

Supplementary Table S1. Gene ontology (GO) enrichment analysis showing the most significant biological processes in which PEMF modulated proteins were involved.

#term ID	term description	observed	ger background	ξ strength	false discover	matching proteins in the nnetwork
GO:0006979	Response to oxidative stress	6	368	1.51	0.00014	SIRT2,EPAS1,HSPA1A,MAPK8,SOD2,PON2
GO:0034599	Cellular response to oxidative stress	5	224	1.64	0.00038	SIRT2,EPAS1,HSPA1A,MAPK8,SOD2
GO:0009628	Response to abiotic stimulus	7	1107	1.1	0.00073	SIRT2,EPAS1,TXN,HSPA1A,MAPK8,CDKN1A,SOD2
GO:2000377	Regulation of reactive oxygen species metabolic process	4	143	1.74	0.0019	SIRT2,PON3,CDKN1A,SOD2
GO:0043618	Regulation of transcription from RNA polymerase II promoter in response to stress	3	49	2.08	0.0054	SIRT2,EPAS1,HSPA1A
GO:0009636	Response to toxic substance	4	229	1.54	0.0074	PON3,TXN,SOD2,PON2
GO:0051173	Positive regulation of nitrogen compound metabolic process	8	3166	0.7	0.0259	SIRT2,EPAS1,CYCS,TXN,HSPA1A,MAPK8,CDKN1A,SOD2
GO:0051098	Regulation of binding	4	375	1.32	0.0404	SIRT2,TXN,MAPK8,CDKN1A
GO:0051101	Regulation of DNA binding	3	124	1.68	0.0404	SIRT2,TXN,MAPK8
GO:0051247	Positive regulation of protein metabolic process	6	1512	0.89	0.0404	SIRT2,CYCS,TXN,HSPA1A,MAPK8,CDKN1A
GO:0097201	Negative regulation of transcription from RNA polymerase II promoter in response to stress	2	14	2.45	0.0404	SIRT2,HSPA1A
GO:0031399	Regulation of protein modification process	6	1560	0.88	0.0443	SIRT2,EPAS1,TXN,HSPA1A,MAPK8,CDKN1A
GO:0033554	Cellular response to stress	6	1572	0.88	0.0443	SIRT2,EPAS1,HSPA1A,MAPK8,CDKN1A,SOD2
GO:0044093	Positive regulation of molecular function	6	1587	0.87	0.0443	SIRT2,CYCS,TXN,HSPA1A,MAPK8,CDKN1A
GO:0007005	Mitochondrion organization	4	445	1.25	0.0458	EPAS1,HSPA1A,MAPK8,SOD2
GO:0009314	Response to radiation	4	444	1.25	0.0458	TXN,MAPK8,CDKN1A,SOD2
GO:0010941	Regulation of cell death	6	1651	0.85	0.0458	SIRT2,TXN,HSPA1A,MAPK8,CDKN1A,SOD2
GO:0031667	Response to nutrient levels	4	461	1.23	0.0458	SIRT2,MAPK8,CDKN1A,SOD2
GO:0051246	Regulation of protein metabolic process	7	2622	0.72	0.0458	SIRT2,EPAS1,CYCS,TXN,HSPA1A,MAPK8,CDKN1A
GO:0070887	Cellular response to chemical stimulus	7	2609	0.72	0.0458	SIRT2,EPAS1,PON3,TXN,HSPA1A,MAPK8,SOD2
GO:0097193	Intrinsic apoptotic signaling pathway	3	166	1.55	0.0465	CYCS,CDKN1A,SOD2
GO:1904706	Negative regulation of vascular associated smooth muscle cell proliferation	2	25	2.2	0.0487	CDKN1A,SOD2