

**Additional file 7. Differentially expressed genes with function unknown or that cannot be included within a class.**

Gene and biological function	Symbol	GenBank	Unigene	M	LOR
↑(5) Gamma-glutamyl hydrolase (conjugase, foylpolymagglutamyl hydrolase) <i>Lysosome exopeptidase</i>	<b>GGH</b>	U55206	78619	2.03	8.41
↑(14) Hypothetical gene supported by AF131741 <i>Unknown function</i>	<b>LOC441052</b>	AF131741	535012	1.58	3.92
↑(16) Phosphoglycerate mutase 1 (brain) <i>Glycolysis</i>	<b>PGAM1</b>	J04173	447492	1.55	4.33
↑(31) Zinc finger CCCH type domain containing 1 <i>Unknown function</i>	<b>ZC3HDC1</b>	AL13725	12646	1.30	2.43
↑(32) Microsomal glutathione S-transferase 3 <i>Glutathione transferase activity</i>	<b>MGST3</b>	AF026977	191734	1.30	2.93
↑(37) Hematological and neurological expressed 1 <i>Haematopoietic cells and neurological development</i>	<b>HN1</b>	NM_016185	532803	1.27	2.59
↑(40) Chromosome 13 open reading frame 12 (C13orf12) <i>Unknown function</i>	<b>C13orf12</b>	NM_015932	268742	1.25	2.49
↑(53) Adaptor-related protein complex 2, sigma 1 subunit <i>Clathrin cage assembly and endocytosis regulator</i>	<b>AP2S1</b>	X97074	119591	1.17	2.00
↑ (60) ATPase, H <sup>+</sup> transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 <i>ATPase-dependent proton transport</i>	<b>ATP6V1B2</b>	L35249	295917	1.11	1.70
↑ (66) DKFZp564J157 protein <i>Unknown function</i>	<b>DKFZp564J157</b>	AL122042	426359	1.07	1.40
↑(68) Transmembrane protein 14C <i>Unknown function</i>	<b>TMEM14C</b>	AF151028	519557	1.06	1.38
↑ (75) EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1) <i>Repressed during capillary morphogenesis</i>	<b>EFEMP1</b>	U03877	76224	1.03	1.17
↑(77) Peroxisomal long-chain acyl-coA thioesterase <i>Acyl-CoA methabolism</i>	<b>ZAP128</b>	AK001939	446685	1.03	1.14
↑(80) Hypothetical protein LOC348262 <i>Unknown function</i>	<b>LOC348262</b>	AK000852	514632	1.02	1.14
↑(81) ATP citrate lyase <i>Synthesis of cytosolic acetyl-CoA</i>	<b>ACLY</b>	X64330	387567	1.02	1.15
↑ (89) Esterase D/formylglutathione hydrolase <i>Unknown function</i>	<b>ESD</b>	AF112219	432491	0.98	0.78
↑ (104) Major vault protein <i>Drug resistance</i>	<b>MVP</b>	X79882	513488	0.94	0.48
↑ (139) Hypothetical protein LOC116068 <i>Cell wall catabolism</i>	<b>LOC116068</b>	AL137315	136235	0,82	0,07
↑(140) Aminopeptidase puromycin sensitive <i>Zinc metallopeptidase possibly involved in proteolytic events regulating the cell cycle</i>	<b>NPEPPS</b>	AJ132583	443837	0.81	0.03
↓ (4) Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A <i>Control of cell cycle and cell growth</i>	<b>APOBEC3B APOBEC3A</b>	AL022318	226307	-1.25	2.36
↓ (5) Sperm associated antigen 6	<b>SPAG6</b>	AF079363	527698	-1.23	2.47

<i>Control of sperm flagellar motility and structural integrity</i>					
<b>↓(11) Folate receptor 2 (fetal)</b> <i>Member of the folate receptor (FOLR) family</i>	<b>FOLR2</b>	AF000380	433159	-1.15	1.84
<b>↓(22) Apolipoprotein A-I</b> <i>High-density lipoprotein binding and lipoprotein metabolism</i>	<b>APOA1</b>	X02162	93194	-1.05	0.93
<b>↓(24) Hypothetical gene supported by AL133018</b> <i>Unknown function</i>	<b>LOC401018</b>	AL133018	534786	-1.05	0.85
<b>↓(28) Glycine N-methyltransferase</b> <i>Regulation of methionine metabolism</i>	<b>GNMT</b>	X62250	144914	-1.03	1.08
<b>↓(29) Myotubularin related protein 8</b> <i>Hydrolytic enzyme involved in phospholipids and protein amino acid dephosphorylation</i>	<b>MTMR8</b>	AF073482	442892	-1.02	0.82
<b>↓(30) PTD013 protein/ RWD domain containing 1</b> <i>Unknown function</i>	<b>RWDD1</b>	NM_016104	532164	-1.02	1.01
<b>↓(34) Hypothetical protein FLJ10769</b> <i>Unknown function</i>	<b>FLJ10769</b>	AK001631	408324	-1.00	0.99
<b>↓(40) Leucine-rich repeats and calponin homology (CH) domain containing 4</b> <i>Putative receptor with unknown function</i>	<b>LRCH4</b>	AF053356	125742	-0.94	0.72
<b>↓(41) Cytochrome P450, family 2, subfamily C, polypeptide 18</b> <i>Protein localized to the endoplasmic reticulum. Specific substrate not yet determined</i>	<b>CYP2C18</b>	M61853	511872	-0.94	0.16
<b>↓(43) Hypothetical protein MGC11332</b> <i>Tetracycline transport</i>	<b>MGC11332</b>	U79290	98798	-0.93	0.64
<b>↓(46) Hypothetical protein FLJ11142</b> <i>Unknown function</i>	<b>FLJ11142</b>	AL133606	98704	-0.91	0.51
<b>↓(49) Putative lymphocyte G0/G1 switch gene</b> <i>Unknown function</i>	<b>G0S2</b>	M69199	432132	-0.89	0.05
<b>↓(52) Vitelliform macular dystrophy (Best disease, bestrophin)</b> <i>Ion transport</i>	<b>VMD2</b>	AF057170	132319	-0.87	0.33
<b>↓(57) Spectrin repeat containing, nuclear envelope 1</b> <i>Nuclear and Golgi complex organization</i>	<b>SYNE1</b>	AL049548	12967	-0.83	0.08
<b>↓(59) Hypothetical protein MGC27085</b> <i>Unknown function</i>	<b>MGC27085</b>	BC028610	120277	-0.82	0.06

M = differential expression ratio after dye-swap normalization; LOR=log odds ratio: all genes with LOR > 0 were considered significantly down-regulated (M<0) or up-regulated (M>0); in italics biological functions are reported; Each gene is univocally identifiable by a number ranging from 1 to 141 with an up-arrow meaning the up-regulation and from 1 to 58 with a down-arrow meaning the down-regulation in SSc-MVEC.