

Additional file 6. Differentially expressed genes involved in regulation of protein synthesis and mitochondrial functions.

Gene and biological function	Symbol	GenBank	Unigene	M	LOR
PROTEIN SYNTHESIS					
↑(7) Eukaryotic translation elongation factor 1 beta 2 <i>Regulates transfer of aminoacylated tRNA to ribosome</i>	EEF1B2	X60656	421608	1.84	7.48
↑(9) Ribosomal protein L38 <i>Structural constituent of ribosome</i>	RPL38	Z26876	380953	1.70	5.20
↑(15) Ribosomal protein L12 <i>Structural constituent of ribosome</i>	RPL12	AF037643	408054	1.57	4.27
↑(22) Ribosomal protein L9 <i>Structural constituent of ribosome</i>	RPL9	U09953	412370	1.41	2.76
↑(27) Ribosomal protein S20 <i>Structural constituent of ribosome</i>	RPS20	L06498	8102	1.34	2.33
↑(43) Ribosomal protein L23a <i>Structural constituent of ribosome</i>	RPL23A	U37230	184776	1.23	2.35
↑(48) Ribosomal protein L10 <i>Structural constituent of ribosome</i>	RPL10	M64241	401929	1.20	0.82
↑(50) Ribosomal protein L7 <i>Structural constituent of ribosome</i>	RPL7	X57958	421257	1.18	1.89
↑(67) Ribosomal protein S5 <i>Structural constituent of ribosome</i>	RPS5	U14970	378103	1.07	0.49
↑(74) Ribosomal protein S10 (RPS10) <i>Structural constituent of ribosome</i>	RPS10	U14972	406620	1.03	0.86
↑(82) Ribosomal protein L10a <i>Structural constituent of ribosome</i>	RPL10A	NM_007104	14834	1.02	0.90
↑(107) Ribosomal protein L14 <i>Structural constituent of ribosome</i>	RPL14	D87735	446522	0.94	0.63
↑(122) Integrin beta 4 binding protein <i>Translation initiation factor</i>	ITGB4B P	AF022229	534326	0.89	0.38
↑(126) Nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs) <i>Ribosome biogenesis and assembly</i>	NOLA2	AK000486	27222	0.89	0.16
↑(134) Eukaryotic translation initiation factor 4 gamma, 1 <i>Recognition of mRNA cap, recruitment of mRNA to the ribosome</i>	EIF4G1	AF104913	433750	0.84	0.17
MITOCHONDRIAL FUNCTIONS					
↑ 52 NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) <i>Oxidative phosphorylation</i>	NDUFS5	AF047434	472185	1.17	2.03
↑ 62 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa <i>Oxidative phosphorylation</i>	NDUFA 8	NM_014222	495039	1.10	1.62
↑ 63 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 <i>ATPase activity, proton transport</i>	ATP5G1	X69907	80986	1.09	1.54
↑ 73 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa <i>Oxidative phosphorylation</i>	NDUFA 6	AF047182	274416	1.03	1.20
↑ 87 Ubiquinol-cytochrome c reductase hinge	UQCRH	Y00764	481571	1.00	0.84

protein <i>Oxidative phosphorylation</i>					
↑ 91 Solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 <i>Ion transport and pH regulation in mitochondrion, microsomes, endoplasmic reticulum</i>	SLC9A6	AF030409	62185	0.98	0.56
↑ 105 Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 <i>Transport of phosphate into the mitochondrial matrix</i>	SLC25A3	NM_005888	290404	0.94	0.43
↑ 127 Translocase of inner mitochondrial membrane 8 homolog B (yeast) <i>Protein translocation through mitochondrial membrane</i>	TIMM8B	NM_012459	279915	0.87	0.28
↑ 133 cytochrome c oxidase subunit VIa polypeptide 1 <i>Oxidative phosphorylation</i>	COX6A1	AL021546	497118	0.84	0.16
↑ 148 Succinate dehydrogenase complex, subunit D, integral membrane protein <i>Regulation of the activity of mitochondrial complex II</i>	SDHD	AB006202	356270	0.82	0.05

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.