



**Supplementary Figure 3.** Single nucleus transcriptomic characteristics including cell type distribution and gene expression patterns in the hippocampi of mice with maternal separation and social isolation. A-C: Identified cell types by Seurat analysis from single nucleus RNA sequencing in mouse hippocampi and cell type distribution between the groups. Graph theory-based cell type clustering of D is presented. The identified cell types classified in the CTL included neurons, which appeared the most at 92.1% compared to the MS and the maternal separation with social isolation group (SS). E: Heatmap showing the gene expression patterns for the top 20 genes in each cluster. Dot plot showing the top 20 genes per cluster. The size of each dot represents the percentage of the gene per each cluster. Color represents the average expression levels (N=The hippocampi of 3 mice each were included in the CTL, MS, and SS). CTL, control group; MS, maternal separation group; SS, social isolation after maternal separation group.