

## **Supplementary Information Guide**

**Supplementary Table 1.** Sample metadata.

**Supplementary Table 2.** PLAC-seq, ATAC-seq, and RNA-seq data processing metrics.

**Supplementary Table 3.** Enriched GO terms for genes participating in cell type-specific chromatin interactions.

**Supplementary Table 4.** TF motif enrichment at cell type-specific distal interacting regions.

**Supplementary Table 5.** TF motif enrichment at distal interacting regions associated with WCGNA modules for each cell type.

**Supplementary Table 6.** Super interactive promoters for each cell type.

**Supplementary Table 7.** Genes and enriched GO terms for distinct developmental trajectories.

**Supplementary Table 8.** TF motif enrichment at distal interacting regions for distinct developmental trajectories.

**Supplementary Table 9.** Cell type-specific enrichment for chromatin interactions between biological processes and human-gained enhancers.

**Supplementary Table 10.** Target gene annotation for enhancers participating in chromatin interactions.

**Supplementary Table 11.** Target gene annotation for complex neuropsychiatric disorder- and trait-associated GWAS SNPs participating in chromatin interactions.

**Supplementary Table 12.** Enriched GO terms for genes linked to complex neuropsychiatric disorder- and trait-associated GWAS SNPs.

**Supplementary Table 13.** sgRNA sequences used for functional validation.