Supplemental Table 5. GO enrichment analysis using DAVID.

Annotation Cluster 1	Enrichment Score: 14.80200293054414	FDR
GOTERM_CC_FAT	GO:0031012~extracellular matrix	9.40E-19
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	9.55E-19
GOTERM_CC_FAT	GO:0044421~extracellular region part	2.46E-16
GOTERM_CC_FAT	GO:0005576~extracellular region	5.71E-15
GOTERM_CC_FAT	GO:0044420~extracellular matrix part	5.39E-10
SP_PIR_KEYWORDS	extracellular matrix	1.25E-09
GOTERM_CC_FAT	GO:0005604~basement membrane	7.12E-07
GOTERM_CC_FAT	GO:0005615~extracellular space	7.39E-04

Annotation Cluster 2	Enrichment Score: 14.147487208836116	FDR
GOTERM_BP_FAT	GO:0007155~cell adhesion	2.46E-16
GOTERM_BP_FAT	GO:0022610~biological adhesion	2.46E-16
SP_PIR_KEYWORDS	cell adhesion	0.025515

Annotation Cluster 3	Enrichment Score: 13.70044833136665	FDR
GOTERM_BP_FAT	GO:0001568~blood vessel development	1.06E-15
GOTERM_BP_FAT	GO:0001944~vasculature development	3.35E-15
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	4.31E-09
GOTERM_BP_FAT	GO:0001525~angiogenesis	1.00E-04

Annotation Cluster 4	Enrichment Score: 5.785860565510054	
UP_SEQ_FEATURE	signal peptide	9.13E-05
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	1.06E-04
SP_PIR_KEYWORDS	signal	2.90E-04
SP_PIR_KEYWORDS	glycoprotein	6.37E-04
SP_PIR_KEYWORDS	Secreted	0.006588

Annotation Cluster 5	Enrichment Score: 5.25703476873765	
GOTERM_BP_FAT	GO:0001501~skeletal system development	6.86E-06
GOTERM_BP_FAT	GO:0060348~bone development	0.012791
GOTERM_BP_FAT	GO:0001503~ossification	0.015579

Annotation Cluster 6	Enrichment Score: 5.247721231541801	
INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation conserved site	4.96E-06
INTERPRO	IPR001881:EGF-like calcium-binding	1.56E-04
INTERPRO	IPR013032:EGF-like region, conserved site	3.79E-04
INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	0.001369
INTERPRO	IPR013091:EGF calcium-binding	0.0024
SMART	SM00179:EGF_CA	0.002814
INTERPRO	IPR000742:EGF-like, type 3	0.022781
SP_PIR_KEYWORDS	egf-like domain	0.027095

Annotation Cluster 7	Enrichment Score: 5.194303618388618	FDR
GOTERM_MF_FAT	GO:0030247~polysaccharide binding	5.23E-05
GOTERM_MF_FAT	GO:0001871~pattern binding	5.23E-05
GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	0.007879
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	0.008057