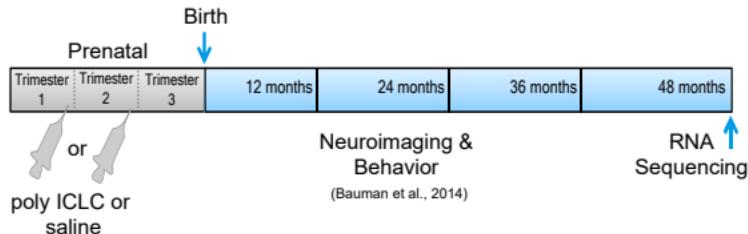
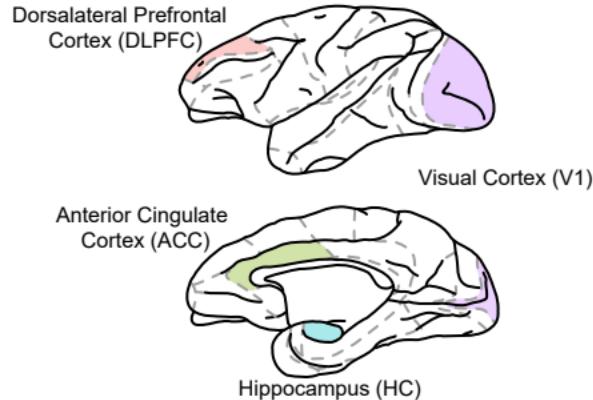


A

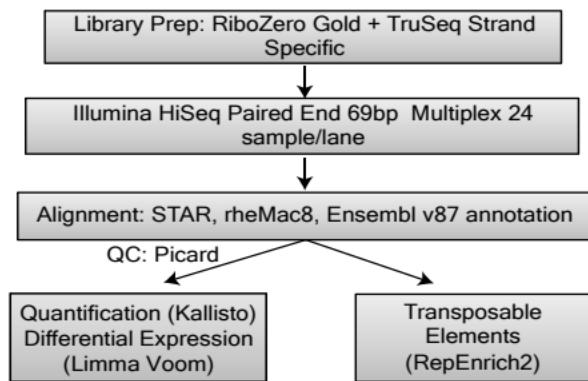
Experimental Timeline

**B**

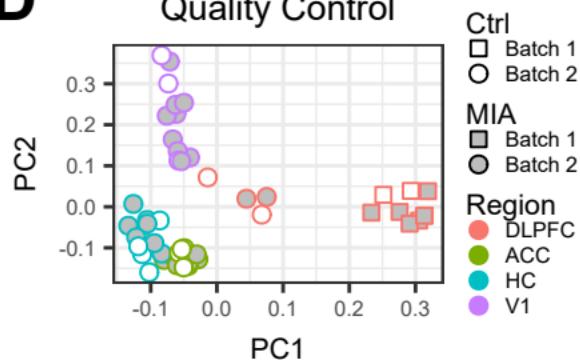
Brain Regions Profiled

**C**

RNA-Sequencing Pipeline

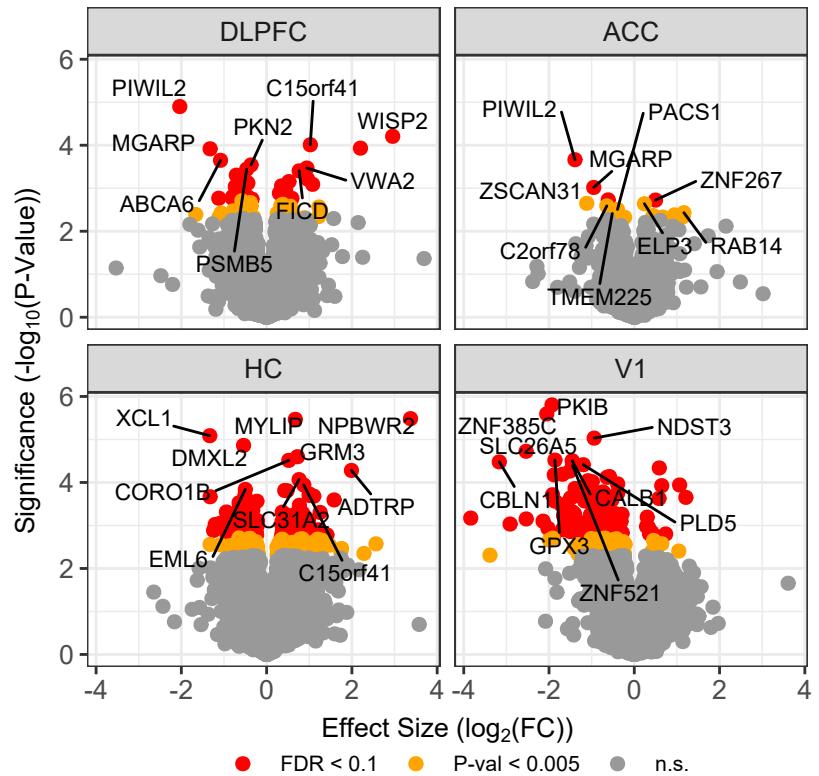
**D**

Quality Control

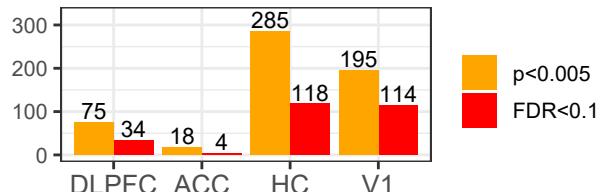


(Figure 1)

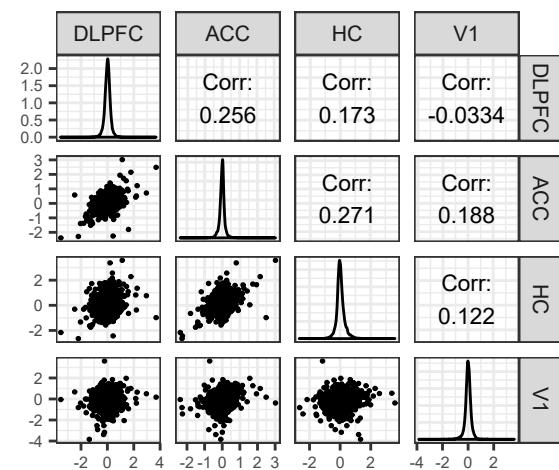
A Regional Differential Gene Expression



B # DE Genes by Region

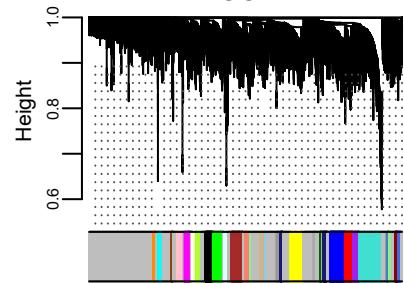


C All Genes logFC Correlation



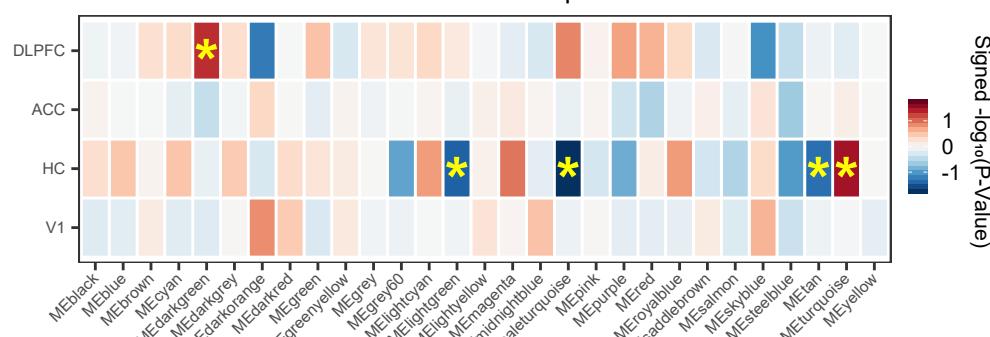
D

WGCNA



E

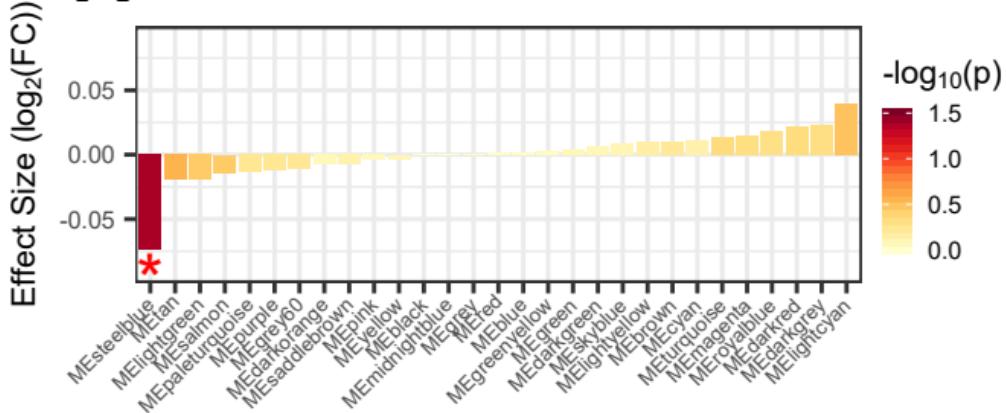
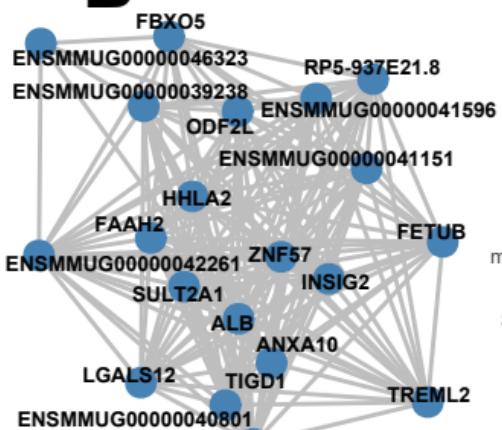
Module Differential Expression



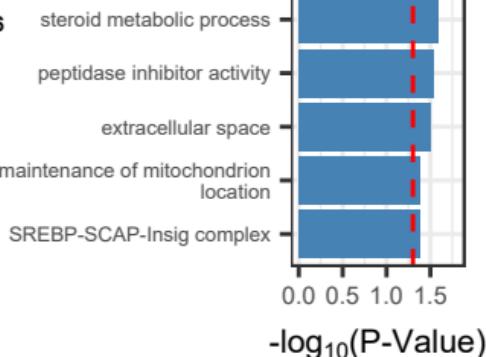
(Figure 2)

A

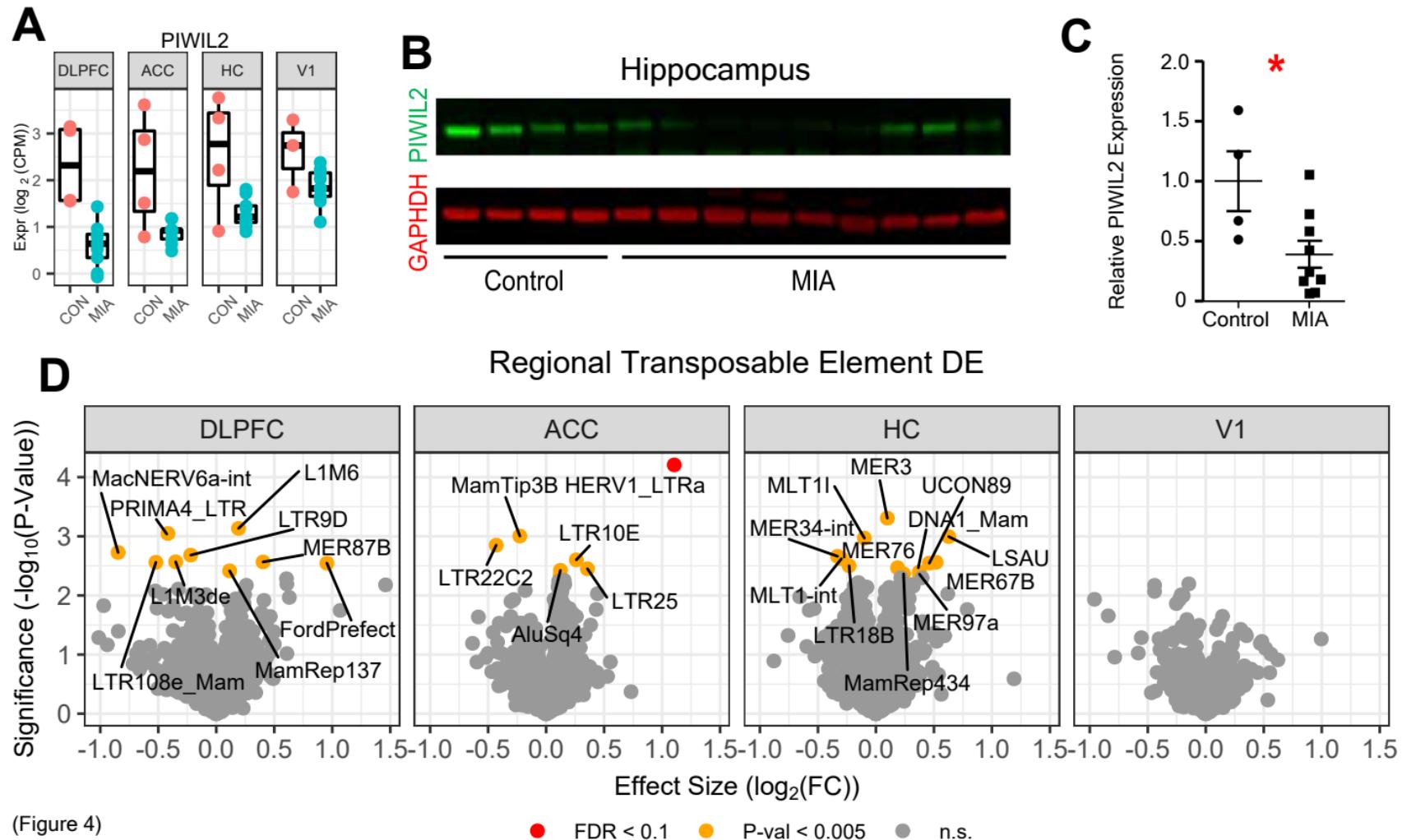
Combined Module DE

**B****C**

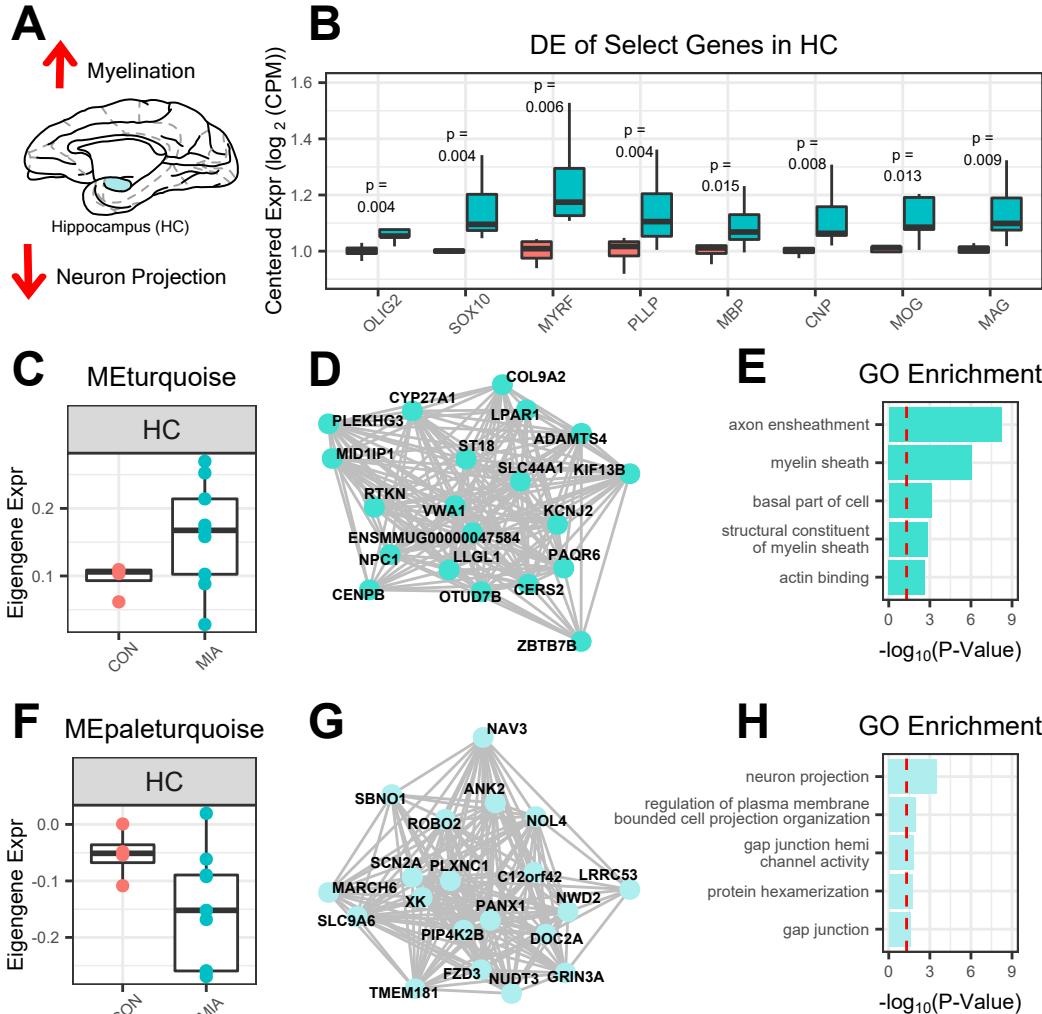
GO Enrichment



(Figure 3)



(Figure 4)



(Figure 5)

A

Disease MIA Overlap

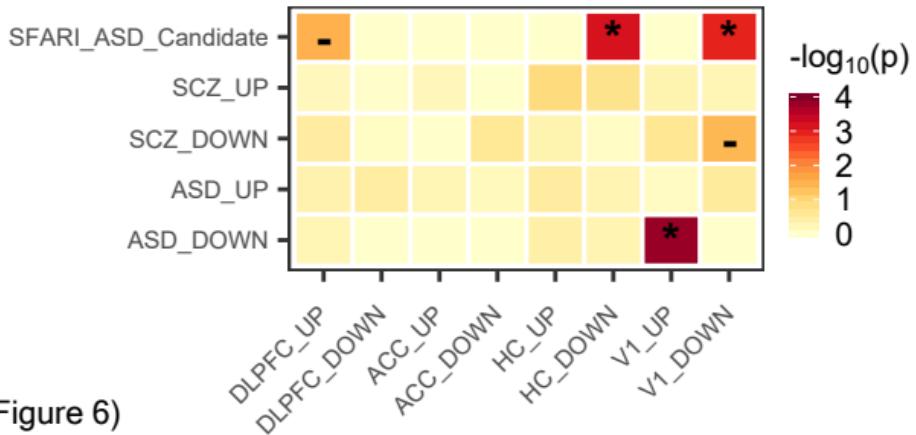
DGE rank in Disease



DGE rank in MIA

B

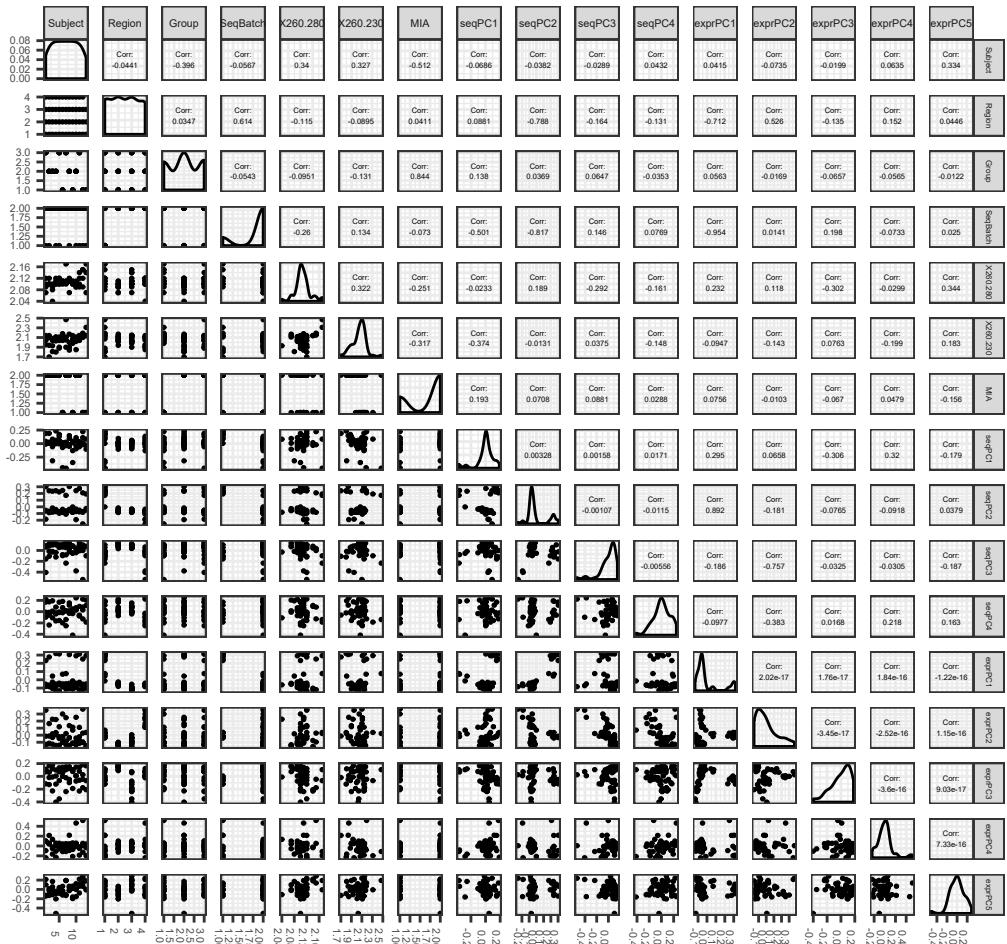
Disease Enrichment



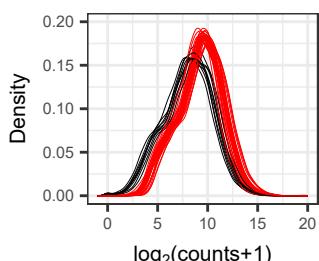
(Figure 6)

A

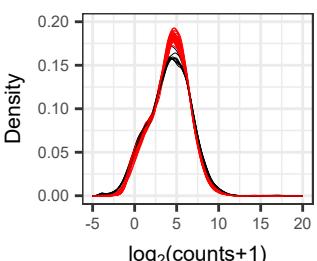
Trait Correlations -- |Pearson's rho|

**B**

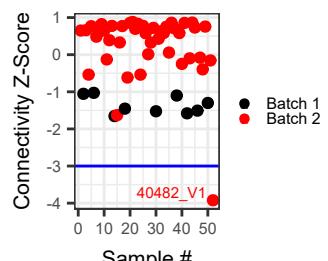
Pre-Normalization

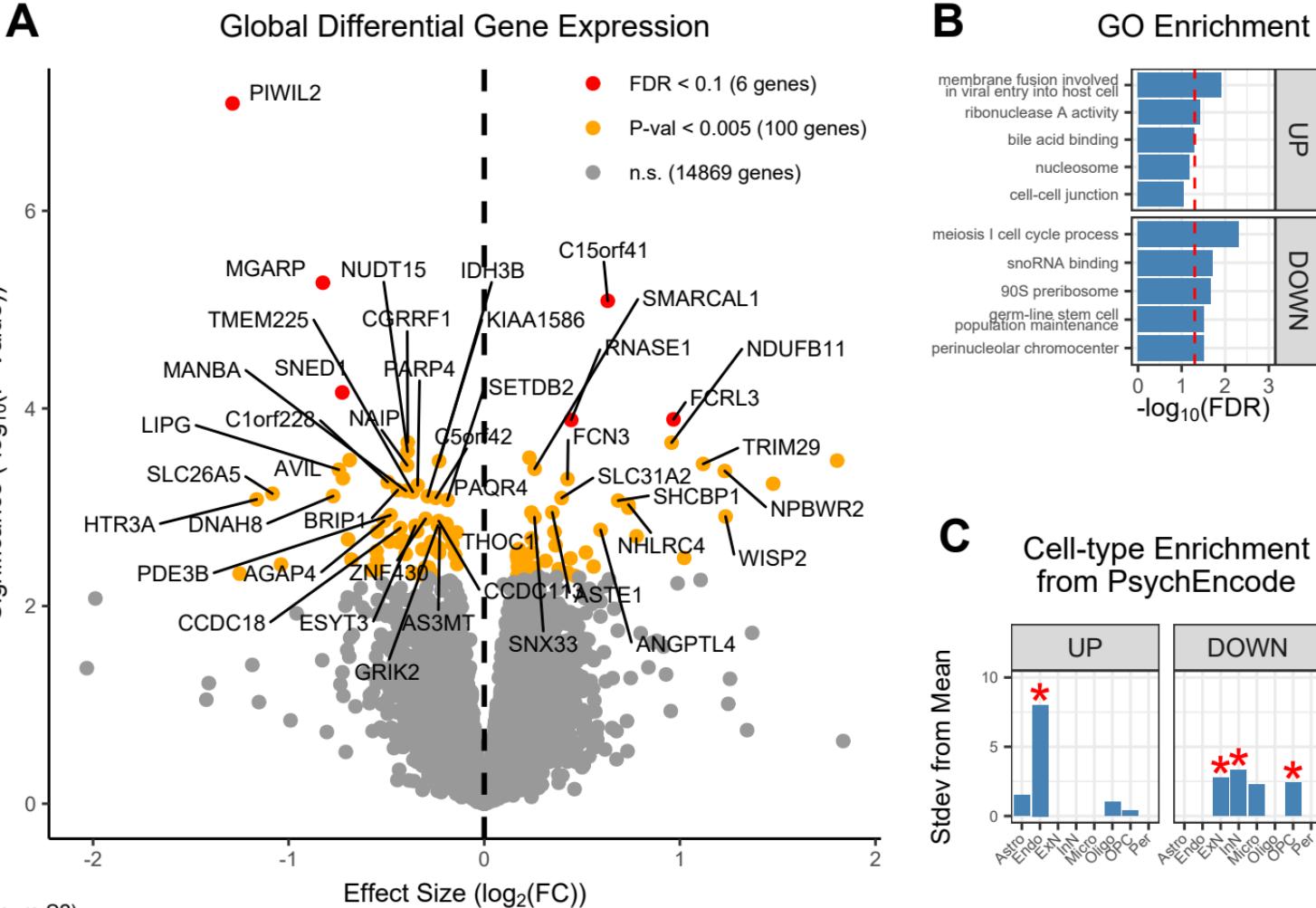
**C**

Post-Normalization

**D**

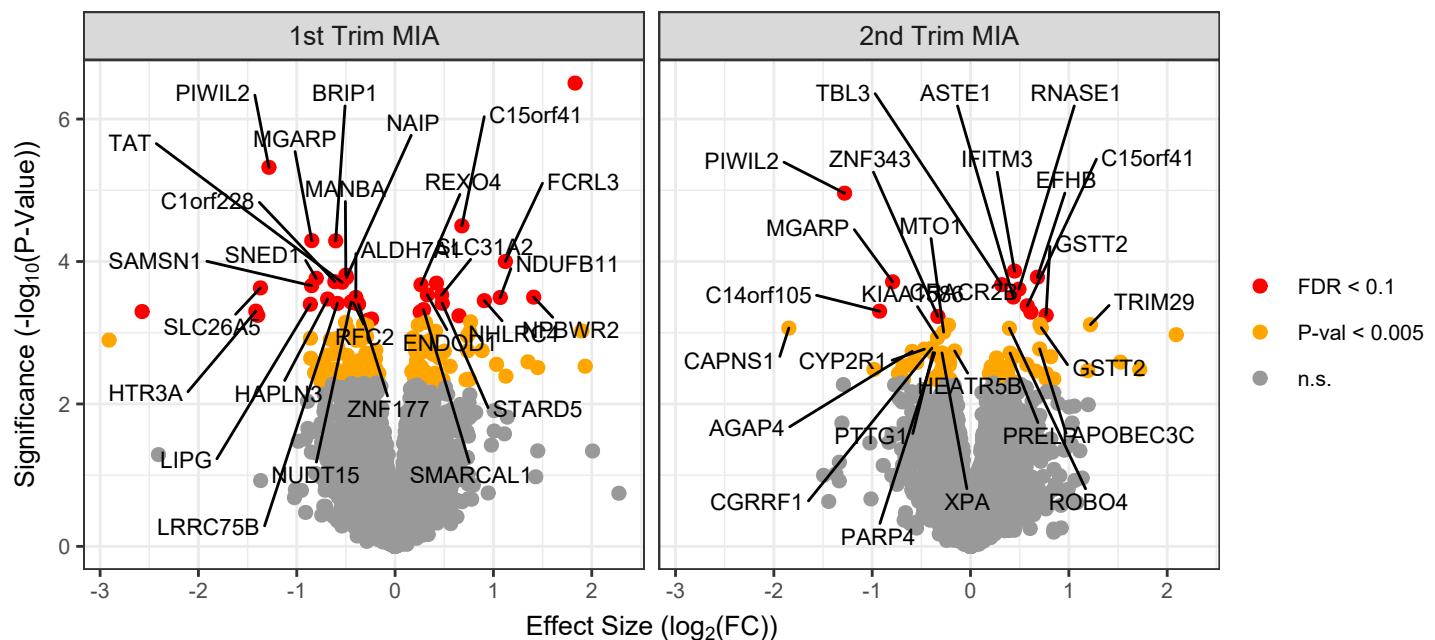
Outlier Removal



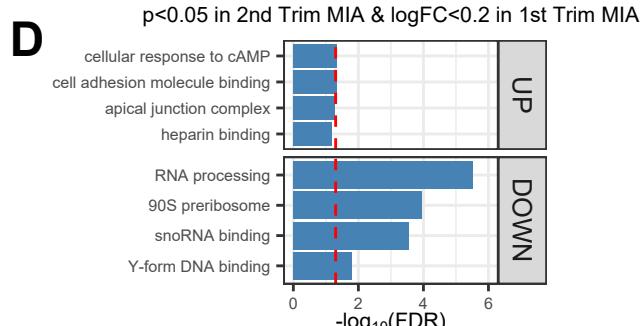
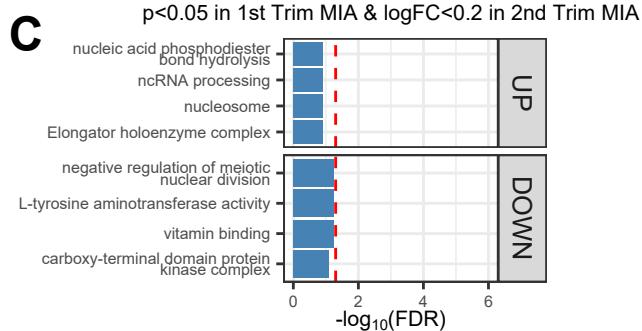
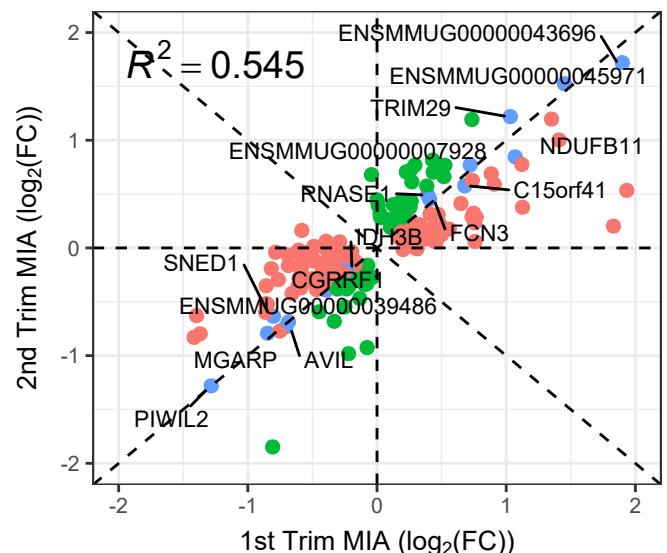


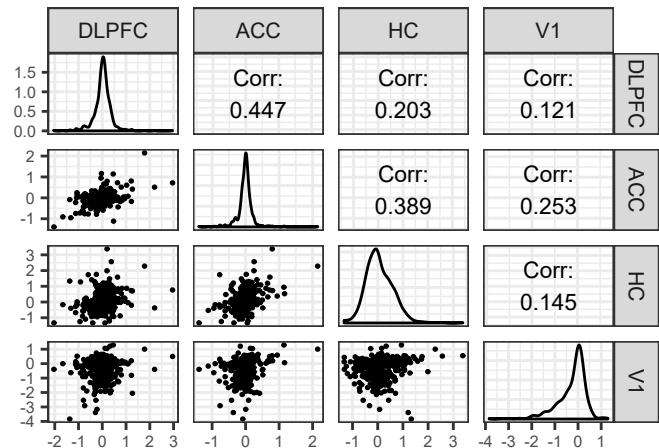
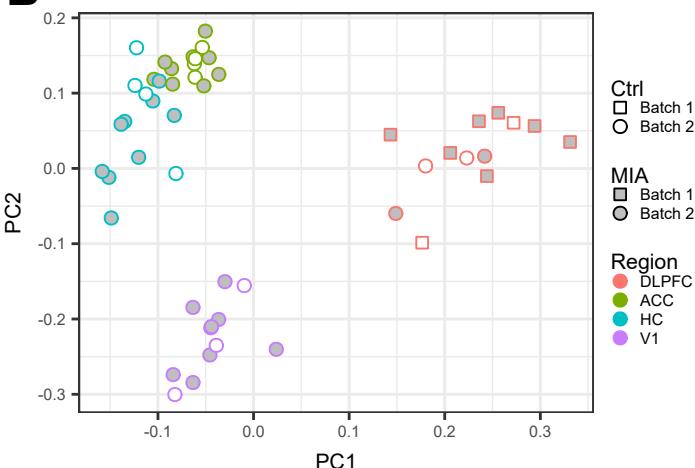
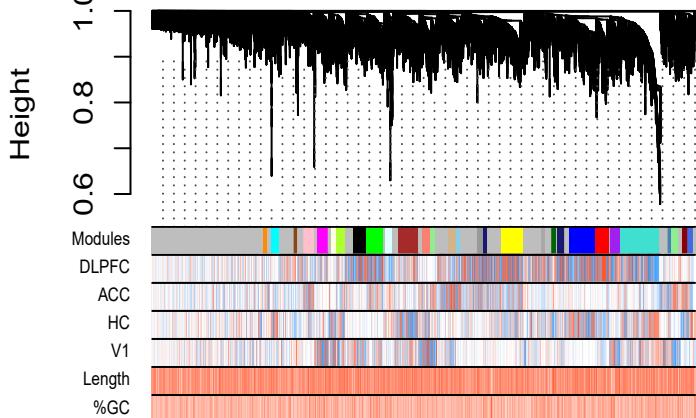
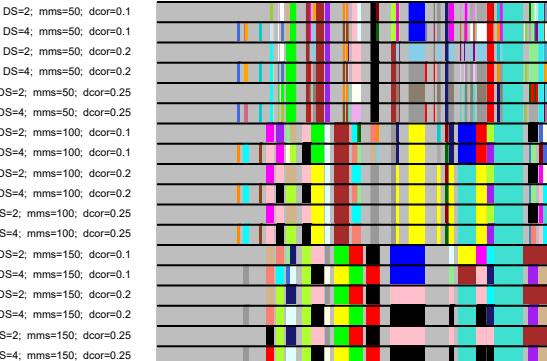
(Figure S2)

A Differential Gene Expression

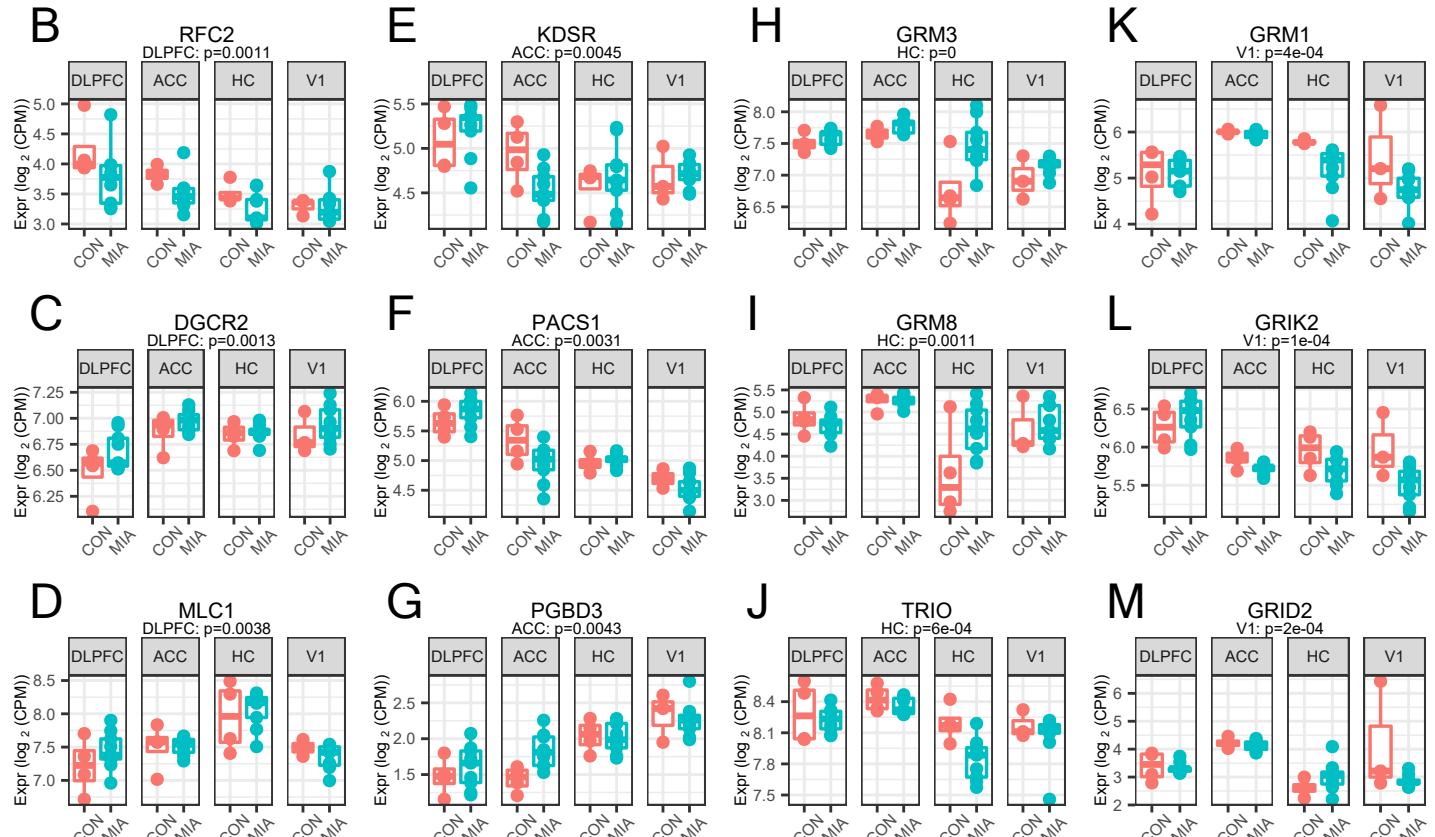
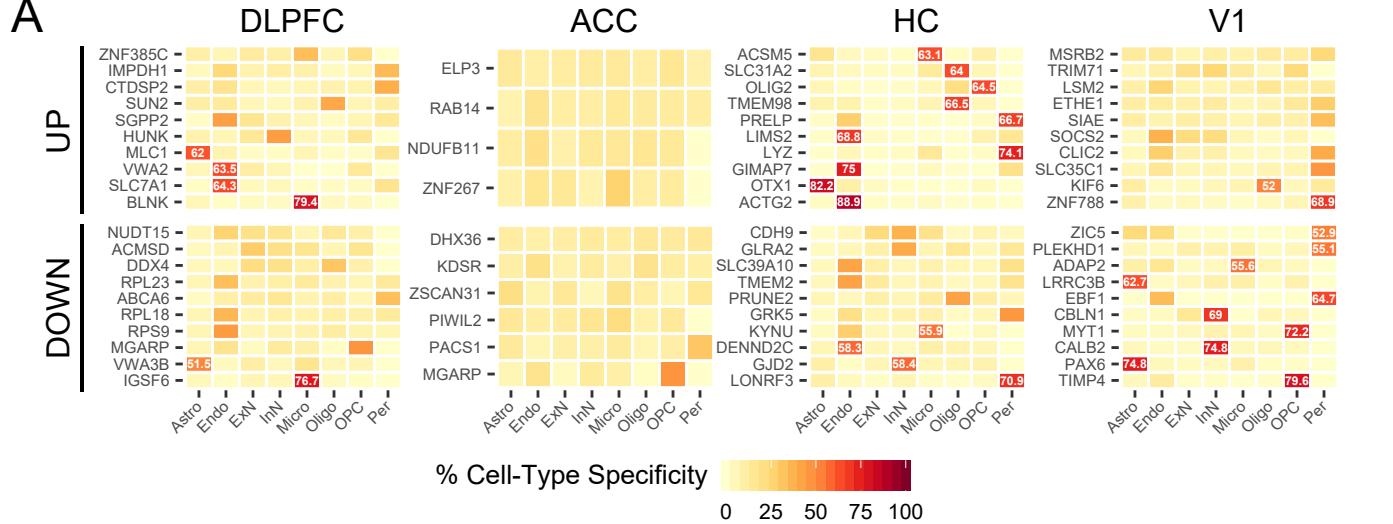


B Correlation of DE Genes



A p < 0.005 Genes logFC Correlation**B** Post SeqPC Regression**C** WGCNA**D**

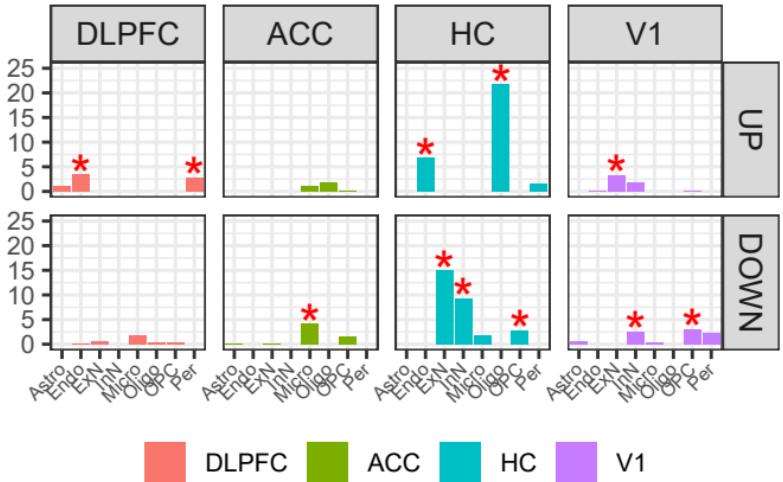
(Figure S4)



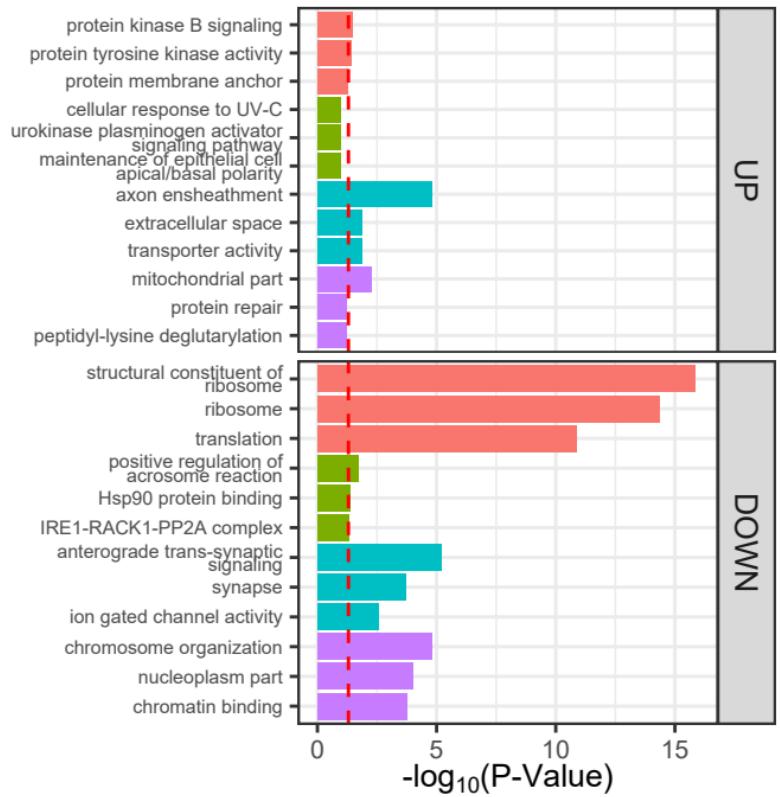
(Figure S5)

A

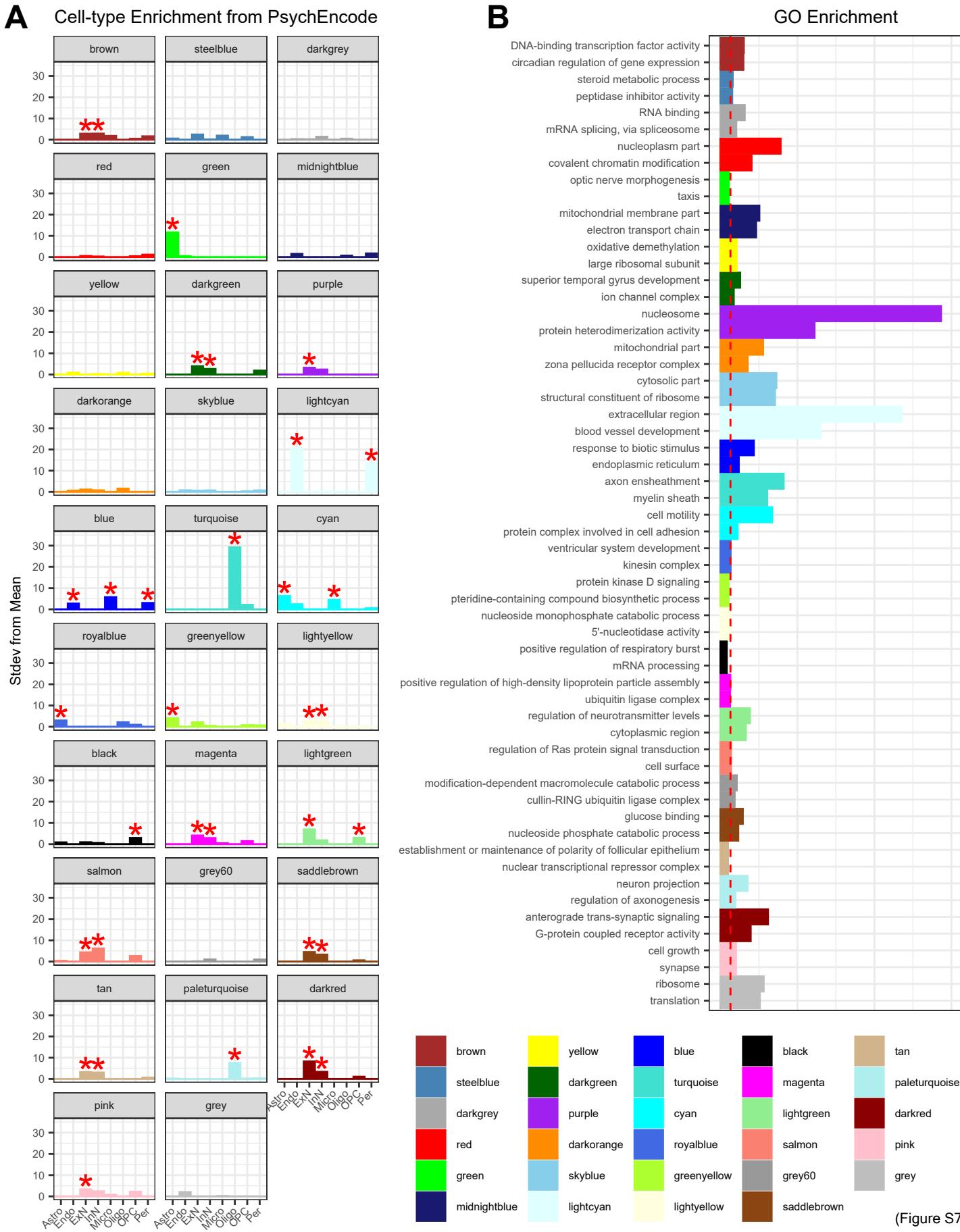
Cell-type Enrichment from PsychEncode

**B**

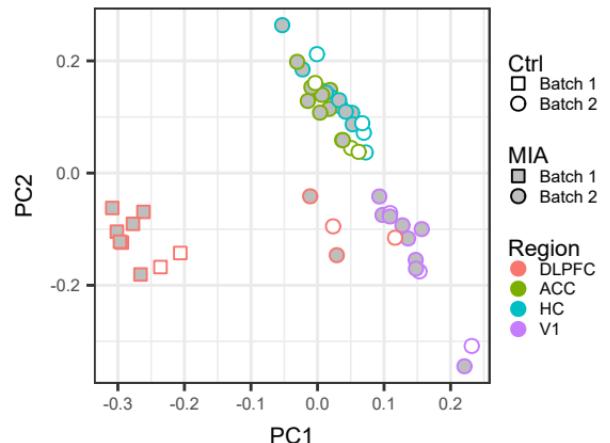
GO Enrichment



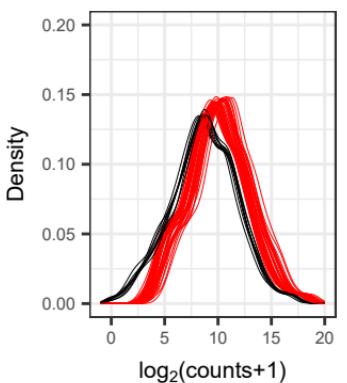
(Figure S6)



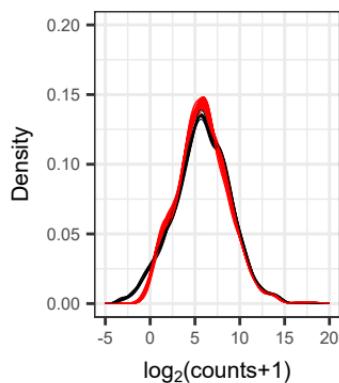
A TE Quality Control



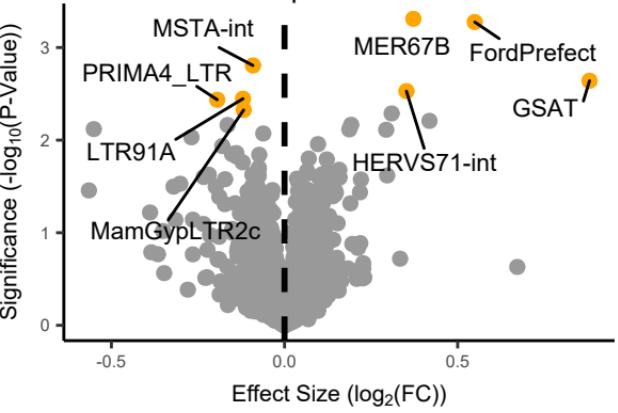
B Pre-Normalization



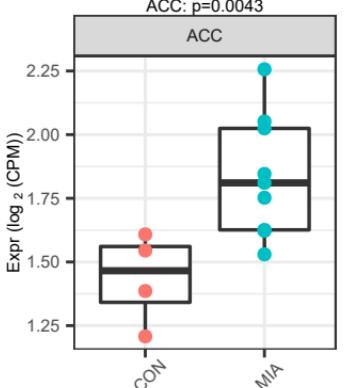
C Post-Normalization



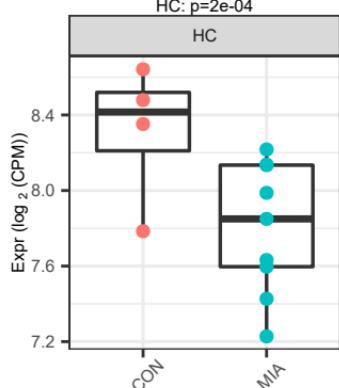
D Global Transposable Element DE



E PGBD3

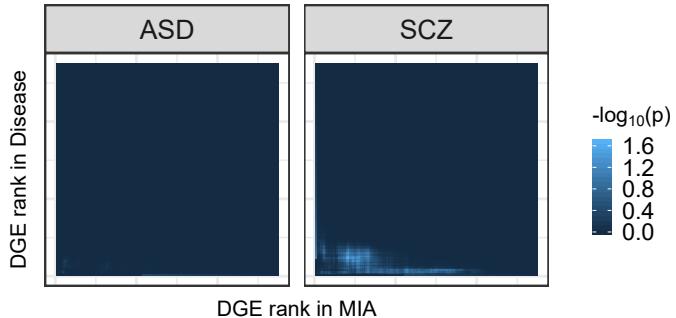


F PGBD5

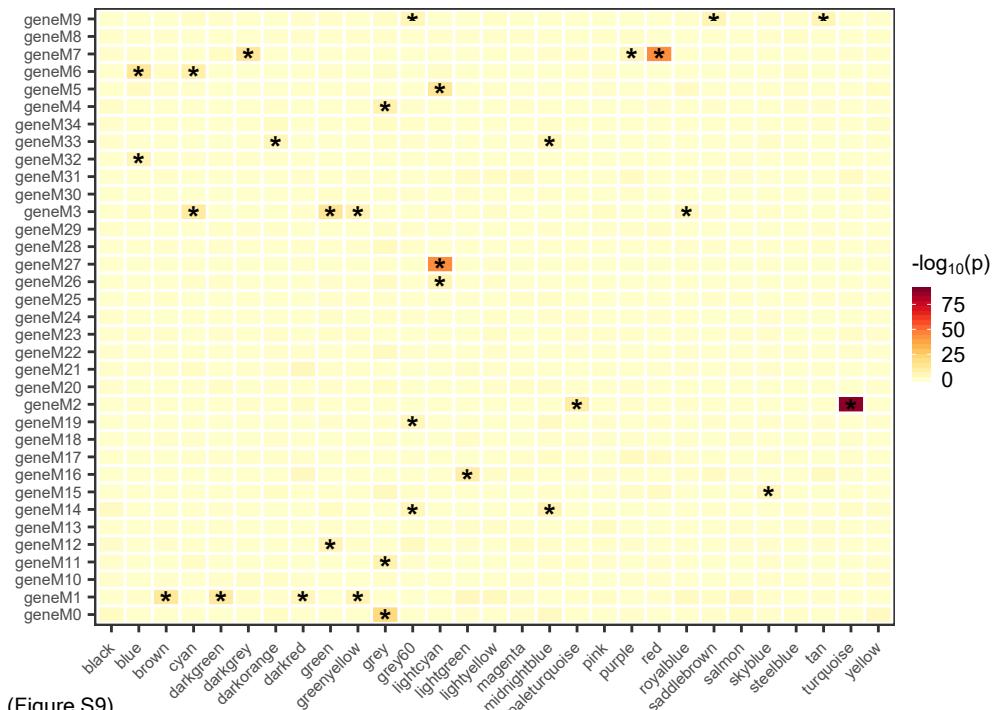


(Figure S8) ● P-val < 0.005 (8 TEs) ● n.s. (1287 TEs)

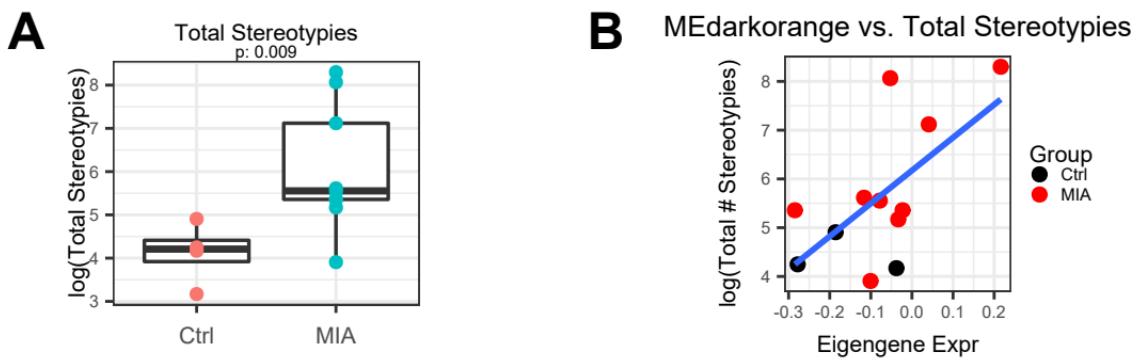
A DLPFC Disease MIA Overlap



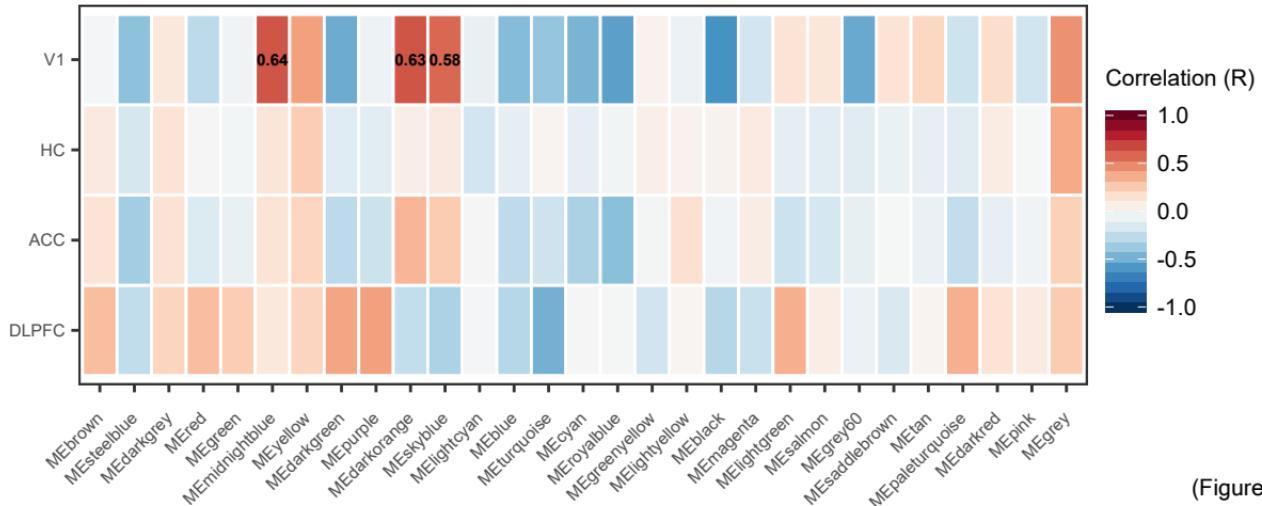
B PsychEncode Module Overlap



(Figure S9)



C Module Eigengene Stereotypes Correlation



(Figure S10)