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| GSE number | Author | Sample type | Sample size | Titles | Notes |
| GSE59288 | Liu et al. | Prefrontal cortex | ASD=34, Ctrl=38 | Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism | RNA-seq RAW data |
| GSE64018 | Parikshak et al. | Prefrontal cortex and cerebellum | ASD=12, Ctrl=12 | Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism | Obtained DEGs list from original article  |
| GSE28521 | Voineagu et al. | Prefrontal cortex, Cerebellum, and Temporal cortex | ASD=10, Ctrl=10 | Transcriptomic Analysis of Autism Brain Reveals Convergent Molecular Pathology | Microarray data |
| GSE18123 | Kong SW et al. | Whole blood | ASD=170, Ctrl=115 | Blood gene expression signatures distinguish autism spectrum disorders from controls | Microarray data |
| GSE25507 | Alter MD et al. | Peripheral blood lymphocytes | ASD=82, Ctrl=64 | Autism and increased paternal age-related changes in global levels of gene expression regulation | Microarray data |
| GSE42133 | Pramparo T et al. | Peripheral blood Leukocyte | ASD=91, Ctrl=56 | Disrupted functional networks in autism underlie early brain mal-development and provide accurate classification | Microarray data |
| GSSE89594 | Kimura R et al. | peripheral blood | ASD=32, Ctrl=54 | Integrative network analysis reveals biological pathways associated with Williams syndrome | Microarray data |

Table S1 Details of the gene expression profiles obtained from GEO DataSets