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Table S1: The statistical significance of the GO term enrichment analysis

GO ID	**Description**	**pvalue**	**Category**	**source**
GO:0030198	extracellular matrix organization	7.84E-19	BP	DEGs
GO:0043062	extracellular structure organization	8.82E-19	BP	DEGs
GO:0051897	positive regulation of protein kinase B signaling	5.37E-13	BP	DEGs
GO:0048660	regulation of smooth muscle cell proliferation	8.85E-12	BP	DEGs
GO:0048659	smooth muscle cell proliferation	1.18E-11	BP	DEGs
GO:0033002	muscle cell proliferation	1.96E-11	BP	DEGs
GO:0007517	muscle organ development	2.05E-11	BP	DEGs
GO:0051896	regulation of protein kinase B signaling	5.27E-11	BP	DEGs
GO:0140014	mitotic nuclear division	8.31E-11	BP	DEGs
GO:1901342	regulation of vasculature development	1.05E-10	BP	DEGs
GO:0062023	collagen-containing extracellular matrix	4.3E-24	CC	DEGs
GO:0005604	basement membrane	5.72E-08	CC	DEGs
GO:0005788	endoplasmic reticulum lumen	6.49E-07	CC	DEGs
GO:0045121	membrane raft	8.22E-07	CC	DEGs
GO:0098857	membrane microdomain	8.76E-07	CC	DEGs
GO:0043292	contractile fiber	1.79E-06	CC	DEGs
GO:0098589	membrane region	1.95E-06	CC	DEGs
GO:0000779	condensed chromosome, centromeric region	1.5E-05	CC	DEGs
GO:0030016	myofibril	2.91E-05	CC	DEGs
GO:0042383	sarcolemma	5.02E-05	CC	DEGs
GO:0005539	glycosaminoglycan binding	4.37E-17	MF	DEGs
GO:0005201	extracellular matrix structural constituent	5.82E-16	MF	DEGs
GO:0008201	heparin binding	2.74E-14	MF	DEGs
GO:1901681	sulfur compound binding	9.47E-12	MF	DEGs
GO:0005178	integrin binding	3.09E-11	MF	DEGs
GO:0019838	growth factor binding	1.05E-08	MF	DEGs
GO:0043394	proteoglycan binding	2.82E-07	MF	DEGs
GO:0061134	peptGO IDase regulator activity	4.86E-07	MF	DEGs
GO:0017171	serine hydrolase activity	9.5E-07	MF	DEGs
GO:0048018	receptor ligand activity	1.38E-06	MF	DEGs
GO:0051897	positive regulation of protein kinase B signaling	1.32E-13	BP	Hub genes
GO:0043491	protein kinase B signaling	2.28E-12	BP	Hub genes
GO:0033002	muscle cell proliferation	7.42E-12	BP	Hub genes
GO:0051896	regulation of protein kinase B signaling	1.17E-11	BP	Hub genes

GO:0070371	ERK1 and ERK2 cascade	1.86E-11	BP	Hub genes
GO:0009612	response to mechanical stimulus	2.14E-11	BP	Hub genes
GO:0048660	regulation of smooth muscle cell proliferation	5.22E-11	BP	Hub genes
GO:0048659	smooth muscle cell proliferation	5.91E-11	BP	Hub genes
GO:0046777	protein autophosphorylation	9.23E-11	BP	Hub genes
GO:0018108	peptGO IDyl-tyrosine phosphorylation	1.2E-10	BP	Hub genes
GO:0005819	spindle	9.49E-08	CC	Hub genes
GO:0031091	platelet alpha granule	1.05E-06	CC	Hub genes
GO:0062023	collagen-containing extracellular matrix	3.55E-06	CC	Hub genes
GO:0031093	platelet alpha granule lumen	4.75E-06	CC	Hub genes
GO:0098687	chromosomal region	5.36E-06	CC	Hub genes
GO:0000152	nuclear ubiquitin ligase complex	1.87E-05	CC	Hub genes
GO:0000922	spindle pole	3.25E-05	CC	Hub genes
GO:0005680	anaphase-promoting complex	7E-05	CC	Hub genes
GO:0000775	chromosome, centromeric region	8.46E-05	CC	Hub genes
GO:0000779	condensed chromosome, centromeric region	8.71E-05	CC	Hub genes
GO:0005178	integrin binding	4.9E-09	MF	Hub genes
GO:0045236	CXCR chemokine receptor binding	6.65E-09	MF	Hub genes
GO:0005539	glycosaminoglycan binding	2.32E-08	MF	Hub genes
GO:0043394	proteoglycan binding	2.77E-07	MF	Hub genes
GO:0042379	chemokine receptor binding	3.17E-07	MF	Hub genes
GO:0008201	heparin binding	3.18E-07	MF	Hub genes
GO:1901681	sulfur compound binding	8.34E-07	MF	Hub genes
GO:0004713	protein tyrosine kinase activity	9.86E-07	MF	Hub genes
GO:0019838	growth factor binding	1.04E-06	MF	Hub genes
GO:0008009	chemokine activity	1.35E-06	MF	Hub genes