

Additional file 5. Differentially expressed genes involved in stimulus transduction, DNA/RNA organization, transcription.

Gene and biological function	Symbol	GenBank	Unigene	M	LOR
STIMULUS TRANSDUCTION					
↑(24) Gap junction protein, alpha 1, 43kDa (connexin 43) <i>Activates the gap junction molecular complex. Positive regulation of I-kB kinase/NF-kB cascade</i>	GJA1	NM_000165	74471	1.39	3.55
↑(26) Hippocalcin-like 1 <i>Calcium-dependent regulation of cell-signaling</i>	HPCAL1	AK000596	467696	1.36	3.36
↑(30) Cofilin 1 (non-muscle) <i>Rho phosphorylates LIM kinases, which phosphorylate cofilin, thus blocking endothelial migratory signals</i>	CFL1	X95404	180370	1.31	1.99
↑(33) Ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) <i>Small GTPase-mediated signal transduction</i>	RAC2	Z82188	517601	1.30	2.90
↑(38) Serum/glucocorticoid regulated kinase <i>Protein serine/threonine kinase activity</i>	SGK	AJ000512	296323	1.27	1.27
↑(54) Ras-GTPase-activating protein SH3-domain-binding protein <i>Ras protein signal transduction</i>	G3BP	U32519	3353	1.16	0.25
↑(55) Interleukin 6 signal transducer (gp130, oncostatin M receptor) <i>Signal transducer which is part of many cytokine-receptor complex</i>	IL6ST	AL049265	532082	1.15	1.83
↑(61) Rho GDP dissociation inhibitor (GDI) beta <i>Inhibits dissociation of GDP from Rho, thus blocking Rho-dependent signal transductions</i>	ARHGDI2	L20688	504877	1.10	1.09
↑(70) Guanine nucleotide binding protein (G protein), gamma 10 <i>G-protein-coupled receptor protein signalling pathway</i>	GNG10	U31383	534196	1.05	1.30
↑(71) Peroxiredoxin 4 (PRDX4) <i>Regulatory role in activation of NF-kB: depletion of NFkB activity</i>	PRDX4	U25182	83383	1.05	1.28
↑(83) Ras homolog gene family, member A <i>GTP binding, GTPase activity, Rho protein signal transduction</i>	RHOA	L09159	247077	1.02	1.10
↑(85) Dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) <i>Inactivation of MAP kinase by de-phosphorylation: Cell growth inhibition, pro-apoptotic</i>	DUSP3	AL049417	181046	1.01	0.22
↑(93) ADP-ribosylation factor 4 <i>GTP binding, GTPase activity. Small GTPase-mediated signal transduction</i>	ARF4	NM_001660	148330	0.97	0.51
↑(95) Guanine nucleotide binding protein (G protein), beta polypeptide 1 <i>GTP binding, GTPase activity. Small GTPase-mediated signal transduction</i>	GNB1	X04526	430425	0.96	0.68
↑(98) Tyrosine 3-monooxygenase/tryptophan 5-	YWHAE	U54778	513851	0.95	0.71

monooxygenase activation protein, epsilon polypeptide <i>Regulates signal transduction by binding to phosphoserine-containing proteins</i>					
↑(101) Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform <i>Inactivation of MAP kinase by de-phosphorylation Cell growth inhibition, pro-apoptotic</i>	PPP2CA	M60483	483408	0.95	0.45
↑(102) Histidine triad nucleotide binding protein 1 <i>PKC-interacting protein: inhibition of PKC</i>	HINT1	U51004	483305	0.95	0.68
↑(106) V-akt murine thymoma viral oncogene homolog 1 <i>MAPK signalling pathway. Toll-like receptor signalling pathway. Jak-STAT signalling pathway</i>	AKT1	M63167	525622	0.94	0.40
↑(115) MAP kinase interacting serine/threonine kinase 2 <i>Directly phosphorylated by ERK and MAPK. Regulation of protein synthesis by phosphorylation of eukaryotic translation initiation factor 4E</i>	MKNK2/GPRK7	AL137615	515032	0.90	0.47
↑(116) ADP-ribosylation factor 1 <i>GTP binding, GTPase activity. Small GTP-ase mediated signal transduction</i>	ARF1	AK000620	286221	0.90	0.44
↑(117) Zyxin <i>Messenger in the signal transduction pathways that mediates adhesion-stimulated changes in gene expression</i>	ZYX	X95735	490415	0.90	0.42
↑(129) Parkinson disease (autosomal recessive, early onset) 7 <i>Involved in Ras protein signal transduction</i>	PARK7	AF021819	419640	0.85	0.23
↑(135) Exostoses (multiple) 1 <i>Signal transduction involved in the negative regulation of cell cycle</i>	EXT1	NM_000127	492618	0.83	0.11
↑(141) Dual specificity phosphatase 1 <i>Inactivates target kinases by de-phosphorylation of both phosphoserine/threonine and phosphotyrosine residues. Inactivation of MAPK/ ERK, SAPK/JNK, p38</i>	DUSP1	NM_004417	171695	0.80	0.002
↓(9) Plexin B1 <i>Binding of semaphorin 4D to PLXNB1 stimulates tyrosine kinase activity of MET, by acting as a GTPase-activating protein for a member of the RAS superfamily</i>	PLXNB1	AJ011414	476209	-1.19	1.99
↓(23) Mitogen-activated protein kinase kinase kinase 1 <i>Specific mammalian STE20-like protein serine/threonine kinase, involved in many cellular signalling cascades</i>	MAP4K1	U66464	95424	-1.05	1.20
↓(37) 5-hydroxytryptamine (serotonin) receptor 1F Member of the G-protein-coupled receptor super-family. Coupled with activation of Erk/ MAPK pathways	HTR1F	L05597	248136	-0.97	0.83
↓(47) RAB5B, member RAS oncogene family <i>Small, monomeric GTPase, belonging to the RAS Super-family</i>	RAB5B	X54871	77690	-0.90	0.37

↓(50) HIV-1 Rev binding protein-like <i>Member of a family of signal transducers with Extensive networking abilities, including Eps15-homology domain-mediate binding with SH3-containing proteins</i>	HRBL				
		AF053356	521083	-0.88	0.35
↓(51) Ropporin, raphilin associated protein 1 <i>Protein shown to interact with Rho signalling pathway through raphilin</i>	ROPN1	AL133624	458304	-0.87	0.35
DNA/RNA ORGANIZATION					
↑(5) Shwachman-Bodian-Diamond syndrome <i>Rna metabolism</i>	SBDS/CGI-97	AK001779	110445	2.14	9.24
↑(10) Enolase 1, (alpha) <i>Regulation of transcription</i>	ENO1	M14328	517145	1.67	5.79
↑(25) H3 histone, family 3B (H3.3B) <i>Genome stabilization. Nucleosome assembly</i>	H3F3B	Z48950	180877	1.37	3.41
↑(86) Pituitary tumor-transforming 1 <i>Control of DNA replication and chromosome cycle and regulation of chromosome segregation</i>	PTTG1	AJ223953	350966	1.01	0.66
↑(90) Polymerase (RNA) II (DNA directed) polypeptide L, 7. 6kDa <i>Regulation of transcription</i>	POLR2L	U37690	441072	0.98	0.53
↑(94) Thioredoxin-like 4A <i>Component of the spliceosome complex</i>	TXNL4A	AF023612	465498	0.96	0.73
↑(103) Suppressor of Ty 16 homolog (S. cerevisiae) <i>Nucleosome dys-assembly</i>	SUPT16H	NM_007192	213724	0.94	0.62
↑(111) Heterogeneous nuclear ribonucleoprotein K <i>DNA and RNA binding, chromatin remodelling, transcription and splicing</i>	HNRPK	X72727	522257	0.92	0.31
↑(118) Aurora-A kinase interacting protein <i>Inhibitor of Aurora-A kinases, that regulate structure and function of centrosomes and spindle</i>	AKIP	AK000615	472535	0.89	0.38
↑(120) Structure specific recognition protein 1 <i>Nucleosome dys-assembly and chromatin transcription elongation factor</i>	SSRP1	M86737	523680	0.89	0.36
↑(121) RNA polymerase II associated protein 1 <i>Function unknown</i>	RPAP1	AB037824	371045	0.89	0.36
↑(137) 5'-nucleotidase, cytosolic III <i>Regulation of nucleotide catabolism</i>	NT5C3	AF151067	487933	0.83	0.13
↓(7) TruB pseudouridine (psi) synthase homolog 2 (E.coli) <i>RNA modifications, control of telomerase activity</i>	TRUB2	AF131848	98541	-1.23	2.38
↓(14) Arginine vasopressin-induced 1 (AVPI1) <i>Positive regulator of cell cycle</i>	AVPI1	AF131791	23918	-1.12	1.73
↓(21) Chromosome 1 open reading frame 34 <i>Function unknown</i>	C1orf34	AK000220	112949	-1.05	1.28
↓(26) Myogenic factor 5 <i>Regulation of transcription from RNA polymerase II promoter</i>	MYF5	X14894	178023	-1.04	0.25
↓(38) Trinucleotide repeat containing 4 <i>Regulation of alternative splicing</i>	TNRC4	U80759	26047	-0.96	0.71
↓(42) DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 <i>Putative RNA elicase, involved in RNA processing and metabolism</i>	DDX41	AK001255	484288	-0.94	0.58

TRANSCRIPTION					
↑(45) Basic transcription factor 3, like 3 <i>Transcription factor</i>	BTF3L3	M90356	181967/447132	1.21	2.14
↑(56) Interleukin enhancer binding factor 2, 45kDa <i>Transcription factor required for expression of Interleukin2 (IL-2) gene</i>	ILF2	U10323	75117	1.15	1.89
↑(84) High mobility group AT-hook 1 <i>Regulator of inducible genes transcription</i>	HMGA1	L17131	518805	1.01	0.11
↑(125) Basic transcription factor 3, like 1 Transcription factor	BTF3L1	M90354	181965	0.89	0.36
↓(1) GATA binding protein 6 <i>Transcription factor, control of vWF expression</i>	GATA6	X95701	514746	-2.19	8.77
↓(2) SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) <i>Transcription factor (unknown function in endothelial cell)</i>	SOX9	NM_000346	2316	-1.99	7.44
↓(10) Runt-related transcription factor 2 <i>Member of the Ig-loop family of transcription factors, regulates endothelial cell migration and invasion</i>	RUNX2	L40992	122116	-1.16	1.48
↓(12) Nuclear factor of activated T-cells 5, tonicity-responsive <i>Transcription factor, important in regulation of gene expression during osmotic stress</i>	NFAT5	AF089824	371987	-1.14	1.51
↓(15) SRY (sex determining region Y)-box 5 pseudogene <i>Transcription factor (unknown function in endothelial cell)</i>	SOX5P	AF032454	248220	-1.12	1.45
↓(16) Forkhead box A2 <i>Transcription factor</i>	FOXA2	AB028021	155651	-1.10	1.59
↓(39) Sine oculis homeobox homolog 4 (Drosophila) <i>Transcription factor which binds to AU- rich elements</i>	SIX4	NM_017420	279004	-0.95	0.43
↓(44) Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) <i>Transcription factor, activated by a wide variety of stimuli. Complete and persistent inhibition of NF-kB has been linked directly to apoptosis, delayed cell growth and anti-angiogenesis</i>	NFKB2	S76638	73090	-0.93	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.

