

Table SI. Top 10 DEGs identified by RNA-sequencing analysis.

Gene symbol	log ₂ Fold change	P-value	adj. P-value (FDR)	KEGG pathway enrichment	GO biological process
BTG2	2.0324	1.67x10 ⁻⁸⁴	5.03x10 ⁻⁸⁰	p53 signaling (hsa04115)	Regulation of cell cycle (GO: 0051726)
CDKN1A	2.2949	2.43x10 ⁻⁸⁰	3.65x10 ⁻⁷⁶	Cell cycle (hsa04110)	Cell cycle arrest (GO: 0007050)
FDXR	1.5857	7.17x10 ⁻⁶²	7.18x10 ⁻⁵⁸	Metabolic pathways (hsa01100)	Electron transport (GO: 0006118)
COL17A1	1.7197	2.64x10 ⁻⁵⁹	1.98x10 ⁻⁵⁵	ECM-receptor interaction (hsa04512)	Collagen fibril organization (GO: 0030199)
PTPRU	1.4035	1.90x10 ⁻⁵⁷	1.14x10 ⁻⁵³	Cell adhesion (hsa04514)	Protein dephosphorylation (GO: 0006470)
TAGLN	-1.8891	2.11 x10 ⁻⁴⁸	7.91x10 ⁻⁴⁵	Vascular smooth muscle (hsa05410)	Actin cytoskeleton (GO: 0015629)
CDKN1C	-2.1359	1.06 x10 ⁻⁴⁵	2.66x10 ⁻⁴²	Cell cycle (hsa04110)	Response to organic substance (GO: 0010033)
NEK2	-1.3301	1.10 x10 ⁻³⁶	1.44x10 ⁻³³	Cell cycle (hsa04110)	Anatomical structure development (GO: 0048856)
HMGB1P5	-1.4506	2.04 x10 ⁻³⁵	2.37x10 ⁻³²	Pseudogene	Pseudogene
ASPM	-1.4724	1.09 x10 ⁻³⁴	1.21x10 ⁻³¹	Focal adhesion (hsa04510)	Cell migration (GO: 0016477)
NOX1	1.5804	0.00001939	0.0021	ROS pathway (hsa04152)	NADPH oxidase activity (GO: 0004497)

The top 10 DEGs, comprising both upregulated and downregulated genes, were selected based on p-values. The list also includes a gene of interest (NOX1). Adjusted P-values (FDR) were calculated using the Benjamini-Hochberg method. KEGG pathway and GO biological process annotations were sourced from their respective databases. DEGs, differentially expressed genes; FDR, false discovery rate; KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology.