

Supplementary Table9: Enrichment analysis and tumor-related pathways.

gene Set	description	enrichmentRatio	pValue	FD	DB
hsa04512	ECM-receptor interaction	10.10875	3.17E-13	9.45E-11	pathway_KEGG
hsa04510	Focal adhesion	4.816522	8.21E-09	1.22E-06	pathway_KEGG
hsa04151	PI3K-Akt signaling pathway	3.471367	5.01E-08	4.97E-06	pathway_KEGG
hsa04974	Protein digestion and absorption	7.410033	6.89E-07	5.13E-05	pathway_KEGG
hsa05165	Human papillomavirus infection	3.030262	1.14E-05	0.000681	pathway_KEGG
hsa05205	Proteoglycans in cancer	3.684771	2.15E-05	0.001066	pathway_KEGG
hsa05414	Dilated cardiomyopathy (DCM)	5.222734	4.75E-05	0.002023	pathway_KEGG
hsa04810	Regulation of actin cytoskeleton	3.388508	5.47E-05	0.002039	pathway_KEGG
hsa05410	Hypertrophic cardiomyopathy (HCM)	5.004178	0.00073	0.000512	pathway_KEGG
hsa05144	Malaria	6.422029	0.00096	0.000812	pathway_KEGG
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	5.108432	0.00092	0.0010621	pathway_KEGG
GO:0043062	extracellular structure organization	7.487673	0	0	geneontology_Biological_Process
GO:00301	extracellular matrix organization	8.588012	0	0	geneontology_Biological_Pro

98					cess
GO:0		4.5102	2.2	4.2	geneontology_
0015	skeletal system development	86	2E-	0E-	Biological_Pro
01			13	10	cess
GO:0		3.9878	2.9	4.2	geneontology_
0485	blood vessel morphogenesis	57	7E-	0E-	Biological_Pro
14			13	10	cess
GO:0		10.875	8.1	9.2	geneontology_
0329	collagen metabolic process	71	3E-	0E-	Biological_Pro
63			13	10	cess
GO:0		4.4931	1.0	1.0	geneontology_
0015	ossification	44	9E-	3E-	Biological_Pro
03			10	07	cess
GO:0		14.378	1.3	1.0	geneontology_
0359	endodermal cell differentiation	95	0E-	5E-	Biological_Pro
87			10	07	cess
GO:0		5.2737	4.1	2.3	geneontology_
0902	regulation of cellular response to growth factor stimulus	83	5E-	8E-	Biological_Pro
87			10	07	cess
GO:0		13.041	4.1	2.3	geneontology_
0017	endoderm formation	37	7E-	8E-	Biological_Pro
06			10	07	cess
GO:0		15.448	4.2	2.3	geneontology_
0329	collagen biosynthetic process	45	1E-	8E-	Biological_Pro
64			10	07	cess
GO:0		3.6960	9.0	4.5	geneontology_
0015	angiogenesis	43	5E-	0E-	Biological_Pro
25			10	07	cess
GO:0		3.5817	9.5	4.5	geneontology_
0485	embryonic morphogenesis	26	3E-	0E-	Biological_Pro
98			10	07	cess
GO:0		9.7104	2.5	1.1	geneontology_
0074	endoderm development	57	9E-	3E-	Biological_Pro
92			09	06	cess
GO:0		7.5128	4.0	1.6	geneontology_
0017	formation of primary germ layer	27	0E-	2E-	Biological_Pro
04			09	06	cess
GO:0		4.1233	1.6	6.1	geneontology_
0315	cell-substrate adhesion	74	2E-	2E-	Biological_Pro
89			08	06	cess
GO:0		5.1281	3.1	1.1	geneontology_
0016	osteoblast differentiation	56	9E-	3E-	Biological_Pro
49			08	05	cess
GO:0	transmembrane receptor protein	4.0861	4.1	1.3	geneontology_

0071	serine/threonine kinase signaling	75	1E-	7E-	Biological_Pro
78	pathway		08	05	cess
GO:0		4.7058	4.7	1.4	geneontology_
0614	connective tissue development	37	3E-	9E-	Biological_Pro
48			08	05	cess
GO:0		5.1954	6.8	1.9	geneontology_
0071	transforming growth factor beta receptor	04	5E-	8E-	Biological_Pro
79	signaling pathway		08	05	cess
GO:0		4.5881	6.9	1.9	geneontology_
0715	cellular response to transforming growth	91	9E-	8E-	Biological_Pro
60	factor beta stimulus		08	05	cess
GO:0		4.4762	1.0	2.6	geneontology_
0715	response to transforming growth factor	84	2E-	2E-	Biological_Pro
59	beta		07	05	cess
GO:0		13.156	1.0	2.6	geneontology_
0107	regulation of collagen metabolic process	1	2E-	2E-	Biological_Pro
12			07	05	cess
GO:0		6.1938	1.5	3.8	geneontology_
0902	negative regulation of cellular response	2	5E-	1E-	Biological_Pro
88	to growth factor stimulus		07	05	cess
GO:0		3.2512	1.8	4.2	geneontology_
0074	sensory organ development	69	1E-	6E-	Biological_Pro
23			07	05	cess
GO:0		5.1668	1.9	4.3	geneontology_
0603	bone development	82	2E-	6E-	Biological_Pro
48			07	05	cess
GO:0		3.0753	2.9	6.5	geneontology_
0075	heart development	54	9E-	1E-	Biological_Pro
07			07	05	cess
GO:0		4.6610	3.1	6.5	geneontology_
0900	regulation of transmembrane receptor	19	0E-	1E-	Biological_Pro
92	protein serine/threonine kinase signaling		07	05	cess
GO:0		7.8430	4.7	9.5	geneontology_
0226	extracellular matrix disassembly	61	1E-	3E-	Biological_Pro
17			07	05	cess
GO:0		2.9853	5.3	0.0	geneontology_
0420	wound healing	09	1E-	001	Biological_Pro
60			07	04	cess
GO:0		13.217	6.4	0.0	geneontology_
0329	regulation of collagen biosynthetic	01	0E-	001	Biological_Pro
65	process		07	17	cess
GO:0		25.489	6.4	0.0	geneontology_
0702	protein heterotrimerization	95	3E-	001	Biological_Pro
08			07	17	cess

GO:2 0001 81	negative regulation of blood vessel morphogenesis	6.5973 99	7.5 4E- 07	0.0 001 33	geneontology_ Biological_Pro cess
GO:0 0487 29	tissue morphogenesis	2.8439 2	8.1 7E- 07	0.0 001 4	geneontology_ Biological_Pro cess
GO:0 0073 69	gastrulation	4.9221 97	9.0 4E- 07	0.0 001 5	geneontology_ Biological_Pro cess
GO:0 0016 54	eye development	3.6551 63	1.0 5E- 06	0.0 001 7	geneontology_ Biological_Pro cess
GO:0 1500 63	visual system development	3.6414 21	1.1 1E- 06	0.0 001 75	geneontology_ Biological_Pro cess
GO:0 0488 80	sensory system development	3.6008 11	1.3 2E- 06	0.0 002 02	geneontology_ Biological_Pro cess
GO:0 0170 15	regulation of transforming growth factor beta receptor signaling pathway	6.1624 05	1.5 1E- 06	0.0 002 25	geneontology_ Biological_Pro cess
GO:0 0512 16	cartilage development	4.6955 17	1.6 0E- 06	0.0 002 32	geneontology_ Biological_Pro cess
GO:1 9038 44	regulation of cellular response to transforming growth factor beta stimulus	6.0298 81	1.8 8E- 06	0.0 002 66	geneontology_ Biological_Pro cess
GO:0 0359 04	aorta development	9.0630 93	2.2 0E- 06	0.0 003 04	geneontology_ Biological_Pro cess
GO:1 9013 43	negative regulation of vasculature development	5.8414 47	2.5 8E- 06	0.0 003 48	geneontology_ Biological_Pro cess
GO:0 0465 78	regulation of Ras protein signal transduction	4.1335 05	3.3 6E- 06	0.0 004 43	geneontology_ Biological_Pro cess
GO:0 0457 65	regulation of angiogenesis	3.6879 08	3.5 3E- 06	0.0 004 55	geneontology_ Biological_Pro cess
GO:0 0060 24	glycosaminoglycan biosynthetic process	8.4966 5	3.6 7E- 06	0.0 004 61	geneontology_ Biological_Pro cess
GO:1 9013	regulation of vasculature development	3.5024 36	3.7 6E-	0.0 004	geneontology_ Biological_Pro

42			06	62	cess
GO:0		8.3232	4.3	0.0	geneontology_
0060	aminoglycan biosynthetic process		1E-	005	Biological_Pro
23		49	06	08	cess
GO:0		8.3232	4.3	0.0	geneontology_
0712	cellular response to amino acid stimulus		1E-	005	Biological_Pro
30		49	06	08	cess
GO:0		6.1421	4.7	0.0	geneontology_
0165	negative regulation of angiogenesis		1E-	005	Biological_Pro
25		57	06	45	cess
GO:0		3.1276	6.0	0.0	geneontology_
0016	ameboidal-type cell migration		0E-	006	Biological_Pro
67		01	06	79	cess
GO:0		5.9278	6.5	0.0	geneontology_
0020	chondrocyte differentiation		2E-	007	Biological_Pro
62		95	06	24	cess
GO:0		7.8430	6.8	0.0	geneontology_
0488	artery morphogenesis		4E-	007	Biological_Pro
44		61	06	44	cess
GO:0		3.3368	7.3	0.0	geneontology_
0510	regulation of small GTPase mediated signal transduction		9E-	007	Biological_Pro
56		66	06	89	cess
GO:0		11.764	8.7	0.0	geneontology_
0359	aorta morphogenesis		7E-	009	Biological_Pro
09		59	06	19	cess
GO:0		9.1502	9.0	0.0	geneontology_
0105	negative regulation of endothelial cell migration		8E-	009	Biological_Pro
96		38	06	35	cess
GO:0		4.0323	9.5	0.0	geneontology_
0487	skeletal system morphogenesis		9E-	009	Biological_Pro
05		08	06	69	cess
GO:0		6.3724	1.0	0.0	geneontology_
0608	artery development		5E-	010	Biological_Pro
40		87	05	43	cess
GO:0		6.2851	1.1	0.0	geneontology_
0302	glycosaminoglycan metabolic process		8E-	011	Biological_Pro
03		93	05	49	cess
GO:0		8.7038	1.2	0.0	geneontology_
0301	collagen fibril organization		8E-	012	Biological_Pro
99		85	05	32	cess
GO:1		10.924	1.3	0.0	geneontology_
9030	regulation of extracellular matrix organization		9E-	013	Biological_Pro
53		26	05	03	cess
GO:0	cell-matrix adhesion	3.9001	1.4	0.0	geneontology_

0071		02	0E-	013	Biological_Pro
60			05	03	cess
GO:0		3.6588	1.4	0.0	geneontology_
0604	mesenchyme development		9E-	013	Biological_Pro
85		44	05	56	cess
GO:0		8.4966	1.5	0.0	geneontology_
0702	protein trimerization		2E-	013	Biological_Pro
06		5	05	62	cess
GO:0		6.0370	1.6	0.0	geneontology_
0060	aminoglycan metabolic process		4E-	014	Biological_Pro
22		93	05	53	cess
GO:0		10.547	1.7	0.0	geneontology_
0181	peptide cross-linking		2E-	015	Biological_Pro
49		57	05	015	cess
GO:0		14.161	1.9	0.0	geneontology_
0107	positive regulation of collagen metabolic process		2E-	016	Biological_Pro
14		08	05	24	cess
GO:0		14.161	1.9	0.0	geneontology_
0329	positive regulation of collagen biosynthetic process		2E-	016	Biological_Pro
67		08	05	24	cess
GO:0		3.7367	2.2	0.0	geneontology_
0303	negative regulation of cell migration		8E-	018	Biological_Pro
36		47	05	95	cess
GO:0		3.9215	2.7	0.0	geneontology_
0487	mesenchymal cell differentiation		0E-	022	Biological_Pro
62		31	05	02	cess
GO:0		2.5826	2.7	0.0	geneontology_
0072	small GTPase mediated signal transduction		2E-	022	Biological_Pro
64		82	05	02	cess
GO:0		6.4736	2.9	0.0	geneontology_
0305	regulation of BMP signaling pathway		3E-	023	Biological_Pro
10		38	05	33	cess
GO:0		5.5279	3.3	0.0	geneontology_
0603	bone morphogenesis		7E-	026	Biological_Pro
49		41	05	47	cess
GO:0		9.2690	3.7	0.0	geneontology_
0305	collagen catabolic process		6E-	029	Biological_Pro
74		73	05	17	cess
GO:0		18.538	4.2	0.0	geneontology_
0302	chondroitin sulfate biosynthetic process		6E-	032	Biological_Pro
06		15	05	12	cess
GO:0		18.538	4.2	0.0	geneontology_
0506	chondroitin sulfate proteoglycan biosynthetic process		6E-	032	Biological_Pro
50		15	05	12	cess

GO:0			4.4	0.0	geneontology_
0488	inner ear development	4.3471	4E-	033	Biological_Pro
39		23	05	04	cess
GO:0			4.4	0.0	geneontology_
0305	negative regulation of BMP signaling pathway	8.9964	9E-	033	Biological_Pro
14		53	05	04	cess
GO:0			4.6	0.0	geneontology_
0426	muscle cell differentiation	3.0302	1E-	033	Biological_Pro
92		74	05	45	cess
GO:2			4.7	0.0	geneontology_
0001	negative regulation of cell motility	3.4986	3E-	033	Biological_Pro
46		21	05	87	cess
GO:0			4.8	0.0	geneontology_
0512	negative regulation of cellular component movement	3.3103	0E-	033	Biological_Pro
71		83	05	96	cess
GO:0			5.8	0.0	geneontology_
0072	integrin-mediated signaling pathway	5.1552	8E-	041	Biological_Pro
29		71	05	12	cess
GO:0			7.0	0.0	geneontology_
0106	epithelial cell migration	3.1995	8E-	048	Biological_Pro
31		75	05	88	cess
GO:0			7.3	0.0	geneontology_
0905	sensory organ morphogenesis	3.5631	4E-	050	Biological_Pro
96		11	05	03	cess
GO:0			7.4	0.0	geneontology_
0901	epithelium migration	3.1862	2E-	050	Biological_Pro
32		44	05	03	cess
GO:0			7.5	0.0	geneontology_
0712	cellular response to acid chemical	3.7997	3E-	050	Biological_Pro
29		44	05	13	cess
GO:0			7.6	0.0	geneontology_
0329	regulation of actin filament-based process	2.9082	9E-	050	Biological_Pro
70		49	05	62	cess
GO:0			8.1	0.0	geneontology_
0106	negative regulation of epithelial cell migration	6.6085	6E-	053	Biological_Pro
33		05	05	07	cess
GO:0			8.8	0.0	geneontology_
0303	positive regulation of cell migration	2.5943	1E-	053	Biological_Pro
35		97	05	89	cess
GO:0			8.9	0.0	geneontology_
0034	chondrocyte morphogenesis involved in endochondral bone morphogenesis	15.686	4E-	053	Biological_Pro
14		12	05	89	cess
GO:0			8.9	0.0	geneontology_
0034	growth plate cartilage morphogenesis	15.686	4E-	053	Biological_Pro
		12			

22			05	89	cess
GO:0	growth plate cartilage chondrocyte	15.686	8.9	0.0	geneontology_
0034	morphogenesis	12	4E-	053	Biological_Pro
29			05	89	cess
GO:0	chondrocyte morphogenesis	15.686	8.9	0.0	geneontology_
0901		12	4E-	053	Biological_Pro
71			05	89	cess
GO:0	tissue migration	3.1340	8.9	0.0	geneontology_
0901		1	5E-	053	Biological_Pro
30			05	89	cess
GO:0	negative regulation of locomotion	3.1340	8.9	0.0	geneontology_
0400		1	5E-	053	Biological_Pro
13			05	89	cess
GO:0	positive regulation of protein kinase B	4.0055	9.3	0.0	geneontology_
0518	signaling	64	7E-	055	Biological_Pro
97			05	85	cess
GO:0	body morphogenesis	7.8430	0.0	0.0	geneontology_
0101		61	001	059	Biological_Pro
71				25	cess
GO:0	positive regulation of locomotion	2.4897	0.0	0.0	geneontology_
0400		16	001	061	Biological_Pro
17			05	18	cess
GO:0	face morphogenesis	10.195	0.0	0.0	geneontology_
0603		98	001	061	Biological_Pro
25			07	57	cess
GO:0	endochondral bone morphogenesis	6.2606	0.0	0.0	geneontology_
0603		89	001	066	Biological_Pro
50			16	25	cess
GO:0	muscle organ development	2.7956	0.0	0.0	geneontology_
0075		72	001	070	Biological_Pro
17			25	48	cess
GO:0	metanephros development	5.2966	0.0	0.0	geneontology_
0016		13	001	070	Biological_Pro
56			26	48	cess
GO:2	positive regulation of cell motility	2.5237	0.0	0.0	geneontology_
0001		57	001	071	Biological_Pro
47			28	26	cess
GO:0	platelet activation	3.8409	0.0	0.0	geneontology_
0301		51	001	075	Biological_Pro
68			37	06	cess
GO:0	endothelial cell migration	3.5567	0.0	0.0	geneontology_
0435		37	001	077	Biological_Pro
42			42	12	cess
GO:0	camera-type eye development	3.1303	0.0	0.0	geneontology_

0430		45	001	084	Biological_Pro
10			56	1	cess
GO:0		3.7636	0.0	0.0	geneontology_
0435	ear development		001	087	Biological_Pro
83		17	64	37	cess
GO:0		3.1031	0.0	0.0	geneontology_
0301	regulation of Wnt signaling pathway		001	090	Biological_Pro
11		24	71	44	cess
GO:0		2.4687	0.0	0.0	geneontology_
0512	positive regulation of cellular component movement		001	090	Biological_Pro
72		6	73	5	cess
GO:1		2.3896	0.0	0.0	geneontology_
9051	cell surface receptor signaling pathway involved in cell-cell signaling		001	096	Biological_Pro
14		83	86	38	cess
GO:0		9.1035	0.0	0.0	geneontology_
0435	negative regulation of blood vessel endothelial cell migration		001	096	Biological_Pro
37		53	88	73	cess
GO:0		2.5158	0.0	0.0	geneontology_
0020	morphogenesis of an epithelium		001	101	Biological_Pro
09		91	98	07	cess
GO:0		4.9137	0.0	0.0	geneontology_
0901	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway		002	106	Biological_Pro
01		25	13	26	cess
GO:0		12.744	0.0	0.0	geneontology_
0302	chondroitin sulfate metabolic process		002	106	Biological_Pro
04		97	17	26	cess
GO:0		12.744	0.0	0.0	geneontology_
0506	chondroitin sulfate proteoglycan metabolic process		002	106	Biological_Pro
54		97	17	26	cess
GO:0		12.744	0.0	0.0	geneontology_
0034	chondrocyte development involved in endochondral bone morphogenesis		002	106	Biological_Pro
33		97	17	26	cess
GO:0		2.5776	0.0	0.0	geneontology_
0072	Ras protein signal transduction		002	106	Biological_Pro
65		35	18	26	cess
GO:0		4.8552	0.0	0.0	geneontology_
0432	response to amino acid		002	112	Biological_Pro
00		29	32	14	cess
GO:0		3.8915	0.0	0.0	geneontology_
0105	regulation of endothelial cell migration		002	118	Biological_Pro
94		95	47	72	cess
GO:0		8.4966	0.0	0.0	geneontology_
0020	chondrocyte development		002	124	Biological_Pro
63		5	64	54	cess

GO:0			0.0	0.0	geneontology_
0603	head morphogenesis	8.4966	002	124	Biological_Pro
23		5	64	54	cess
GO:0			0.0	0.0	geneontology_
0612	retina vasculature development in	11.995	002	126	Biological_Pro
98	camera-type eye	27	8	72	cess
GO:1			0.0	0.0	geneontology_
9001	extracellular regulation of signal	11.995	002	126	Biological_Pro
15	transduction	27	8	72	cess
GO:1			0.0	0.0	geneontology_
9001	extracellular negative regulation of signal	11.995	002	126	Biological_Pro
16	transduction	27	8	72	cess
GO:0			0.0	0.0	geneontology_
0850	extracellular matrix assembly	11.995	002	126	Biological_Pro
29		27	8	72	cess
GO:0			0.0	0.0	geneontology_
0034	growth plate cartilage chondrocyte	11.995	002	126	Biological_Pro
18	differentiation	27	8	72	cess
GO:0			0.0	0.0	geneontology_
0310	actomyosin structure organization	3.5269	002	129	Biological_Pro
32		11	89	81	cess
GO:0			0.0	0.0	geneontology_
0519	positive regulation of nervous system	2.4398	002	130	Biological_Pro
62	development	44	93	49	cess
GO:0			0.0	0.0	geneontology_
0485	eye morphogenesis	4.1335	003	142	Biological_Pro
92		05	23	79	cess
GO:0			0.0	0.0	geneontology_
0305	BMP signaling pathway	4.0965	003	151	Biological_Pro
09		99	45	49	cess
GO:0			0.0	0.0	geneontology_
0487	smooth muscle tissue development	11.328	003	154	Biological_Pro
45		87	54	26	cess
GO:0			0.0	0.0	geneontology_
0511	smooth muscle cell differentiation	6.2424	003	158	Biological_Pro
45		37	66	14	cess
GO:0			0.0	0.0	geneontology_
0465	positive regulation of Ras protein signal	6.1175	004	175	Biological_Pro
79	transduction	88	09	47	cess
GO:0			0.0	0.0	geneontology_
0108	regulation of cell-substrate adhesion	3.3781	004	178	Biological_Pro
10		86	18	06	cess
GO:0			0.0	0.0	geneontology_
0301	positive regulation of Wnt signaling	4.3853	004	195	Biological_Pro
0301	pathway	68			

77			66	55	cess
GO:0		2.5894	0.0	0.0	geneontology_
0485	embryonic organ development		004	195	Biological_Pro
68		55	66	55	cess
GO:0		7.4970	0.0	0.0	geneontology_
0060	proteoglycan metabolic process		004	201	Biological_Pro
29		44	84	28	cess
GO:0		3.3182	0.0	0.0	geneontology_
0017	morphogenesis of a branching structure		004	201	Biological_Pro
63		18	87	28	cess
GO:0		2.9195	0.0	0.0	geneontology_
0018	kidney development		005	215	Biological_Pro
22		54	25	18	cess
GO:0		4.2930	0.0	0.0	geneontology_
0020	sprouting angiogenesis		005	219	Biological_Pro
40		44	38	07	cess
GO:0		3.8234	0.0	0.0	geneontology_
0717	response to BMP		005	230	Biological_Pro
72		92	74	59	cess
GO:0		3.8234	0.0	0.0	geneontology_
0717	cellular response to BMP stimulus		005	230	Biological_Pro
73		92	74	59	cess
GO:0		2.6278	0.0	0.0	geneontology_
0075	hemostasis		006	240	Biological_Pro
99		3	02	14	cess
GO:0		2.7345	0.0	0.0	geneontology_
0329	regulation of actin cytoskeleton organization		006	245	Biological_Pro
56		54	19	19	cess
GO:0		7.0805	0.0	0.0	geneontology_
0019	blood vessel remodeling		006	247	Biological_Pro
74		42	35	87	cess
GO:0		7.0805	0.0	0.0	geneontology_
0603	cartilage development involved in endochondral bone morphogenesis		006	247	Biological_Pro
51		42	35	87	cess
GO:0		4.7581	0.0	0.0	geneontology_
0344	substrate adhesion-dependent cell spreading		006	250	Biological_Pro
46		24	46	55	cess
GO:0		9.7104	0.0	0.0	geneontology_
0605	cartilage morphogenesis		006	254	Biological_Pro
36		57	62	81	cess
GO:0		3.1682	0.0	0.0	geneontology_
0518	regulation of protein kinase B signaling		007	274	Biological_Pro
96		42	18	51	cess
GO:0	glycosaminoglycan catabolic process	6.8891	0.0	0.0	geneontology_

0060		76	007	274	Biological_Pro
27			23	51	cess
GO:0	negative regulation of Wnt signaling	3.7001	0.0	0.0	geneontology_
0301	pathway	54	007	275	Biological_Pro
78			29	02	cess
GO:0	Wnt signaling pathway	2.4007	0.0	0.0	geneontology_
0160		15	007	275	Biological_Pro
55			35	73	cess
GO:0	positive regulation of small GTPase	5.4621	0.0	0.0	geneontology_
0510	mediated signal transduction	32	007	280	Biological_Pro
57			58	62	cess
GO:1	mucopolysaccharide metabolic process	5.4621	0.0	0.0	geneontology_
9035		32	007	280	Biological_Pro
10			58	62	cess
GO:0	chondrocyte differentiation involved in	9.2690	0.0	0.0	geneontology_
0034	endochondral bone morphogenesis	73	007	288	Biological_Pro
13			96	98	cess
GO:0	response to acid chemical	2.6631	0.0	0.0	geneontology_
0011		29	008	288	Biological_Pro
01			03	98	cess
GO:0	negative regulation of interleukin-17	15.293	0.0	0.0	geneontology_
0327	production	97	008	288	Biological_Pro
00			06	98	cess
GO:0	chondroitin sulfate catabolic process	15.293	0.0	0.0	geneontology_
0302		97	008	288	Biological_Pro
07			06	98	cess
GO:0	cell-cell signaling by wnt	2.3809	0.0	0.0	geneontology_
1987		29	008	288	Biological_Pro
38			07	98	cess
GO:0	renal system development	2.7729	0.0	0.0	geneontology_
0720		65	008	302	Biological_Pro
01			5	55	cess
GO:0	positive regulation of neurogenesis	2.3614	0.0	0.0	geneontology_
0507		67	008	312	Biological_Pro
69			83	57	cess
GO:0	epithelial cell proliferation	2.5237	0.0	0.0	geneontology_
0506		57	009	319	Biological_Pro
73			12	85	cess
GO:0	myofibril assembly	5.2737	0.0	0.0	geneontology_
0302		83	009	319	Biological_Pro
39			15	85	cess
GO:0	aminoglycan catabolic process	6.5358	0.0	0.0	geneontology_
0060		85	009	321	Biological_Pro
26			25	1	cess

GO:0010632	regulation of epithelial cell migration	3.064366	0.046	0.072	geneontology_Biological_Process
GO:0030166	proteoglycan biosynthetic process	8.866069	0.049	0.072	geneontology_Biological_Process
GO:00002576	platelet degranulation	3.884183	0.045	0.026	geneontology_Biological_Process
GO:0060537	muscle tissue development	2.482787	0.076	0.055	geneontology_Biological_Process
GO:0061138	morphogenesis of a branching epithelium	3.226576	0.086	0.055	geneontology_Biological_Process
GO:0060841	venous blood vessel development	13.90361	0.092	0.055	geneontology_Biological_Process
GO:0034309	primary alcohol biosynthetic process	13.90361	0.092	0.055	geneontology_Biological_Process
GO:0040037	negative regulation of fibroblast growth factor receptor signaling pathway	13.90361	0.092	0.055	geneontology_Biological_Process
GO:0035023	regulation of Rho protein signal transduction	3.84754	0.011	0.077	geneontology_Biological_Process
GO:0060324	face development	6.217061	0.066	0.005	geneontology_Biological_Process
GO:0072175	epithelial tube formation	3.776289	0.055	0.025	geneontology_Biological_Process
GO:0060562	epithelial tube morphogenesis	2.650955	0.083	0.0415	geneontology_Biological_Process
GO:00101718	positive regulation of epithelial to mesenchymal transition	6.069036	0.003	0.097	geneontology_Biological_Process
GO:0045666	positive regulation of neuron differentiation	2.530917	0.012	0.097	geneontology_Biological_Process
GO:00443	wound healing, spreading of cells	8.156784	0.013	0.0415	geneontology_Biological_Process

19			15	97	cess
GO:0			0.0	0.0	geneontology_
0905	epiboly involved in wound healing	8.1567	013	415	Biological_Pro
05		84	15	97	cess
GO:0			0.0	0.0	geneontology_
0018	epithelial to mesenchymal transition	3.7076	014	444	Biological_Pro
37		29	13	29	cess
GO:0			0.0	0.0	geneontology_
0019	lymphangiogenesis	12.744	014	446	Biological_Pro
46		97	35	42	cess
GO:0			0.0	0.0	geneontology_
0109	regulation of macrophage cytokine production	12.744	014	446	Biological_Pro
35		97	35	42	cess
GO:0			0.0	0.0	geneontology_
0075	blood coagulation	2.4955	014	463	Biological_Pro
96		2	99	74	cess
GO:0			0.0	0.0	geneontology_
0072	Rho protein signal transduction	3.0896	015	463	Biological_Pro
66		91	08	83	cess
GO:0			0.0	0.0	geneontology_
0905	epiboly	7.8430	015	465	Biological_Pro
04		61	31	92	cess
GO:0			0.0	0.0	geneontology_
0309	regulation of vascular endothelial growth factor receptor signaling pathway	7.8430	015	465	Biological_Pro
47		61	31	92	cess
GO:0					geneontology_
0310	extracellular matrix	7.7208	0	0	Cellular_Comp
12		57			onent
GO:0					geneontology_
0620	collagen-containing extracellular matrix	8.6217	0	0	Cellular_Comp
23		82			onent
GO:0			5.7	1.3	geneontology_
0055	collagen trimer	16.753	7E-	6E-	Cellular_Comp
81		42	15	12	onent
GO:0			1.3	2.3	geneontology_
0057	endoplasmic reticulum lumen	6.6440	0E-	0E-	Cellular_Comp
88		9	13	11	onent
GO:0			6.6	9.4	geneontology_
0056	basement membrane	11.536	9E-	7E-	Cellular_Comp
04		14	11	09	onent
GO:0			7.1	8.4	geneontology_
0444	extracellular matrix component	15.065	6E-	4E-	Cellular_Comp
20		09	10	08	onent
GO:0			5.0	5.1	geneontology_
	complex of collagen trimers	25.192			

0986		17	5E-	0E-	Cellular_Comp
44			09	07	onent
GO:0		3.2585	1.5	1.3	geneontology_
0701	anchoring junction		2E-	4E-	Cellular_Comp
61		45	07	05	onent
GO:0		32.389	1.9	1.3	geneontology_
0055	fibrillar collagen trimer		5E-	8E-	Cellular_Comp
83		94	07	05	onent
GO:0		32.389	1.9	1.3	geneontology_
0986	banded collagen fibril		5E-	8E-	Cellular_Comp
43		94	07	05	onent
GO:0		15.115	2.7	1.7	geneontology_
0083	integrin complex		6E-	8E-	Cellular_Comp
05		3	07	05	onent
GO:0		3.2122	3.6	2.1	geneontology_
0059	adherens junction		2E-	3E-	Cellular_Comp
12		25	07	05	onent
GO:0		13.741	5.5	3.0	geneontology_
0986	protein complex involved in cell adhesion		8E-	3E-	Cellular_Comp
36		19	07	05	onent
GO:0		3.3175	4.2	0.0	geneontology_
0059	focal adhesion		0E-	002	Cellular_Comp
25		68	06	05	onent
GO:0		3.2997	4.5	0.0	geneontology_
0059	cell-substrate adherens junction		4E-	002	Cellular_Comp
24		79	06	05	onent
GO:0		3.4396	4.6	0.0	geneontology_
0432	receptor complex		4E-	002	Cellular_Comp
35		39	06	05	onent
GO:0		3.2734	5.1	0.0	geneontology_
0300	cell-substrate junction		0E-	002	Cellular_Comp
55		51	06	12	onent
GO:0		6.6440	2.5	0.0	geneontology_
0310	platelet alpha granule		4E-	009	Cellular_Comp
91		9	05	96	onent
GO:0		4.9830	0.0	0.0	geneontology_
0432	apical junction complex		001	071	Cellular_Comp
96		67	99	54	onent
GO:0		6.9407	0.0	0.0	geneontology_
0310	platelet alpha granule lumen		002	071	Cellular_Comp
93		01	11	54	onent
GO:0		2.8919	0.0	0.0	geneontology_
0312	cell leading edge		002	071	Cellular_Comp
52		59	12	54	onent

GO:0005796	Golgi lumen	5.668239	0.00226	0.007266	geneontology_Cellular_Component
GO:0009897	plasma membrane protein complex	2.491534	0.00315	0.009681	geneontology_Cellular_Component
GO:0005432	lysosomal lumen	6.073113	0.00441	0.012988	geneontology_Cellular_Component
GO:0009989	external side of plasma membrane	3.098168	0.00862	0.02438	geneontology_Cellular_Component
GO:0003002	lamellipodium	3.491131	0.01113	0.030146	geneontology_Cellular_Component
GO:0009852	side of membrane	2.459995	0.01151	0.030146	geneontology_Cellular_Component
GO:0005052	extracellular matrix structural constituent	12.63706	0	0	geneontology_Molecular_Function
GO:0005055	collagen binding	15.7942	1.4E-15	6.8E-13	geneontology_Molecular_Function
GO:0005030	extracellular matrix structural constituent conferring tensile strength	20.59373	1.6E-12	5.0E-10	geneontology_Molecular_Function
GO:0004847	platelet-derived growth factor binding	34.54981	2.0E-10	4.7E-08	geneontology_Molecular_Function
GO:0001983	growth factor binding	7.143757	2.3E-09	4.3E-07	geneontology_Molecular_Function
GO:0005051	integrin binding	6.301814	1.2E-07	1.9E-05	geneontology_Molecular_Function
GO:0005055	glycosaminoglycan binding	5.288236	1.4E-07	1.9E-05	geneontology_Molecular_Function
GO:0004339	proteoglycan binding	12.66826	9.1E-07	0.0009	geneontology_Molecular_Function
GO:0005058	extracellular matrix binding	9.652009	1.3E-07	0.0001	geneontology_Molecular_Function

40			06	45	ction
GO:1			2.5	0.0	geneontology_
9016	sulfur compound binding	4.5243	1E-	002	Molecular_Fun
81		79	06	38	ction
GO:0			1.0	0.0	geneontology_
0082	heparin binding	5.0611	7E-	009	Molecular_Fun
01		7	05	2	ction
GO:0			5.5	0.0	geneontology_
0463	SMAD binding	5.9498	2E-	043	Molecular_Fun
32		69	05	67	ction
GO:0			8.6	0.0	geneontology_
0050	guanyl-nucleotide exchange factor activity	3.1443	0E-	062	Molecular_Fun
85		56	05	84	ction
GO:0			9.6	0.0	geneontology_
0300	extracellular matrix structural constituent conferring compression resistance	15.512	6E-	065	Molecular_Fun
21		16	05	53	ction
GO:0			0.0	0.0	geneontology_
0020	protease binding	4.2489	002	167	Molecular_Fun
20		82	64	34	ction
GO:0			0.0	0.0	geneontology_
0019	fibronectin binding	10.341	005	309	Molecular_Fun
68		44	22	88	ction
GO:0			0.0	0.0	geneontology_
0302	carbohydrate binding	3.3722	007	433	Molecular_Fun
46		08	75	27	ction
GO:0			0.0	0.0	geneontology_
0012	DNA-binding transcription repressor activity, RNA polymerase II-specific	3.1105	008	442	Molecular_Fun
27		11	37		ction
GO:0			0.0	0.0	geneontology_
0199	cytokine binding	3.9847	008	444	Molecular_Fun
55		75	88	01	ction
