

Figure

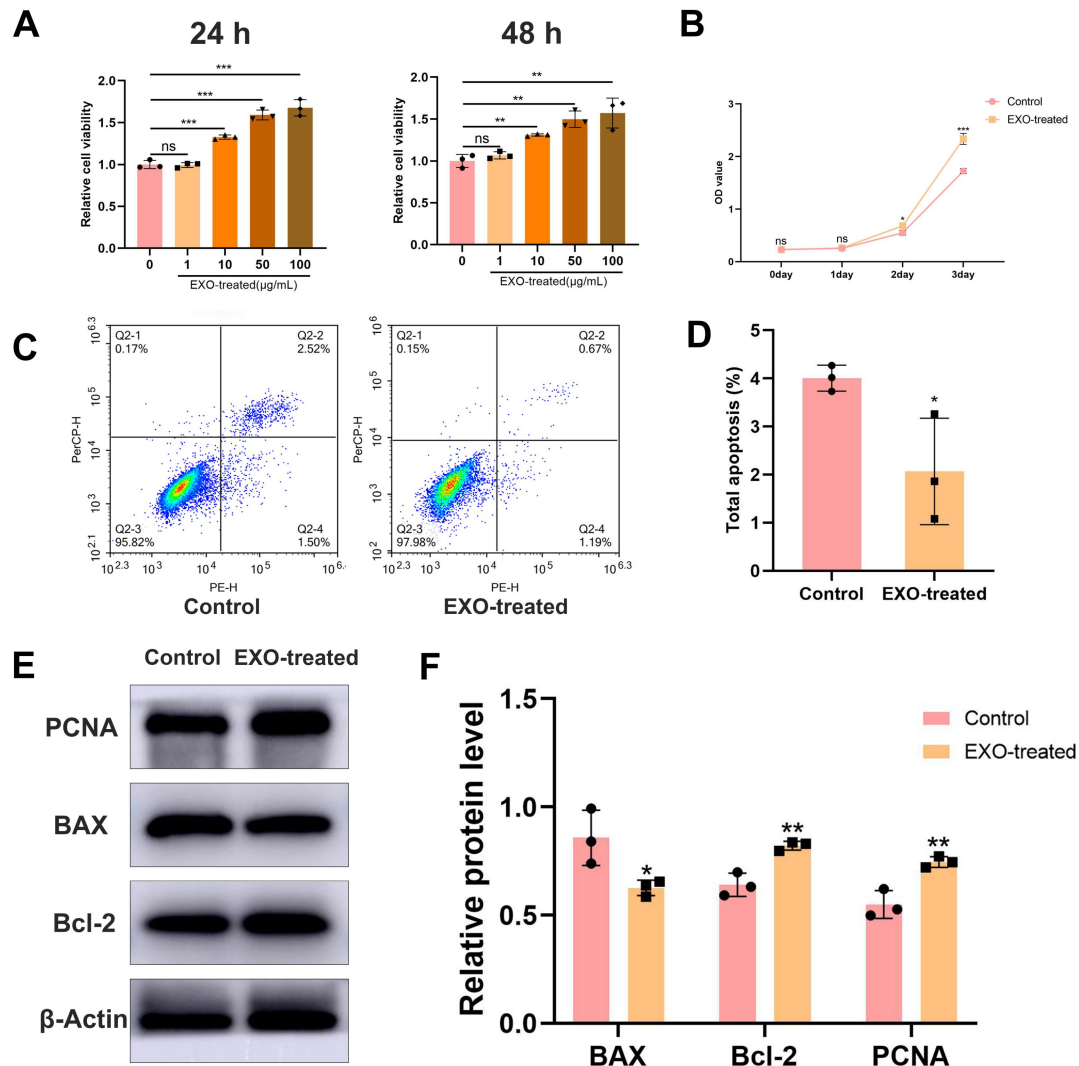


Fig. S1 The effect of EC-exosomes on proliferation and apoptosis phenotypes of Schwann cells.

A The proliferation of Schwann cells treated with EC-exosomes of different concentration (1, 10, 50 and 100 μg/mL) for 24 and 48 h was detected by CCK8 assay. The data are expressed as mean ± SD (n=3). **B** Cell growth curve was detected by CCK-8 assay in 50 μg/mL EXO-treated and control groups. The data are expressed as mean ± SD (n=3). **C** Schwann cell apoptotic levels determined by flow cytometry assay. The data are expressed as mean ± SD (n=3). **D** Statistical results of cell apoptotic. The data are expressed as mean ± SD (n=3). **E** The protein levels of proliferation-related protein (PCNA) and apoptosis-related protein (BAX and Bcl2) were analyzed by WB following incubation of Schwann cells to EC-exosomes for 24 h. **F** Quantification of PCNA, BAX and Bcl2 levels in EXO-treated and control groups. The data are expressed as mean ± SD (n=3). ns = not significant, *p < 0.05, **p < 0.01, ***p < 0.001.

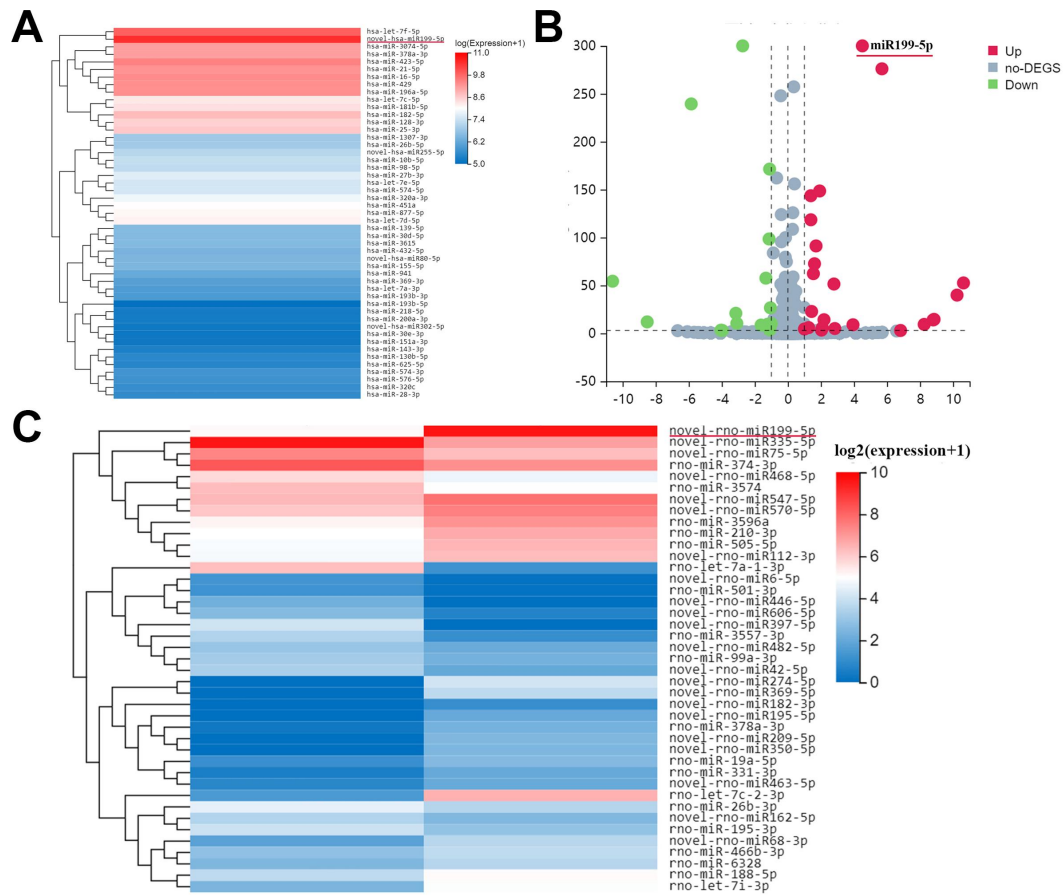


Fig. S2 The microRNA sequencing results of EC-exosomes and EXO-treated Schwann cells. **A** The heat map showed the main microRNAs composition of EC-exosomes. **B** Volcano plots showed the up-regulated microRNAs (red), down-regulated microRNAs (green) and non-changing microRNAs (gray) between EXO-treated Schwann cells and control Schwann cells. **C** The heat map displayed the expression ratios of different microRNAs between control group and EXO-treated group.

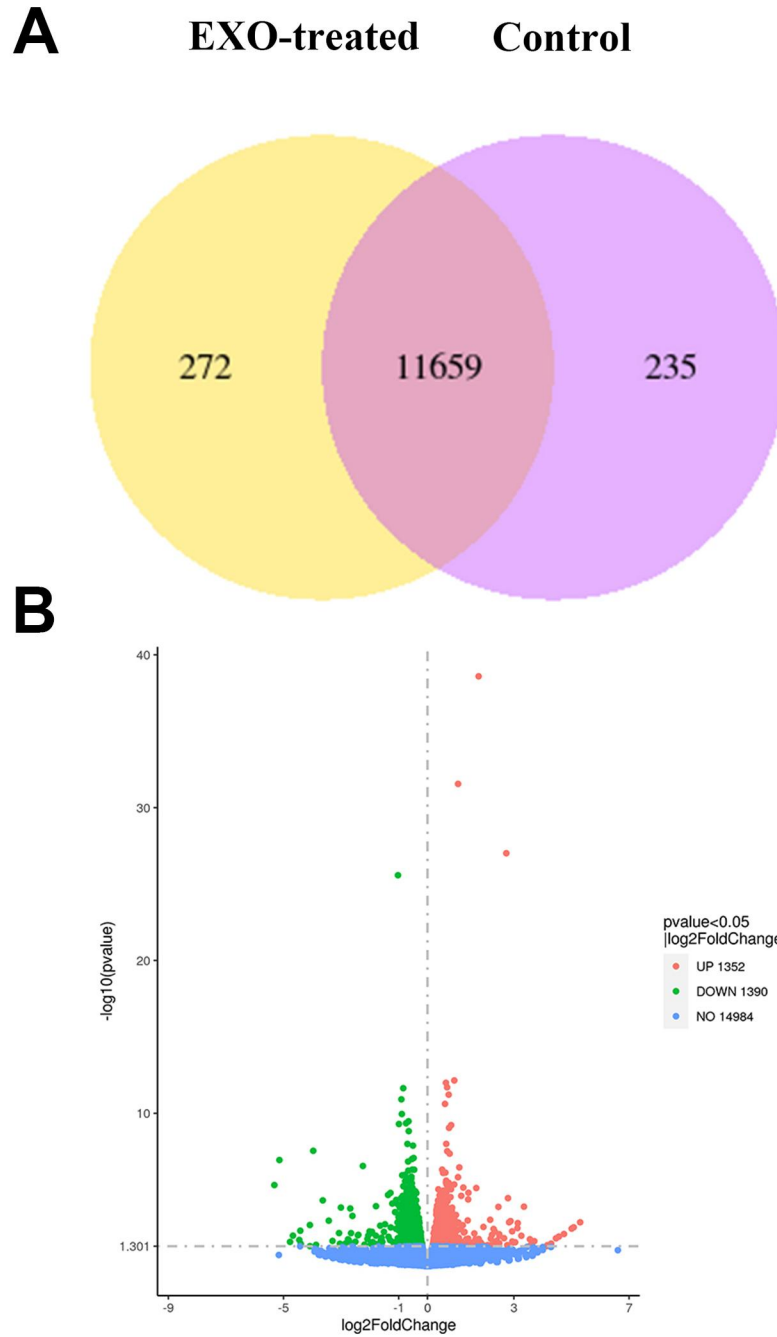


Fig. S3 Transcriptome profiles of Schwann cells. **A** Different genes were detected in EXO-treated and control groups on a co-expression Venn diagram. **B** Volcano plots showed the up-regulated genes (red), down-regulated genes (green) and non-changing genes (blue) between EXO-treated Schwann cells and control Schwann cells.

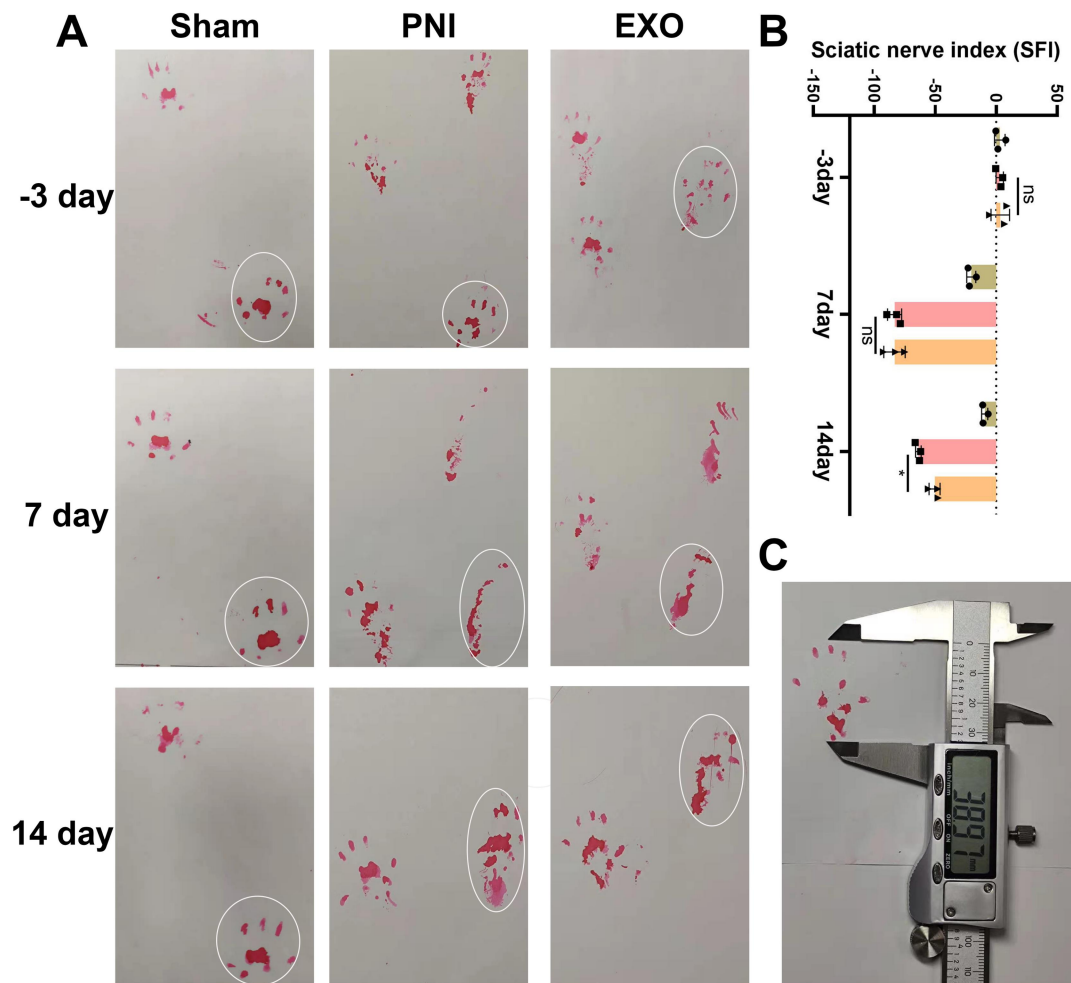


Fig. S4 Functional analysis of the regenerated sciatic nerves. **A** Representative images of footprints in sham, PNI, and EXO groups at 3 days before, 7 days following, and 14 days following operation. **B** Sciatic nerve function index (SFI) analysis in each group. The data are expressed as mean $\pm$ SD (n=3). **C** Representative image of the footprint measurement method. ns = not significant, * $p < 0.05$.

Table**Table S1 The primer sequences of the genes related.**

Primer name	Primer sequence
GAPDH-F	GACATGCCGCCTGGAGAAAC
GAPDH-R	AGCCCAGGATGCCCTTTAGT
VEGFA-F	AGAAAGCCCATGAAGTGGTGA
VEGFA-R	GCTGGCTTTGGTGAGGTTTG
VEGFB-F	AGCCACCAGAAGAAAGTGGT
VEGFB-R	TTGGCTGTGTTCTTCCAGGG
GDNF-F	GGAGACCGGATCCGAGGTG
GDNF-R	GCGCTTCGAGAAGCCTCTTA
CNTF-F	TTCGCAGAGCAAACACCTCT
CNTF-R	AGGCCCTGATGTTTTACATAAGATT
Gal-3-F	GGAGGAGCACTAACCAGGAAA
Gal-3-R	CCGGATAGGCACTAGGAGGA
LIF-F	CGCCCAACATGACGGATTTCT
LIF-R	TTGTTGCACAGACGGCAAAG
MCP-1-F	TAGCATCCACGTGCTGTCTC
MCP-1-R	CAGCCGACTCATTGGGATCA
GDF15-F	CTGCTGTTCTGCTGCTCT
GDF15-R	ACCCCAATCGCACCTCT
CCN1-F	GCATTCCTCTGTGTCCCAA
CCN1-R	TCCGTGCCAAAGACAGGAAG
JunD-F	GAAAGTCCTCAGCCACGTCA
JunD-R	CGTAGGACTGGGGGTACAGA
TXNIP-F	GACCTTGGACTACTTGCGCT
TXNIP-R	GGCAGACACTGGTGCCATTA
KLF10-F	GACCGTCCCAGCATTCTGTT
KLF10-R	TGTGTGACGGATGACACTGG