

**Additional file 2. Differentially expressed genes involved in angiogenesis.**

Gene and biological function	Symbol	GenBank	Unigene	M	LOR
<b>CELL MIGRATION/INVASION</b>					
↑(1) <b>Metallothionein 1A (functional)</b> <i>Regulation of Zn and Cu availability</i>	<b>MT1A</b>	K01383	440939	3.25	23.81
↑(2) <b>Plasminogen activator, tissue</b> <i>Degradation of provisional fibrin matrix</i>	<b>PLAT</b>	M15518	491582	2.23	11.50
↑(6) <b>Angiopoietin-like 4</b> <i>Positive regulation of angiogenesis</i>	<b>ANGPTL4</b>	NM_016109	9613	1.97	8.75
↑(8) <b>Connective tissue growth factor</b> <i>Positive regulation of angiogenesis, ECM synthesis</i>	<b>CTGF</b>	X78947	410037	1.80	6.71
↑(10) <b>Enolase 1, (alpha)</b> <i>Binding of plasminogen, ECM degradation</i>	<b>ENO1</b>	M14328	517145	1.67	5.79
↑(19) <b>Metallothionein 2A</b> <i>Regulation of Zn and Cu availability</i>	<b>MT2A</b>	V00594	418241	1.50	2.44
↑(20) <b>Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)</b> <i>Protease inhibition, ECM stabilization</i>	<b>SPOCK</b>	AF231124	124611	1.46	3.15
↑(21) <b>Metallothionein 1E (functional)</b> <i>Regulation of Zn and Cu availability</i>	<b>MT1E</b>	M10942	534330	1.43	2.20
↑(23) <b>Cyclin D1 (PRAD1: parathyroid adenomatosis 1)</b> <i>Cytokinesis, invasion</i>	<b>CCND1</b>	X59798	523852	1.40	2.83
↑(34) <b>Calpain 2, (m/II) large subunit</b> <i>Proteolysis and peptidolysis, cytoskeletal Remodelling, invasion</i>	<b>CAPN2</b>	M23254	350899	1.28	2.58
↑(42) <b>Macrophage migration inhibitory factor (glycosylation- inhibiting factor)</b> <i>Positive regulation of angiogenesis</i>	<b>MIF</b>	L19686	407995	1.24	2.43
↑(46) <b>WD repeat domain 1 (WDR1)</b> <i>Cytoskeletal remodelling, mitotic cell rounding</i>	<b>WDR1</b>	AF020056	128548	1.21	2.24
↑(47) <b>Metallothionein 1B (functional)</b> <i>Regulation of Zn and Cu availability</i>	<b>MT1B</b>	M13485	36102	1.20	0.16
↑(51) <b>Interleukin 8</b> <i>Positive regulation of angiogenesis</i>	<b>IL8</b>	M17017	624	1.18	2.05
↑(69) <b>A disintegrin and metalloproteinase domain 15 (metargidin)</b> <i>Proteolysis and peptidolysis</i>	<b>ADAM15</b>	U41767	312098	1.06	1.32
↑(88) <b>ARP3 actin-related protein 3 homolog (yeast)</b> <i>Cell motility, control of actin polymerization</i>	<b>ACTR3</b>	NM_005721	433512	1.00	0.96
↑(96) <b>Actinin, alpha 4</b> <i>Cell motility, cytoskeleton dysregulation</i>	<b>ACTN4</b>	U48734	270291	0.96	0.79
↑(99) <b>Nuclear receptor subfamily 2, group F, member 2</b> <i>Positive regulator of angiopoietin-1</i>	<b>NR2F2</b>	M64497	347991	0.95	0.54
↑(108) <b>Alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)</b> <i>Proteolysis</i>	<b>ANPEP</b>	M22324	1239	0.93	0.27
↑(112) <b>Plasminogen activator, urokinase</b> <i>ECM and provisional fibrin matrix degradation</i>	<b>PLAU</b>	X02419/	77274	0.92	0.42
↑(124) <b>Actin related protein 2/3 complex, subunit 2, 34kDa</b> <i>Cell motility, control of actin polymerization</i>	<b>ARPC2</b>	U50523	529303	0.89	0.23
↑(130) <b>Hepatoma-derived growth factor (high-mobility group protein 1-like)</b> <i>Positive regulation of angiogenesis</i>	<b>HDGF</b>	L24521	506748	0.84	0.21

↓(9) <b>Plexin B1</b> <i>Semaphorin receptor activity and binding, cell migration</i>	<b>PLXNB1</b>	AJ011414	476209	-1.19	1.99
↓(18) <b>Kallikrein 12</b> <i>Positive regulation of EC migration and of capillary morphogenesis</i>	<b>KLK12</b>	AF135025	411572	-1.08	1.39
<b>PROLIFERATION</b>					
↑(1) <b>Metallothionein 1A (functional)</b> <i>Regulation of Zn and Cu availability</i>	<b>MT1A</b>	K01383	440939	3.25	23.81
↑(8) <b>Connective tissue growth factor</b> <i>Positive regulation of angiogenesis, ECM synthesis</i>	<b>CTGF</b>	X78947	410037	1.80	6.71
↑(19) <b>Metallothionein 2A</b> <i>Regulation of Zn and Cu availability</i>	<b>MT2A</b>	V00594	418241	1.50	2.44
↑(20) <b>Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)</b> <i>Calcium ion binding: cell proliferation</i>	<b>SPOCK</b>	AF231124	124611	1.46	3.15
↑(21) <b>Metallothionein 1E (functional)</b> <i>Regulation of Zn and Cu availability</i>	<b>MT1E</b>	M10942	534330	1.43	2.20
↑(23) <b>Cyclin D1 (PRAD1: parathyroid adenomatosis 1)</b> <i>G1/S transition of mitotic cell cycle</i>	<b>CCND1</b>	X59798	523852	1.40	2.83
↑(47) <b>Metallothionein 1B (functional)</b> <i>Regulation of Zn and Cu availability</i>	<b>MT1B</b>	M13485	36102	1.20	0.16
↑(76) <b>Cysteine-rich protein 1 (intestinal)</b> <i>Zn-binding protein. Mediation of MT activity (?)</i>	<b>CRIP1</b>	D42123	70327	1.03	0.85
↑(112) <b>Plasminogen activator, urokinase</b> <i>EC proliferation, release of ECM-growth factors</i>	<b>PLAU</b>	X02419/	77274	0.92	0.42
↑(114) <b>Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)</b> <i>Regulation of purine metabolism</i>	<b>HPRT1</b>	M31642	412707	0.91	0.54
↑(130) <b>Hepatoma-derived growth factor (high-mobility group protein 1-like)</b> <i>Positive regulator of EC proliferation</i>	<b>HDGF</b>	L24521	506748	0.84	0.21
↑(136) <b>Midkine (neurite growth-promoting factor 2)</b> <i>Positive regulator of EC proliferation</i>	<b>MDK</b>	X55110	82045	0.83	0.12
<b>ADHESION</b>					
↓(6) <b>Kallikrein 9</b> <i>Positive regulator of EC proliferation</i>	<b>KLK9</b>	AF135026	448942	-1.23	2.45
↓(18) <b>Kallikrein 12</b> <i>Positive regulator of EC proliferation</i>	<b>KLK12</b>	AF135025	411572	-1.08	1.39
↓(19) <b>Kallikrein 11</b> <i>Positive regulator of EC proliferation</i>	<b>KLK11</b>	AB012917	57771	-1.08	1.39
<b>ADHESION</b>					
↑(8) <b>Connective tissue growth factor</b> <i>Positive regulation of angiogenesis, ECM synthesis</i>	<b>CTGF</b>	X78947	410037	1.80	6.71
↑(12) <b>Vinculin</b> <i>Cytoskeletal actin-cell membrane, cell-cell, cell-ECM interaction</i>	<b>VCL</b>	NM_014000	75350	1.65	5.63
↑(13) <b>Laminin receptor 1 (ribosomal protein SA, 67 kDa)</b> <i>Cell attachment to ECM</i>	<b>LAMR1</b>	U43901	374553	1.63	5.42
↑(17) <b>Profilin 1</b> <i>Fibronectin adhesion, focal conctat formation,</i>	<b>PFN1</b>	J03191	494691	1.54	4.51

<i>cytoskeleton organization</i>					
↑(20) <b>Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)</b> <i>Cell adhesion</i>	<b>SPOCK</b>	AF231124	124611	1.46	3.15
↑(23) <b>Cyclin D1 (PRAD1: parathyroid adenomatosis 1)</b> <i>Inside-out regulation of Rho-GTPases: cytoskeleton organization, adhesion</i>	<b>CCND1</b>	X59798	523852	1.40	2.83
↑(30) <b>Cofilin 1 (non-muscle)</b> <i>Actin cytoskeleton organization</i>	<b>CFL1</b>	X95404	180370	1.31	1.99
↑(65) <b>Calsyntenin 1</b> <i>Cell adhesion</i>	<b>CLSTN1</b>	AB020718	518451	1.07	1.41
↑(69) <b>A disintegrin and metalloproteinase domain 15 (metargidin)</b> <i>Cell-cell, cell-ECM adhesion</i>	<b>ADAM15</b>	U41767	312098	1.06	1.32
↑(117) <b>Zyxin</b> <i>Cell adhesion at focal contacts, actin cytoskeleton organization</i>	<b>ZYX</b>	X95735	490415	0.90	0.42
↑(122) <b>Integrin beta 4 binding protein</b> <i>Linking of basal lamina to the intermediate filament cytoskeleton in hemidesmosomes</i>	<b>ITGB4BP</b>	AF022229	534326	0.89	0.38
↓(27) <b>Desmoglein 2 (DSG2)</b> <i>Codherin cell adhesion molecule, homophilic cell adhesion</i>	<b>DSG2</b>	Z26317	412597	-1.04	1.15
↓(32) <b>Tenascin N</b> <i>ECM-integrin/syndecan interaction</i>	<b>TNN</b>	AL049689	156369	-1.01	0.43
↓(33) <b>Glycoprotein IX (platelet)</b> <i>Part of a cell surface receptor for von Willebrand factor</i>	<b>GP9</b>	X52997	1144	-1.00	0.83
↓(54) <b>Immunoglobulin superfamily, member 1</b> <i>Cell-cell interaction, cell-surface recognition</i>	<b>IGSF1</b>	AB002362	22111	-0.86	0.29
<b>ANGIOGENESIS INHIBITORS</b>					
↑ (11) <b>Pentaxin-related gene, rapidly induced by IL-1 beta</b> <i>Inhibitory binding of FGF-2</i>	<b>PTX3</b>	M31166	546280	1.66	5.19
↑ (72) <b>Peptidylprolyl isomerase A (cyclophilin A)-like</b> <i>Biphasic mediator of EC activation/dysfunction</i>	<b>PPIAL</b>	AL021395	272279	1.05	0.01
<b>ANGIOGENESIS UNKNOWN FUNCTIONS</b>					
↓ (17) <b>CD1B antigen, b polypeptide</b> <i>Pro-angiogenesis, induced by VEGF</i>	<b>CD1B</b>	M28826	1310	-1.09	1.52

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.