

Supplementary Information for Spinal Cord Injury Affects Gene Expression of Transmembrane Proteins in Tissue and Release of Extracellular Vesicle in Blood: In Silico and *In Vivo* Analysis

Yasmin Mirzaalikhan, M.Sc.^{1,2,3}, Nasim Eslami, Ph.D.¹, Amin Izadi, M.Sc.⁴, Faezeh Shekari, Ph.D.^{5,6*} ,
Sahar Kiani, Ph.D.^{1,3*} 

1. Department of Stem Cells and Developmental Biology, Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran
2. Department of Developmental Biology, University of Science and Culture, Tehran, Iran
3. Department of Brain and Cognitive Sciences, Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran
4. Department of Embryology, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran
5. Department of Molecular Systems Biology, Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran
6. Advanced Therapy Medicinal Product Technology Development Center, Royan Institute for Stem Cell Biology and Technology, Academic Center for Education, Culture, and Research, Tehran, Iran



Fig.S1: DNA microarray data selection. The microarray datasets related to spinal cord injury are selected according to the type of sample, stage of injury, and region of injury.

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*Corresponding Addresses: P.O.Box: 16635-148, Department of Molecular Systems Biology, Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran

P.O.Box: 16635-148, Department of Stem Cells and Developmental Biology, Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran

Emails: faezehshekari@royaninstitute.org, sahar_kiani@royaninstitute.org

Table S1: Sample selection in each dataset

Dataset	GSE464	GSE2599	GSE45006	GSE46988
Phase				
Acute	4 samples intact 4 samples 7d PI	-	4 samples sham injury 4 samples 7d PI	4 samples intact 4 samples 7d PI
Subacute	4 samples intact 4 samples 28d PI	3 samples control 3 samples 35d PI	4 samples sham injury 4 samples 14d PI	-

From each dataset in both injury phases, a control group and a post-injury group were selected, and the number of samples in each group is given in the table.

Table S2: Animal procedures groups

Groups	Condition	State	Samples
1	Control	Intact	3
2	Sham	Laminectomy (7 day)	3
3	Sham	Laminectomy (14 day)	3
4	SCI	Acute (7 day)	3
5	SCI	Subacute (14 day)	3

Table S3: BBB score in acute and subacute groups

BBB score	After injury	7 d PI	14 d PI
Rat number			
1	0	1.5	-
2	0.5	4	-
3	0.5	2	-
4	0.5	5	9.5
5	0.5	1.5	2
6	1	5	8.5

BBB; Basso, Beattie, and Bresnahan, d; Day, and PI; Post Injury.

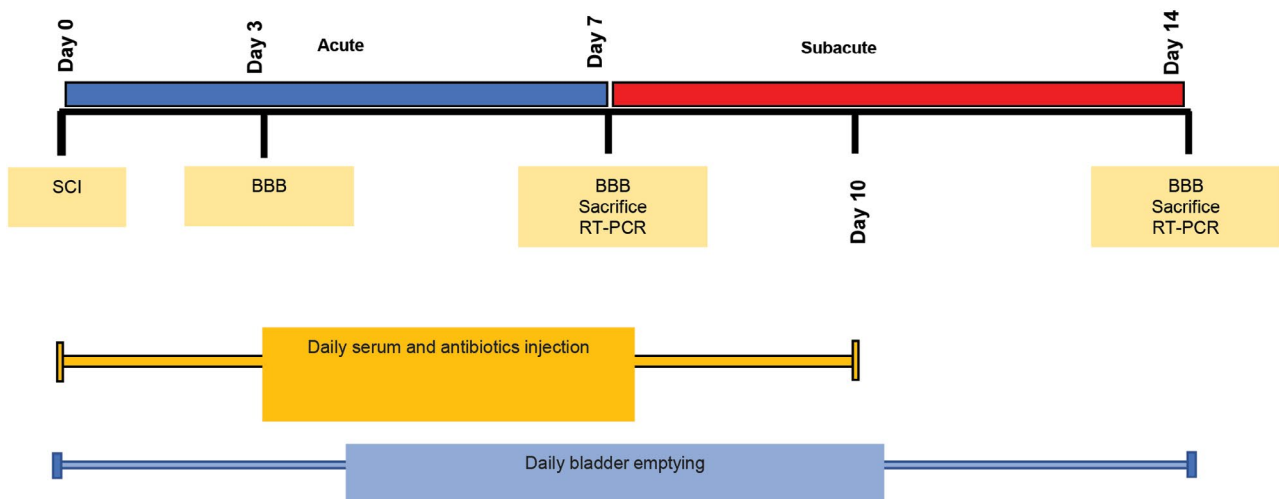


Fig.S2: Timeline of the experiment. As the picture depicts, SCI surgery is considered as day 0. One week after that acute group and after 2 weeks subacute group have sacrificed. Caring and other assessments have performed in the following weeks. SCI; Spinal cord injury, BBB; Basso, beattie, and bresnahan, and RT-PCR; Real time polymerase chain reaction.

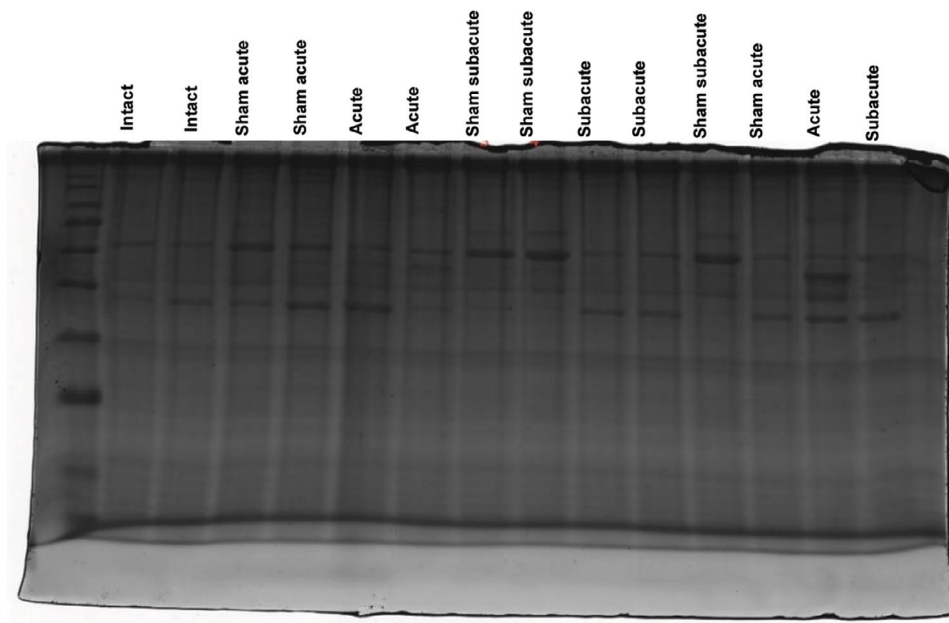


Fig.S3: SDS-PAGE was used to obtain high-resolution separation of complex mixtures of proteins.

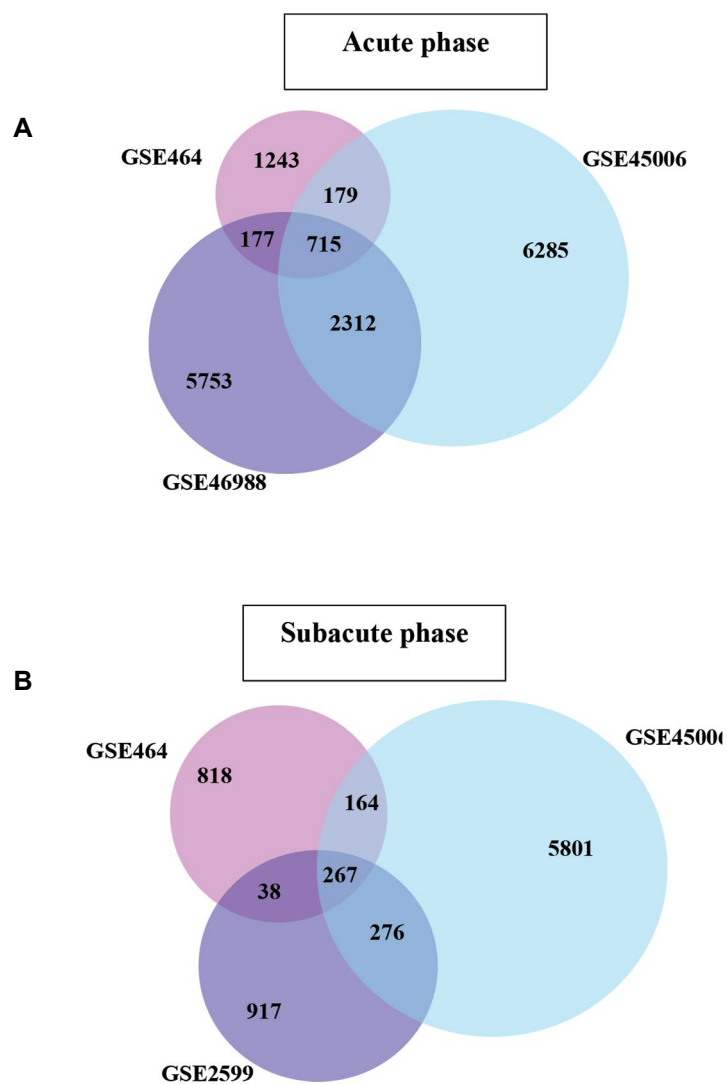


Fig.S4: Overlapped DEGs in the acute and subacute phases. In acute and subacute phases, differentially expressed genes were shared across the three datasets, and genes that were common to at least two datasets were selected. DEGs; Differentially Expressed Genes.

Table S4: Primers sequences

Gene name	Primer sequences (5'-3')	Accession number	Annealing temperature (°C)	Amplicon size (bp)	T _M (°C)
<i>Enpp3</i>	F: GTATCCAGAGTCGCACGGCA R: AGGAGCCATTGACAGCCACA	NM_019370	60	197	62
<i>Cd63</i>	F: GCATCAAGAAGCGTCGGGGA R: ACAGCGAGCCAGCAGTAGTC	XM_008765024	59	194	63
<i>Cxcr4</i>	F: GGCCGTCTATGTGGGTGTCT R: AGGACAGGATGACGATGCC	NM_022205	60	191	62
<i>Kcna1</i>	F: CCCGAGAAGGAGTACCAGCG R: AATGGTGCCCGTGAAGTCCT	XM_039107020	60	174	62
<i>Scn1a</i>	F: TTCCCCGAGACGCAATAGCA R: GGAGGATCTGCTGGTTTGGC	NM_030875	58	196	61
<i>Nrg1</i>	F: CACCTTTCCCTCTTCGGGCT R: AGGAAGCAGCGTGGACTCG	NM_001271118	59	154	61
<i>Grm1</i>	F: ACGGCGAGAGTGGAATGGATGC R: TCGCAGAAGCAGACCACAACCC	NM_001114330	60	169	65

T_M; Melting temperature.

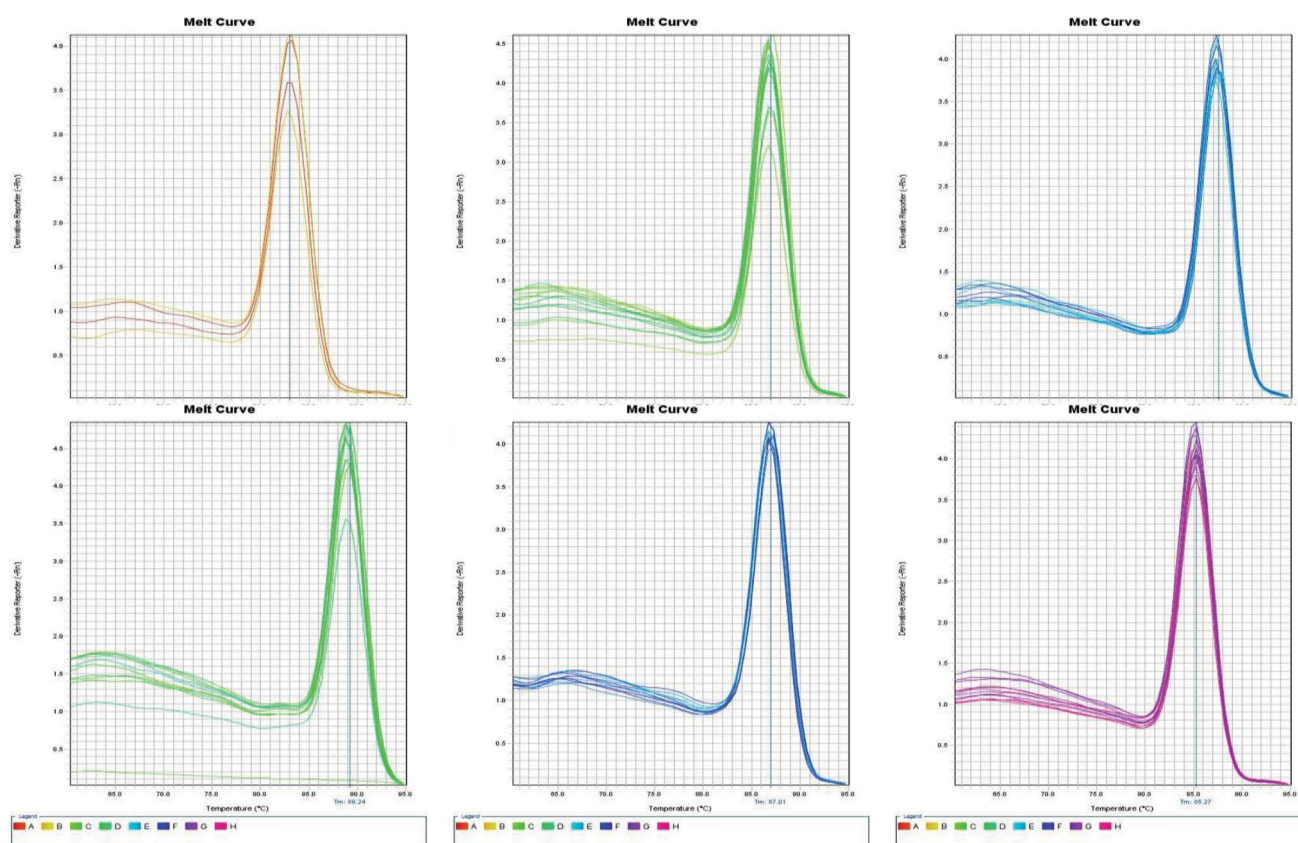


Fig.S5: Melting curve for the quantitative real-time polymerase chain reaction (PCR) of RNA samples treated with DNase I and reverse transcribed to cDNA.