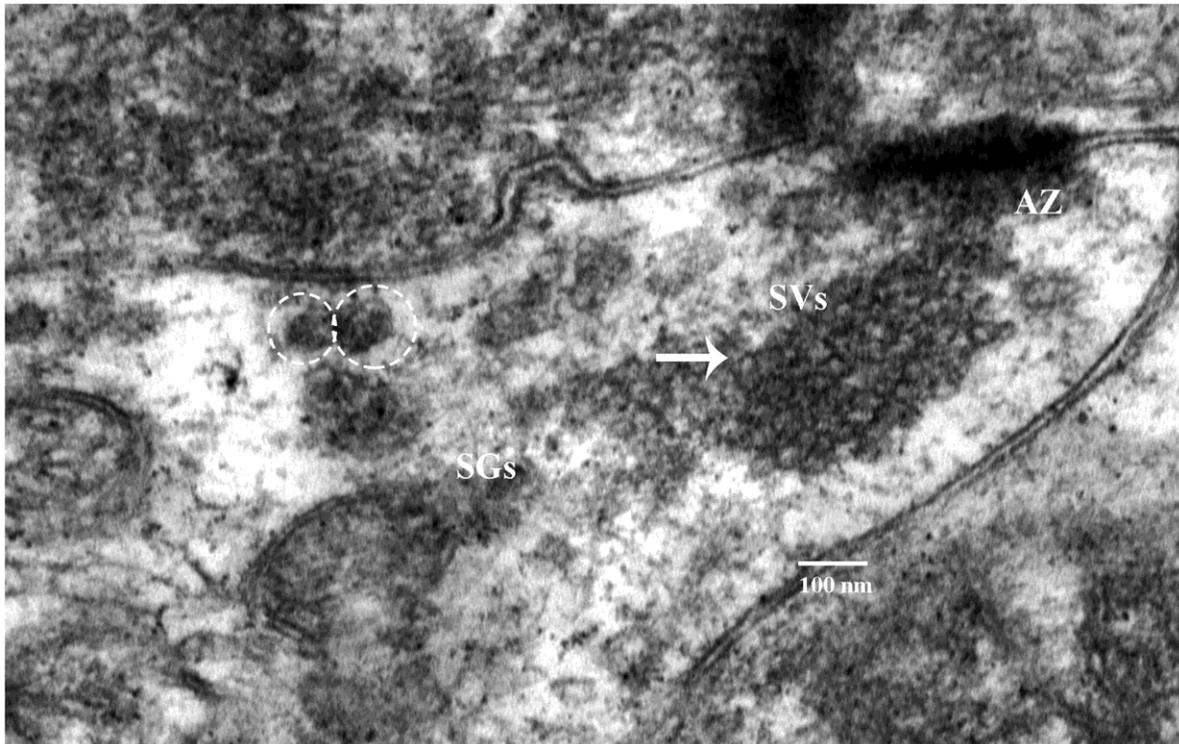
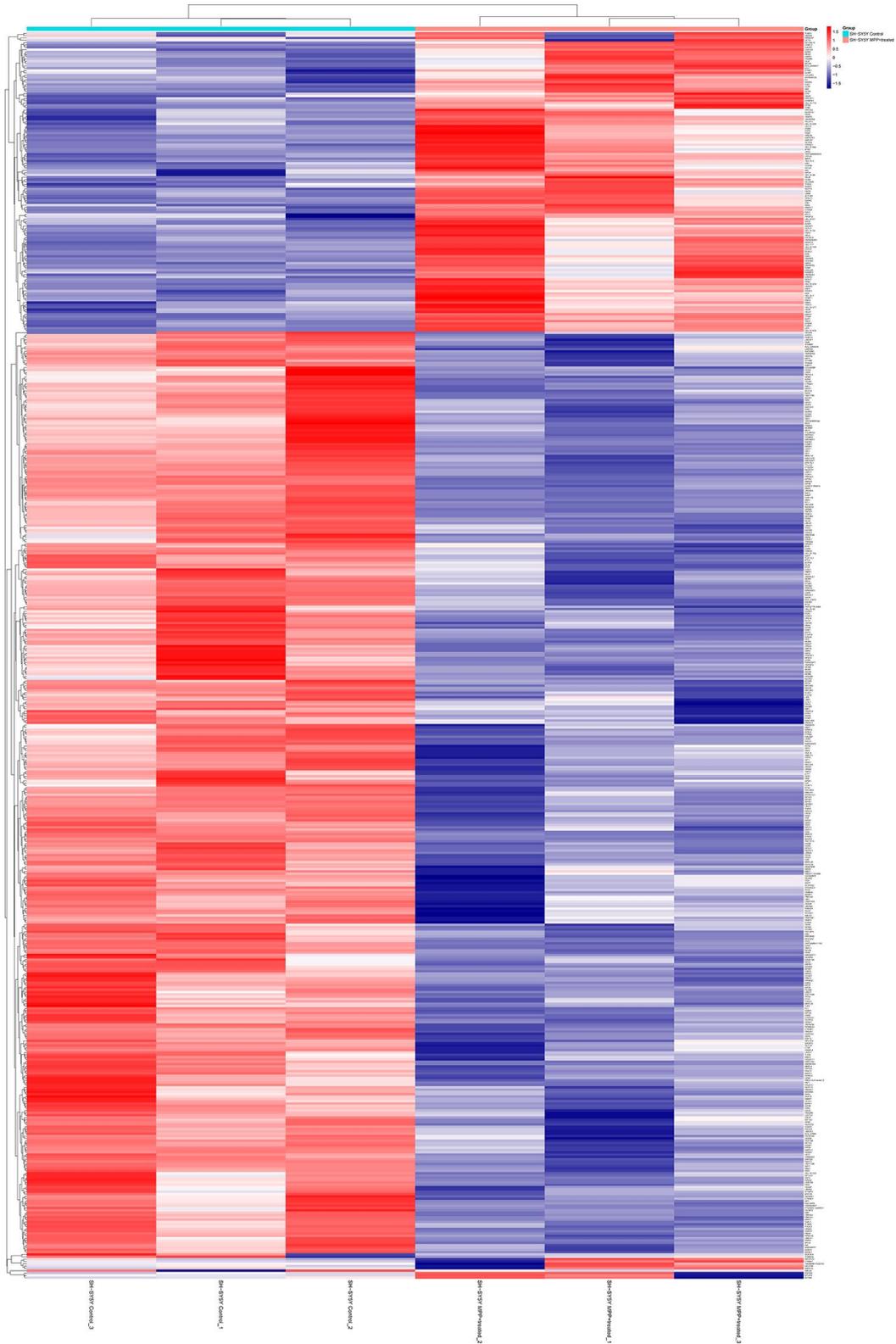


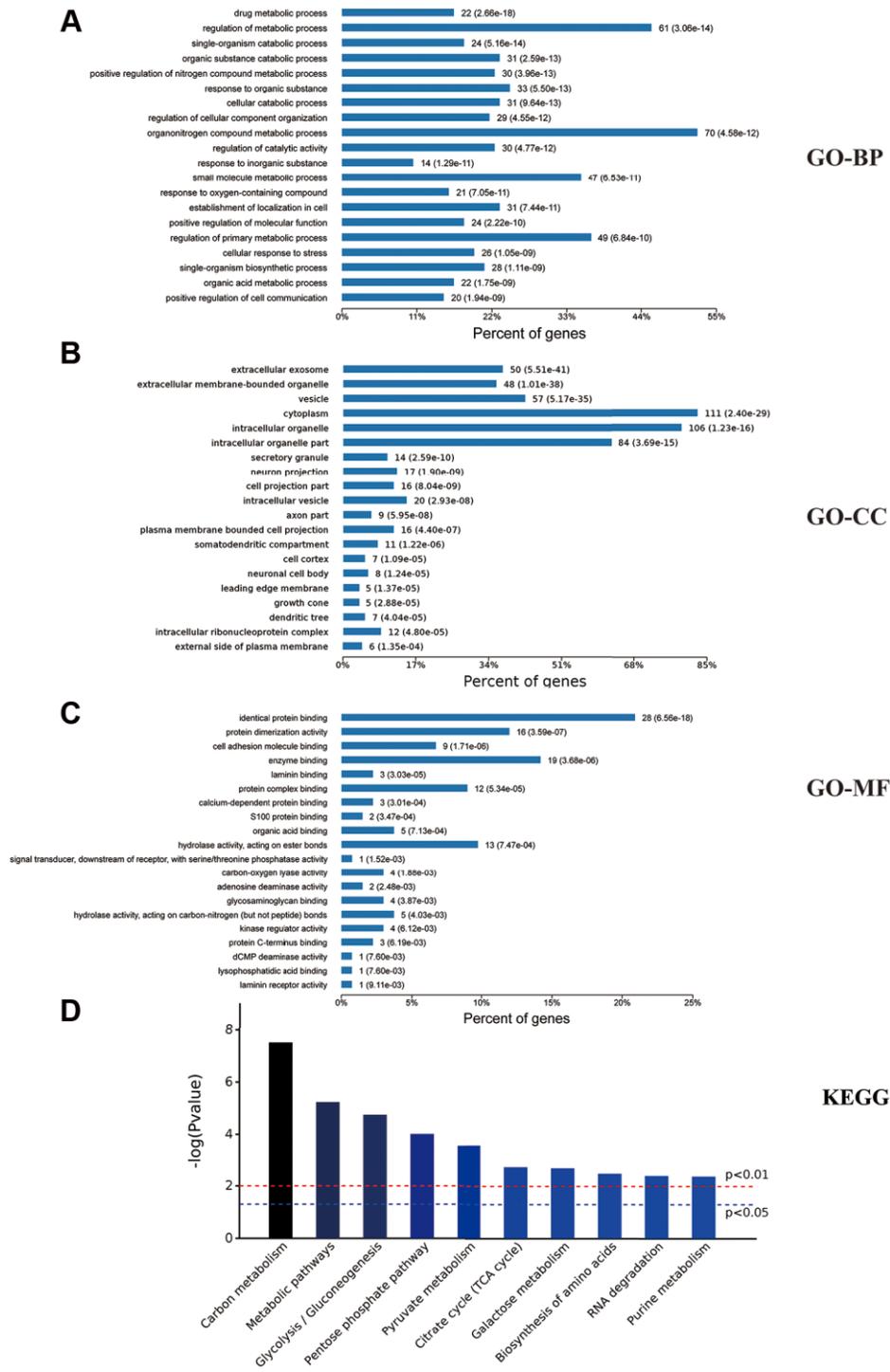
SUPPLEMENTARY FIGURES



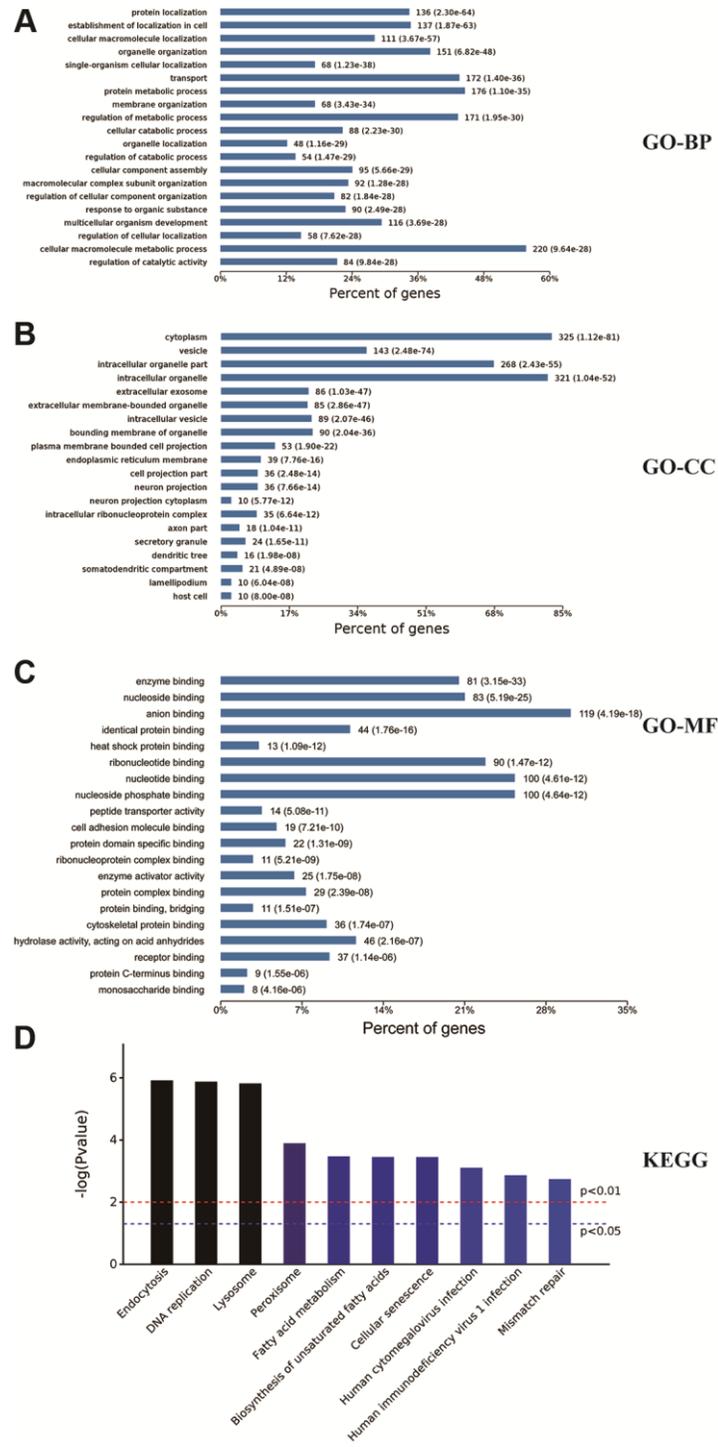
Supplementary Figure 1. Electron microscopy image of dense-core SGs of neurons in SN. The existence of SGs was captured using electron microscopy. Several dense-core SGs are present at the border of synaptic vesicle clusters. SVs: Synaptic vesicles; AZ: Active zone; SGs: Secretory granules.



Supplementary Figure 2. Heatmap analysis using complete linkage hierarchical clustering of the significantly differentially expressed proteins between the control and MPP⁺ groups. Cluster 1 represents significantly up-regulated proteins in and MPP⁺ treated groups, cluster 2 represents significantly down-regulated proteins. *N* = 3.



Supplementary Figure 3. Enrichment analysis of significantly up-regulated expressed proteins in the secretory granules enriched samples of control and MPP⁺ groups. The secretory granules enriched samples of control and MPP⁺ treated SH-sy5Y cells were separated via sucrose density gradient centrifugation, and sent for the mass spectrometry analysis. 145 proteins were identified as significantly increased with the fold of change (FC \geq 1.5, $P < 0.05$, $N = 3$). And Gene ontology and Kyoto Encyclopedia of genes and genomes pathways analysis was conducted to these proteins. (A) Gene ontology biological processes (BP). (B) Gene ontology cellular components (CC). (C) Gene ontology molecular functions (MF). (D) Kyoto Encyclopedia of genes and genomes pathways.



Supplementary Figure 4. Enrichment analysis of significantly down-regulated expressed proteins in the secretory granules enriched samples of control and MPP⁺ groups. The secretory granules enriched samples of control and MPP⁺ treated SH-sy5Y cells were separated via sucrose density gradient centrifugation, and sent for the mass spectrometry analysis. 576 proteins were identified as significantly decreased with the fold of change (FC \geq 1.5, $P < 0.05$). And Gene ontology and Kyoto Encyclopedia of genes and genomes pathways analysis was conducted to these proteins. (A) Gene ontology biological processes (BP). (B) Gene ontology cellular components (CC). (C) Gene ontology molecular functions (MF). (D) Kyoto Encyclopedia of genes and genomes pathways.