

Morinda officinalis saponins promote osteogenic differentiation

Table S1. The result of GO enrichment including BP and MP from the DEGs

Function	ID	Description	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0003177	pulmonary valve development	21/18866	4.772E-07	0.0013285	0.0011267	BMP4/HEY1/SMAD6/STRA6/TNFRSF1B	5
	GO:0036293	response to decreased oxygen levels	371/18866	1.168E-06	0.0016257	0.0013788	ANKRD1/CITED2/CPEB1/CXCR4/DDAH1/DDIT4/EDN1/EGLN3/HILPDA/MYB/NDNF/OXTR/PMAIP1/RGCC	14
	GO:0070482	response to oxygen levels	396/18866	2.507E-06	0.0023268	0.0019733	ANKRD1/CITED2/CPEB1/CXCR4/DDAH1/DDIT4/EDN1/EGLN3/HILPDA/MYB/NDNF/OXTR/PMAIP1/RGCC	14
	GO:0001666	response to hypoxia	359/18866	4.492E-06	0.0024075	0.0020418	ANKRD1/CITED2/CPEB1/CXCR4/DDAH1/DDIT4/EDN1/EGLN3/HILPDA/MYB/NDNF/PMAIP1/RGCC	13
	GO:0071456	cellular response to hypoxia	208/18866	5.144E-06	0.0024075	0.0020418	ANKRD1/CITED2/CPEB1/DDAH1/EDN1/EGLN3/HILPDA/NDNF/PMAIP1/RGCC	10
	GO:0003007	heart morphogenesis	258/18866	5.439E-06	0.0024075	0.0020418	ADAMTS1/ADGRG6/ANKRD1/BMP4/CITED2/HEY1/PKP2/S1PR1/SMAD6/SOX17/SYNPO2L	11
	GO:0048863	stem cell differentiation	264/18866	6.767E-06	0.0024075	0.0020418	BMP4/EDN1/KBTBD8/KIT/MYB/PRICKLE1/SEMA6A/SEMA6D/SHC4/SOX17/SOX6	11
	GO:0003184	pulmonary valve morphogenesis	17/18866	7.574E-06	0.0024075	0.0020418	BMP4/HEY1/SMAD6/STRA6	4
	GO:0036294	cellular response to decreased oxygen levels	218/18866	7.783E-06	0.0024075	0.0020418	ANKRD1/CITED2/CPEB1/DDAH1/EDN1/EGLN3/HILPDA/NDNF/PMAIP1/RGCC	10
	GO:1905314	semi-lunar valve development	37/18866	9.252E-06	0.0025759	0.0021846	BMP4/HEY1/SMAD6/STRA6/TNFRSF1B	5
	GO:1905207	regulation of cardiocyte differentiation	66/18866	1.201E-05	0.0030406	0.0025787	BMP4/EDN1/PRICKLE1/RGS4/SOX17/SOX6	6
	GO:0071453	cellular response to oxygen levels	235/18866	1.498E-05	0.003399	0.0028827	ANKRD1/CITED2/CPEB1/DDAH1/EDN1/EGLN3/HILPDA/NDNF/PMAIP1/RGCC	10
	GO:0071902	positive regulation of protein serine/threonine kinase activity	345/18866	1.587E-05	0.003399	0.0028827	ADRB2/BMP4/CEMIP/CXCR4/DUSP5/EDN1/KIT/LPAR3/NEK10/NGF/NTF3/RGCC	12
	GO:0001558	regulation of cell growth	420/18866	2.387E-05	0.0046153	0.0039141	BDKRB1/CDKN2C/CXCR4/EDN1/HBEGF/LPAR3/NGF/NPPB/RGS4/SEMA6A/SEMA6D/SOCS2/SOX17	13
	GO:0050769	positive regulation of neurogenesis	485/18866	2.487E-05	0.0046153	0.0039141	ANKRD1/BMP4/CXCR4/KIT/LPAR3/MYB/NDNF/NGF/ROR1/SEMA6A/SOCS2/TNFRSF1B/TOX/ZNF804A	14
	GO:0071560	cellular response to transforming growth factor beta stimulus	252/18866	2.73E-05	0.0047505	0.0040288	ANKRD1/CITED2/EDN1/ID1/LDLRAD4/SMAD6/SMAD9/SMURF2/SOX6/ZNF703	10
	GO:0045926	negative regulation of growth	254/18866	2.92E-05	0.0047827	0.0040561	ADRB2/BDKRB1/BMP4/CDKN2C/NPPB/RGS4/SEMA6A/SEMA6D/SOCS2/SOX17	10
	GO:0071559	response to transforming growth factor beta	258/18866	3.335E-05	0.0051413	0.0043602	ANKRD1/CITED2/EDN1/ID1/LDLRAD4/SMAD6/SMAD9/SMURF2/SOX6/ZNF703	10
	GO:0045446	endothelial cell differentiation	117/18866	3.509E-05	0.0051413	0.0043602	ATOH8/BMP4/CXCR4/HEY1/ID1/S1PR1/SOX17	7
	GO:0050954	sensory perception of mechanical stimulus	173/18866	6.119E-05	0.0084483	0.0071648	ATP8B1/CEMIP/CXCR4/KIT/MBP/ROR1/TFAP2A/USP53	8
	GO:0003205	cardiac chamber development	174/18866	6.373E-05	0.0084483	0.0071648	ADAMTS1/ADGRG6/BMP4/CITED2/HEY1/PKP2/SMAD6/STRA6	8
	GO:0003206	cardiac chamber morphogenesis	131/18866	7.217E-05	0.0086822	0.0073632	ADAMTS1/ADGRG6/BMP4/CITED2/HEY1/PKP2/SMAD6	7
	GO:0043405	regulation of MAP kinase activity	342/18866	7.336E-05	0.0086822	0.0073632	BMP4/CXCR4/DUSP5/DUSP8/EDN1/KIT/LPAR3/NEK10/NGF/NTF3/RGS4	11
	GO:0048762	mesenchymal cell differentiation	229/18866	7.485E-05	0.0086822	0.0073632	BMP4/EDN1/HEY1/KBTBD8/LDLRAD4/RGCC/SEMA6A/SEMA6D/ZNF703	9

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	GO:0003158	endothelium development	135/18866	8.725E-05	0.009509	0.0080644	ATO8/BMP4/CXCR4/HEY1/ID1/S1PR1/SOX17	7
	GO:0060485	mesenchyme development	290/18866	8.88E-05	0.009509	0.0080644	BMP4/CITED2/EDN1/HEY1/KBTBD8/ LDLRAD4/RGCC/SEMA6A/SEMA6D/ZNF703	10
	GO:0003073	regulation of systemic arterial blood pressure	95/18866	9.562E-05	0.0098597	0.0083618	ADRB2/DDAH1/EDN1/NPPB/OXTR/SLC2A5	6
	GO:0003170	heart valve development	61/18866	0.0001088	0.0108168	0.0091735	BMP4/HEY1/SMAD6/STRA6/TNFRSF1B	5
	GO:0016049	cell growth	490/18866	0.0001147	0.0110069	0.0093347	BDKRB1/CDKN2C/CXCR4/EDN1/HBEGF/LPAR3/ NGF/NPPB/RGS4/SEMA6A/SEMA6D/SOCS2/SOX17	13
	GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	34/18866	0.0001333	0.0119667	0.0101487	EDN1/F2RL2/LPAR3/S1PR1	4
MF	GO:0070412	R-SMAD binding	23/18352	3.026E-05	0.0070382	0.0063918	ANKRD1/LDLRAD4/RGCC/SMAD6	4
	GO:0046332	SMAD binding	79/18352	3.943E-05	0.0070382	0.0063918	ANKRD1/LDLRAD4/RGCC/SMAD6/ SMAD9/SMURF2	6
	GO:0005539	glycosaminoglycan binding	232/18352	0.0005459	0.064967	0.0589999	ADAMTS1/ADAMTS15/BMP4/CEMIP/ CXCL6/HBEGF/NDNF/TNFAIP6	8
	GO:0048018	receptor ligand activity	487/18352	0.0018027	0.1128224	0.10246	BMP4/CCL20/CXCL6/EDN1/FGF5/HBEGF/ NGF/NPPB/NTF3/SEMA6A/SEMA6D	11
	GO:0030546	signaling receptor activator activity	492/18352	0.0019526	0.1128224	0.10246	BMP4/CCL20/CXCL6/EDN1/FGF5/HBEGF/ NGF/NPPB/NTF3/SEMA6A/SEMA6D	11
	GO:0008201	heparin binding	169/18352	0.0023412	0.1128224	0.10246	ADAMTS1/ADAMTS15/BMP4/CXCL6/ HBEGF/NDNF	6
	GO:0008330	protein tyrosine/threonine phosphatase activity	10/18352	0.0027127	0.1128224	0.10246	DUSP5/DUSP8	2
	GO:0032052	bile acid binding	10/18352	0.0027127	0.1128224	0.10246	AKR1C1/AKR1C2	2
	GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	11/18352	0.0032983	0.1128224	0.10246	DDAH1/PADI1	2
	GO:0004032	alditol:NADP+ 1-oxidoreductase activity	12/18352	0.0039374	0.1128224	0.10246	AKR1C1/AKR1C2	2
	GO:0005165	neurotrophin receptor binding	12/18352	0.0039374	0.1128224	0.10246	NGF/NTF3	2
	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	13/18352	0.004629	0.1128224	0.10246	DUSP5/DUSP8	2
	GO:0030548	acetylcholine receptor regulator activity	13/18352	0.004629	0.1128224	0.10246	LYPD6/LYPD6B	2
	GO:0099602	neurotransmitter receptor regulator activity	13/18352	0.004629	0.1128224	0.10246	LYPD6/LYPD6B	2
	GO:1901681	sulfur compound binding	262/18352	0.0050388	0.1128224	0.10246	ADAMTS1/ADAMTS15/BMP4/CXCL6/ HBEGF/NDNF/PTGES	7
	GO:0033549	MAP kinase phosphatase activity	14/18352	0.0053725	0.1128224	0.10246	DUSP5/DUSP8	2
	GO:0070411	I-SMAD binding	14/18352	0.0053725	0.1128224	0.10246	SMAD6/SMAD9	2
	GO:0005126	cytokine receptor binding	271/18352	0.0060354	0.1197027	0.1087084	CCL20/CXCL6/NGF/NTF3/SMAD6/ SMURF2/SOCS2	7
	GO:0045125	bioactive lipid receptor activity	16/18352	0.0070113	0.1257985	0.1142443	LPAR3/S1PR1	2
	GO:0031406	carboxylic acid binding	212/18352	0.0070475	0.1257985	0.1142443	AKR1C1/AKR1C2/CEMIP/DDAH1/ EGLN3/TNFAIP6	6
	GO:0043177	organic acid binding	224/18352	0.0091159	0.1549706	0.140737	AKR1C1/AKR1C2/CEMIP/DDAH1/ EGLN3/TNFAIP6	6
	GO:0008083	growth factor activity	162/18352	0.0095943	0.1556896	0.1413899	BMP4/FGF5/HBEGF/NGF/NTF3	5
	GO:0005123	death receptor binding	20/18352	0.0108729	0.1687657	0.1532651	NGF/NTF3	2

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GO:0008106	alcohol dehydrogenase (NADP+) activity	21/18352	0.0119552	0.1731651	0.1572604	AKR1C1/AKR1C2	2
GO:0098631	cell adhesion mediator activity	60/18352	0.0121264	0.1731651	0.1572604	MADCAM1/NEXN/PKP2	3
GO:0005540	hyaluronic acid binding	22/18352	0.0130827	0.1796362	0.1631371	CEMIP/TNFAIP6	2
GO:0030215	semaphorin receptor binding	23/18352	0.0142547	0.1884788	0.1711675	SEMA6A/SEMA6D	2
GO:0005160	transforming growth factor beta receptor binding	24/18352	0.0154703	0.1904446	0.1729528	SMAD6/SMURF2	2
GO:0070696	transmembrane receptor protein serine/threonine kinase binding	24/18352	0.0154703	0.1904446	0.1729528	BMP4/SMAD6	2
GO:0001965	G-protein alpha-subunit binding	26/18352	0.0180294	0.2011404	0.1826662	LPAR3/RGS4	2

Table S2. The result of KEGG enrichment from the DEGs

ID	Description	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04350	TGF-beta signaling pathway	94/8115	0.0014218	0.1491827	0.138030287	BMP4/ID1/SMAD6/SMAD9/SMURF2	5
hsa04015	Rap1 signaling pathway	210/8115	0.002491	0.1491827	0.138030287	EFNA4/FGF5/ID1/KIT/LPAR3/NGF/PLCB4	7
hsa04924	Renin secretion	69/8115	0.0031891	0.1491827	0.138030287	ADRB2/EDN1/GUCY1A2/PLCB4	4
hsa04080	Neuroactive ligand-receptor interaction	353/8115	0.0038008	0.1491827	0.138030287	ADRB2/BDKRB1/EDN1/F2RL2/LPAR3/LYPD6/LYPD6B/OXTR/S1PR1	9
hsa04020	Calcium signaling pathway	240/8115	0.0052076	0.1635191	0.151294915	ADRB2/BDKRB1/CXCR4/FGF5/NGF/OXTR/PLCB4	7
hsa04072	Phospholipase D signaling pathway	148/8115	0.0099075	0.2460824	0.227686046	CYTH3/KIT/LPAR3/PLCB4/SHC4	5
hsa04061	Viral protein interaction with cytokine and cytokine receptor	100/8115	0.0117809	0.2460824	0.227686046	CCL20/CXCL6/CXCR4/TNFRSF1B	4
hsa04151	PI3K-Akt signaling pathway	354/8115	0.0126935	0.2460824	0.227686046	DDIT4/EFNA4/FGF5/KIT/LPAR3/MYB/NGF/NTF3	8
hsa04010	MAPK signaling pathway	294/8115	0.0150276	0.2460824	0.227686046	DUSP5/DUSP8/EFNA4/FGF5/KIT/NGF/NTF3	7
hsa04014	Ras signaling pathway	232/8115	0.0166325	0.2460824	0.227686046	EFNA4/FGF5/KIT/NGF/NTF3/SHC4	6
hsa04668	TNF signaling pathway	112/8115	0.0172414	0.2460824	0.227686046	CCL20/CXCL6/EDN1/TNFRSF1B	4
hsa04360	Axon guidance	182/8115	0.022419	0.2933146	0.271387335	CXCR4/EFNA4/SEMA6A/SEMA6D/TRPC4	5
hsa04062	Chemokine signaling pathway	192/8115	0.0274618	0.3316535	0.306860108	CCL20/CXCL6/CXCR4/PLCB4/SHC4	5
hsa04270	Vascular smooth muscle contraction	134/8115	0.0308559	0.3460269	0.320158954	EDN1/GUCY1A2/NPPB/PLCB4	4
hsa04915	Estrogen signaling pathway	138/8115	0.0338572	0.3543722	0.327880368	HBEGF/KRT34/PLCB4/SHC4	4
hsa04610	Complement and coagulation cascades	85/8115	0.039441	0.3804648	0.352022455	BDKRB1/F2RL2/F3	3
hsa05224	Breast cancer	147/8115	0.0412163	0.3804648	0.352022455	FGF5/HEY1/KIT/SHC4	4
hsa04060	Cytokine-cytokine receptor interaction	295/8115	0.0462678	0.3804648	0.352022455	BMP4/CCL20/CXCL6/CXCR4/NGF/TNFRSF1B	6
hsa04970	Salivary secretion	93/8115	0.0493109	0.3804648	0.352022455	ADRB2/GUCY1A2/PLCB4	3