

Supplementary materials

Supplementary Figure 1

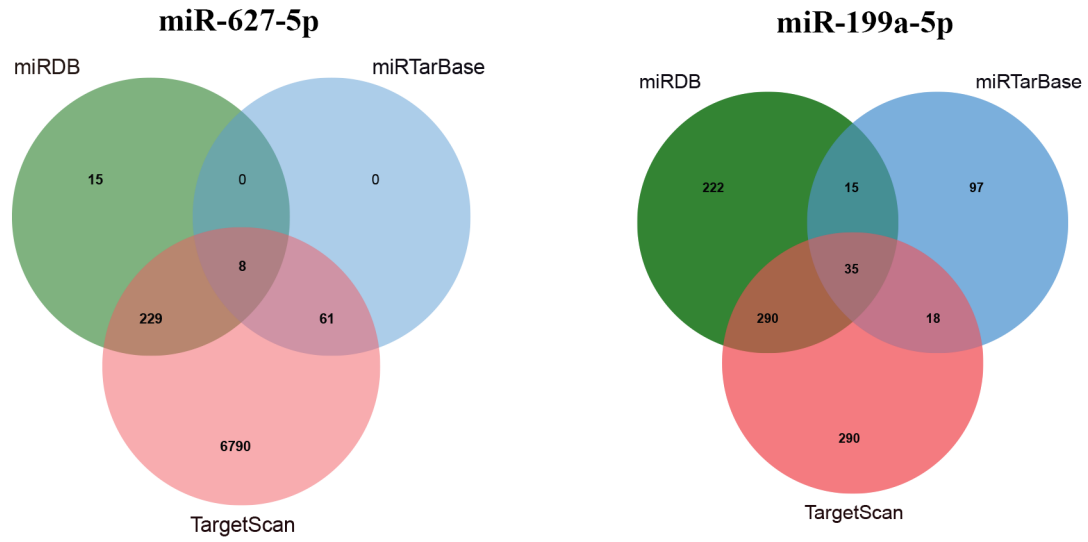


Figure S1 Venn diagram of target genes for miR-627-5p and miR-199a-5p.

Supplementary Table 1 The primer sequences used for quantitative real-time polymerase chain reaction

Primers	Classification	Sequence (5'-3')
hsa-miR-627-5p	F	CAGTGCAGGGTCCGAGGTAT
	R	GTGAGTCTCTAAGAAAAGAGGAGTCGT
	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCCTCTTT
hsa-miR-199a-5p	F	CCCAGTGTTTCAGACTACCTGTTC
	R	CAGTGCAGGGTCCGAGGTAT
	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGAACAGGT
RNA, U6 small nuclear (U6)	F	CTCGCTTCGGCAGCACA
	R	AACGCTTCACGAATTTGCGT
	RT	AACGCTTCACGAATTTGCGT

F: Forward; R: Reverse; RT: Reverse transcription.

Supplementary Table 2 Correlations between serum miR-627-5p and miR-199a-5p expression levels and clinicopathological features in advanced colorectal adenoma patients

Variable	Number, <i>n</i> (%)	miR-627-5p		miR-199a-5p	
		Median (IQR)	<i>P</i> value	Median (IQR)	<i>P</i> value
Age	< 65	30 (50.00%)	2.28 (1.27-3.72)	0.75	2.34 (1.42-3.92)
	≥ 65	30 (50.00%)	2.12 (1.37-2.98)		2.43 (1.73-3.94)
Gender	Male	42 (70.00%)	2.47 (1.97-3.92)	0.41	2.83 (2.31-3.44)
	Female	18 (30.00%)	1.96 (1.27-3.06)		2.60 (1.67-5.71)
No. of adenomas	< 3	35 (58.33%)	1.90 (1.27-3.32)	0.49	2.37 (1.46-3.90)
	≥ 3	25 (41.67%)	2.39 (1.40-3.49)		2.28 (1.74-3.91)
Histology	TA	35 (58.33%)	2.41 (1.30-3.97)	0.20	2.72 (1.73-5.03)
	TVA	24 (40%)	1.96 (1.41-2.86)		2.16 (1.41-3.31)
Intraepithelial neoplasia	Mild grade	51 (85.00%)	3.89 (3.06-4.49)	0.10	3.82 (2.04-7.42)
	High grade	9 (15.00%)	1.36 (1.24-2.11)		3.57 (1.34-5.77)

IQR: Interquartile range; TA: Tubular adenoma; TVA: Villous tubular adenoma.

Supplementary Table 3 KEGG enrichment analysis of the predicted targets of miR-627-5p and miR-199a-5p

ID	Description	Gene Ratio	P value	Q value	Count
hsa05226	Gastric cancer	6/30	0.000	0.001	6
hsa05225	Hepatocellular carcinoma	6/30	0.000	0.001	6
hsa05217	Basal cell carcinoma	4/30	0.000	0.002	4
hsa05205	Proteoglycans in cancer	6/30	0.000	0.002	6
hsa04550	Signaling pathways regulating pluripotency of stem cells	5/30	0.000	0.003	5
hsa05224	Breast cancer	5/30	0.000	0.003	5
hsa04150	mTOR signaling pathway	5/30	0.000	0.003	5
hsa04934	Cushing syndrome	5/30	0.000	0.003	5
hsa04390	Hippo signaling pathway	5/30	0.000	0.003	5
hsa04916	Melanogenesis	4/30	0.000	0.005	4
hsa04110	Cell cycle	4/30	0.001	0.010	4
hsa05165	Human papillomavirus infection	6/30	0.001	0.010	6
hsa05211	Renal cell carcinoma	3/30	0.002	0.016	3
hsa04218	Cellular senescence	4/30	0.002	0.017	4
hsa05212	Pancreatic cancer	3/30	0.003	0.017	3
hsa05220	Chronic myeloid leukemia	3/30	0.003	0.017	3
hsa05161	Hepatitis B	4/30	0.003	0.017	4
hsa04310	Wnt signaling pathway	4/30	0.003	0.017	4
hsa04010	MAPK signaling pathway	5/30	0.004	0.022	5
hsa05222	Small cell lung cancer	3/30	0.005	0.023	3
hsa05206	MicroRNAs in cancer	5/30	0.005	0.024	5
hsa05215	Prostate cancer	3/30	0.005	0.024	3

hsa05167	Kaposi sarcoma-associated herpesvirus infection	4/30	0.005	0.024	4
hsa01523	Antifolate resistance	2/30	0.006	0.024	2
hsa05166	Human T-cell leukemia virus 1 infection	4/30	0.008	0.033	4
hsa05010	Alzheimer disease	5/30	0.011	0.042	5
hsa04380	Osteoclast differentiation	3/30	0.012	0.043	3
hsa04068	FOXO signaling pathway	3/30	0.012	0.044	3

mTOR: Mammalian/mechanistic target of rapamycin; MAPK: Mitogen-activated protein kinases; FOXO: Forkhead box O.

Supplementary Table 4 GO enrichment analysis of the predicted targets of miR-627-5p and miR-199a-5p

Ontology	ID	Description	Gene Ratio	P value	Q value	Count
BP	GO: 0042698	Ovulation cycle	5/43	0.000	0.001	5
BP	GO: 0071560	Cellular response to transforming growth factor beta stimulus	7/43	0.000	0.001	7
BP	GO: 0090092	Regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	7/43	0.000	0.001	7
BP	GO: 0071559	Response to transforming growth factor beta	7/43	0.000	0.001	7
BP	GO: 0022602	Ovulation cycle process	4/43	0.000	0.001	4
BP	GO: 0090287	Regulation of cellular response	7/43	0.000	0.001	7

		to growth factor stimulus				
BP	GO: 0048608	Reproductive structure development	8/43	0.000	0.001	8
BP	GO: 0007179	Transforming growth factor beta receptor signaling pathway	6/43	0.000	0.001	6
BP	GO: 0061458	Reproductive system development	8/43	0.000	0.001	8
BP	GO: 0048568	Embryonic organ development	8/43	0.000	0.001	8
BP	GO: 0060562	Epithelial tube morphogenesis	7/43	0.000	0.001	7
BP	GO: 0017015	Regulation of transforming growth factor beta receptor signaling pathway	5/43	0.000	0.001	5
BP	GO: 1903844	Regulation of cellular response to transforming growth factor beta stimulus	5/43	0.000	0.001	5
BP	GO: 0007178	Transmembrane receptor protein serine/threonine kinase signaling pathway	7/43	0.000	0.001	7
BP	GO: 0046777	Protein autophosphorylation	6/43	0.000	0.001	6
BP	GO: 0001837	Epithelial to mesenchymal transition	5/43	0.000	0.002	5
BP	GO: 2001242	Regulation of intrinsic apoptotic signaling pathway	5/43	0.000	0.003	5
BP	GO: 0001558	Regulation of cell growth	7/43	0.000	0.003	7
BP	GO: 0001942	Hair follicle development	4/43	0.000	0.003	4

BP	GO: 0010634	Positive regulation of epithelial cell migration	5/43	0.000	0.003	5
BP	GO: 0001892	Embryonic placenta development	4/43	0.000	0.003	4
BP	GO: 0022404	Molting cycle process	4/43	0.000	0.003	4
BP	GO: 0022405	Hair cycle process	4/43	0.000	0.003	4
BP	GO: 0098773	Skin epidermis development	4/43	0.000	0.003	4
BP	GO: 0060317	Cardiac epithelial to mesenchymal transition	3/43	0.000	0.003	3
BP	GO: 0048732	Gland development	7/43	0.000	0.003	7
BP	GO: 0048511	Rhythmic process	6/43	0.000	0.003	6
BP	GO: 0045648	Positive regulation of erythrocyte differentiation	3/43	0.000	0.003	3
BP	GO: 0062012	Regulation of small molecule metabolic process	7/43	0.000	0.003	7
BP	GO: 2001243	Negative regulation of intrinsic apoptotic signaling pathway	4/43	0.000	0.003	4
BP	GO: 0007565	Female pregnancy	5/43	0.000	0.003	5
BP	GO: 0071542	Dopaminergic neuron differentiation	3/43	0.000	0.003	3
BP	GO: 0046545	Development of primary female sexual characteristics	4/43	0.000	0.003	4
BP	GO: 0062014	Negative regulation of small molecule metabolic process	4/43	0.000	0.003	4
BP	GO: 0006473	Protein acetylation	5/43	0.000	0.003	5
BP	GO: 0001667	Ameboidal-type cell migration	7/43	0.000	0.003	7

BP	GO: 0050769	Positive regulation of neurogenesis	7/43	0.000	0.003	7
BP	GO: 1902895	Positive regulation of pri-mirna transcription by RNA polymerase II	3/43	0.000	0.003	3
BP	GO: 0016049	Cell growth	7/43	0.000	0.003	7
BP	GO: 0060070	Canonical Wnt signaling pathway	6/43	0.000	0.003	6
BP	GO: 0042303	Molting cycle	4/43	0.000	0.003	4
BP	GO: 0042633	Hair cycle	4/43	0.000	0.003	4
BP	GO: 0071902	Positive regulation of protein serine/threonine kinase activity	6/43	0.000	0.003	6
BP	GO: 0002064	Epithelial cell development	5/43	0.000	0.004	5
BP	GO: 0046660	Female sex differentiation	4/43	0.000	0.004	4
BP	GO: 0070997	Neuron death	6/43	0.000	0.004	6
BP	GO: 0044706	Multi-multicellular organism process	5/43	0.000	0.004	5
BP	GO: 0030218	Erythrocyte differentiation	4/43	0.000	0.004	4
BP	GO: 0045137	Development of primary sexual characteristics	5/43	0.000	0.004	5
BP	GO: 0048762	Mesenchymal cell differentiation	5/43	0.000	0.004	5
BP	GO: 0010631	Epithelial cell migration	6/43	0.000	0.004	6
BP	GO: 0097191	Extrinsic apoptotic signaling pathway	5/43	0.000	0.004	5
BP	GO: 0090132	Epithelium migration	6/43	0.000	0.004	6

BP	GO: 0022612	Gland morphogenesis	4/43	0.000	0.004	4
BP	GO: 2001234	Negative regulation of apoptotic signaling pathway	5/43	0.000	0.004	5
BP	GO: 0007595	Lactation	3/43	0.000	0.004	3
BP	GO: 0090130	Tissue migration	6/43	0.000	0.004	6
BP	GO: 0030111	Regulation of Wnt signaling pathway	6/43	0.000	0.004	6
BP	GO: 0045646	Regulation of erythrocyte differentiation	3/43	0.000	0.004	3
BP	GO: 0034101	Erythrocyte homeostasis	4/43	0.000	0.004	4
BP	GO: 0006984	ER-nucleus signaling pathway	3/43	0.000	0.004	3
BP	GO: 1902893	Regulation of pri-mirna transcription by RNA polymerase II	3/43	0.000	0.004	3
BP	GO: 0001701	In utero embryonic development	6/43	0.000	0.004	6
BP	GO: 0072175	Epithelial tube formation	4/43	0.000	0.004	4
BP	GO: 0061614	Pri-mirna transcription by RNA polymerase II	3/43	0.000	0.004	3
BP	GO: 0043543	Protein acylation	5/43	0.000	0.004	5
BP	GO: 0030198	Extracellular matrix organization	6/43	0.000	0.005	6
BP	GO: 0050678	Regulation of epithelial cell proliferation	6/43	0.000	0.005	6
BP	GO: 0043062	Extracellular structure organization	6/43	0.000	0.005	6
BP	GO: 0045926	Negative regulation of growth	5/43	0.000	0.005	5

BP	GO: 2000027	Regulation of animal organ morphogenesis	5/43	0.000	0.005	5
BP	GO: 0033483	Gas homeostasis	2/43	0.000	0.005	2
BP	GO: 0003007	Heart morphogenesis	5/43	0.000	0.005	5
BP	GO: 0030879	Mammary gland development	4/43	0.000	0.005	4
BP	GO: 0051055	Negative regulation of lipid biosynthetic process	3/43	0.000	0.005	3
BP	GO: 0001503	Ossification	6/43	0.000	0.005	6
BP	GO: 2001233	Regulation of apoptotic signaling pathway	6/43	0.000	0.005	6
BP	GO: 0051058	Negative regulation of small gtpase mediated signal transduction	3/43	0.000	0.005	3
BP	GO: 0006983	ER overload response	2/43	0.000	0.005	2
BP	GO: 0071901	Negative regulation of protein serine/threonine kinase activity	4/43	0.000	0.005	4
BP	GO: 0035148	Tube formation	4/43	0.000	0.006	4
BP	GO: 0016331	Morphogenesis of embryonic epithelium	4/43	0.000	0.006	4
BP	GO: 0045785	Positive regulation of cell adhesion	6/43	0.000	0.006	6
BP	GO: 0030099	Myeloid cell differentiation	6/43	0.000	0.006	6
BP	GO: 0002262	Myeloid cell homeostasis	4/43	0.000	0.006	4
BP	GO: 0032507	Maintenance of protein location in cell	3/43	0.000	0.006	3
BP	GO: 0007548	Sex differentiation	5/43	0.000	0.006	5

BP	GO: 0001890	Placenta development Regulation of cell	4/43	0.000	0.006	4
BP	GO: 0010649	communication by electrical coupling Maintenance of protein	2/43	0.000	0.006	2
BP	GO: 0035437	localization in endoplasmic reticulum	2/43	0.000	0.006	2
BP	GO: 0051403	Stress-activated MAPK cascade	5/43	0.000	0.006	5
BP	GO: 0010976	Positive regulation of neuron projection development	5/43	0.000	0.006	5
BP	GO: 0060485	Mesenchyme development	5/43	0.000	0.006	5
BP	GO: 0097193	Intrinsic apoptotic signaling pathway	5/43	0.000	0.006	5
BP	GO: 0055088	Lipid homeostasis	4/43	0.001	0.006	4
BP	GO: 0043518	Negative regulation of DNA damage response, signal transduction by p53 class mediator	2/43	0.001	0.006	2
BP	GO: 0034976	Response to endoplasmic reticulum stress	5/43	0.001	0.006	5
BP	GO: 0050673	Epithelial cell proliferation	6/43	0.001	0.006	6
BP	GO: 0060828	Regulation of canonical Wnt signaling pathway	5/43	0.001	0.006	5
BP	GO: 0051348	Negative regulation of transferase activity	5/43	0.001	0.006	5
BP	GO: 0051090	Regulation of DNA-binding	6/43	0.001	0.006	6

		transcription factor activity				
BP	GO: 0061180	Mammary gland epithelium development	3/43	0.001	0.007	3
BP	GO: 0031098	Stress-activated protein kinase signaling cascade	5/43	0.001	0.007	5
BP	GO: 0010632	Regulation of epithelial cell migration	5/43	0.001	0.007	5
BP	GO: 0010934	Macrophage cytokine production	2/43	0.001	0.007	2
BP	GO: 0086103	G protein-coupled receptor signaling pathway involved in heart process	2/43	0.001	0.007	2
BP	GO: 0003205	Cardiac chamber development	4/43	0.001	0.007	4
BP	GO: 1901983	Regulation of protein acetylation	3/43	0.001	0.007	3
BP	GO: 0003198	Epithelial to mesenchymal transition involved in endocardial cushion formation	2/43	0.001	0.007	2
BP	GO: 0010715	Regulation of extracellular matrix disassembly	2/43	0.001	0.007	2
BP	GO: 1903524	Positive regulation of blood circulation	3/43	0.001	0.007	3
BP	GO: 0000271	Polysaccharide biosynthetic process	3/43	0.001	0.008	3
BP	GO: 1905330	Regulation of morphogenesis of an epithelium	4/43	0.001	0.008	4
BP	GO: 0061298	Retina vasculature	2/43	0.001	0.008	2

		development in camera-type eye				
		Positive regulation of blood vessel endothelial cell migration				
BP	GO: 0043536	vessel endothelial cell migration	3/43	0.001	0.008	3
BP	GO: 1901214	Regulation of neuron death	5/43	0.001	0.008	5
BP	GO: 0003151	Outflow tract morphogenesis	3/43	0.001	0.008	3
BP	GO: 0001936	Regulation of endothelial cell proliferation	4/43	0.001	0.008	4
		Negative regulation of canonical Wnt signaling pathway				
BP	GO: 0090090	canonical Wnt signaling pathway	4/43	0.001	0.008	4
BP	GO: 0051235	Maintenance of location	5/43	0.001	0.008	5
		Mammary gland alveolus development				
BP	GO: 0060749	Mammary gland alveolus development	2/43	0.001	0.008	2
		Mammary gland lobule development				
BP	GO: 0061377	Mammary gland lobule development	2/43	0.001	0.008	2
		Negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway				
BP	GO: 1902176	oxidative stress-induced intrinsic apoptotic signaling pathway	2/43	0.001	0.008	2
BP	GO: 0001570	Vasculogenesis	3/43	0.001	0.009	3
		Negative regulation of cell growth				
BP	GO: 0030308	Negative regulation of cell growth	4/43	0.001	0.009	4
		Positive regulation of cholesterol efflux				
BP	GO: 0010875	Positive regulation of cholesterol efflux	2/43	0.001	0.009	2
BP	GO: 0032092	Positive regulation of protein	3/43	0.001	0.009	3

		binding				
		Negative regulation of transforming growth factor beta receptor signaling pathway				
BP	GO: 0030512		3/43	0.001	0.009	3
		Positive regulation of cell adhesion mediated by integrin				
BP	GO: 0033630		2/43	0.001	0.009	2
		Histone H4-K16 acetylation				
BP	GO: 0043984		2/43	0.001	0.009	2
		Negative regulation of fatty acid biosynthetic process				
BP	GO: 0045717		2/43	0.001	0.009	2
		Labyrinthine layer blood vessel development				
BP	GO: 0060716		2/43	0.001	0.009	2
		Beta-catenin destruction complex disassembly				
BP	GO: 1904886		2/43	0.001	0.009	2
		Regulation of MAP kinase activity				
BP	GO: 0043405		5/43	0.001	0.009	5
		Endothelial cell proliferation				
BP	GO: 0001935		4/43	0.001	0.010	4
		Negative regulation of cellular response to transforming growth factor beta stimulus				
BP	GO: 1903845		3/43	0.001	0.010	3
		Midbrain development				
BP	GO: 0030901		3/43	0.001	0.010	3
		Roof of mouth development				
BP	GO: 0060021		3/43	0.001	0.010	3
		Regulation of response to endoplasmic reticulum stress				
BP	GO: 1905897		3/43	0.001	0.010	3
		Maintenance of protein location				
BP	GO: 0045185		3/43	0.001	0.011	3
		Negative regulation of protein				
BP	GO: 1901984		2/43	0.001	0.011	2

		acetylation				
BP	GO: 2000810	Regulation of bicellular tight junction assembly	2/43	0.001	0.011	2
BP	GO: 0001666	Response to hypoxia	5/43	0.001	0.011	5
BP	GO: 0062197	Cellular response to chemical stress	5/43	0.001	0.011	5
BP	GO: 0006109	Regulation of carbohydrate metabolic process	4/43	0.001	0.011	4
BP	GO: 0045216	Cell-cell junction organization	4/43	0.001	0.011	4
BP	GO: 0007589	Body fluid secretion	3/43	0.001	0.011	3
BP	GO: 0003272	Endocardial cushion formation	2/43	0.001	0.011	2
BP	GO: 0034123	Positive regulation of toll-like receptor signaling pathway	2/43	0.001	0.011	2
BP	GO: 0036003	Positive regulation of transcription from RNA polymerase II promoter in response to stress	2/43	0.001	0.011	2
BP	GO: 0086064	Cell communication by electrical coupling involved in cardiac conduction	2/43	0.001	0.011	2
BP	GO: 0016051	Carbohydrate biosynthetic process	4/43	0.001	0.011	4
BP	GO: 1901216	Positive regulation of neuron death	3/43	0.001	0.011	3
BP	GO: 0014020	Primary neural tube formation	3/43	0.001	0.011	3
BP	GO: 0045833	Negative regulation of lipid	3/43	0.001	0.011	3

		metabolic process				
BP	GO: 0050810	Regulation of steroid biosynthetic process	3/43	0.001	0.011	3
BP	GO: 0051651	Maintenance of location in cell	4/43	0.001	0.011	4
BP	GO: 0060571	Morphogenesis of an epithelial fold	2/43	0.001	0.011	2
BP	GO: 0010810	Regulation of cell-substrate adhesion	4/43	0.001	0.011	4
BP	GO: 0043255	Regulation of carbohydrate biosynthetic process	3/43	0.001	0.011	3
BP	GO: 0036293	Response to decreased oxygen levels	5/43	0.001	0.011	5
BP	GO: 0008585	Female gonad development	3/43	0.002	0.011	3
BP	GO: 0030178	Negative regulation of Wnt signaling pathway	4/43	0.002	0.011	4
BP	GO: 0019217	Regulation of fatty acid metabolic process	3/43	0.002	0.011	3
BP	GO: 0042632	Cholesterol homeostasis	3/43	0.002	0.011	3
BP	GO: 0045639	Positive regulation of myeloid cell differentiation	3/43	0.002	0.011	3
BP	GO: 0000188	Inactivation of MAPK activity	2/43	0.002	0.011	2
BP	GO: 0055092	Sterol homeostasis	3/43	0.002	0.012	3
BP	GO: 0008406	Gonad development	4/43	0.002	0.012	4
BP	GO: 0045666	Positive regulation of neuron differentiation	5/43	0.002	0.012	5
BP	GO: 0043583	Ear development	4/43	0.002	0.012	4
BP	GO: 0010923	Negative regulation of	3/43	0.002	0.012	3

		phosphatase activity				
		Regulation of oxidative				
BP	GO: 1902175	stress-induced intrinsic apoptotic signaling pathway	2/43	0.002	0.012	2
BP	GO: 0001841	Neural tube formation	3/43	0.002	0.012	3
BP	GO: 0010894	Negative regulation of steroid biosynthetic process	2/43	0.002	0.013	2
BP	GO: 0031069	Hair follicle morphogenesis	2/43	0.002	0.013	2
BP	GO: 0060071	Wnt signaling pathway, planar cell polarity pathway	3/43	0.002	0.013	3
BP	GO: 0031346	Positive regulation of cell projection organization	5/43	0.002	0.013	5
BP	GO: 0032373	Positive regulation of sterol transport	2/43	0.002	0.013	2
BP	GO: 0032376	Positive regulation of cholesterol transport	2/43	0.002	0.013	2
BP	GO: 0070482	Response to oxygen levels	5/43	0.002	0.013	5
BP	GO: 0006641	Triglyceride metabolic process	3/43	0.002	0.013	3
BP	GO: 0090100	Positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	3/43	0.002	0.013	3
BP	GO: 0090175	Regulation of establishment of planar polarity	3/43	0.002	0.013	3
BP	GO: 1901653	Cellular response to peptide	5/43	0.002	0.013	5
BP	GO: 0035305	Negative regulation of dephosphorylation	3/43	0.002	0.013	3

BP	GO: 0005976	Polysaccharide metabolic process	3/43	0.002	0.013	3
BP	GO: 0003209	Cardiac atrium morphogenesis	2/43	0.002	0.013	2
BP	GO: 0033137	Negative regulation of peptidyl-serine phosphorylation	2/43	0.002	0.013	2
BP	GO: 0045939	Negative regulation of steroid metabolic process	2/43	0.002	0.013	2
BP	GO: 0061082	Myeloid leukocyte cytokine production	2/43	0.002	0.013	2
BP	GO: 0045765	Regulation of angiogenesis	5/43	0.002	0.013	5
BP	GO: 0001938	Positive regulation of endothelial cell proliferation	3/43	0.002	0.013	3
BP	GO: 0010644	Cell communication by electrical coupling	2/43	0.002	0.014	2
BP	GO: 1902230	Negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	2/43	0.002	0.014	2
BP	GO: 0051402	Neuron apoptotic process	4/43	0.002	0.014	4
BP	GO: 0006469	Negative regulation of protein kinase activity	4/43	0.002	0.014	4
BP	GO: 1903828	Negative regulation of cellular protein localization	3/43	0.002	0.014	3
BP	GO: 0048730	Epidermis morphogenesis	2/43	0.002	0.015	2
BP	GO: 1901797	Negative regulation of signal transduction by p53 class	2/43	0.003	0.015	2

		mediator				
BP	GO: 0031398	Positive regulation of protein ubiquitination	3/43	0.003	0.016	3
BP	GO: 0043588	Skin development	5/43	0.003	0.016	5
BP	GO: 0048872	Homeostasis of number of cells	4/43	0.003	0.016	4
BP	GO: 0043516	Regulation of DNA damage response, signal transduction by p53 class mediator	2/43	0.003	0.016	2
BP	GO: 1901617	Organic hydroxy compound biosynthetic process	4/43	0.003	0.016	4
BP	GO: 0001736	Establishment of planar polarity	3/43	0.003	0.016	3
BP	GO: 0007164	Establishment of tissue polarity	3/43	0.003	0.016	3
BP	GO: 0003203	Endocardial cushion morphogenesis	2/43	0.003	0.016	2
BP	GO: 0007435	Salivary gland morphogenesis	2/43	0.003	0.016	2
BP	GO: 0030947	Regulation of vascular endothelial growth factor receptor signaling pathway	2/43	0.003	0.016	2
BP	GO: 0034390	Smooth muscle cell apoptotic process	2/43	0.003	0.016	2
BP	GO: 0034391	Regulation of smooth muscle cell apoptotic process	2/43	0.003	0.016	2
BP	GO: 0045922	Negative regulation of fatty acid metabolic process	2/43	0.003	0.016	2

BP	GO: 0060674	Placenta blood vessel development	2/43	0.003	0.016	2
BP	GO: 0001838	Embryonic epithelial tube formation	3/43	0.003	0.016	3
BP	GO: 0061448	Connective tissue development	4/43	0.003	0.016	4
BP	GO: 0043406	Positive regulation of MAP kinase activity	4/43	0.003	0.016	4
BP	GO: 0001704	Formation of primary germ layer	3/43	0.003	0.016	3
BP	GO: 0030326	Embryonic limb morphogenesis	3/43	0.003	0.016	3
BP	GO: 0035113	Embryonic appendage morphogenesis	3/43	0.003	0.016	3
BP	GO: 0003230	Cardiac atrium development	2/43	0.003	0.016	2
BP	GO: 0071634	Regulation of transforming growth factor beta production	2/43	0.003	0.016	2
BP	GO: 0033673	Negative regulation of kinase activity	4/43	0.003	0.017	4
BP	GO: 0062208	Positive regulation of pattern recognition receptor signaling pathway	2/43	0.003	0.017	2
BP	GO: 1905314	Semi-lunar valve development	2/43	0.003	0.017	2
BP	GO: 0090596	Sensory organ morphogenesis	4/43	0.003	0.017	4
BP	GO: 0001933	Negative regulation of protein phosphorylation	5/43	0.003	0.017	5
BP	GO: 1901342	Regulation of vasculature	5/43	0.003	0.017	5

		development				
		Positive regulation of				
BP	GO: 0051091	DNA-binding transcription factor activity	4/43	0.003	0.017	4
BP	GO: 0003206	Cardiac chamber morphogenesis	3/43	0.003	0.017	3
BP	GO: 0010508	Positive regulation of autophagy	3/43	0.003	0.017	3
BP	GO: 0019218	Regulation of steroid metabolic process	3/43	0.003	0.017	3
BP	GO: 0010595	Positive regulation of endothelial cell migration	3/43	0.003	0.017	3
BP	GO: 0007223	Wnt signaling pathway, calcium modulating pathway	2/43	0.003	0.017	2
BP	GO: 0032885	Regulation of polysaccharide biosynthetic process	2/43	0.003	0.017	2
BP	GO: 0071604	Transforming growth factor beta production	2/43	0.003	0.017	2
BP	GO: 1905898	Positive regulation of response to endoplasmic reticulum stress	2/43	0.003	0.017	2
BP	GO: 0090101	Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	3/43	0.003	0.017	3
BP	GO: 0007431	Salivary gland development	2/43	0.004	0.018	2
BP	GO: 1902229	Regulation of intrinsic	2/43	0.004	0.018	2

		apoptotic signaling pathway in response to DNA damage				
BP	GO: 0006638	Neutral lipid metabolic process	3/43	0.004	0.019	3
BP	GO: 0006639	Acylglycerol metabolic process	3/43	0.004	0.019	3
BP	GO: 0038083	Peptidyl-tyrosine autophosphorylation	2/43	0.004	0.019	2
BP	GO: 1902042	Negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	2/43	0.004	0.019	2
BP	GO: 0043542	Endothelial cell migration	4/43	0.004	0.020	4
BP	GO: 1903322	Positive regulation of protein modification by small protein conjugation or removal	3/43	0.004	0.020	3
BP	GO: 0072595	Maintenance of protein localization in organelle	2/43	0.004	0.020	2
BP	GO: 0031333	Negative regulation of protein-containing complex assembly	3/43	0.004	0.020	3
BP	GO: 0051346	Negative regulation of hydrolase activity	5/43	0.004	0.020	5
BP	GO: 0008631	Intrinsic apoptotic signaling pathway in response to oxidative stress	2/43	0.004	0.021	2
BP	GO: 0045823	Positive regulation of heart contraction	2/43	0.004	0.021	2

BP	GO: 0086004	Regulation of cardiac muscle cell contraction	2/43	0.004	0.021	2
BP	GO: 0001738	Morphogenesis of a polarized epithelium	3/43	0.004	0.021	3
BP	GO: 0032881	Regulation of polysaccharide metabolic process	2/43	0.005	0.021	2
BP	GO: 1903053	Regulation of extracellular matrix organization	2/43	0.005	0.021	2
BP	GO: 0007043	Cell-cell junction assembly	3/43	0.005	0.021	3
BP	GO: 0051592	Response to calcium ion	3/43	0.005	0.021	3
BP	GO: 0042326	Negative regulation of phosphorylation	5/43	0.005	0.022	5
BP	GO: 0003197	Endocardial cushion development	2/43	0.005	0.022	2
BP	GO: 0032722	Positive regulation of chemokine production	2/43	0.005	0.022	2
BP	GO: 0060443	Mammary gland morphogenesis	2/43	0.005	0.022	2
BP	GO: 1904646	Cellular response to amyloid-beta	2/43	0.005	0.022	2
BP	GO: 0035107	Appendage morphogenesis	3/43	0.005	0.022	3
BP	GO: 0035108	Limb morphogenesis	3/43	0.005	0.022	3
BP	GO: 0060041	Retina development in camera-type eye	3/43	0.005	0.022	3
BP	GO: 0048562	Embryonic organ morphogenesis	4/43	0.005	0.022	4
BP	GO: 0035567	Non-canonical Wnt signaling	3/43	0.005	0.022	3

		pathway				
BP	GO: 0010874	Regulation of cholesterol efflux	2/43	0.005	0.022	2
BP	GO: 0032007	Negative regulation of TOR signaling	2/43	0.005	0.022	2
BP	GO: 0032570	Response to progesterone	2/43	0.005	0.022	2
BP	GO: 0061028	Establishment of endothelial barrier	2/43	0.005	0.022	2
BP	GO: 0002224	Toll-like receptor signaling pathway	3/43	0.005	0.022	3
BP	GO: 1903115	Regulation of actin filament-based movement	2/43	0.005	0.023	2
BP	GO: 0061351	Neural precursor cell proliferation	3/43	0.005	0.023	3
BP	GO: 0048754	Branching morphogenesis of an epithelial tube	3/43	0.005	0.023	3
BP	GO: 0018105	Peptidyl-serine phosphorylation	4/43	0.005	0.023	4
BP	GO: 0044843	Cell cycle G1/S phase transition	4/43	0.005	0.023	4
BP	GO: 0010862	Positive regulation of pathway-restricted SMAD protein phosphorylation	2/43	0.005	0.023	2
BP	GO: 0031952	Regulation of protein autophosphorylation	2/43	0.005	0.023	2
BP	GO: 0033628	Regulation of cell adhesion mediated by integrin	2/43	0.005	0.023	2

BP	GO: 0060711	Labyrinthine layer development	2/43	0.006	0.024	2
BP	GO: 0010718	Positive regulation of epithelial to mesenchymal transition	2/43	0.006	0.025	2
BP	GO: 2001236	Regulation of extrinsic apoptotic signaling pathway	3/43	0.006	0.025	3
BP	GO: 0035272	Exocrine system development	2/43	0.006	0.025	2
BP	GO: 0045912	Negative regulation of carbohydrate metabolic process	2/43	0.006	0.025	2
BP	GO: 0021915	Neural tube development	3/43	0.006	0.025	3
BP	GO: 0043535	Regulation of blood vessel endothelial cell migration	3/43	0.006	0.026	3
BP	GO: 0003179	Heart valve morphogenesis	2/43	0.006	0.026	2
BP	GO: 0046580	Negative regulation of Ras protein signal transduction	2/43	0.006	0.026	2
BP	GO: 0050999	Regulation of nitric-oxide synthase activity	2/43	0.006	0.026	2
BP	GO: 0072132	Mesenchyme morphogenesis	2/43	0.006	0.026	2
BP	GO: 0045599	Negative regulation of fat cell differentiation	2/43	0.006	0.027	2
BP	GO: 0071375	Cellular response to peptide hormone stimulus	4/43	0.007	0.027	4
BP	GO: 0032147	Activation of protein kinase activity	4/43	0.007	0.027	4
BP	GO: 0030857	Negative regulation of	2/43	0.007	0.027	2

		epithelial cell differentiation				
BP	GO: 0043010	Camera-type eye development	4/43	0.007	0.027	4
BP	GO: 0032874	Positive regulation of stress-activated MAPK cascade	3/43	0.007	0.027	3
BP	GO: 0018209	Peptidyl-serine modification	4/43	0.007	0.028	4
BP	GO: 0030856	Regulation of epithelial cell differentiation	3/43	0.007	0.028	3
BP	GO: 0042304	Regulation of fatty acid biosynthetic process	2/43	0.007	0.028	2
BP	GO: 0070304	Positive regulation of stress-activated protein kinase signaling cascade	3/43	0.007	0.028	3
BP	GO: 1990138	Neuron projection extension	3/43	0.007	0.028	3
BP	GO: 0086065	Cell communication involved in cardiac conduction	2/43	0.007	0.028	2
BP	GO: 1904645	Response to amyloid-beta	2/43	0.007	0.028	2
BP	GO: 0051099	Positive regulation of binding	3/43	0.007	0.029	3
BP	GO: 1990778	Protein localization to cell periphery	4/43	0.007	0.029	4
BP	GO: 0010921	Regulation of phosphatase activity	3/43	0.007	0.029	3
BP	GO: 0050680	Negative regulation of epithelial cell proliferation	3/43	0.007	0.029	3
BP	GO: 0002011	Morphogenesis of an epithelial sheet	2/43	0.008	0.030	2
BP	GO: 0007566	Embryo implantation	2/43	0.008	0.030	2

BP	GO: 1900408	Negative regulation of cellular response to oxidative stress	2/43	0.008	0.030	2
BP	GO: 1903202	Negative regulation of oxidative stress-induced cell death	2/43	0.008	0.030	2
BP	GO: 0043525	Positive regulation of neuron apoptotic process	2/43	0.008	0.031	2
BP	GO: 0098930	Axonal transport	2/43	0.008	0.031	2
BP	GO: 0048736	Appendage development	3/43	0.008	0.031	3
BP	GO: 0060173	Limb development	3/43	0.008	0.031	3
BP	GO: 0090288	Negative regulation of cellular response to growth factor stimulus	3/43	0.008	0.031	3
BP	GO: 0032515	Negative regulation of phosphoprotein phosphatase activity	2/43	0.008	0.031	2
BP	GO: 0035904	Aorta development	2/43	0.008	0.031	2
BP	GO: 1902883	Negative regulation of response to oxidative stress	2/43	0.008	0.031	2
BP	GO: 0001959	Regulation of cytokine-mediated signaling pathway	3/43	0.008	0.031	3
BP	GO: 2001235	Positive regulation of apoptotic signaling pathway	3/43	0.008	0.031	3
BP	GO: 0048638	Regulation of developmental growth	4/43	0.008	0.031	4
BP	GO: 0003170	Heart valve development	2/43	0.009	0.031	2

BP	GO: 0042733	Embryonic digit morphogenesis	2/43	0.009	0.031	2
BP	GO: 0043954	Cellular component maintenance	2/43	0.009	0.031	2
BP	GO: 1902041	Regulation of extrinsic apoptotic signaling pathway via death domain receptors	2/43	0.009	0.031	2
BP	GO: 0050770	Regulation of axonogenesis	3/43	0.009	0.032	3
BP	GO: 0060393	Regulation of pathway-restricted SMAD protein phosphorylation	2/43	0.009	0.032	2
BP	GO: 2001244	Positive regulation of intrinsic apoptotic signaling pathway	2/43	0.009	0.032	2
BP	GO: 0061138	Morphogenesis of a branching epithelium	3/43	0.009	0.032	3
BP	GO: 0031589	Cell-substrate adhesion	4/43	0.009	0.032	4
BP	GO: 0055008	Cardiac muscle tissue morphogenesis	2/43	0.009	0.032	2
BP	GO: 0007369	Gastrulation	3/43	0.009	0.032	3
BP	GO: 0010565	Regulation of cellular ketone metabolic process	3/43	0.009	0.032	3
BP	GO: 0043534	Blood vessel endothelial cell migration	3/43	0.009	0.032	3
BP	GO: 0001885	Endothelial cell development	2/43	0.009	0.033	2
BP	GO: 0002066	Columnar/cuboidal epithelial cell development	2/43	0.009	0.033	2
BP	GO: 0033344	Cholesterol efflux	2/43	0.009	0.033	2

BP	GO: 0060135	Maternal process involved in female pregnancy	2/43	0.009	0.033	2
BP	GO: 0035265	Organ growth	3/43	0.009	0.033	3
BP	GO: 0010038	Response to metal ion	4/43	0.009	0.033	4
BP	GO: 0035308	Negative regulation of protein dephosphorylation	2/43	0.010	0.034	2
BP	GO: 0060389	Pathway-restricted SMAD protein phosphorylation	2/43	0.010	0.034	2
BP	GO: 0045862	Positive regulation of proteolysis	4/43	0.010	0.034	4
BP	GO: 0007219	Notch signaling pathway	3/43	0.010	0.034	3
BP	GO: 0032768	Regulation of monooxygenase activity	2/43	0.010	0.034	2
BP	GO: 2000378	Negative regulation of reactive oxygen species metabolic process	2/43	0.010	0.034	2
BP	GO: 0060759	Regulation of response to cytokine stimulus	3/43	0.010	0.034	3
BP	GO: 0006694	Steroid biosynthetic process	3/43	0.010	0.035	3
BP	GO: 0048839	Inner ear development	3/43	0.010	0.035	3
BP	GO: 0051216	Cartilage development	3/43	0.010	0.035	3
BP	GO: 0071300	Cellular response to retinoic acid	2/43	0.010	0.035	2
BP	GO: 0043112	Receptor metabolic process	3/43	0.010	0.035	3
BP	GO: 0016239	Positive regulation of macroautophagy	2/43	0.011	0.035	2
BP	GO: 0032642	Regulation of chemokine	2/43	0.011	0.035	2

		production				
BP	GO: 0071479	Cellular response to ionizing radiation	2/43	0.011	0.035	2
BP	GO: 1904888	Cranial skeletal system development	2/43	0.011	0.035	2
BP	GO: 1901654	Response to ketone	3/43	0.011	0.035	3
BP	GO: 1901888	Regulation of cell junction assembly	3/43	0.011	0.035	3
BP	GO: 0001763	Morphogenesis of a branching structure	3/43	0.011	0.035	3
BP	GO: 0002221	Pattern recognition receptor signaling pathway	3/43	0.011	0.035	3
BP	GO: 0010952	Positive regulation of peptidase activity	3/43	0.011	0.035	3
BP	GO: 0060038	Cardiac muscle cell proliferation	2/43	0.011	0.036	2
BP	GO: 0006879	Cellular iron ion homeostasis	2/43	0.011	0.036	2
BP	GO: 0008088	Axo-dendritic transport	2/43	0.011	0.036	2
BP	GO: 0032370	Positive regulation of lipid transport	2/43	0.011	0.036	2
BP	GO: 0032374	Regulation of cholesterol transport	2/43	0.011	0.036	2
BP	GO: 0043967	Histone H4 acetylation	2/43	0.011	0.036	2
BP	GO: 0001654	Eye development	4/43	0.011	0.036	4
BP	GO: 1903708	Positive regulation of hemopoiesis	3/43	0.011	0.036	3
BP	GO: 0032371	Regulation of sterol transport	2/43	0.011	0.036	2

BP	GO: 0033627	Cell adhesion mediated by integrin	2/43	0.011	0.036	2
BP	GO: 0033692	Cellular polysaccharide biosynthetic process	2/43	0.011	0.036	2
BP	GO: 0045739	Positive regulation of DNA repair	2/43	0.011	0.036	2
BP	GO: 0150063	Visual system development	4/43	0.012	0.037	4
BP	GO: 0046890	Regulation of lipid biosynthetic process	3/43	0.012	0.037	3
BP	GO: 0031331	Positive regulation of cellular catabolic process	4/43	0.012	0.037	4
BP	GO: 0045766	Positive regulation of angiogenesis	3/43	0.012	0.037	3
BP	GO: 0035303	Regulation of dephosphorylation	3/43	0.012	0.038	3
BP	GO: 0003208	Cardiac ventricle morphogenesis	2/43	0.012	0.038	2
BP	GO: 1903779	Regulation of cardiac conduction	2/43	0.012	0.038	2
BP	GO: 0006869	Lipid transport	4/43	0.012	0.038	4
BP	GO: 0048880	Sensory system development	4/43	0.012	0.038	4
BP	GO: 0031396	Regulation of protein ubiquitination	3/43	0.012	0.038	3
BP	GO: 0043393	Regulation of protein binding	3/43	0.012	0.038	3
BP	GO: 0050679	Positive regulation of epithelial cell proliferation	3/43	0.012	0.038	3
BP	GO: 0070555	Response to interleukin-1	3/43	0.012	0.038	3

BP	GO: 0034121	Regulation of toll-like receptor signaling pathway	2/43	0.012	0.038	2
BP	GO: 0043507	Positive regulation of JUN kinase activity	2/43	0.012	0.038	2
BP	GO: 0086003	Cardiac muscle cell contraction	2/43	0.012	0.038	2
BP	GO: 1901215	Negative regulation of neuron death	3/43	0.012	0.038	3
BP	GO: 0042493	Response to drug	4/43	0.012	0.038	4
BP	GO: 0007254	JNK cascade	3/43	0.013	0.038	3
BP	GO: 0001707	Mesoderm formation	2/43	0.013	0.038	2
BP	GO: 0032602	Chemokine production	2/43	0.013	0.038	2
BP	GO: 0043523	Regulation of neuron apoptotic process	3/43	0.013	0.038	3
BP	GO: 0060415	Muscle tissue morphogenesis	2/43	0.013	0.039	2
BP	GO: 0048332	Mesoderm morphogenesis	2/43	0.013	0.040	2
BP	GO: 0070830	Bicellular tight junction assembly	2/43	0.013	0.040	2
BP	GO: 1903201	Regulation of oxidative stress-induced cell death	2/43	0.013	0.040	2
BP	GO: 0007517	Muscle organ development	4/43	0.014	0.040	4
BP	GO: 0030433	Ubiquitin-dependent ERAD pathway	2/43	0.014	0.041	2
BP	GO: 0006826	Iron ion transport	2/43	0.014	0.041	2
BP	GO: 0043407	Negative regulation of MAP kinase activity	2/43	0.014	0.041	2
BP	GO: 0120192	Tight junction assembly	2/43	0.014	0.041	2

BP	GO: 1900034	Regulation of cellular response to heat	2/43	0.014	0.041	2
BP	GO: 0070828	Heterochromatin organization	2/43	0.014	0.042	2
BP	GO: 0019915	Lipid storage	2/43	0.015	0.043	2
BP	GO: 0032869	Cellular response to insulin stimulus	3/43	0.015	0.043	3
BP	GO: 2001020	Regulation of response to DNA damage stimulus	3/43	0.015	0.043	3
BP	GO: 0022617	Extracellular matrix disassembly	2/43	0.015	0.044	2
BP	GO: 0120193	Tight junction organization	2/43	0.015	0.044	2
BP	GO: 0048705	Skeletal system morphogenesis	3/43	0.015	0.044	3
BP	GO: 0014855	Striated muscle cell proliferation	2/43	0.015	0.044	2
BP	GO: 0048644	Muscle organ morphogenesis	2/43	0.015	0.044	2
BP	GO: 0055117	Regulation of cardiac muscle contraction	2/43	0.015	0.044	2
BP	GO: 0071277	Cellular response to calcium ion	2/43	0.015	0.044	2
BP	GO: 2001021	Negative regulation of response to DNA damage stimulus	2/43	0.015	0.044	2
BP	GO: 0007160	Cell-matrix adhesion	3/43	0.015	0.044	3
BP	GO: 0043161	Proteasome-mediated ubiquitin-dependent protein catabolic process	4/43	0.016	0.044	4

BP	GO: 0001649	Osteoblast differentiation	3/43	0.016	0.044	3
BP	GO: 0045913	Positive regulation of carbohydrate metabolic process	2/43	0.016	0.045	2
BP	GO: 0043297	Apical junction assembly	2/43	0.016	0.045	2
BP	GO: 0110110	Positive regulation of animal organ morphogenesis	2/43	0.016	0.045	2
BP	GO: 0071453	Cellular response to oxygen levels	3/43	0.016	0.046	3
BP	GO: 0071695	Anatomical structure maturation	3/43	0.016	0.046	3
BP	GO: 1904018	Positive regulation of vasculature development	3/43	0.016	0.046	3
BP	GO: 0019216	Regulation of lipid metabolic process	4/43	0.016	0.046	4
BP	GO: 0034637	Cellular carbohydrate biosynthetic process	2/43	0.016	0.046	2
BP	GO: 2000106	Regulation of leukocyte apoptotic process	2/43	0.016	0.046	2
BP	GO: 0060560	Developmental growth involved in morphogenesis	3/43	0.017	0.046	3
BP	GO: 0032872	Regulation of stress-activated MAPK cascade	3/43	0.017	0.046	3
BP	GO: 0048588	Developmental cell growth	3/43	0.017	0.046	3
BP	GO: 0032436	Positive regulation of proteasomal ubiquitin-dependent protein	2/43	0.017	0.046	2

		catabolic process				
BP	GO: 0055072	Iron ion homeostasis	2/43	0.017	0.046	2
BP	GO: 0034329	Cell junction assembly	4/43	0.017	0.046	4
BP	GO: 0010594	Regulation of endothelial cell migration	3/43	0.017	0.046	3
BP	GO: 0014068	Positive regulation of phosphatidylinositol 3-kinase signaling	2/43	0.017	0.047	2
BP	GO: 0070302	Regulation of stress-activated protein kinase signaling cascade	3/43	0.017	0.047	3
BP	GO: 0008625	Extrinsic apoptotic signaling pathway via death domain receptors	2/43	0.018	0.048	2
BP	GO: 0043506	Regulation of JUN kinase activity	2/43	0.018	0.048	2
BP	GO: 0010876	Lipid localization	4/43	0.018	0.048	4
BP	GO: 1903320	Regulation of protein modification by small protein conjugation or removal	3/43	0.018	0.048	3
BP	GO: 0001843	Neural tube closure	2/43	0.018	0.049	2
BP	GO: 0071216	Cellular response to biotic stimulus	3/43	0.018	0.049	3
BP	GO: 0009314	Response to radiation	4/43	0.019	0.050	4
BP	GO: 0043434	Response to peptide hormone	4/43	0.019	0.050	4
BP	GO: 0060606	Tube closure	2/43	0.019	0.050	2
BP	GO: 0106027	Neuron projection	2/43	0.019	0.050	2

		organization				
BP	GO: 1900407	Regulation of cellular response to oxidative stress	2/43	0.019	0.050	2
CC	GO: 0005925	Focal adhesion	6/41	0.000	0.011	6
CC	GO: 0030055	Cell-substrate junction	6/41	0.000	0.011	6
CC	GO: 1990909	Wnt signalosome	2/41	0.000	0.011	2
CC	GO: 0005667	Transcription regulator complex	5/41	0.002	0.049	5
MF	GO: 0035035	Histone acetyltransferase binding	3/43	0.000	0.005	3
MF	GO: 0031625	Ubiquitin protein ligase binding	6/43	0.000	0.005	6
MF	GO: 0044389	Ubiquitin-like protein ligase binding	6/43	0.000	0.005	6
MF	GO: 0002039	P53 binding	3/43	0.000	0.017	3
MF	GO: 0042813	Wnt-activated receptor activity	2/43	0.001	0.017	2
MF	GO: 0046982	Protein heterodimerization activity	5/43	0.001	0.023	5
MF	GO: 0017147	Wnt-protein binding	2/43	0.002	0.049	2

BP: Biological process; GO: Gene ontology; ER: Endoplasmic reticulum; MAPK: Mitogen-activated protein kinases; ERAD: ER-associated degradation; MAP: Mitogen-activated protein