

Supplementary Material

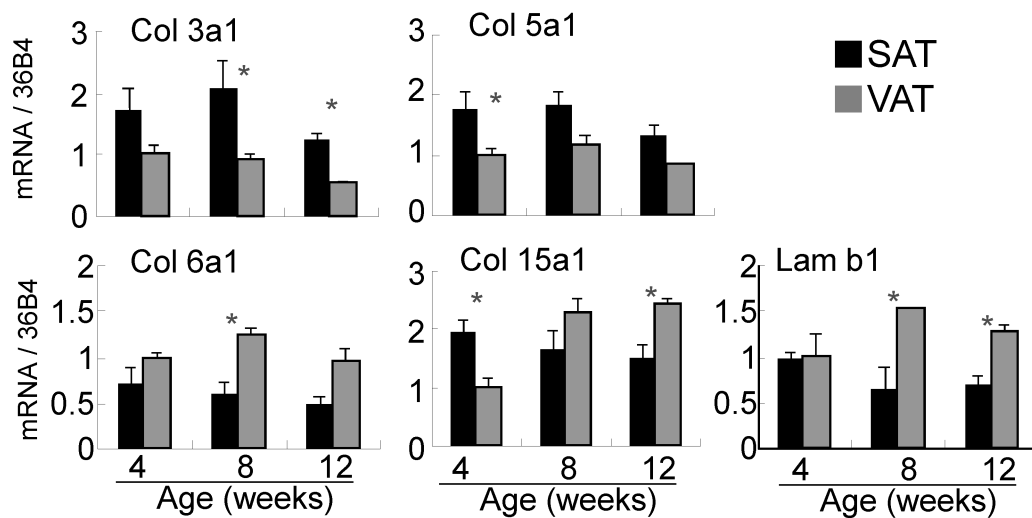


Figure S1. Differential expression of major ECM in adipose tissues by real-time PCR
Quantified mRNA of ECM was normalized by 36B4. Relative values to VAT at 4 weeks of age are presented as the mean \pm S.E.M. of five animals. *: $p < 0.05$, compared with the value of the VAT.

Table S1. Primer sets and probes used for TaqMan Gene Expression Assay

Product numbers given by the manufacturer are listed.

Table S2. Functional annotation clustering for VAT-high genes.

Clustering analysis was performed for VAT-high genes, and eight clusters with highest enrichment score were shown.

Table S3. Functional annotation clustering for SAT-high genes

Clustering analysis was performed for SAT-high genes, and eight clusters with highest enrichment score were shown.

Table S1.

Primer sets and probes used for TaqMan Gene Expression Assay

Rat;

<u>Gene</u>	<u>Product Number</u>
PPAR γ	Rn00440945_m1
aFABP4	Rn00670361_m1
Col 1a1	Rn01463869_g1
Col 3a1	Rn01437683_m1
Col 4a1	Rn01482928_m1
Col 5a1	Rn00593170_m1
Col 6a1	Rn01429558_g1
Col 15a1	Rn01439585_m1
Lam b1	Rn01473698_m1
Lam c1	Rn01758926_m1
FN1	Rn00569575_m1
36B4	Rn00821065_g1

Mouse;

<u>Gene</u>	<u>Product Number</u>
PPAR γ	Mm01184323_m1
aFABP4	Mm00445880_m1
Col 1a1	Mm00801666_g1
Col 3a1	Mm00802331_m1
Col 4a1	Mm01210125_m1
Col 5a1	Mm00489342_m1
Col 6a1	Mm00487160_m1
Col 15a1	Mm00456584_m1
Lam b1	Mm00801853_m1
Lam c1	Mm00711820_m1
FN1	Mm00692666_m1
36B4	Mm00725448_s1

Table S2.

Functional annotation clustering for VAT-high genes

Cluster	Enrichment Score	Term
1	2.5236	GO:0001501~skeletal system development GO:0060348~bone development GO:0048705~skeletal system morphogenesis GO:0001503~ossification GO:0008083~growth factor activity GO:0051216~cartilage development
2	2.3261	GO:0044421~extracellular region part GO:0005578~proteinaceous extracellular matrix GO:0031012~extracellular matrix extracellular matrix
3	2.0198	GO:0005576~extracellular region signal signal peptide Secreted disulfide bond disulfide bond glycoprotein glycosylation site:N-linked (GlcNAc...)
4	1.3334	GO:0016477~cell migration GO:0051674~localization of cell GO:0048870~cell motility GO:0035295~tube development GO:0006928~cell motion GO:0048514~blood vessel morphogenesis GO:0001568~blood vessel development GO:0001944~vasculature development GO:0001525~angiogenesis GO:0007166~cell surface receptor linked signal transduction
5	1.3192	GO:0030097~hemopoiesis GO:0048534~hemopoietic or lymphoid organ development GO:0002520~immune system development GO:0042592~homeostatic process
6	1.2848	GO:0005977~glycogen metabolic process GO:0044042~glucan metabolic process GO:0006073~cellular glucan metabolic process GO:0006112~energy reserve metabolic process GO:0044264~cellular polysaccharide metabolic process GO:0005976~polysaccharide metabolic process GO:0015980~energy derivation by oxidation of organic compounds GO:0006006~glucose metabolic process GO:0019318~hexose metabolic process GO:0005996~monosaccharide metabolic process GO:0006091~generation of precursor metabolites and energy
7	1.2097	cell adhesion GO:0022610~biological adhesion GO:0007155~cell adhesion GO:0016337~cell-cell adhesion
8	1.1851	GO:0035295~tube development GO:0030324~lung development GO:0030323~respiratory tube development GO:0060541~respiratory system development

Table S3.

Functional annotation clustering for SAT-high genes

Cluster	Enrichment Score	Term
1	7.5224	GO:0031012~extracellular matrix GO:0005578~proteinaceous extracellular matrix extracellular matrix GO:0030198~extracellular matrix organization GO:0043062~extracellular structure organization
2	7.0550	signal peptide signal Secreted glycoprotein glycosylation site:N-linked (GlcNAc...) disulfide bond
3	3.0728	GO:0030247~polysaccharide binding GO:0001871~pattern binding GO:0030246~carbohydrate binding GO:0005539~glycosaminoglycan binding GO:0008201~heparin binding
4	3.0580	IPR008160:Collagen triple helix repeat collagen trimer domain:Collagen-like hydroxylation
5	2.7770	propeptide:Activation peptide GO:0008233~peptidase activity GO:0070011~peptidase activity, acting on L-amino acid peptides IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site zymogen Protease IPR001254:Peptidase S1 and S6, chymotrypsin/Hap GO:0004252~serine-type endopeptidase activity SM00020:Tryp_Sp IPR001314:Peptidase S1A, chymotrypsin GO:0008236~serine-type peptidase activity GO:0017171~serine hydrolase activity PIRSF001135:trypsin Serine protease GO:0006508~proteolysis GO:0004175~endopeptidase activity domain:Peptidase S1 hydrolase active site:Charge relay system serine proteinase
6	2.7379	GO:0007155~cell adhesion GO:0022610~biological adhesion cell adhesion
7	2.4317	GO:0005509~calcium ion binding GO:0046872~metal ion binding GO:0043169~cation binding GO:0043167~ion binding GO:0046914~transition metal ion binding
8	2.3878	IPR008160:Collagen triple helix repeat GO:0030198~extracellular matrix organization collagen GO:0005581~collagen GO:0044420~extracellular matrix part GO:0043062~extracellular structure organization GO:0005583~fibrillar collagen GO:0005201~extracellular matrix structural constituent rno04512:ECM-receptor interaction Pyrrolidone carboxylic acid GO:0030199~collagen fibril organization IPR000885:Fibrillar collagen, C-terminal SM00038:COLFI rno04510:Focal adhesion GO:0048730~epidermis morphogenesis GO:0001503~ossification GO:0043588~skin development GO:0060348~bone development short sequence motif:Cell attachment site GO:0005198~structural molecule activity GO:0008544~epidermis development GO:0007398~ectoderm development GO:0048729~tissue morphogenesis rno04810:Regulation of actin cytoskeleton