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# **Supplemental Data**

# Pleiotropic Meta-Analysis of Cognition, Education, and

## Schizophrenia Differentiates Roles of Early

## Neurodevelopmental and Adult Synaptic Pathways

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### Figure S1: Preliminary Analysis and ASSET Meta Analysis Workflow

*Note:* Summary statistics data was first consolidated in Stage 1 of the analysis, followed by performing preliminary genetic correlations to evaluate global genetic correlations across the traits of interests, i.e. cognition, education and schizophrenia. ASSET meta-analysis was carried during Stage 2 of the analysis followed by functional characterization of loci, genes and pathways obtained from the ASSET results.



### Figure S2: GWAS Loci Functional Characterization Workflow

*Note:* Functional characterization involved using tools such as MAGMA for gene-based and competitive pathway analysis, S-Predixcan was carried out to identify eQTL profiles in the brain, driven by ASSET metaanalysis, and GNOVA was utilized to examine localized genetic correlations of subsets identified by ASSET. A myriad of annotation databases were used including, GTEX7, CommonMind Consortium, DLPFC expression, and Drug pathway annotations. The FUMA annotation pipeline was also used to identify significant independent genomic loci from the ASSET meta-analysis, which also enabled loci lookups with more recent GWASs.



#### Figure S3: MAGMA Gene property tissue expression results for ASSET Subsets

*Note:* Colored bars indicate –log10P values for MAGMA gene property analysis. Both concordant and discordant ASSET subsets include genes highly expressed across brain tissue.

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Multi-Site Collaborative Study for Genotype-Phenotype Associations in Alzheimer's Disease (GENADA): phs000219.v1.p1

Long Life Family Study (LLFS): phs000397.v1.p1

Genetics of Late Onset Alzheimer's Disease Study (LOAD): phs000168.v1.p1

Minnesota Center for Twin and Family Research (MCTFR): phs000620.v1.p1

Philadelphia Neurodevelopmental Cohort (PNC): phs000607.v1.p1

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