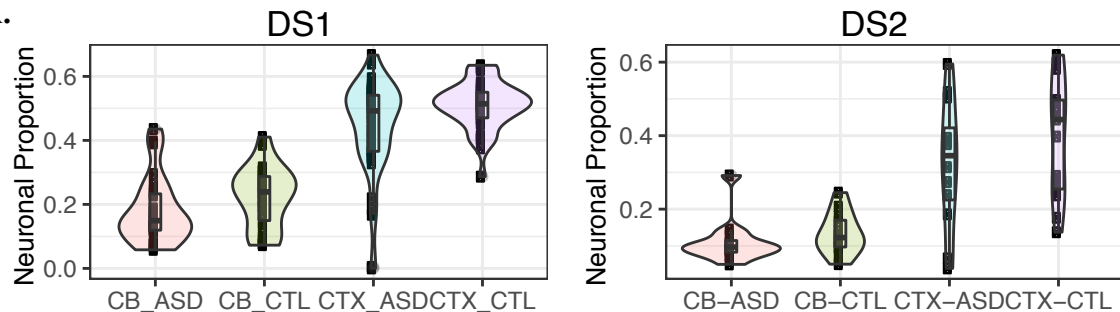
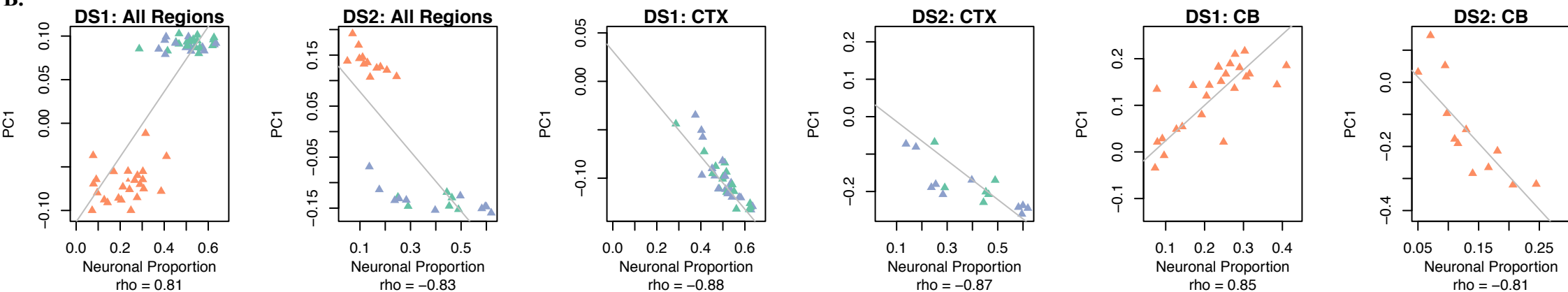


Supplementary Figure 6

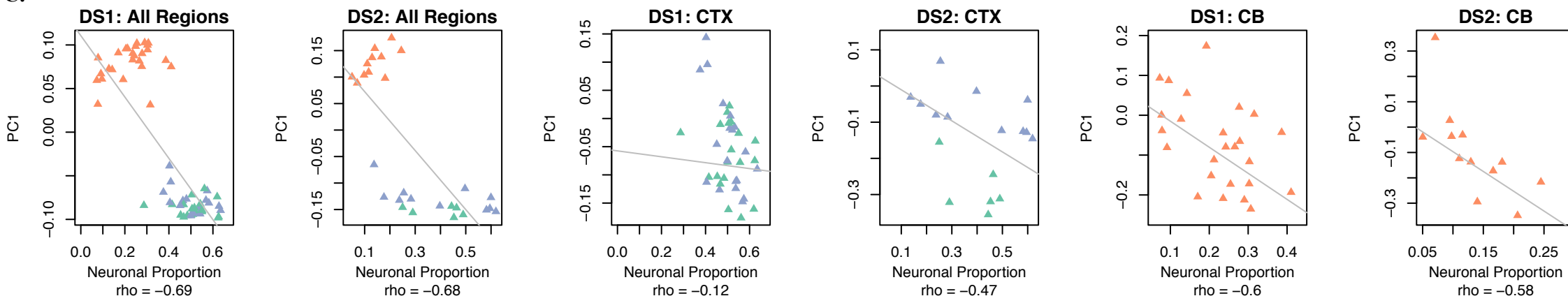
A.



B.



C.



Supplementary Figure 6. Estimated proportion of neurons in DS1 and DS2. (A) Boxplots displaying the estimated proportion of neurons across brain regions and pheno-types, in DS1 (*left*) and DS2 (*right*). Boxplots were generated using the `geom_boxplot` and `geom_violin` functions in R; the horizontal line represents the median, boxes extend between the first and third quartiles, and whiskers extend to 1.5 IQR (inter-quartile range) from the box. Notches mark $\pm 1.5 \text{ IQR} / \sqrt{n}$, where n represents the number of data points. (B) Scatterplots of first principal component values of gene expression data (PC1, y-axis) vs. estimated proportion of neurons. (C) Scatterplots of first principal component values of circRNA expression data (PC1, y-axis) vs. estimated proportion of neurons. All neuronal proportion estimates are based on reference transcriptome data from Zhang et al. 2016.