

Supporting Information

Quantitative proteomic analysis identifies proteins and pathways related to neuronal development in differentiated SH-SY5Y neuroblastoma cells.

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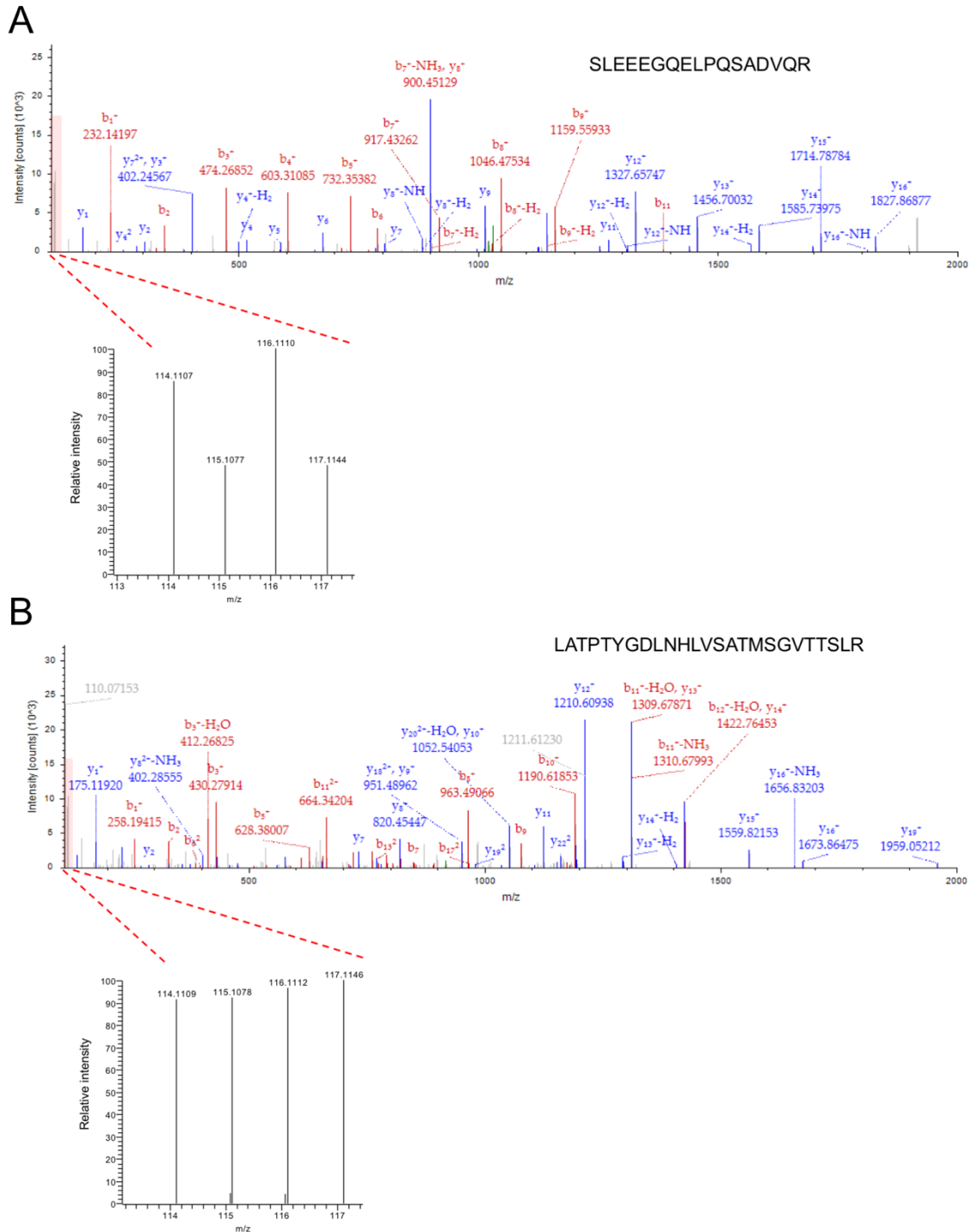


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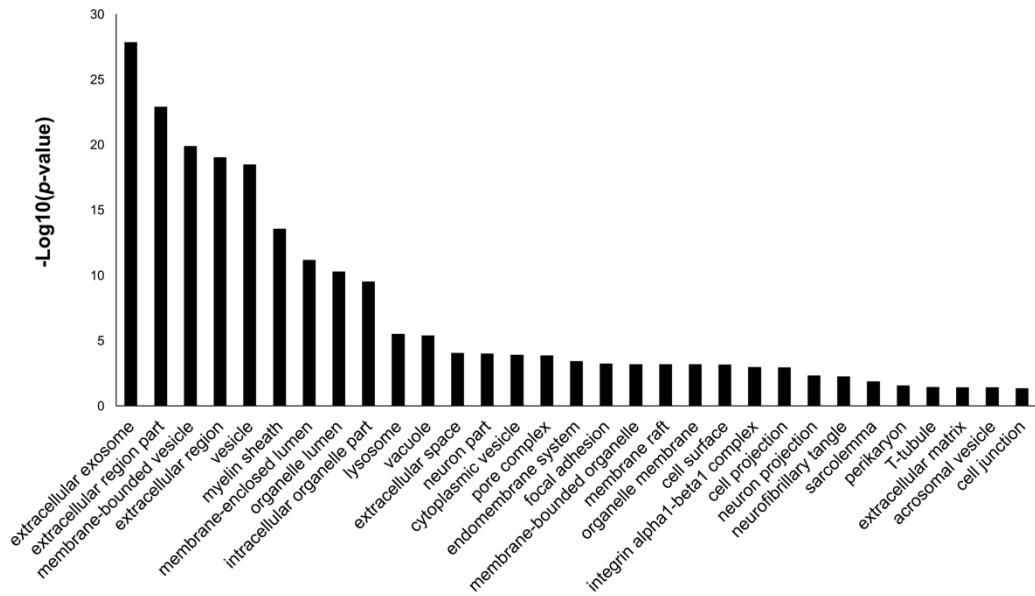


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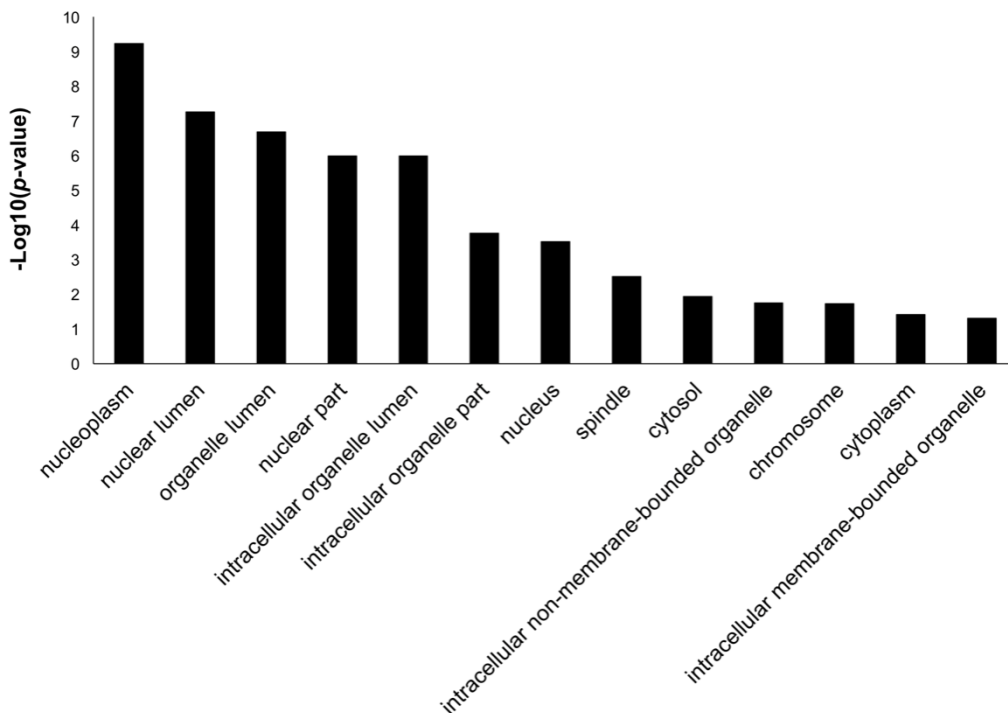


Fig. S3. GO analysis (cellular component terms) of the downregulated proteins from total proteome (without phosphopeptide enrichment) data set. Only terms with p values less than 0.01 are shown.

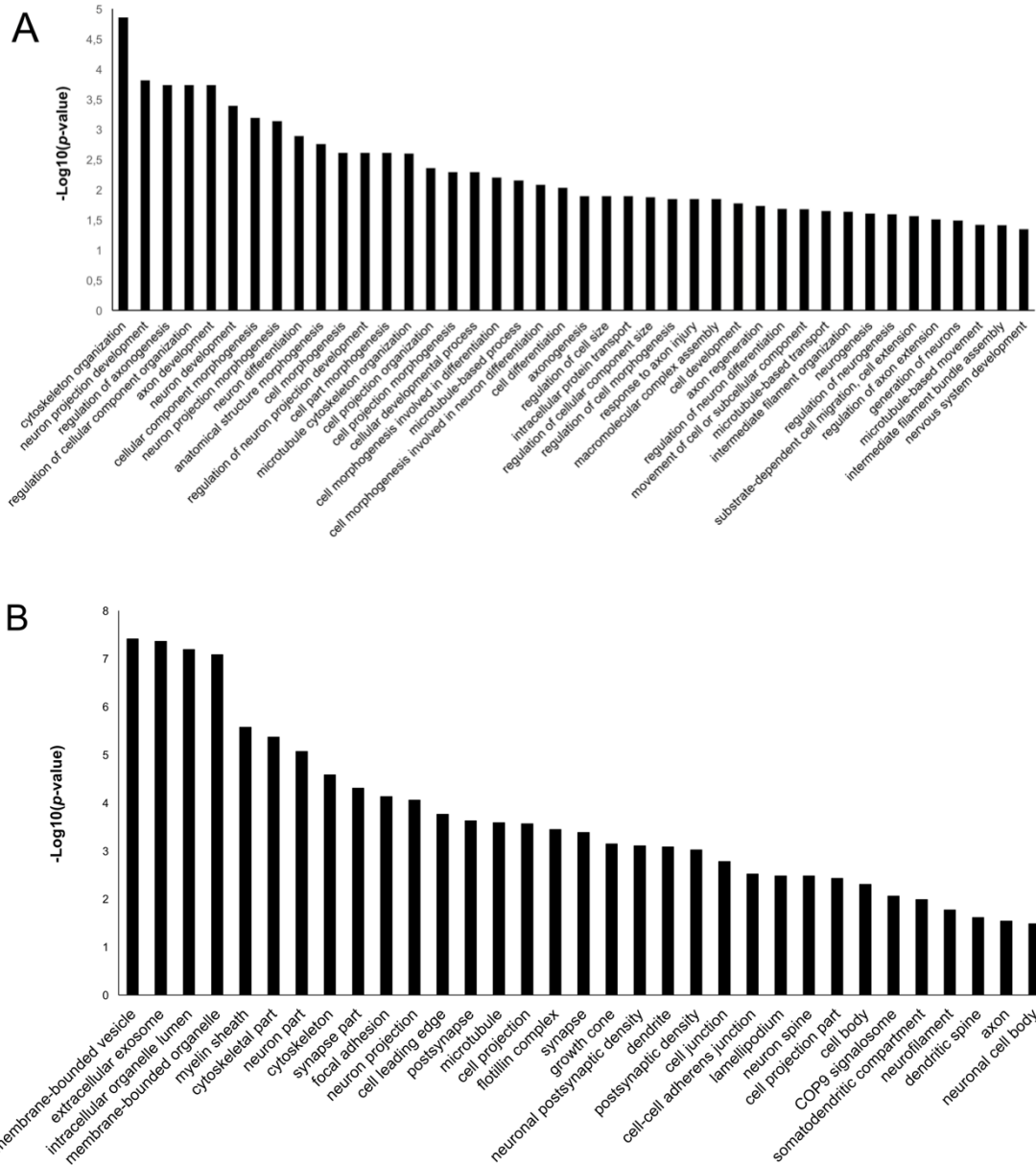


Fig. S4. GO analysis of the upregulated proteins from phosphopeptide enrichment data set. (A) Biological process. (B) Cellular component. Only terms with p values less than 0.01 are shown.

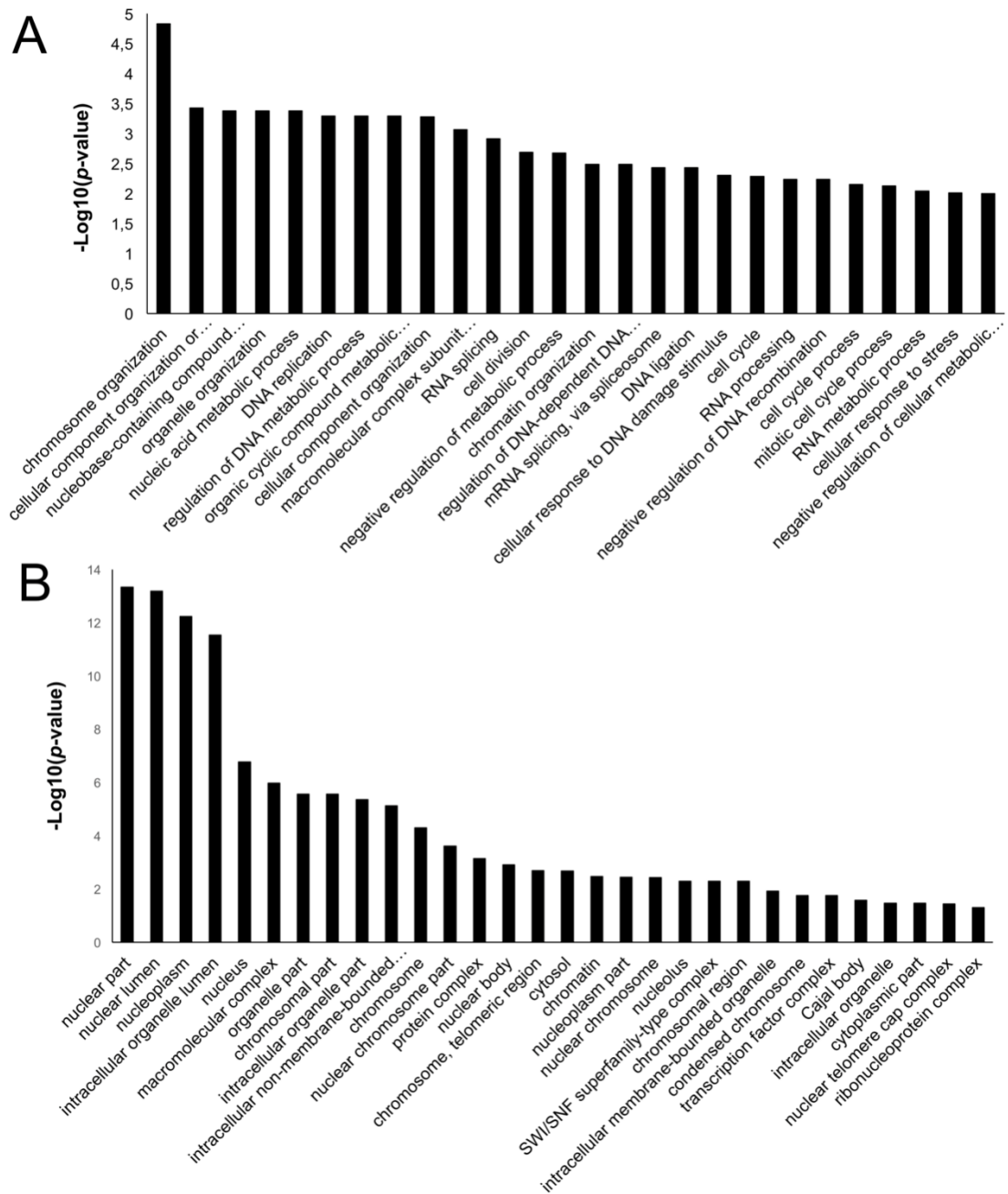


Fig. S5. GO analysis of the downregulated proteins from phosphopeptide enrichment data set. (A) Biological process. (B) Cellular component. Only terms with p values less than 0.01 are shown.

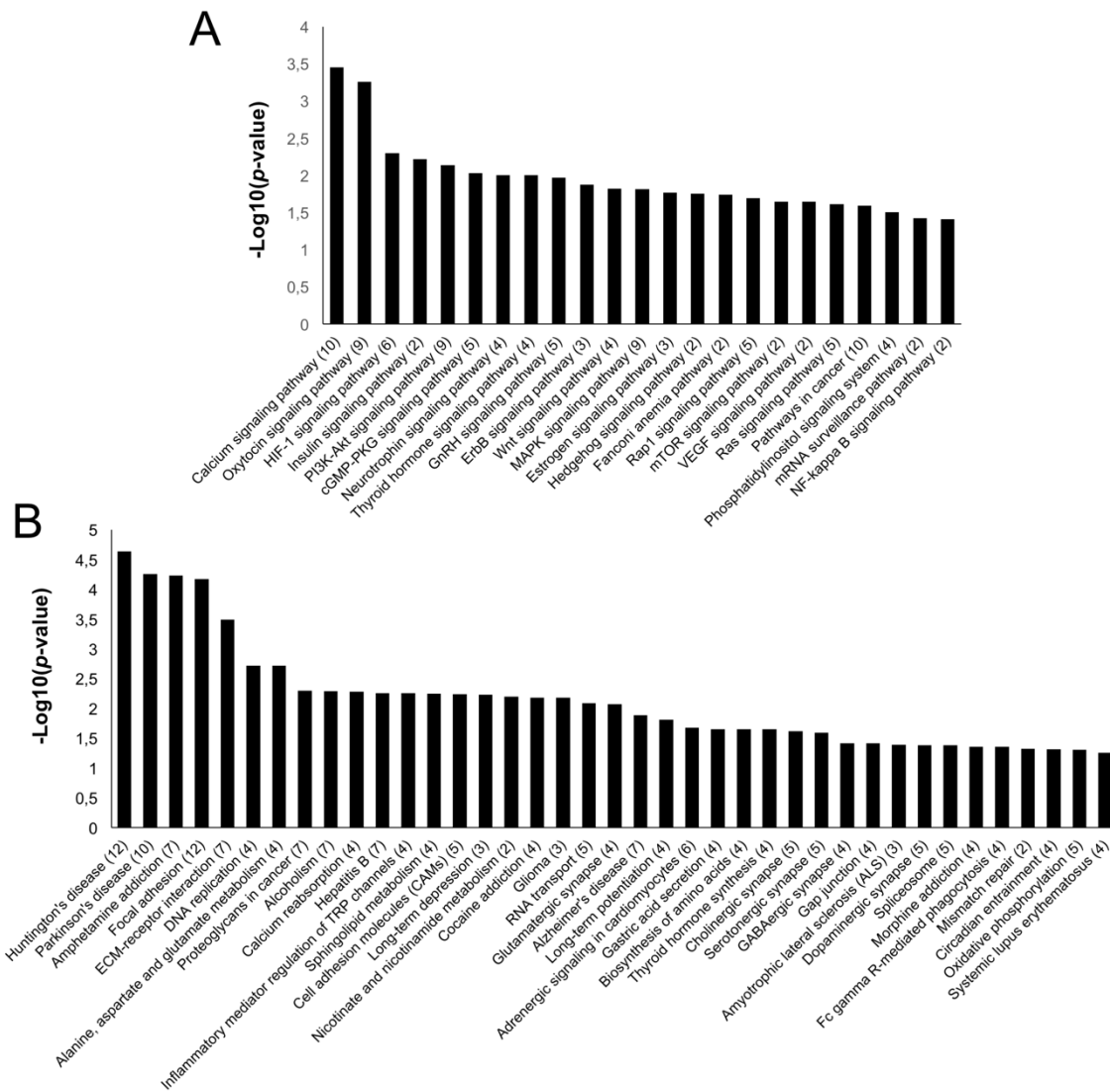


Fig. S6. KEGG pathways enrichment analysis of regulated proteins in interactive network. (A) Signaling pathways enrichment. (B) Pathways enrichment of processes related to neuron phenotype. Only terms with p values less than 0.01 are shown. Number of proteins involved in each pathway are indicated in parenthesis.