

Supplementary information to:

Original article:

**ANTIDEPRESSANT-LIKE AND NEUROPROTECTIVE EFFECTS OF
PINE NEEDLE EXTRACTS: EVIDENCE FROM BEHAVIORAL,
TRANSCRIPTOMIC, AND BIOCHEMICAL STUDIES**

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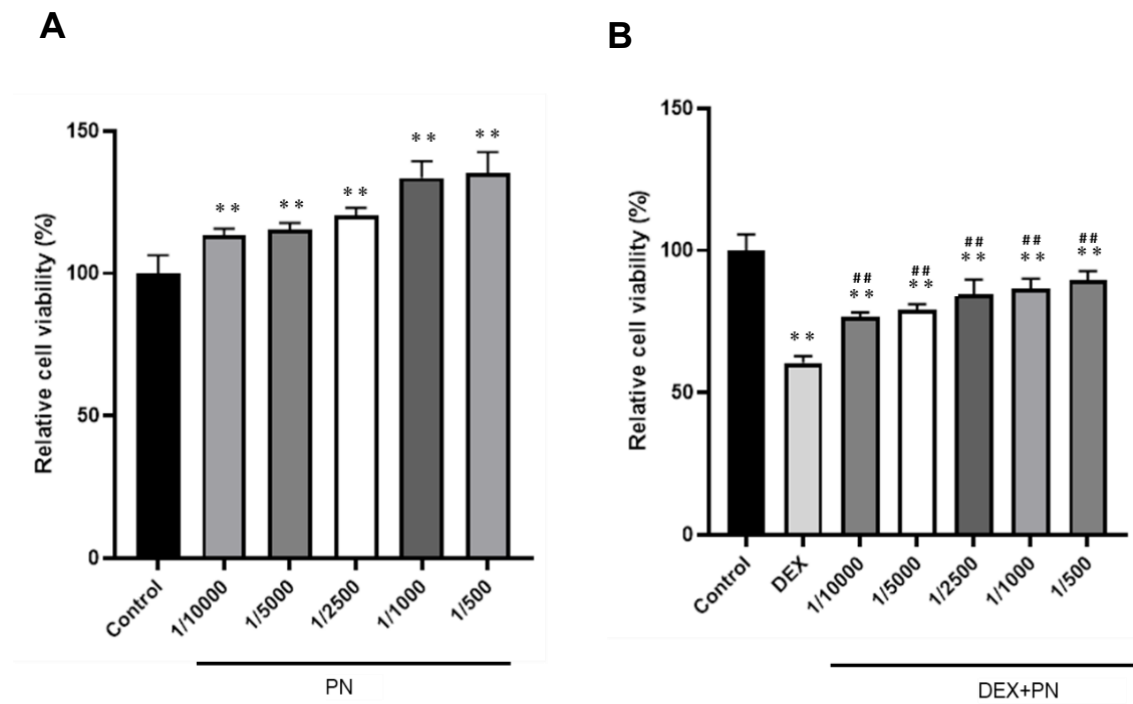
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Supplementary Figure 1: Effect of pine needle extract (PN) on **A**) cell viability and **B**) dexamethasone (DEX)-induced changes in human neuroblastoma SH-SY5Y cells. SH-SY5Y cells were treated with PN for 48 h to evaluate cell viability. SH-SY5Y cells were pretreated with PN for 1 h and then treated with 250 μ M DEX for 48 h to evaluate neuroprotection. Statistical significance was assessed using one-way ANOVA followed by Tukey's post-hoc test. Each bar represents the mean \pm SEM ($n = 5$ independent experiments). ** p value < 0.01 vs. control cells, ### p value < 0.01 vs. DEX-treated cells.

Supplementary Table 1: Detailed heatmap data showing differentially expressed genes (DEGs) categorized into four groups:

- Downregulated in LPS and Upregulated in PN
- Upregulated in LPS and Downregulated in PN

For each group, the table includes the associated Gene Ontology (GO) terms, log p-values (enrichment significance), Enrichment scores, the number of DEGs, and the list of DEGs. This comprehensive dataset provides detailed insights into gene expression patterns underlying the effects of PN and LPS treatment.

GO term	GO no.	Downregulated in LPS				Upregulated in PN			
		LogP	Enrichment	No. of DEGs	List of DEGs	LogP	Enrichment	No. of DEGs	List of DEGs
fatty acid biosynthetic process	GO:0006633	-2.4	3.1	8	ALOX12 ALOX5 CYP1A1 CYP3A4 EDN2 PTGDS TBXAS1 AKR1C3	-2	2.7	8	ALOX12 GPX4 LTC4S MIF PRKAA1 TBXAS1 HACD1 ALOXE3
inflammatory response	GO:0006954	-9	3.1	38	AHSG ALOX5 BMP2 CD36 CD40LG CCR3 CCR4 IL1B IL1RN IL9 IL13 IDO1 CXCL9 SERPINA1 PTGDR PTGER2 RARRES2 S100A8 SELE SELP TNF TNFRSF1A TNFSF4 CXCR4 AOC3 CD96 NOD1 AGR2 IL36RN NOX1 CHIA IL36B TLR8 UGT1A1 GSDMC ZC3H12A H2BC1 NLRP9	-2.6	1.8	26	TMEM258 CASP8 CD36 CD44 S1PR3 ITGAM MIF NFKBIB PTGER1 RELA CCL25 SLC11A1 TGFB1 TLR1 MAPKAPK2 LY86 SMPDL3B PYCARD TLR7 PXK GSDMD IL1F10 IL17RC IL33 IL34 NLRP9
cranial nerve development	GO:0021545	-2.6	4.3	6	HOXA1 HOXB1 ATP8B1 SIX1 SLC38A8 TIFAB	-2.3	3.8	6	EPHB1 MAFB ACKR3 SLITRKB NAV2 DRGX
regulation of epithelial cell differentiation	GO:0030856	-5.3	4.1	15	AQP3 CEACAM1 BMP2 FOXO3 GDF2 IL1B IL13 KRT84 TNF TNFRSF1A WNT10B KRT36 GDF3 ESRP1 OSR1	-2.4	2.6	11	CEACAM1 CDH5 CYP27B1 S1PR3 EXTL3 FRZB NCOA3 KLF7 ATOH8 OSR1 SPRED2
carbohydrate homeostasis	GO:0033500	-2.1	2.3	11	ALOX5 CASR GCGR CMKLR2 HK2 FOXA1 LE	-2.1	2.2	12	CASR FKBP1B IGFBP5 PRKAA1 RBM4 SRF TCF7L2 T

					P SER- PINF1 CCN4 SLC12A7 OBP2A				GFB1 KLF7 NR1D1 MBD5 A DGRF5
T cell activa- tion	GO:0042110	-3	2.4	17	CD3E TNFSF8 CTSL IF NA1 IFNA5 IL7 IDO1 LE P MSN RORC STAT4 T NFSF4 WNT10B TNFSF 14 TNFSF18 TMEM98 FNE	-3.1	2.3	19	CASP8 RUNX2 CD4 CD8A CD44 FKBP1B IT- PKB SLC11A1 SPI1 SRF TG FB1 TP53 TOX MAFB CCR9 FOXP1 APBB1P ENTPD7 PRR7
glucose home- ostasis	GO:0042593	-2.1	2.3	11	ALOX5 CASR GCGR C MKLR2 HK2 FOXA1 LE P SER- PINF1 CCN4 SLC12A7 OBP2A	-2.1	2.2	12	CASR FKBP1B IGFBP5 PR KAA1 RBM4 SRF TCF7L2 T GFB1 KLF7 NR1D1 MBD5 A DGRF5
innate immune response	GO:0045087	-3.7	2	33	ARG1 C2 DEFA1 CFD HLA- B HPX IFNA1 IFNA5 KL RC2 LGALS3 RARRES 2 S100A8 TNF APOL1 OASL NOD1 IL36RN IL 36B TLR8 SLC46A2 CA RD9 ULBP1 NEURL3 P GLYRP3 RNF166 APO- BEC3H SLC30A8 DEFB 128 WFDC9 NLRP9 IFN E LILRA5 DEFB131A	-2.9	1.8	34	SERPING1 CYP27B1 FAU HLA- B ITGAM RPSA MIF RELA RNASE3 SLC11A1 TLR1 TP 53 ADAM15 LY86 PQBP1 IF ITM2 PLEKHM2 SMPDL3B PY- CARD ZDHC1 TLR7 TRIM 68 SPIRE1 GSDMD RNF39 COLEC12 IL33 TIFA TRIM6 IL34 DEFB128 STXBP4 NLR P9 STING1
defense re- sponse to Gram-nega- tive bacterium	GO:0050829	-2.1	3.1	7	DEFA1 RARRES2 SEL P NOD1 DEFB128 LCE 3B LCE3C	-2.3	3.1	8	CD4 RNASE3 RPS19 SLC1 1A1 PY- CARD GSDMD TSLP DEFB 128
regulation of cell activation	GO:0050865	-4.5	2.2	31	ALOX12 ARG1 CEA- CAM1 CD3E CD19 TNF SF8 CD40LG HLA- DOB IL1B IL7 IL13 IDO1 KLRC2 LEP LGALS3 S ELP SMARCD2 TNF TN FSF4 WNT10B TNFSF1	-2.5	1.8	28	ACTA2 ALOX12 CEA- CAM1 CAPN3 CD4 CDKN1 A GP5 IGF1 IT- PKB MIF PRKAA1 SPI1 TGF B1 CST7 NR1D1 TOX RNF4

					4 TNFSF18 MMRN1 IL36 MZB1 BTNL2 SLC46A2 ZC3H12A PGLYRP3 TIGIT LILRA5				1 PAXIP1 RABGEF1 PY-CARD SH3KBP1 AM-BRA1 VSIR TSLP IL33 ZBTB46 PIK3R6 ADGRF5
cellular response to cytokine stimulus	GO:0071345	-3.1	1.9	31	CEA-CAM1 CXCR5 CCR3 CCR4 CCR8 EDN2 HK2 HPX IFNA1 IFNA5 IL1B IL7 IL9 IL13 LEP CXCL9 ROR2 PRL STAT4 TFF2 TNF TNFRSF1A CXCR4 OASL TNFSF18 IL36 RBMX TEX14 ZC3H12A IFNE LILRA5	-2.4	1.7	32	ABCA1 CEA-CAM1 CD4 CD44 EPHB1 RELA RPS16 CCL25 SELPLG SRSF7 SPI1 TP53 NR1D1 ST18 ST3GAL6 IFITM2 CCR9 PTP4A3 FOXP1 RABGEF1 PY-CARD ACKR3 ABCG4 IL1F10 IL17RC TSLP IL33 TIFA TRIM6 IL34 STXBP4 STING1
neuron fate specification	GO:0048665	-2.2	5.4	4	FOXA1 HOXD10 SIX1 TLX3	n/a			
astrocyte development	GO:0014002	-2.1	5.1	4	IL1B ROR2 S100A8 TNF	n/a			
neurotransmitter receptor internalization	GO:0099590					-2.4	8.8	3	AP2S1 CACNG2 CACNG7
regulation of cell growth	GO:0001558					-3.7	2.3	23	CEA-CAM1 BMPR2 CDKN1A CYP27B1 EXTL3 FRZB IGF1 IGFBP5 IGFBP7 ING1 RYK SRF SUPV3L1 TGFB1 TP53 URI1 ADAM15 CEP43 FAM107A TWF2 FOXP1 CACNG7 RTN4R
regulation of nervous system development	GO:0051960					-3	2.1	23	BMPR2 EPHB1 MBD1 RELA RYK SRF TGFB1 TIAM1 TP53 CST7 NR1D1 TWF2 TRAK1 PARD3 LRRN1 CTDSP1

									CLSTN2 RTN4R SLI-TRK6 NKX6-2 IL33 IL34 LINGO2
dendrite morphogenesis	GO:0048813					-3	4.4	7	EPHB1 MEF2A KLF7 WASL ABI1 TRAK1 SHANK1
nerve development	GO:0021675					-2.5	3.3	8	EPHB1 GABRA5 NTF3 MAFB ACKR3 SLI-TRK6 NAV2 DRGX
regulation of glial cell differentiation	GO:0045685					-2.5	3.6	7	MBD1 RELA TGFB1 NR1D1 NKX6-2 IL33 IL34
glial cell proliferation	GO:0014009					-2.3	5.6	4	NFIA TP53 IL33 IL34
brain development	GO:0007420					-2.2	1.6	30	APAF1 COL3A1 COX6B1 EMX2 EPHB1 GPX4 GRIN2C ITGAM PBX3 RFX4 RYK ATXN1 STIL SRF SSTR2 TP53 CDK5R2 TOX MAFB TACC3 NCOA6 LHX6 FOXP1 CEND1 MEIS3 SHROOM4 RTN4R FAT4 DNAJC30 SLC32A1
regulation of gliogenesis	GO:0014013					-2.2	2.9	8	MBD1 RELA TGFB1 TP53 NR1D1 NKX6-2 IL33 IL34

GO term	GO no.	Upregulated in LPS				Downregulated in PN			
		LogP	Enrichment	No. of DEGs	List of DEGs	LogP	Enrichment	No. of DEGs	List of DEGs
response to virus	GO:0009615	-2.7	2.1	19	ADAR DEFA1 DEFA3 GSDME HSP90AA1 IFI16 STMN1 MBL2 NCBP1 XPR1 TBKBP1 NT5C3A POLR3K USP29 ZC3H12A ZBP1 TRIM56 UNC13D SERINC5	-4.6	2.4	28	ADAR ADARB1 ARF1 BCL2L1 BNIP3L CALR AP1S1 DDX1 DDX3X EEF1G EIF5A FMR1 HIF1A HSP90AA1 RPSA STMN1 PCBP2 TPT1 DCLK1 XPR1 RB1CC1 TOMM70 ZMYND11 HNRNPUL1 LSM14A GPAM UBL7 DHX36
regulation of cell cycle process	GO:0010564	-2.6	1.7	31	BID CXCR5 CDC42 CENPE DB1 ECT2 FHL1 HSPA1A MKI67 TIMELESS TAOK2 ROCK2 ADAMTS1 KIF20B TTI1 KLHL21 BTN2A2 GIPC1 TPX2 OR1A2 NUSAP1 SPDL1 RIOK2 NCAPG CEP97 ATAD5 CDT1 DOT1L WDR62 CENATAC ZC3H12D	-4	1.8	43	AKT1 APBB2 APC ATRX BCL2L1 CALM1 CALR CCNG1 CCNH CDC42 CLTC DCTN1 DDX3X DYNC1H1 EIF4G1 H2AX HNRNPU CDK16 CDK17 CDK14 PTEN RAD21 RDY UBE2E2 ZNF207 RAE1 RAB11A BUB3 TAOK2 PSME3 PLK2 ZWINT FAM107A PLCB1 ATXN10 ANKRD17 BAM1 FBXW7 AMBRA1 MTA3 WNK1 MAP9 PPP1R9B
carbohydrate catabolic process	GO:0016052	-2.6	3.1	9	CHIT1 FUT1 MPI PGK2 TKTL1 NEU3 NUDT5 OGDHL GLB1L3	-2.3	2.7	10	ALDOC HEXB HK1 OGDH PGK1 PKM RB1CC1 GABARAPL1 WIPI2 ATG2B
positive regulation of defense response	GO:0031349	-3.9	2.3	24	KLK3 FABP4 HSPA1A HSP90AA1 IFI16 IRAK2 KLRC1 MBL2 MEFV NPAS2 PAK3 UCN IL1RL1 PJA2 HEXIM1 CD226 CD160 STAP1 USP29 ZBP1 TRIM56 OTULIN NLRP12 REG3G	-2	1.7	23	CD47 CD81 CNR1 CREBBP CTSS DDX3X GRN HMG B1 HSP90AA1 HSPD1 LAMP1 MEF2C PAK1 CX3CL1 SFPQ PLA2G7 MATR3 PJA2 TOMM70 ANKRD17 LSM14A AKIRIN2 RTN4

regulation of actin cytoskeleton organization	GO:0032956	-6.1	3.1	25	CDC42 CCN2 ECT2 STMN1 MET MYOC NEB PAK3 RGS4 CL21 TPM1 TAOK2 ROCK2 AVIL CDC42EP4 RND1 SNX9 MAGEL2 KIRREL1 CARMIL1 LMO3 CRACD XIRP2 MTPN ARPIN	-6.9	2.9	31	ADD2 ADD3 ARF1 CAPZA2 CD47 CDC42 FLNA MTOR GPM6B STMN1 PAK1 PFN1 PFN2 PIK3CA RD3 CX3CL1 SPTAN1 SPTBN1 TPM1 CDK5R1 TAOK2 ARPC3 ARPC2 ABI2 CORO2B NCKAP1 FAM107A CYFIP1 CYFIP2 STAU2 MTPN
regulation of stress fiber assembly	GO:0051492	-2.8	3.7	8	CDC42 CCN2 STMN1 MET MYOC TPM1 ROCK2 CARMIL1	-2.6	3.1	9	CD47 CDC42 MTOR STMN1 PAK1 PFN1 PFN2 TPM1 CORO2B
cytoskeleton-dependent cytokinesis	GO:0061640	-2.8	3.3	9	ECT2 STMN1 MTMR4 ROCK2 EXOC5 ZNF365 KIF4A NUSAP1 SNX9	-3.1	3.1	11	ANK3 APC ARF1 STMN1 ORC4 SPTBN1 ACTR3 ZNF365 SPIRE1 EXOC4 MAP9
negative regulation of intracellular signal transduction	GO:1902532	-2.7	1.8	30	BID ESR1 GSTP1 HELLS HSPA1A IFI16 IGBP1 ISL1 STMN1 MEFV MET MMP3 MYOC SERPINB3 VDAC2 RANBP9 BTN2A2 HYOU1 PRAME TXNDC12 IN-SIG2 RRN3 NLRP2 YJU2 MAPKAP1 ATAD5 ZC3H12A WDR24 NLRP12 ADGRG3	-8.7	2.4	54	AKT1 APOE BCL2L1 CALR CRY2 CSNK1A1 DDX3X DUSP8 EPHA4 MTOR HIF1A HSPA5 ITPR1 STMN1 MARK3 NDUFC2 CNOT2 CCN3 PAFAH1B1 PCBP2 SERPINE2 PPIA PPM1A PPM1B PPP2CB PPP6C PRKACA PRKACB PRKAR1A PRKAR1B MAP2K5 PTEN SKI SOD2 TMBIM6 TPT1 UBE2D1 UCLH1 VCP VDAC2 YWHAZ SYN-GAP1 AKT3 ZMYND11 SIRT3 STRN3 NLK FBXW7 NPLOC4 ASH1L LMO3 SAR1A ARHGAP12 SPRED2
microtubule cytoskeleton organization involved in mitosis	GO:1902850	-4.2	3.9	12	CENPE KPNB1 STMN1 PTPA TPX2 FBXW11 KIF4A NUSAP1 SPDL1 MAP1S WDR62 MZT1	-4.2	3.4	14	DCTN1 DYNC1H1 FLNA GJA1 STMN1 MAP4 PAFAH1B1 VCP ZNF207 RAB11A NUDC PLK2 LSM14A MAP9

negative regulation of response to oxidative stress	GO:1902883	-2.6	11	3	MEAK7 MCTP1 NCOA7	-2.3	8.3	3	GGT7 USP25 OXR1
chemokine binding	GO:0019956	-2.2	5.3	4	CXCR5 CCR6 CCR8 ZFP36	n/a			
cytokine receptor activity	GO:0004896	-2.2	3.2	7	CXCR5 CCR6 CCR8 F3 GFRA1 IL1RL1 IL22RA2	n/a			
cellular response to cytokine stimulus	GO:0071345					-3.8	1.8	43	AKT1 SLC25A5 ATP5F1B CALM1 CD47 CDC42 EIF5A EPHA4 EPHA7 FLNB PDI A3 HIF1A HNRNPU HSPA5 HSP90AB1 HSPD1 KIT LIFR MAT2A NFYB NTRK2 NTRK3 PRKACA MAPK1 MAP2K7 RAF1 CX3CL1 TLE4 UGCG ADAM23 INA EEF1E1 SPOCK2 ACTR3 MRAS PLCB1 WBP1L ABCG4 WNK1 ARID5B VPS26B EPHA6 SLC27A1
positive regulation of dendritic cell cytokine production	GO:0002732					-2.4	9.1	3	DDX1 KIT DHX36
positive regulation of myeloid leukocyte cytokine production involved in immune response	GO:0061081					-2.4	4.7	5	DDX1 KIT NR4A3 RTN4 DHX36
positive regulation of cytokine production	GO:0001819					-2.4	1.7	27	B2M BSG CD81 DDX1 DDX3X HDAC2 HIF1A HK1 HMG1 HSP90AA1 HSPD1 KIT MAPK9 RAB1A RAD21 CX3CL1 SORL1 SPTBN1 NR4A3 TOMM70 AGPAT1 PL

									CB1 AKI- RIN2 SULF2 RTN4 DHX36 SCAMP5
positive regulation of programmed cell death	GO:0043068					-4.7	2.1	37	APBB2 APC BCL2L1 BNIP 3L CDC42 CNR1 DDX3X E1 F5A EPHA7 GRN GRIN2A PDIA3 HMGB1 HSPD1 IGF 2R ITPR1 KCNMA1 MAL M EF2C MAPK9 RPS6 SFPQ SOD2 SP1 SRPK2 TIA1 VD AC1 NCOA1 TSC22D1 CD K5R1 MAGED1 EEF1E1 R BM5 OLFM1 ARL6IP5 FBX W7 CSRNP3
regulation of neu- ron apoptotic pro- cess	GO:0043523					-9	3.8	29	BCL2L1 CDC42 EPHA4 EP HA7 GRN GRIK2 HIF1A ME F2C NTRK2 PIK3CA PRKC G MAP2K7 PTPRZ1 RAD2 1 CX3CL1 SET SOD2 SRP K2 SYN- GAP1 CDK5R1 SIG- MAR1 CHL1 FAIM2 HIPK2 OXR1 FBXW7 AM- BRA1 CPEB4 AGAP2
apoptotic mito- chondrial changes	GO:0008637					-3.9	4.6	9	AKT1 SLC25A4 BCL2L1 B NIP3L HSPD1 PPP2CB SO D2 VDAC2 VPS35
apoptotic signal- ing pathway	GO:0097190					-3.7	2.3	23	BCL2L1 BNIP3L DDX3X P DIA3 ITPR1 PDK2 PRKCA MAPK9 RAF1 CX3CL1 SO D2 TMBIM6 VDAC2 BAG6 CUL1 RB1CC1 RNF41 ARL 6IP5 FASTK FAIM2 HIPK2 CYCS HIPK1

Supplementary Table 2: Top 20 Genes Upregulated by PN Treatment

The top 20 genes upregulated in the hippocampus of mice following oral administration of PN in the TST model. Genes are ranked according to fold-change values obtained through microarray analysis.

Gene Symbol	Description	Fold Change	p Value	Biological Functions
Wipf2	WAS/WASL interacting protein family, member 2	4.57	0.0003	actin binding cytoplasm
Retsat	retinol saturase (all trans retinol 13,14 reductase)	4.00	0.0047	oxidoreductase activity lipid metabolic process
Rpp25	ribonuclease P/MRP 25 subunit	3.84	0.0002	nucleic acid binding rRNA processing
Spi1	spleen focus forming virus (SFFV) proviral integration oncogene	3.61	0.0004	positive regulation of myeloid dendritic cell chemotaxis, lipopolysaccharide-mediated signaling pathway
Ddx26b	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	3.30	0.0008	snRNA 3'-end processing
Rexo1	REX1, RNA exonuclease 1 homolog (<i>S. cerevisiae</i>)	3.07	0.0004	nucleic acid binding hydrolase activity
Ctdsp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	3.01	0.0001	phosphoprotein phosphatase activity myosin phosphatase activity
Mid1	midline 1	2.81	0.0151	positive regulation of stress-activated MAPK cascade
Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	2.77	0.0021	reticulum stress-induced intrinsic apoptotic signaling pathway transmembrane transporter binding
Rpsa	ribosomal protein SA	2.70	0.0075	synapse neuronal cell body
Fcrls	Fc receptor-like S, scavenger receptor	2.66	0.0111	transmembrane signaling receptor activity
Rps16	ribosomal protein S16	2.65	0.0038	translation at presynapse, translation at postsynapse

Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	2.63	0.0167	translation at presynapse, translation at postsynapse
Psm13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	2.62	0.0004	ubiquitin-dependent protein catabolic process
Tmem258	transmembrane protein 258	2.60	0.0028	inflammatory response, epithelial cell apoptotic process
Prr14	proline rich 14	2.57	0.0001	muscle organ development
Rpl23a	ribosomal protein L23A; small nucleolar RNA, C/D box 42B	2.54	0.0359	translation at presynapse, translation at postsynapse
Lrp11	low density lipoprotein receptor-related protein 11	2.52	0.0434	multicellular organismal response to stress, response to immobilization stress
Igfbp7	insulin-like growth factor binding protein 7	2.52	0.0004	insulin-like growth factor binding, growth factor binding
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta sub-complex, 9	2.40	0.0039	proton motive force-driven mitochondrial ATP synthesis

Supplementary Table 3: Top 20 Genes Downregulated by PN Treatment

The top 20 genes downregulated in the hippocampus of mice following oral administration of PN in the TST model. Genes are ranked according to fold-change values obtained through microarray analysis.

Gene Symbol	Description	Fold Change	p Value	Biological Functions
Kcnj16	potassium inwardly-rectifying channel, subfamily J, member 16	-5.72	0.0057	inward rectifier potassium channel activity monoatomic ion transport
Zic1	zinc finger protein of the cerebellum 1	-4.2	0.0122	nervous system development, hippocampus development, RNA polymerase II transcription regulatory region sequence-specific DNA binding
Nt5dc3	5-nucleotidase domain containing 3; 5'-nucleotidase domain containing 3	-2.67	0.0012	5'-nucleotidase activity mitochondrion
Ano2	anoctamin 2	-2.58	0.0262	intracellular calcium activated chloride channel activity, neuron projection
Hells	helicase, lymphoid specific	-2.57	0.0046	ATP binding
Glo1	glyoxalase 1	-2.47	0.0128	GPCR, family 3, extracellular calcium-sensing receptor-related
Fstl1	folliculin-like 1	-2.38	0.0017	lactoylglutathione lyase activity
Zfp729a	zinc finger protein 729a	-2.19	0.0086	pheromone receptor activity
Xlr4b	X-linked lymphocyte-regulated 4B	-2.18	0.0118	dopamine secretion positive regulation of synapse assembly
Isl1	ISL1 transcription factor, LIM/homeodomain	-2.12	0.0009	negative regulation of neuron differentiation negative regulation of inflammatory response
Slc25a31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	-2.03	0.0362	cell differentiation, mitochondrial ATP transmembrane transport
Thoc2	THO complex 2	-2.00	0.0099	negative regulation of neuron projection development

Gstp1	glutathione S-transferase, pi 1	-1.98	0.0002	regulation of stress-activated MAPK cascade, inflammatory response
Cdh19	cadherin 19, type 2	-1.98	0.0128	cell migration, cell-cell adhesion
Rasd1	RAS, dexamethasone-induced 1	-1.98	0.0158	negative regulation of DNA-templated transcription
Lrrc16a	leucine rich repeat containing 16A	-1.98	0.0264	positive regulation of stress fiber assembly
Slc34a1	solute carrier family 34 (sodium phosphate), member 1	-1.98	0.0099	monoatomic ion transport
Cps1	carbamoyl-phosphate synthetase 1	-1.96	0.0364	ATP binding, potassium ion binding
Tbkbp1	TBK1 binding protein 1	-1.94	0.0352	protein binding, zinc ion binding
Cd19	CD19 antigen	-1.93	0.0132	B cell proliferation, regulation of B cell receptor signaling pathway