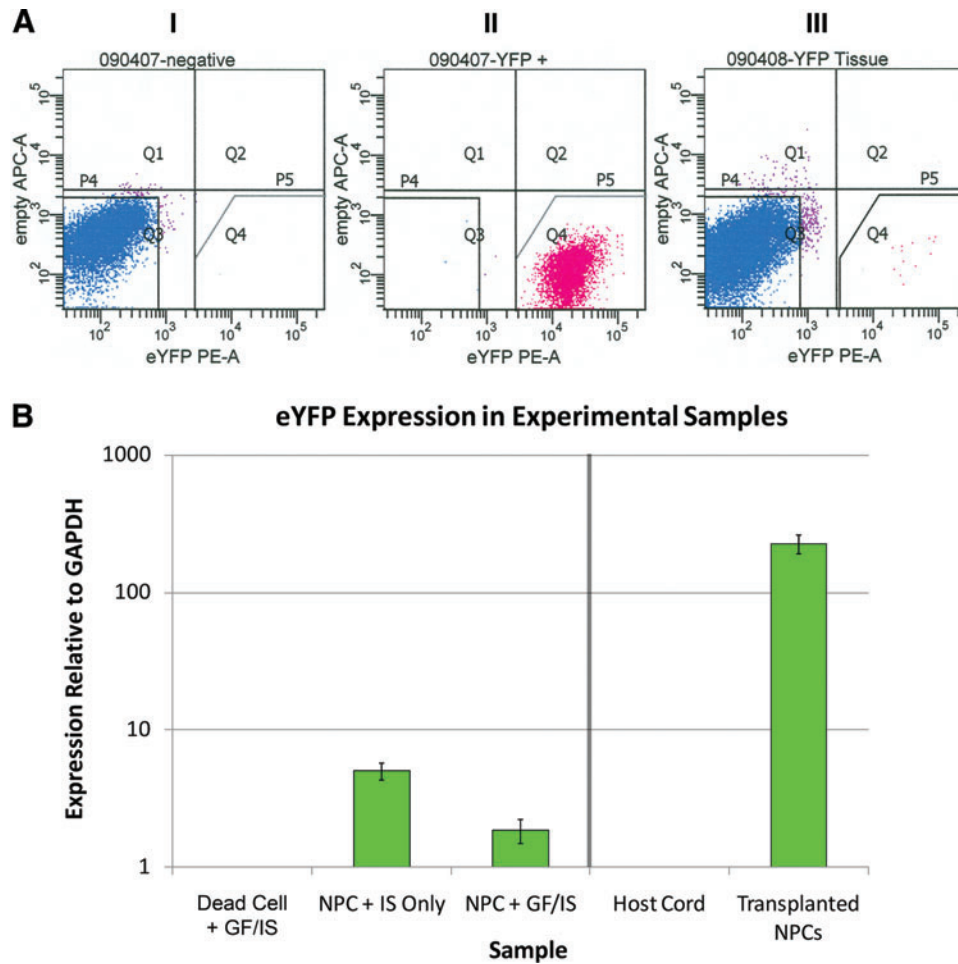# Supplementary Data

SUPPLEMENTARY FIG. S1. Isolation of NPCs from transplanted tissue and verification of transplant success. **(A)** Isolation of *eYFP*-bearing cells using FACS is demonstrated. **I** and **II** denote negative and positive controls, respectively. **III** shows isolation of *eYFP* positive cells from a host spinal cord 1 week post-transplant. **(B)** *eYFP* expression data are shown for experimental specimens on a logarithmic scale. Specificity of *eYFP* primers is demonstrated by lack of expression in the *Dead Cell + GF/IS* group as well as the *eYFP* negative 'Host Cord' FACS specimen.
Sample sizes: *Dead Cell + GF/IS n=4, NPC + IS Only n=3, NPC + GF/IS n=3*; qPCR was performed in quadruplicate.
NPCs, neural precursor cells; *eYFP*, enhanced yellow fluorescent protein; FACS, fluorescent-activated cell sorting; qPCR, quantitative polymerase chain reaction.

SUPPLEMENTARY TABLE S1. SAMPLE SIZES

Group	Sample size (qPCR)	Sample size (Western blot)
Paradigm 1		
NPC transplanted	4	
Control	3	
Paradigm 2		
Uninjured	3	3
Injured no treatment	3	4
Injured + GF/IS	3	3
Dead Cell + GF/IS	4	3
NPC + IS Only	3	3
NPC + GF/IS	3	6
FACS	3	
Paradigm 3		
BMSC transplanted	3[a]	
Control	3	

[a]For this group, 4 animals were transplanted; however, qPCR indicated unsuccessful transplantation for one animal. This animal was excluded from further trophin analysis.

NPC, neural precursor cell; BMSC, bone marrow stromal cell; FACS, fluorescence-activated cell sorting; qPCR, quantitative polymerase chain reaction.

SUPPLEMENTARY TABLE S2. EMPLOYED QUANTITATIVE POLYMERASE CHAIN REACTION PRIMER SEQUENCES

Gene	Forward primer sequence	Reverse primer sequence
GAPDH[a]	GGCAAATTCAACGGCACA	GTTAGTGGGGTCTCGCTCCTG
eGFP	TGACCCTGAAGTTCATCTGCACCA	TCTTGTAGTTGCCGTCGTCCTTGA
eYFP	GAA GTT CAT CTG CAC CAC CGG CAA G	GGTAGCTCAGGTAGTGGTTGTCG
NGF[a]	ACTTCCAGGCCCATGGTACAATCT	TTGATGTCCGTGGCTGTGGTCTTA
BDNF[a]	TGGCAGTGCAGGAGGAATTTCTGA	GCAGAAGGCCTAAGCAACTTGACA
NT3[a]	ACTACGGCAACAGAGACGCTACAA	ATAGCGTTTCCTCCGTGGTGATGT
NT4/5[a]	TGCGTCAGTACTTCTTCGAGACGC	TAGCCTTGCATTCTGAGAGCCAGT
GDNF[a]	AGAATTCCAGAGGGAAAGGTCGCA	TCCTCCTTGGTTTCGTAGCCCAAA
CNTF[a]	TACCAGTGGCAAGCACTGATCGTT	GGCAAAGGCAGAAACTTGGAGCAT
PDGF-A[a]	ATTCCCGCAGTTTGCAAGACCA	CCAGATCAAGAAGTTGGCCGATGT
EGF[a]	TTTCATCCTTTGCCTGGTTGTGCC	AAATTTCCCAGAGCCTAAGAGCCC
bFGF[a]	TTCAAGGATCCCAAGCGGCTCTA	TGTGGGTCGCTCTTCTCCC
LIF[a]	TGCCAATGGGACAGAGAAGACCAA	TACTTGTTGCACAGACGGCAAAGC
IGF-1[a]	TGGCACTCTGCTTGCTCACCTTTA	TTGGTCCACACACGAACTGAAGAG
GGF2[a]	TAGTCACAGCTGGAGTAATGGGCA	TGGCATGCCTGAGGAAGCTGTTAT
TGF-β1[a]	GTGGCCAGATCCTGTCCAAACTAA	CATTAGCACGCGGGTGACTTCTTT
VEGF-A[a]	TATTGCCGTCCAATTGAGACCCTG	GCACACAGGACGGCTTGAAGATATAC
IL-1β	AAGACACGGGTTCCATGGTGAAGT	TGGTACATCAGCACCTCTCAAGCA
IL-6	TGGCTAAGGACCAAGACCATCCAA	AGCACACTAGGTTTGCCGAGTAGA
TNF-α	ACCAGCAGATGGGCTGTACCTTAT	ATGAAATGGCAAATCGGCTGACGG

[a]Denotes that the primer sequence presented was previously published (Hawryluk et al., Stem Cells and Development, 2011).