

Table 2 Functional enrichment analysis for Proteins/genes in protein interaction sub-network

Term	Gene Num.	<i>p</i> value
Multicellular organismal process	152	5.01E-12
Homeostatic process	46	1.01E-09
Cell-cell signaling	44	1.14E-09
Response to chemical stimulus	81	1.36E-09
Regulation of multicellular organismal process	54	4.66E-09
Chemical homeostasis	34	1.64E-08
Response to stress	84	2.98E-08
Wound healing	31	6.02E-08
Response to wounding	42	1.49E-07
Ion homeostasis	27	2.40E-07
Developmental process	107	2.74E-07
Cell proliferation	48	4.31E-07
Cell differentiation	70	6.76E-07
Cell morphogenesis	32	1.36E-06
Localization of cell	29	2.08E-06
Cation homeostasis	20	4.47E-06
Regulation of sequence-specific DNA binding transcription factor activity	16	4.77E-06
Regulation of transcription regulator activity	16	5.84E-06
Response to stimulus	157	6.30E-06
Regulation of cell communication	39	6.88E-06
Protein modification process	65	8.71E-06
MAPKKK cascade	20	8.71E-06
Regulation of signaling	51	1.04E-05
Central nervous system development	26	1.48E-05
Immune system process	51	1.76E-05
Response to drug	18	1.78E-05
Small cell lung cancer	10	5.68E-05
MI:hsa-miR-323-5p	28	1.03E-04
Regulation of actin cytoskeleton	15	1.75E-04
Pathways in cancer	19	3.58E-04

Note: Only annotations with *p* value <0.05 for GO in all levels are listed here