

ECM-related genes demonstrating significant expression changes in the obese WAT compared to lean controls; bold rows indicates genes showing similar expression patterns in preadipocytes cultured with activated macrophages medium (AcMC). An extended version of this table, indicating significant expression changes of ECM-related genes in the three analyzed situations, is provided as online supplementary data on the companion web site associated to the manuscript.

ECM component	Gene ID	Symbol	Name	Obese/lean		AcMC		Tissular fraction	ECM role
				Fold	q-value (%)	Fold	q-value (%)		
Structural proteins									
	1303	COL12A1	collagen, type XII, alpha 1	2.24	1.54	0.67	0.70	—	proper matrix
	1290	COL5A2	collagen, type V, alpha 2	1.79	1.67	1.64	0.26	SVF	proper matrix
	1282	COL4A1	collagen, type IV, alpha 1	1.77	0.39	0.61	0.37	SVF	proper matrix
	1277	COL1A1	collagen, type I, alpha 1	0.64	4.72	0.89	4.77	SVF	proper matrix
Glycoproteins									
	3685	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	2.01	2.44	1.25	3.24	Adipocyte	cell matrix adhesion
	3688	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.96	0.82	—	—	Adipocyte	cell matrix adhesion
	50856	CLEC4A	C-type lectin domain family 4, member A	1.81	3.07	—	—	SVF	cell cell adhesion
	3684	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	1.61	1.00	2.85	0.00	SVF	cell matrix adhesion

3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	1.52	3.65	1.19	3.94	SVF	cell matrix adhesion	
3693	ITGB5	integrin, beta 5	1.48	3.65	—	—	—	cell matrix adhesion	
3912	LAMB1	laminin, beta 1	1.46	4.72	1.59	0.37	—	cell matrix adhesion	
8506	CNTNAP1	contactin associated protein 1	1.26	4.72	0.32	0.00	SVF	cell matrix adhesion	
7148	TNXB	tenascin XB	0.78	1.54	—	—	SVF	cell matrix adhesion	
3959	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.68	2.44	8.00	0.00	Adipocyte	cell cell adhesion	
3956	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	0.64	2.44	3.95	0.00	—	cell matrix adhesion	
563	AZGP1	alpha-2-glycoprotein 1, zinc	0.53	0.00	—	—	Adipocyte	cell matrix adhesion	
Glycosaminoglycans and proteoglycans									
6386	SDCBP	syndecan binding protein (syntenin)	2.48	0.28	0.55	0.01	—	cell cell adhesion	
4060	LUM	lumican	1.67	2.44	2.86	0.00	SVF	proper matrix	
Enzymes									
7980	TFPI2	tissue factor pathway inhibitor 2	1.74	0.00	7.06	0.00	SVF	remodeling	
6184	RPN1	ribophorin I	1.61	0.00	1.88	0.00	—	remodeling	
8038	ADAM12	ADAM metallopeptidase domain 12 (meltrin	1.61	0.00	1.14	3.94	Adipocyte	remodeling	

		alpha)							
4015	LOX	lysyl oxidase	1.53	3.07	—	—	SVF	remodeling	
1520	CTSS	cathepsin S	1.49	3.07	1.80	0.04	SVF	remodeling	
8974	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	1.47	0.00	5.42	0.00	—	remodeling	
22856	CHSY1	carbohydrate (chondroitin) synthase 1	1.44	3.65	—	—	—	remodeling	
115209	OMA1	OMA1 homolog, zinc metallopeptidase (<i>S. cerevisiae</i>)	1.42	0.28	0.27	0.00	—	remodeling	
8754	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	1.41	1.00	1.42	0.50	SVF	remodeling	
55454	GALNACT	chondroitin sulfate GalNAcT-2	1.40	1.29	—	—	SVF	remodeling	
6868	ADAM17	ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha, converting enzyme)	0.79	2.44	1.48	3.94	SVF	remodeling	
10402	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	0.77	3.65	—	—	—	remodeling	
30815	ST6GALN	ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	0.76	3.07	—	—	—	remodeling	
5351	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-	0.76	3.07	3.49	0.00	Adipocyte	remodeling	

8751	ADAM15	dioxygenase 1 ADAM metallopeptidase domain 15 (metargidin)	0.71	0.82	2.34	0.02	SVF	remodeling
1368	CPM	carboxypeptidase M	0.63	1.00	2.63	0.00	Adipocyte	remodeling
Other components								
131566	DCBLD2	discoidin, CUB and LCCL domain containing 2	1.87	1.00	1.50	0.11	—	cell matrix adhesion
11082	ESM1	endothelial cell- specific molecule 1 membrane	1.38	0.28	2.50	0.01	—	proper matrix
9223	MAGI1	associated guanylate kinase, WW and PDZ domain containing 1	0.76	1.67	0.55	0.00	Adipocyte	cell matrix adhesion
8189	SYMPK	symplekin	0.76	3.07	0.40	0.00	Adipocyte	cell cell adhesion
57165	GJA12	gap junction protein, alpha 12, 47kDa	0.75	1.00	0.44	0.00	SVF	cell cell adhesion
2701	GJA4	gap junction protein, alpha 4, 37kDa (connexin 37)	0.74	1.00	—	—	SVF	cell cell adhesion
5549	PRELP	proline/arginine-rich end leucine-rich repeat protein	0.73	3.07	—	—	Adipocyte	cell matrix adhesion
2152	F3	coagulation factor III (thromboplastin, tissue factor)	0.72	1.54	3.51	0.00	—	remodeling

SVF = Stroma Vascular Fraction

The indicated fold variations were measured in the cDNA microarray experiments. Differential expression q-values were computed with the SAM algorithm and are expressed in percentages (%) indicating the global FDR expected in relation with each of the selected genes.