

Table S2 GO enrichment analysis in biological process

GO-BP	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:1901861	GO:1901861	regulation of muscle tissue development	5/47	175/23239	2.72E-05	0.00782418	0.00609908	Igfbp5/Ncam1/Tgfb3/Smad4/Gja1	5
GO:0001649	GO:0001649	osteoblast differentiation	5/47	192/23239	4.23E-05	0.00782418	0.00609908	Igfbp5/Tgfb3/Col1a1/Smad4/Gja1	5
GO:0048762	GO:0048762	mesenchymal cell differentiation	5/47	213/23239	6.92E-05	0.00853643	0.00665429	Tgfb3/Col1a1/Tgfb1i1/Smad4/Gja1	5
GO:0060485	GO:0060485	mesenchyme development	5/47	269/23239	0.00020643	0.01909453	0.0148845	Tgfb3/Col1a1/Tgfb1i1/Smad4/Gja1	5
GO:0051147	GO:0051147	regulation of muscle cell differentiation	4/47	159/23239	0.0002993	0.0221481	0.0172648	Ptbp1/Cxcl12/Cd8/Smad4	4
GO:0016202	GO:0016202	regulation of striated muscle tissue development	4/47	172/23239	0.00040324	0.02324811	0.01812228	Ncam1/Tgfb3/Smad4/Gja1	4
GO:0048634	GO:0048634	regulation of muscle organ development	4/47	176/23239	0.00043983	0.02324811	0.01812228	Ncam1/Tgfb3/Smad4/Gja1	4
GO:0048771	GO:0048771	tissue remodeling	4/47	187/23239	0.00055264	0.02555944	0.019924	Igfbp5/Tgfb3/Ctsk/Gja1	4
GO:0007411	GO:0007411	axon guidance	4/47	223/23239	0.00106546	0.0400798	0.03124286	Cxcl12/Ncam1/Alcam/Smad4	4
GO:0097485	GO:0097485	neuron projection guidance	4/47	224/23239	0.00108324	0.0400798	0.03124286	Cxcl12/Ncam1/Alcam/Smad4	4
GO:0033002	GO:0033002	muscle cell proliferation	4/47	231/23239	0.00121356	0.04081971	0.03181963	Igfbp5/Ncam1/Tgfb3/Gja1	4
GO:0030198	GO:0030198	extracellular matrix organization	4/47	248/23239	0.00157521	0.04822661	0.03759343	Col24a1/Col1a1/Postn/Efemp2	4
GO:0048738	GO:0048738	cardiac muscle tissue development	4/47	253/23239	0.00169445	0.04822661	0.03759343	Ncam1/Tgfb3/Smad4/Gja1	4

Table S3 KEGG enrichment analysis

KEGG	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
mmu04142	mmu04142	Lysosome	5/23	124/8613	1.56E-05	0.001263127	0.001001309	83429/13038/11593/16004/12514	5
mmu05323	mmu05323	Rheumatoid arthritis	4/23	84/8613	6.47E-05	0.002621406	0.002078048	20315/15894/13038/16414	4
mmu04514	mmu04514	Cell adhesion molecules (CAMs)	4/23	171/8613	0.000988848	0.020592632	0.016324243	17967/15894/11658/16414	4
mmu00511	mmu00511	Other glycan degradation	2/23	18/8613	0.00101692	0.020592632	0.016324243	11593/217364	2
mmu04512	mmu04512	ECM-receptor interaction	3/23	86/8613	0.001473384	0.023868824	0.018921355	319480/21923/12842	3
mmu04933	mmu04933	AGE-RAGE signaling pathway in diabetic complications	3/23	101/8613	0.002337462	0.027555859	0.021844151	15894/12842/17128	3
mmu04810	mmu04810	Regulation of actin cytoskeleton	4/23	217/8613	0.002381371	0.027555859	0.021844151	319480/20315/73178/16414	4
mmu04670	mmu04670	Leukocyte transendothelial migration	3/23	115/8613	0.003379856	0.034221045	0.027127794	20315/15894/16414	3

Table S4 Upregulated or downregulated proteins in KEGG enrichment pathways

Rheumatoid arthritis		
	logFC	P.Value
Cxcl12	1.65125169	5.11E-12
Icam1	1.48058856	1.62E-09
CTSk	1.16418106	5.10E-09
Itgb2	1.10142719	1.09E-07

Cell adhesion molecules (CAMs)		
	logFC	P.Value
Ncam1	1.60588612	1.68E-11
Icam1	1.48058856	1.62E-09
Alcam	-1.3401928	4.64E-09
Itgb2	1.10142719	1.09E-07

ECM-receptor interaction		
	logFC	P.Value
Itga11	-2.7695619	2.90E-15
Tnc	1.49813768	4.35E-10
Col1a1	1.18545023	7.59E-09

Regulation of actin cytoskeleton		
	logFC	P.Value
Itga11	-2.7695619	2.90E-15
Cxcl12	1.65125169	5.11E-12
Wasl	1.21424908	3.77E-08
Itgb2	1.10142719	1.09E-07

Leukocyte transendothelial migration		
	logFC	P.Value
Cxcl12	1.65125169	5.11E-12
Icam1	1.48058856	1.62E-09
Itgb2	1.10142719	1.09E-07