

Table SI. GO term and KEGG enrichment analysis in Module 1.

Category/term	Count	P-value
Biological process		
GO: 0007166~cell surface receptor linked signal transduction	6	<0.001
GO: 0030334~regulation of cell migration	6	0.001
GO: 0051130~positive regulation of cellular component organization	6	0.002
GO: 0040012~regulation of locomotion	6	0.002
GO: 0051270~regulation of cell motion	6	0.002
GO: 0051050~positive regulation of transport	6	0.002
GO: 0032309~icosanoid secretion	6	0.004
GO: 0050482~arachidonic acid secretion	6	0.004
GO: 0051496~positive regulation of stress fiber formation	6	0.004
GO: 0007186~G-protein coupled receptor protein signaling pathway	6	0.004
Cellular component		
GO: 0005886~plasma membrane	5	0.013
GO: 0016020~membrane	6	0.0205
Molecular function		
GO:0042277~peptide binding	3	0.002
GO:0008188~neuropeptide receptor activity	2	0.013
GO:0042923~neuropeptide binding	2	0.013
GO:0004930~G-protein coupled receptor activity	3	0.030
GO:0005102~receptor binding	3	0.030
GO:0030594~neurotransmitter receptor activity	2	0.031
GO:0042165~neurotransmitter binding	2	0.034
GO:0008528~peptide receptor activity, G-protein coupled	2	0.037
GO:0001653~peptide receptor activity	2	
KEGG pathway		
hsa04080: Neuroactive ligand-receptor interaction	3	0.007

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table SII. GO term analysis in Module 2.

Category/term	Count	P-value
Biological process		
GO: 0043632~modification-dependent macromolecule catabolic process	4	<0.001
GO: 0019941~modification-dependent protein catabolic process	4	<0.001
GO: 0051603~proteolysis involved in cellular protein catabolic process	4	<0.001
GO: 0044257~cellular protein catabolic process	4	<0.001
GO: 0030163~protein catabolic process	4	<0.001
GO: 0044265~cellular macromolecule catabolic process	4	<0.001
GO: 0009057~macromolecule catabolic process	4	<0.001
GO: 0044248~cellular catabolic process	4	<0.001
GO: 0006508~proteolysis	4	<0.001
GO: 0009056~catabolic process	4	0.001
Molecular function		
GO: 0042803~protein homodimerization activity	2	0.022
GO: 0046983~protein dimerization activity	2	0.036
GO: 0042802~identical protein binding	2	0.042
GO, Gene Ontology.		