Transcriptomic Analysis Reveals PTBP1 as a Key Molecular Signature of Sciatic Nerve Injury Recovery

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Research

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Abstract

Background: Peripheral nerves control motor, sensory, and autonomic functions, so injury can seriously affect a patient's quality of life. There have been studies that have shown that the repair factors are different at different ages, and we have identified a repair hub gene that plays a key role throughout the entire age group.

Methods: From Gene Expression Omnibus database GSE4090, mice of 2 and 24 months of age after sciatic nerve injury were selected from mice transcriptome data of differentially expressed genes in common, and the hub genes were then determined using protein-protein network and MCODE analysis, DAVID biological process, molecular function, and cell component analysis, and the miRWalk analysis of hub genes was performed to verify the key molecule. In mice aged eight weeks of sciatic 2 nerve clamps damage building, on days 0, 1, 4, and 7, sciatic nerve motor and sensory function were evaluated, and sciatic nerve immunofluorescence test was performed to verify PTBP1 expression. The continuous data were expressed as the mean ±SD. An independent t-test was used to compare two groups. A p-value of less than 0.05 was considered statistically significant.

Results: Bioinformatics analysis showed that PTBP1 is one of the key molecules in mouse sciatic nerve repair after injury. The immunofluorescence test verified that the number of positive cells reached a maximum value of 30.6 ±6.4/ROI on day 7 after injury and a minimum value of 17.4 ±7.0/ROI in the control group ($p<0.001$). However, the percentage of PTBP1 positive cells reached a peak of 90.8 ±16.9% at the early stage of injury, i.e., the first day, and then dropped to a minimum of 75.7 ±8.9% on the seventh day in the animal experiment as the repair time gradually increased ($p<0.05$).

Conclusions: PTBP1 plays a key role in the repair of sciatic nerve injury, providing a new strategy for clinical treatment of patients of all ages.

Full Text

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Tables

Due to technical limitations, table 1-2 is only available as a download in the Supplemental Files section.

Figures

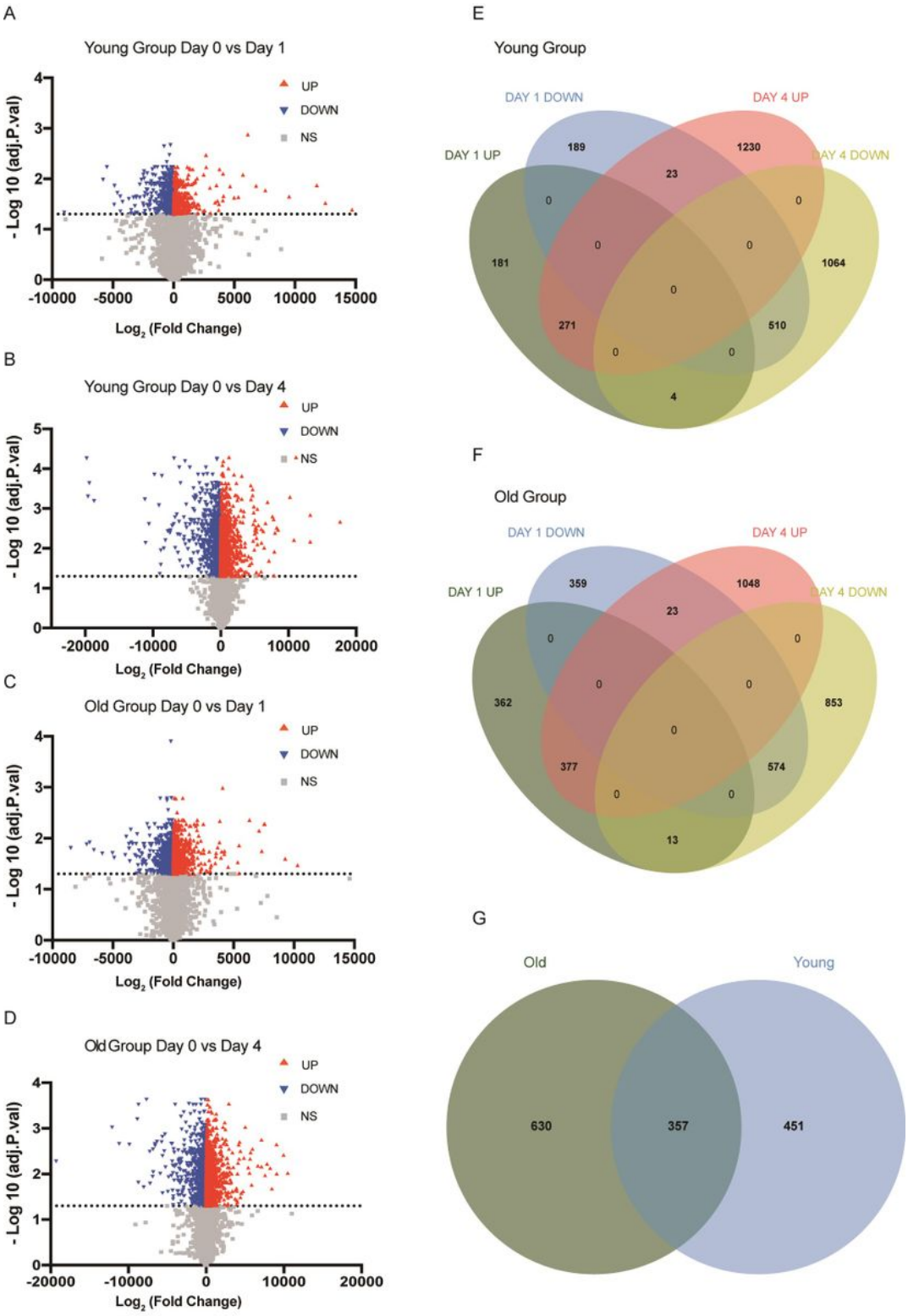

Figure 1

(A) Day 0 vs. day 1 differentially expressed genes in the young group. (B) Day 0 vs. day 4 differentially expressed genes in the young group. (C) Day 0 vs. day 1 differentially expressed genes in the old group. (D) Day 0 vs. day 4 differentially expressed genes in the old group. (E) Venn diagram showing the changing trend of different genes' expression in the young group. (F) Venn diagram showing the

changing trend of different genes' expression in the old group. (G) Venn diagram of differentially expressed genes after sciatic nerve injury in young and old mice.

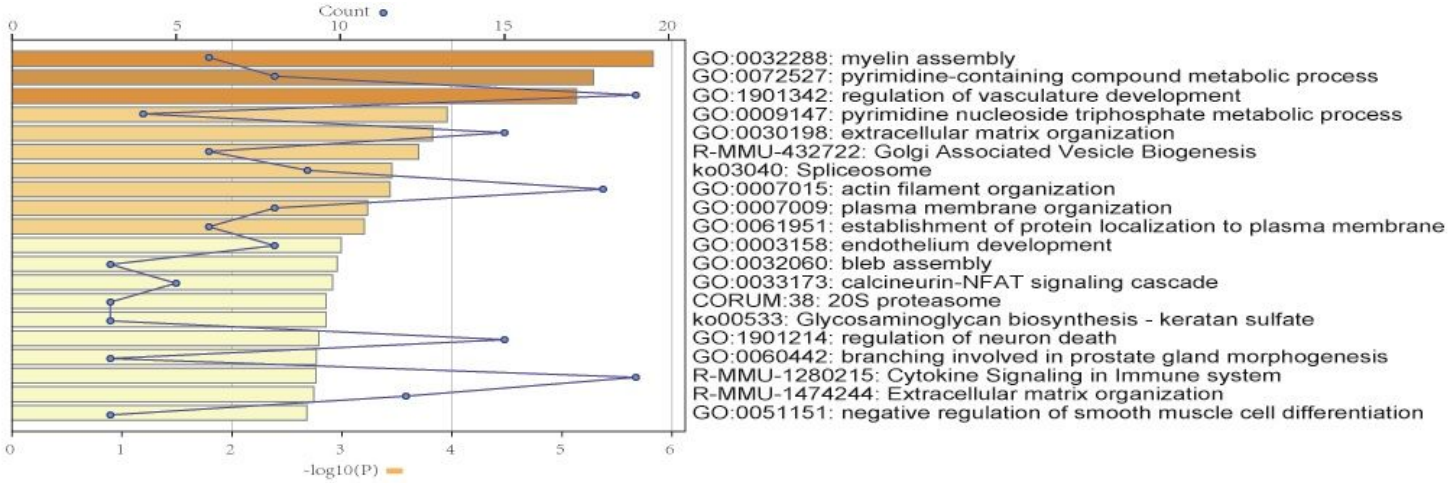

Figure 2

Bar graph of enriched terms across differentially expressed genes, colored by P values. The dots on the line chart represent the number of genes for this term.

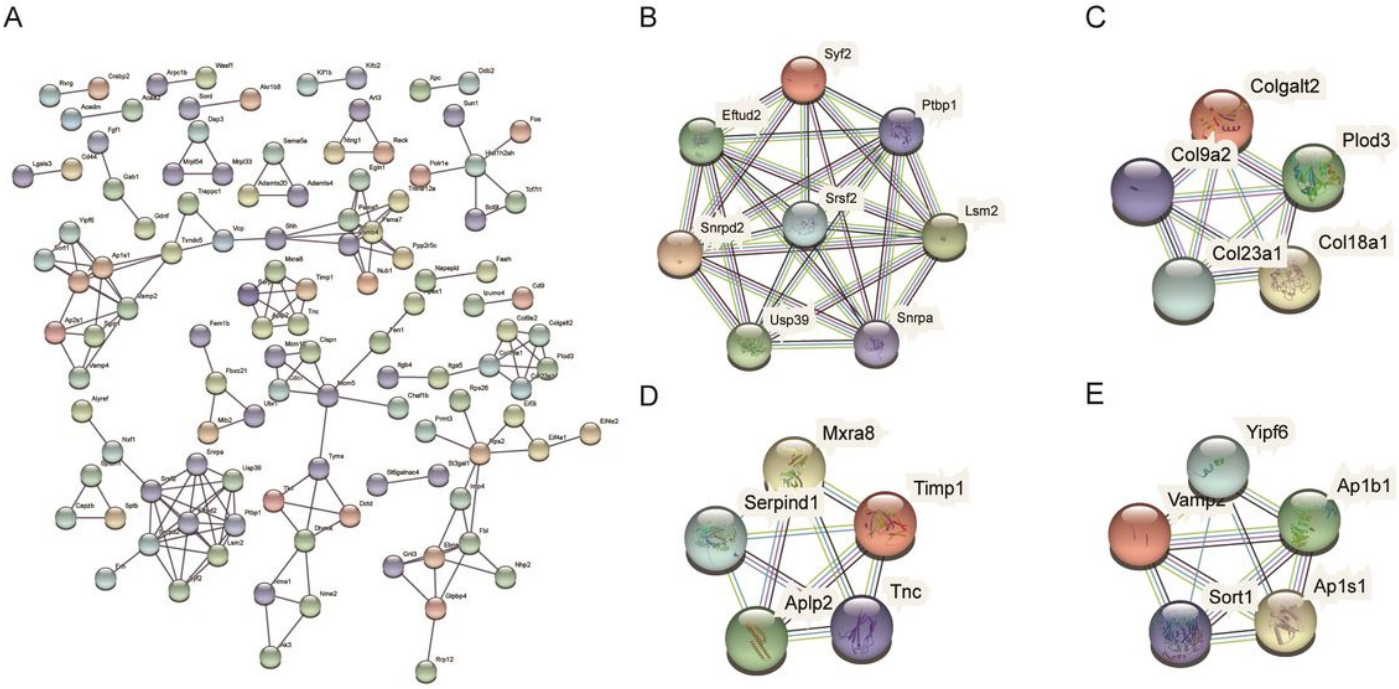

Figure 3

(A) Protein-protein interaction (PPI) network analysis of differentially expressed genes. (B) PPI network of hub genes after MCODE analysis. (C-E) The PPI network of the gene with the second score after MCODE analysis.

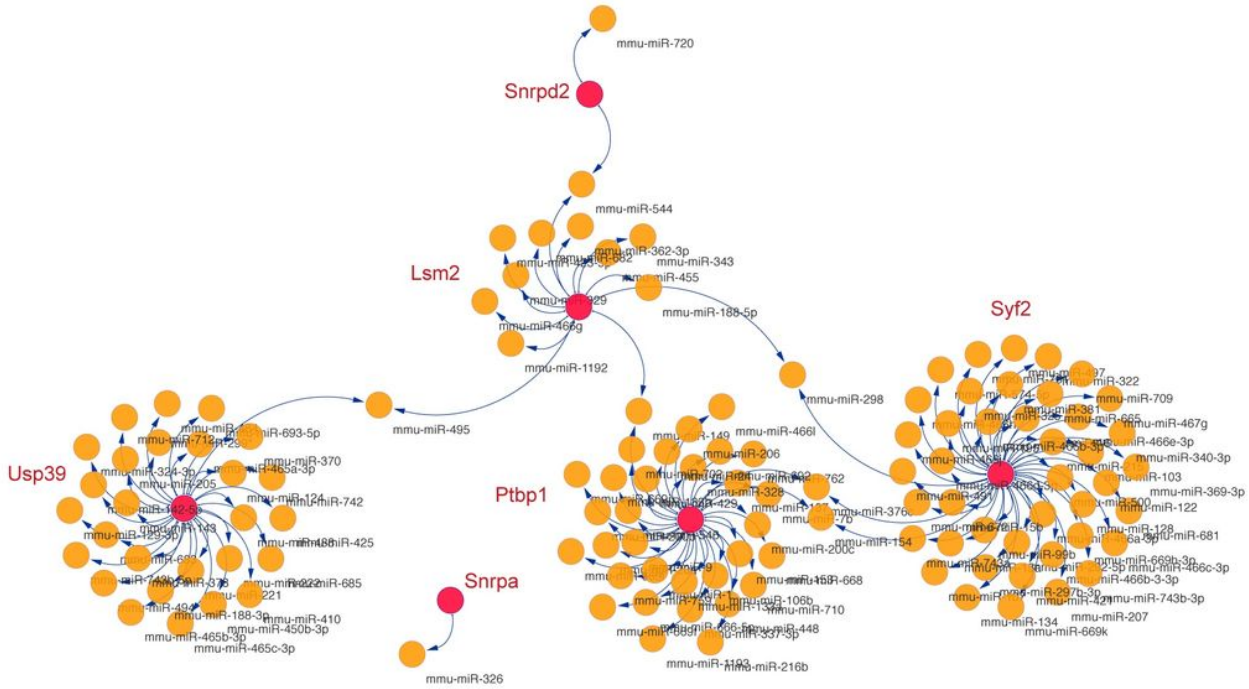

Figure 4

miRWalk 1.0 predicts the microRNAs interacting with hub genes.

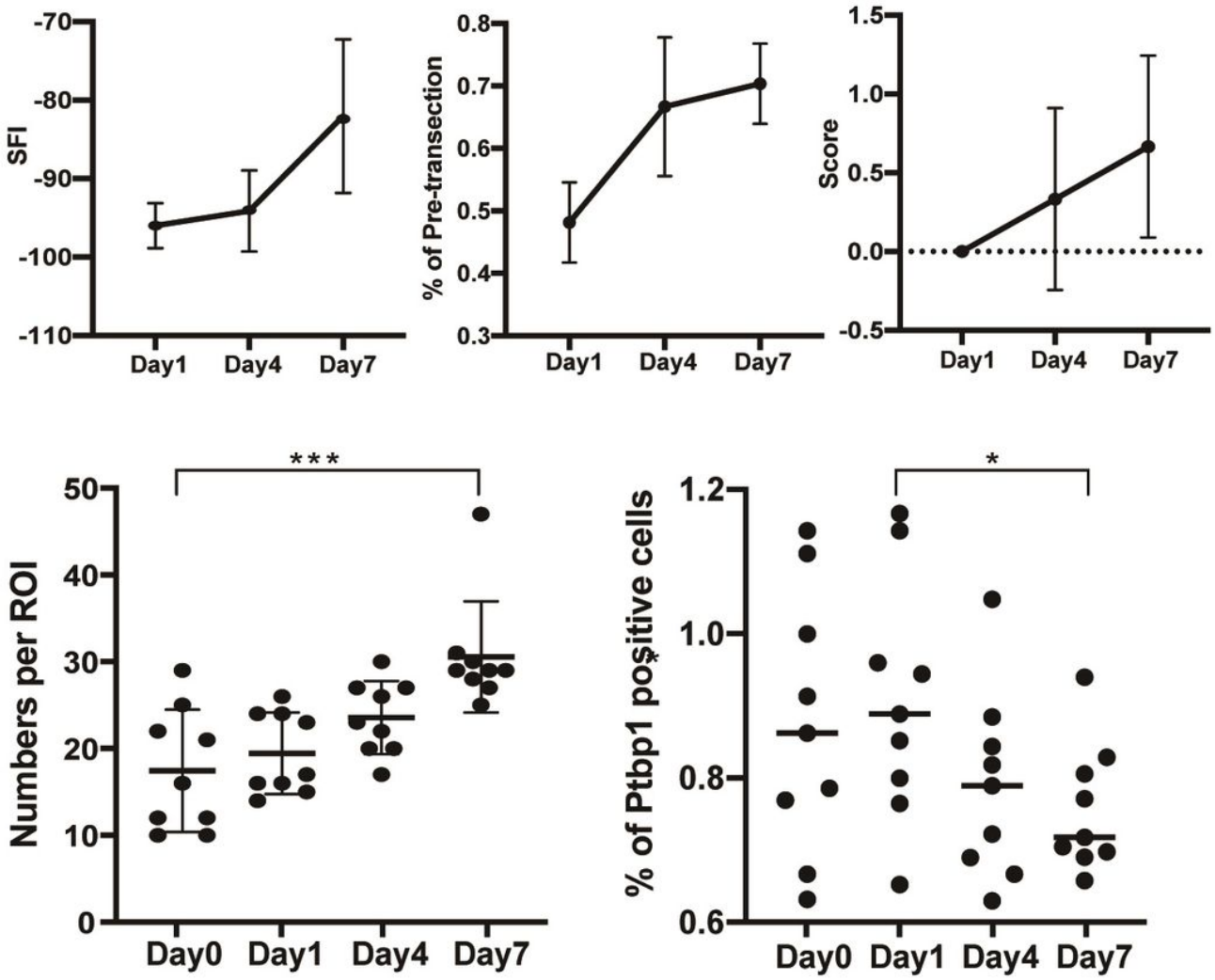

Figure 5

(A) Mice sciatic nerve function index recovery score. (B) Mice five-toe propagation analysis. (C) Sensory function recovery score of mice. (D) Immunofluorescence of frozen sections of mouse sciatic nerve, PTBP1-positive cell count in each region of interest (ROI). (E) Immunofluorescence staining was performed with frozen sections of the sciatic nerve of mice, and the ratio of PTBP1-positive cells in each ROI to the total number of cells was determined. $P < 0.05$, $P < 0.001$.

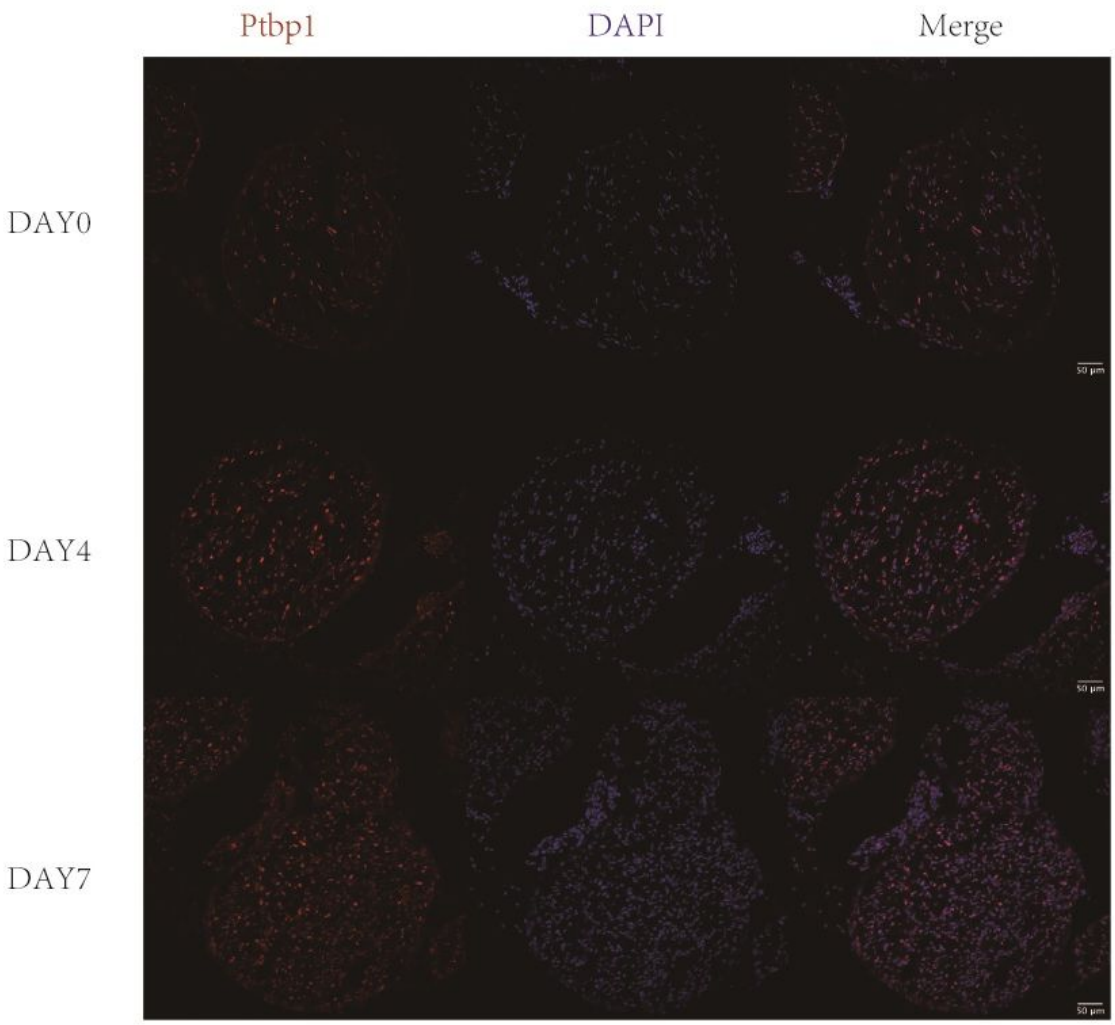

Figure 6

Immunofluorescence sections of mouse sciatic nerve were stained with PTBP1 and 4',6-diamidino-2-phenylindole (DAPI).

Supplementary Files

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- table1.docx
- table2.docx