

Additional file 4. Differentially expressed genes involved in cellular stress and ubiquitination.

Gene and biological function	Symbol	GenBank	Unigene	M	LOR
↑(18) ATX1 antioxidant protein 1 homolog (yeast) <i>Copper chaperone ,produced in response to oxidative stress</i>	ATOX1	BT009786	125213	1.51	4.51
↑(28) Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) <i>Hydrolyzes C-terminal adducts of ubiquitin to generate ubiquitin monomer</i>	UCHL1	X04741	518731	1.33	2.99
↑(35) APC11 anaphase promoting complex subunit 11 homolog (yeast) <i>Contributes to ubiquitin-protein ligase activity</i>	ANAPC11	AF151048	534456	1.28	2.76
↑(41) Ferritin, light polypeptide <i>Regulates Fe homeostasis. Produced upon oxidative stress</i>	FTL	NM_000146	433670	1.25	2.35
↑(49) Peripheral myelin protein 22 (PMP22) <i>Also called gas3, it is produced by endothelial cells under shear stress</i>	PMP22	D11428	372031	1.19	2.13
↑(57) Solute carrier family 38, member 2 <i>Aminoacid transporter. Answer to osmotic stress</i>	SLC38A2	AK001700	221847	1.14	1.28
↑(58) Proteasome (prosome, macropain) 26S subunit, ATPase, 1 <i>Structural member of the proteasoma, wich degrades ubiquitinated proteins</i>	PSMC1	L02426	356654	1.12	1.70
↑(59) FK506 binding protein 4, 59kDa <i>Aminoacid transporter. Answer to osmotic stress. Protein folding and trafficking</i>	FKBP4	M88279	524183	1.12	1.71
↑(78) Proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (PSMD13) <i>Structural member of the proteasoma, wich degrades ubiquitinated proteins</i>	PSMD13	NM_002817	134688	1.03	1.13
↑(79) Peroxiredoxin 1 <i>Protective anti-oxidant enzyme, produced in response to oxidative stress.</i>	PRDX1	X67951	180909	1.02	1.03
↑(97) COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis) <i>One of the eight subunits of the COP9 signalosome, involved in multiple signalling pathways. Interacts with cullin-family proteins thus regulating ubiquitin/protein ligase complexes</i>	COPS6	U70735	15591	0.96	0.26
↑(109) Ubiquitin-conjugating enzyme E2 variant 1 <i>Ubiquitin-coniogating enzyme activity</i>	UBE2V1	AL110132	420529	0.93	0.46
↑(113) Neural precursor cell expressed, developmentally down-regulated 8 <i>COP9 signalosome cleaves this protein from CUL1 subunit of ubiquitin ligases.</i>	NEDD8	D23662	531064	0.91	0.55
↑(119) Peroxisome biogenesis factor 10 <i>Involved in generating peroxisomes, which act as a defence against oxidative stress. Involved in ubiquitin cycle</i>	PEX10	AB013818	546273	0.89	0.04
↑(123) Ubiquitin C <i>Ubiquitination</i>	UBC	M26880	520348	0.89	0.004
↑(128) Valosin-containing protein	VCP	NM_007126	529782	0.87	0.17

<i>ATP-binding protein involved in vescicle transport, proteasome function and peroxisome assembly.Regulates ubiquitin-dependent protein degradation</i>					
↑(131) Cullin 2 <i>Regulation of the ubiquitin cycle, in cooperation with COP9 signalosome</i>	CUL2	U83410	82919	0.84	0.18
↑(132) Proteasome (prosome, macropain) subunit, beta type, 2 <i>Structural member of the proteasoma, which degrades ubiquitinated proteins</i>	PSMB2	D26599	471441	0.84	0.16
↑(141) Dual specificity phosphatase 1 <i>Induced by oxidative/heat stress</i>	DUSP1	NM_004417	171695	0.80	0.002
↓(8) Anaphase promoting complex subunit 10 <i>Mediator of ubiquitination reactions, promotion of ubiquitinated protein catabolism</i>	ANAPC10	AL080090	480876	-1.22	2.29
↓(36) ubiquitin specific protease 21 <i>Removes ubiquitin from ubiquitinated proteins</i>	USP21	AL157417	8015	-0.97	0.81
↓(55) Glutathione peroxidase 2 (gastrointestinal) <i>Induced by oxidative stress</i>	GPX2	X53463	2704	-0.84	0.19

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.

