Table 1. Gene ontology (GO) enrichment analyses of the differentially expressed genes between ABX and control mPFC samples in Fig. 1f.

Table 2. Gene ontology (GO) enrichment analyses of the differentially expressed genes shared by excitatory neuronal subsets in Fig. 2a.

Table 3. Gene ontology (GO) enrichment analyses of the differentially expressed genes shared by multiple cell types in Fig. 2a.

Table 4. Gene ontology (GO) enrichment analyses of the differentially expressed genes in microglia in Fig. 2c.