

Table S1. Details of the transcriptome data using post-mortem brain tissues of ASD and unaffected individuals obtained from GEO DataSets.

| Data type | GSE number | Author | Sample type | Sample size | Titles | Notes |
|--------------|------------|-------------------------|----------------------------------|-----------------|--|-----------------------|
| RNA-seq data | GSE59288 | Liu et al. (2016) | Prefrontal cortex | ASD=34, Ctrl=38 | Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism | RNA-seq RAW data |
| | GSE102741 | Wright et al. (2017) | Prefrontal cortex | ASD=13, Ctrl=39 | Altered expression of histamine signaling genes in autism spectrum disorder. | RNA-seq RAW data |
| | GSE64018 | Parikshak et al. (2014) | Prefrontal cortex and cerebellum | ASD=12, Ctrl=12 | Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism | no available RAW data |
| | GSE30573 | Voineagu et al. (2011) | Prefrontal cortex | ASD=3, Ctrl=3 | Transcriptomic analysis of autistic brain reveals convergent molecular pathology | RNA-seq RAW data |