

SUPPLEMENTARY TABLE

Supplementary Table 1. Enriched GO terms and KEGG pathway that are associated with ECM in top list.

Analysis	Term	Count	-LogP**	Fold enrichment	
Gene Ontology Analysis(David Bioinformatics Resources 6.8, NIAID/NIH)					
GO_BP	GO:0030198 extracellular matrix organization	28	8.40	3.85	
	GO:0030574 collagen catabolic process	14	6.30	5.90	
	GO:0022617 extracellular matrix disassembly	14	5.41	4.97	
	GO:0007160 cell-matrix adhesion	14	4.58	4.19	
	GO:0007155 cell adhesion	33	3.32	1.94	
	GO:0005518 collagen binding	9	2.93	4.23	
GO_MF	GO:0005201 extracellular matrix structural constituent	8	2.03	3.37	
	GO:0031012 extracellular matrix	30	6.44	2.97	
GO_CC	GO:0005578 proteinaceous extracellular matrix	26	5.25	2.84	
	GO:0005615 extracellular space	74	4.29	1.61	
	GO:0005581 collagen trimer	13	4.18	4.14	
	GO:0009986 cell surface	33	2.72	1.78	
	KEGG pathway				
	Hsa04512 ECM-receptor interaction	16	5.71	4.47	
Hsa04510 Focal adhesion	23	4.49	2.71		

GEO data (GSE44765; GSM10990247-9 for test group, GSM109024-3 for control group) was processed with Limma package in R. GO and KEGG pathway were analyzed by using David Bioinformatics resources 6.8. -LogP = Log10P. Value. **p < 0.01.