

**Supplementary Table 1.** The results of KEGG enrichment analysis of genes in three gene modules

KEGG pathway	KEGG ID	P	P <sub>adjust</sub>	Gene module
Long-term potentiation	4720	5.49e-05	0.0016	Black
Regulation of actin cytoskeleton	4810	0.0004	0.0058	Black
Phosphatidylinositol signaling system	4070	0.0016	0.0155	Black
Leishmaniasis	5140	0.0189	0.0520	Black
Focal adhesion	4510	0.0211	0.0520	Black
Hypertrophic cardiomyopathy (HCM)	5410	0.0247	0.0520	Black
Calcium signaling pathway	4020	0.0153	0.0520	Black
Wnt signaling pathway	4310	0.0098	0.0520	Black
Endometrial cancer	5213	0.0102	0.0520	Black
Prostate cancer	5215	0.0281	0.0520	Black
Osteoclast differentiation	4380	2.18e-12	2.57e-10	Blue
Hepatitis C	5160	4.45e-12	2.63e-10	Blue
Toll-like receptor signaling pathway	4620	1.43e-11	5.62e-10	Blue
Neurotrophin signaling pathway	4722	2.87e-10	8.47e-09	Blue
Pancreatic cancer	5212	5.00e-10	1.13e-08	Blue
Non-small cell lung cancer	5223	5.74e-10	1.13e-08	Blue
Leukocyte transendothelial migration	4670	1.01e-09	1.70e-08	Blue
Fc epsilon RI signaling pathway	4664	1.90e-09	2.80e-08	Blue
T cell receptor signaling pathway	4660	4.93e-09	6.46e-08	Blue
Prostate cancer	5215	6.94e-09	8.19e-08	Blue
Protein processing in endoplasmic reticulum	4141	1.51e-09	1.83e-07	Turquoise
Ubiquitin mediated proteolysis	4120	3.86e-08	1.56e-06	Turquoise
Endocytosis	4144	2.98e-08	1.56e-06	Turquoise
Hepatitis C	5160	2.58e-07;	7.80e-06	Turquoise
Cell cycle	4110	7.62e-07	1.84e-05	Turquoise
Neurotrophin signaling pathway	4722	9.86e-07	1.99e-05	Turquoise
Prostate cancer	5215	1.62e-06	2.31e-05	Turquoise
Pathways in cancer	5200	1.58e-06	2.31e-05	Turquoise
Renal cell carcinoma	5211	1.72e-06	2.31e-05	Turquoise
Regulation of actin cytoskeleton	4810	1.98e-06	2.40e-05	Turquoise