Supplementary Figures

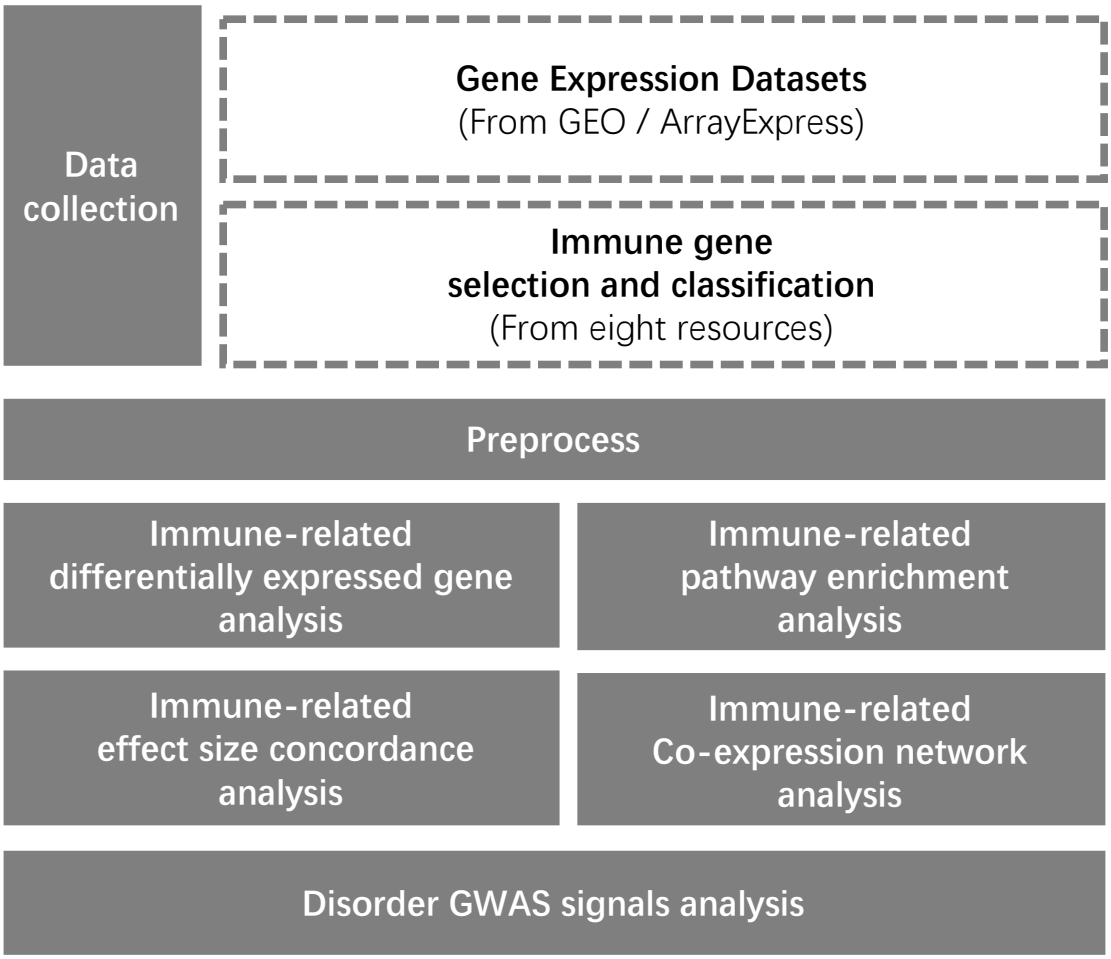

Figure S1. Study design

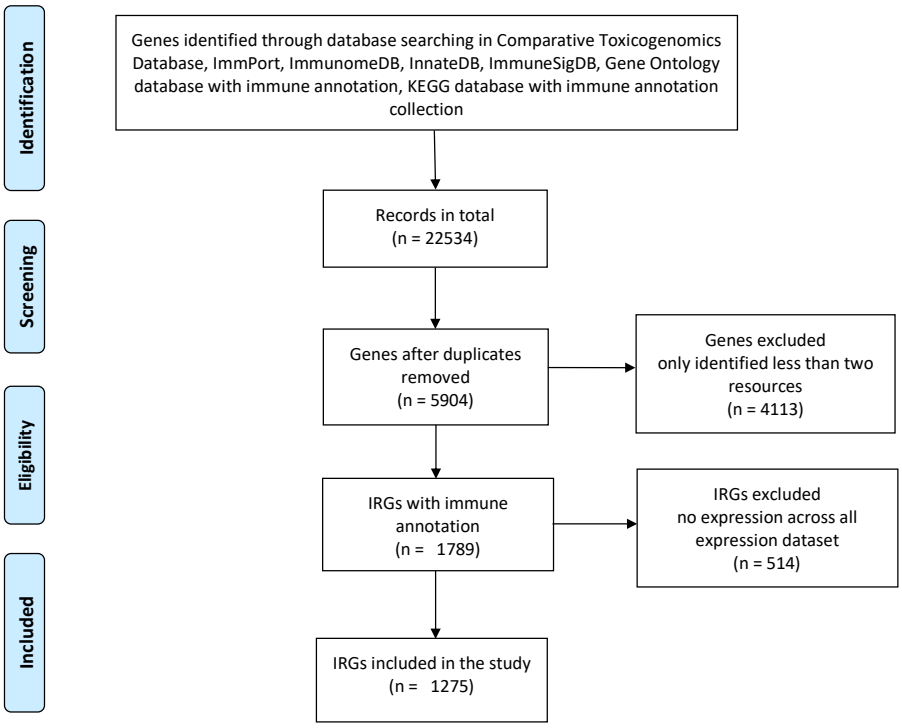

Figure S2. PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) It is an evidence-based minimum set of items aimed at helping authors to report a wide array of systematic reviews and meta-analyses, primarily used to assess the benefits and harms of a health care intervention. PRISMA focuses on ways in which authors can ensure a transparent and complete reporting of this type of research.

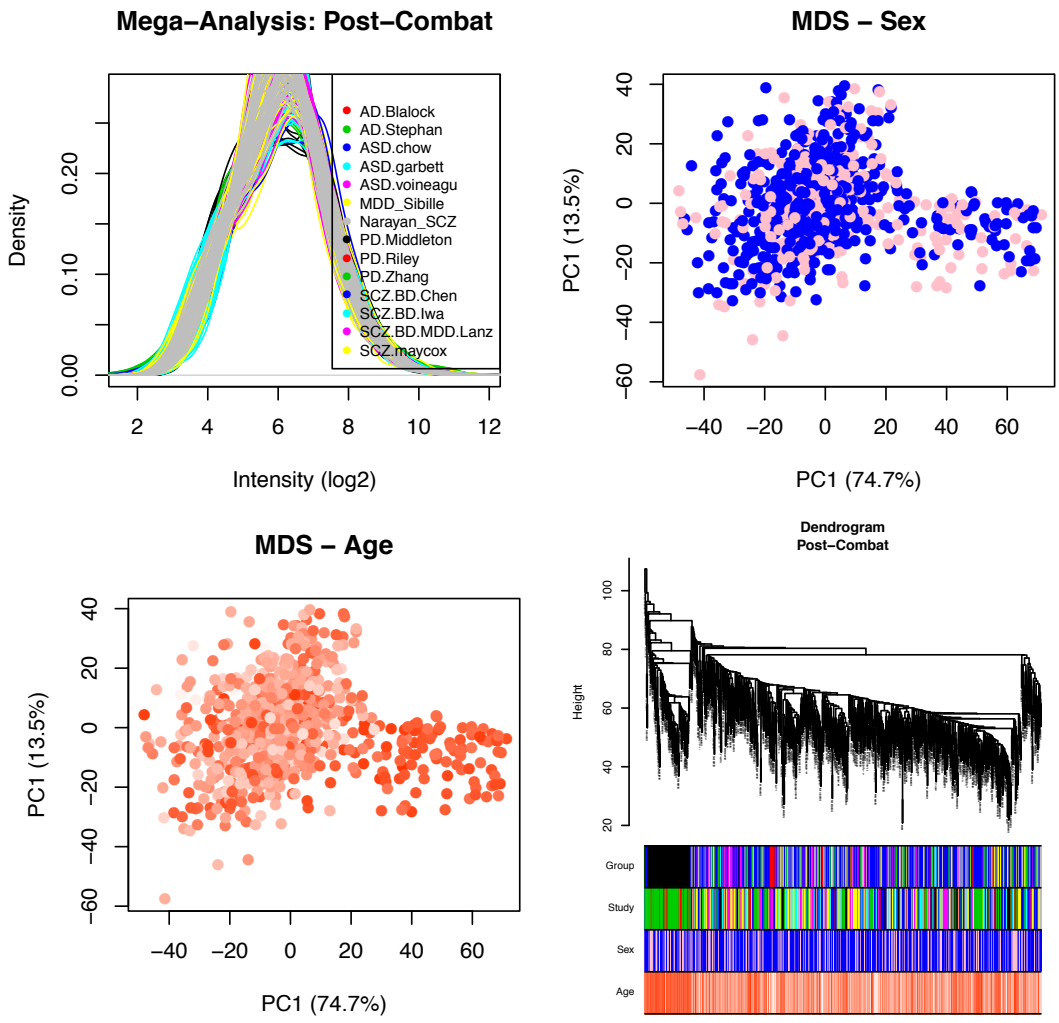

Figure S3. Here we showed post quality control plots including expression distribution and histograms. Outlier detection was determined based on standardized network connectivity z-scores. Multidimensional scaling (MDS) plots show sample clustering by the first two expression principal components.

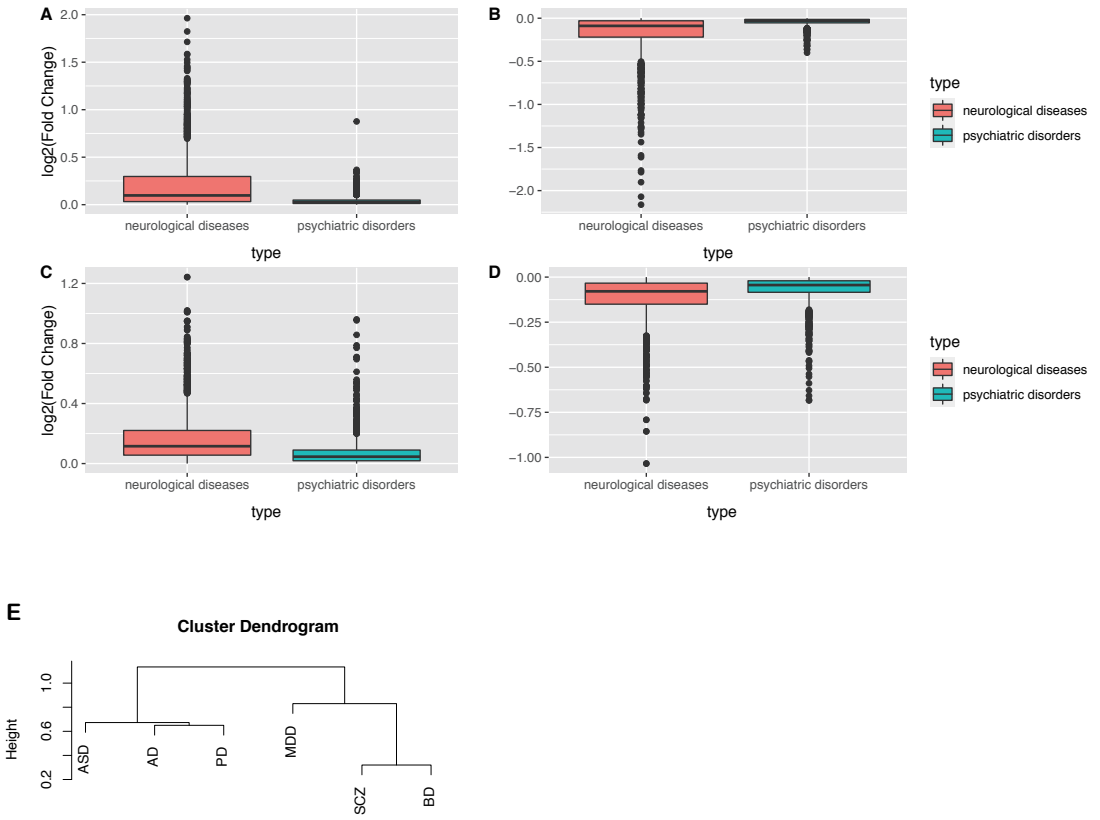

Figure S4. A, B A higher log2-FC in neurological disorders than in psychiatric disorders (t-test p.value < 2.2E-16, Fig. S4). C,D RNA-seq data replicated this observation that average log2-FC of IRGs is higher in neurological disorders than in psychiatric disorders. E. Cluster dendrogram of brain disorders

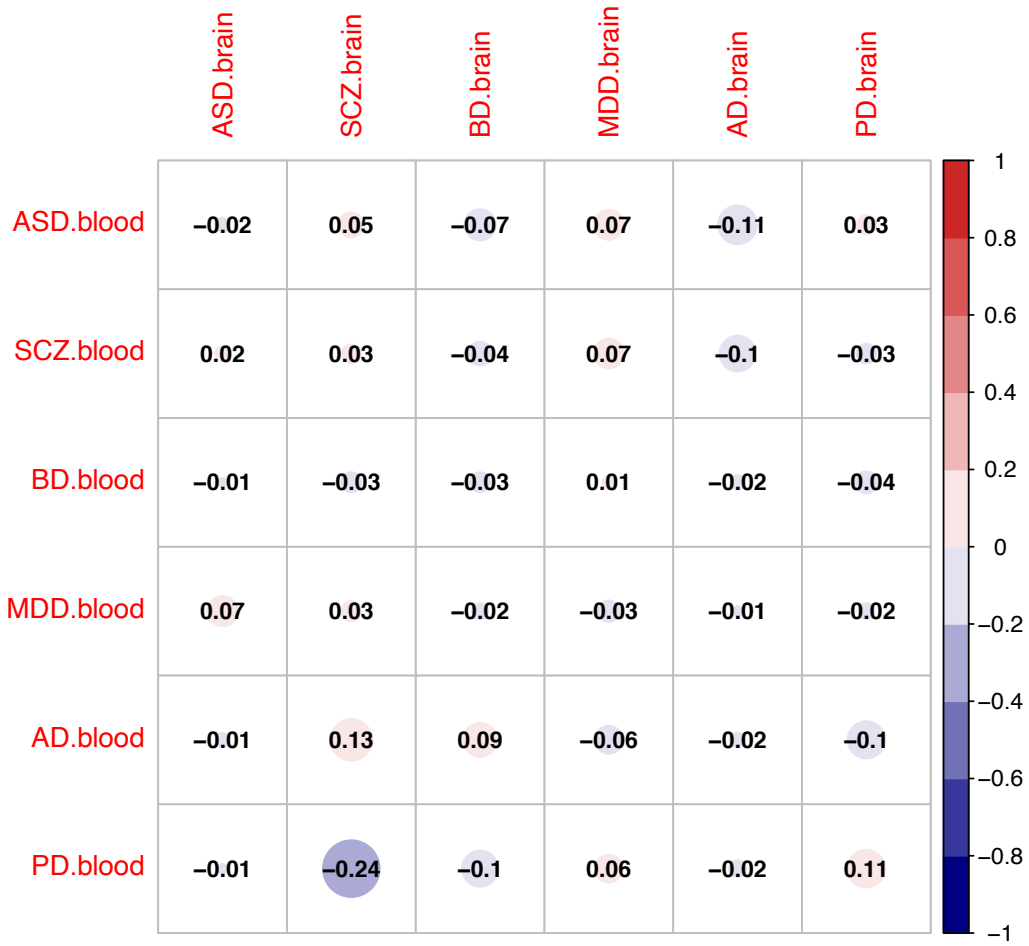

Figure S5. Brain blood correlations across neuropsychiatric disorders. The color of each box indicates the magnitude of the correlation. None of them were significant after Bonferroni correction.

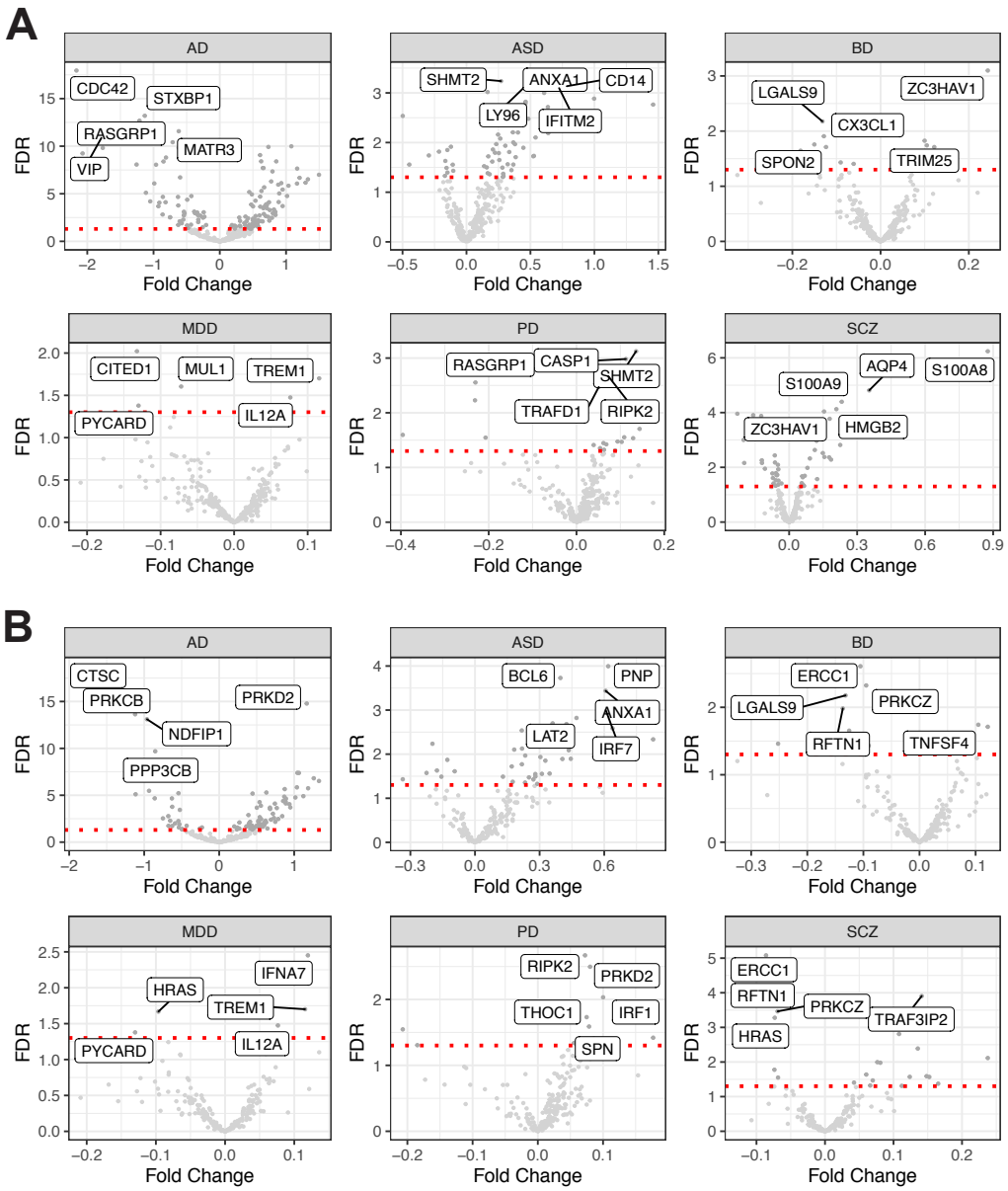

Figure S6. **Disease-specific differential expression of innate and adaptive IRGs.** A. Innate IRGs' volcano plot for each disorder. B Adaptive IRGs' volcano plots for each disorders.

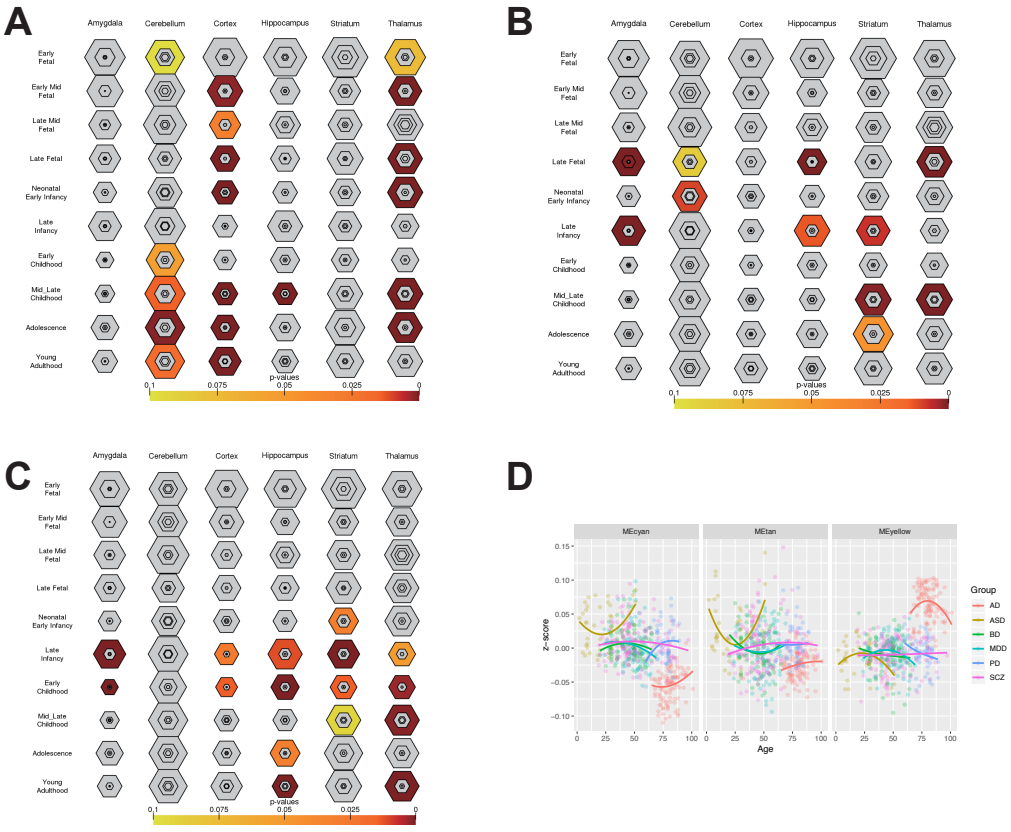

Figure S7. Analysis of enrichment in human brain regions supports the disruption of shared-IRMs. Genes of shared-IRMs are over-represented at multiple pSI levels in brain enriched transcripts calculated from Brainspan. Varying stringencies for enrichment (pSI): are represented by the size of the hexagons going from least specific lists (outer hexagons) to most specific (center). Hexagons scaled to size of gene lists.A Shared-IRM-4 has enriched expression during fetal cortical, cerebellum, and thalamus development. B. Shared-IRM-14 has enriched expression during medium-fetal brain development. C. Shared-IRM-12 has enriched expression during brain development after infancy. D. Eigengene expression of shared-IRMs across age demonstrates distinct and dynamic neural-immune trajectories.

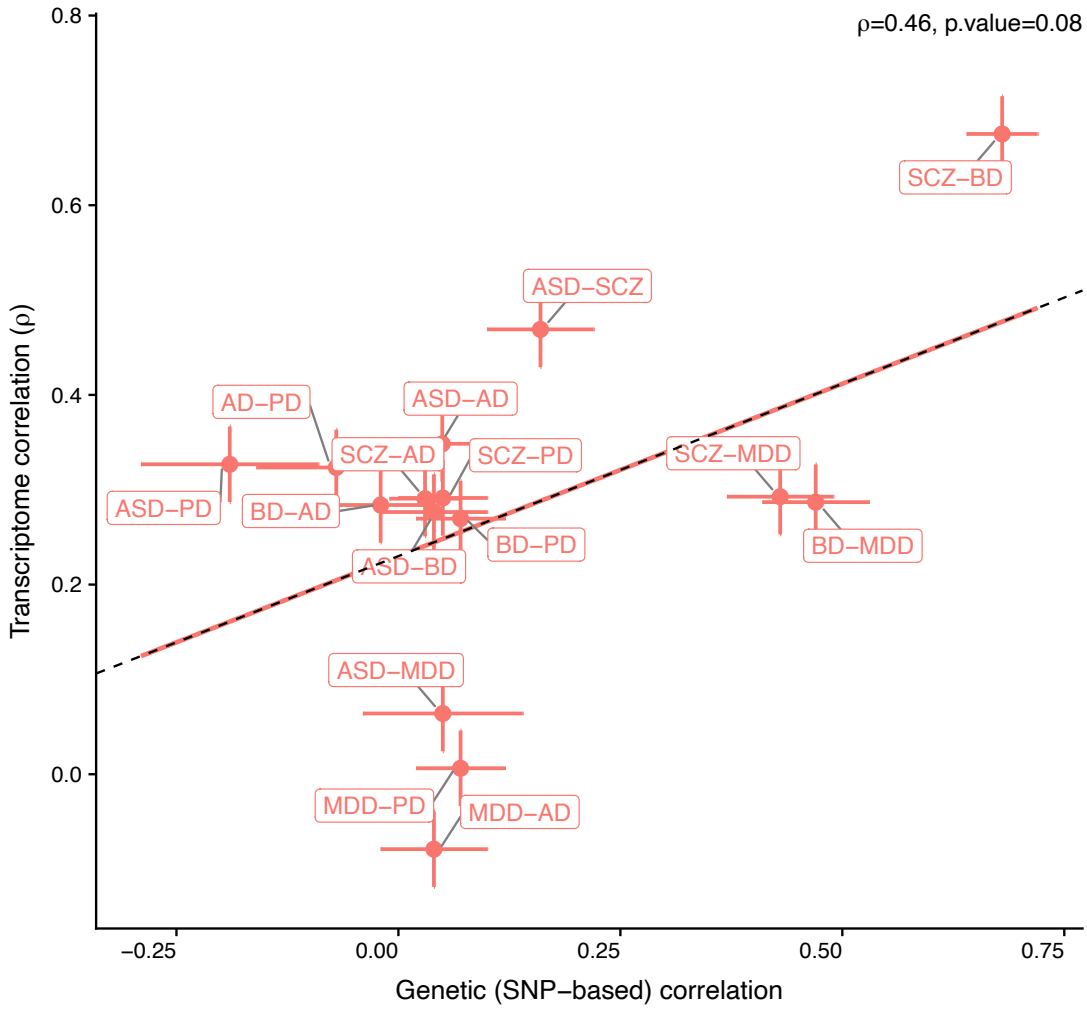

Figure S8. Correlation between transcriptome similarity and genetic overlap.