

Supplementary Table S1

Rank	GO ID	GO Name	Diff Gene Counts in GO	Gene Amount in GO	Enrichment Score	p-value	FDR
1	GO:0006355	regulation of transcription, DNA-dependent	273	1852	3.696985	1.46E-79	5.41E-76
2	GO:0006351	transcription, DNA-dependent	261	1756	3.727709	9.80E-77	1.26E-73
3	GO:0007049	cell cycle	148	565	6.569606	1.02E-76	1.26E-73
4	GO:0006810	transport	257	1712	3.764917	1.89E-76	1.75E-73
5	GO:0051301	cell division	91	333	6.85367	4.47E-49	3.32E-46
6	GO:0007067	mitosis	78	241	8.11715	3.09E-48	1.91E-45
7	GO:0006974	response to DNA damage stimulus	84	361	5.835769	1.58E-39	8.40E-37
8	GO:0006260	DNA replication	51	123	10.39899	3.89E-38	1.81E-35
9	GO:0007275	multicellular organismal development	131	954	3.443888	1.09E-34	4.50E-32
10	GO:0006281	DNA repair	70	291	6.032969	4.29E-34	1.59E-31
11	GO:0007155	cell adhesion	91	500	4.564544	1.02E-33	3.43E-31
12	GO:0016310	phosphorylation	105	684	3.849987	4.38E-32	1.36E-29
13	GO:0006468	protein phosphorylation	97	611	3.98159	6.80E-31	1.94E-28
14	GO:0008152	metabolic process	124	991	3.138153	5.53E-29	1.47E-26
15	GO:0008150	biological_process	620	10237	1.518955	1.06E-28	2.63E-26
16	GO:0007399	nervous system development	65	307	5.310079	2.77E-28	6.43E-26
17	GO:0006397	mRNA processing	57	278	5.142284	3.35E-24	7.31E-22
18	GO:0015031	protein transport	80	538	3.729355	9.15E-24	1.89E-21
19	GO:0043066	negative regulation of apoptotic process	75	480	3.918737	1.11E-23	2.16E-21
20	GO:0006811	ion transport	81	570	3.563988	9.38E-23	1.74E-20

Supplementary Table S2

Rank	Pathway ID	Pathway Name	Outdegree	Indegree	Degree
1	4010	MAPK signaling pathway	5	31	36
2	5200	Pathways in cancer	26	0	26
3	4210	Apoptosis	2	23	25
4	4110	Cell cycle	3	21	24
5	4115	p53 signaling pathway	2	18	20
6	4020	Calcium signaling pathway	5	11	16
7	4310	Wnt signaling pathway	7	8	15
8	4012	ErbB signaling pathway	8	6	14
9	4510	Focal adhesion	7	7	14
10	4350	TGF-beta signaling pathway	4	8	12

Supplementary Table S3

Pathway ID	Pathway Name	Diff Counts	Gene in	Gene Amount in Pathway	Enrichment Score	p-value	FDR	Gene Symbols
4010	MAPK signaling pathway	35		259	3.38917751444749	6.95332957303585E-10	5.63459465401181E-09	Ppp5c Cacna1b Cacna1e Cacna2d1 Cacna2d3 Tak1 Ppp3ca Cdc25b Hras1 Atf4 Fgf14 Mapkapk2 Mapk10 Atf2 Rasa2 Flnb Mapk8 Pdgfra Chuk Ddit3 Fgf21 Gadd45a Map3k2 Rps6ka3 Braf Stk3 Tgfb2 Mef2c Tgfbr1 Cacnb4 Cacng2 Map4k3 Rasa1 Rps6ka5 Dusp6
4360	Axon guidance	31		133	5.84569414897936	2.46808249836573E-15	8.28570553022782E-14	Nfatc1 Sema3a Epha6 Unc5d Hras1 Pak7 Nfat5 Rasa1 Epha5 L1cam Ntn1 Unc5c Robo1 Slit2 Dcc Epha4 Ntn4 Epha7 Met Rock2 Epha3 Plxna4 Plxna3 Sema5a Robo2 Ppp3ca Lrrc4c Ntn1 Rock1 Nrp1 Pak3
4020	Calcium signaling pathway	16		185	2.1690736092464	0.0074160538165082	0.0145231053906619	Pdgfra Itpkb Ppp3ca Plcb4 ErbB4 Cacna1e P2rx3 Plcb1 Slc8a1 Ednra Cacna1b Slc25a5 Pde1a Atp2b1 Ryr3 Plcd4
4350	TGF-beta signaling pathway	15		83	4.53251450727315	1.84122661303045E-06	9.20613306515224E-06	Thbs1 Inhba Tgfbr1 Rock2 Zfyve16 Id3 Rock1 Rps6kb1 Bmpr2 Bmp4 Bmp2 Tgfb2 Id1 Dcn Acvr2a

Supplementary Table S4

Probe Set ID	Gene Symbol	Accession Number	Database Source	Mean Signal of Group rTMS	Mean Signal of Group Blank	d Score	Fold Change	p-value	q-value	Gene Feature
10484276	Neurod1	NM_010894	RefSeq	5.922978	4.717428	7.560285	2.306252	0.000263	0	up
10607156	Dcx	NM_001110222	RefSeq	9.798409	8.495217	4.101576	2.467743	0.002731	0	up
10495964	Neurog2	NM_009718	RefSeq	6.745101	6.085297	6.464297	1.579869	0.000512	0	up
10474312	Pax6	NM_001244198	RefSeq	7.508712	7.09887	2.988355	1.328541	0.006178	8.80E-05	up
10347036	Map2	NM_001039934	RefSeq	9.755172	8.989564	3.065041	1.700086	0.005817	8.80E-05	up
10395074	Myt11	NM_008666	RefSeq	7.953199	7.128191	4.299004	1.771545	0.00236	0	up