

Table S1. Forward and Reverse Primer Pairs

Gene	Forward Primer	Reverse Primer
<i>NCEH1</i>	ggtattgccctttcctcctc	tgaggcccaggaagtgtatc
<i>CKAP2</i>	ctagccacggatccacctaa	tgaacaatttggccacgata
<i>ADAMTS1</i>	tgaatggcgacttcactctg	gaaagtagggatggcggtga
<i>TAGLN</i>	gagcaagctggtaaatagcc	aagaggtcaacggctctggaa
<i>CSF2</i>	cctaccacaaagagccaaa	tattgctgatccctgccagt
<i>VCAM1</i>	atctctctggaccccagat	ttttgccacacatcacagt
<i>MCP1</i>	gctcagccagatgcaattaac	cacttgctgctggtgactct
<i>THBS1</i>	acacgactgcaacaagaacg	ggttggggcaattatccttt
<i>BMP4</i>	accgaatgctgatggctggt	cagaagtgtggcctcgaagt
<i>WISP2</i>	ggctgaggatggagactctg	gaaacgtggccattctccta
<i>CCL26</i>	cctggaagcaggtgcatagt	attcagcggtcaggtcacag
<i>TTR</i>	caagaaggctgctgacgaga	tgtgaacaccacctctgcaa
<i>CSF1</i>	tgattgggaacggacacctg	ctttggcattgggggtgttg
<i>PROCR</i>	cggcttgctaagaaccaaag	ggttgcggatgacttgttt
<i>EMR3</i>	tacgcttccaccatcaccaa	cagccagactccacagatga
<i>RTP4</i>	ctacactggggagaggacca	ggtctgaagctgtgtccctt
<i>DCK</i>	gcaaccaaagtattccacct	ggaaccacctaataccagaa
<i>TOP2A</i>	aatgatgcaggaggccgaaa	aaccaccaaaggcctgaaa
<i>DHRS3</i>	gggaggaggtgtaccagaca	agagagtccaacacggagt
<i>SMC2</i>	gtagcttgggtgctttcgc	gtcactagggcagagagtgc

<i>HSPH1</i>	gaagccgacatggactgtca	aggggggagactgtgaggtt
<i>SMC4</i>	acaacgggtagcagaattgg	acaaggtccagctcagcatc
<i>CENPF</i>	ggcaaaaggcaaaggccag	agcccctctggctcaaattc
<i>GAS2</i>	aaactaccaagcccaccaag	ttgtggaggaccaaaccttc
<i>FABP4</i>	agctgcacttcttttcaccttg	cgcccacttctttcatgtaatca
<i>FBXO32</i>	tggagacacccttcagctct	catccaatcatcaggggaac
<i>RPRM</i>	cgacttctgccttcgggat	cgccctaatgccttctctt
<i>PRUNE2</i>	cttgagactcccgatgaagc	aggccatccccatagtatcc
<i>PDLIM4</i>	tacccagaggacaacaagg	taaagaagctgcctgccaat
<i>H4</i>	acaggccaaagttttgtcg	taaagaagctgcctgccaat
<i>CD14</i>	cagccgacaaccagagagag	tagaccagtcaggcttcgga
<i>FABP5</i>	gatggcaaaaacctcagcat	ttgtgcttctttccatcc
<i>NOV</i>	agcctgaacacctacaagcc	gacgagttgctgtgaggaca
<i>LOC539374</i>	ggagatgggacacttgaggc	cacaaacaggaaactggccg
<i>PTPRR</i>	ttgctgaagtgggatcgtg	atgctggcttcccactcttc
<i>18s rRNA</i>	agaaacggctaccacatcca	caccagacttgcctcca

Table S2. Differentially expressed genes between uniform 28.4 Pa and 3.5 Pa with no gradient \*

<b>Symbol</b>	<b>Description</b>	<b>Gene ID</b>	<b>Ratio</b>	<b>Adjusted p value</b>
PROCR	protein C receptor, endothelial	282005	2.74	0.00027
EMR3	egf-like module-containing mucin-like receptor 3	526347	2.42	0.00106
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	512171	1.86	0.00027
TOP2A	topoisomerase (DNA) II alpha 170kDa	787696	1.58	0.00041
PTPRR	protein tyrosine phosphatase, receptor type, R	536337	1.51	0.00133
AQP1	aquaporin 1 (Colton blood group)	282653	1.47	0.00049
LPIN1	lipin 1	537224	1.45	0.00109
NCEH1	neutral cholesterol ester hydrolase 1	534212	1.42	0.00089
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	506740	1.41	0.00041
NR4A1	nuclear receptor subfamily 4, group A, member 1	528390	1.41	0.00083
SHCBP1	SHC SH2-domain binding protein 1	523367	1.38	0.00107
KIF20A	kinesin family member 20A	527854	1.37	0.00054
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	534849	1.36	0.00086
LOC538402	similar to Protein FAM81A	538402	1.34	0.00238
CASC5	cancer susceptibility candidate 5	787969	1.34	0.00053
CDK1	cyclin-dependent kinase 1	281061	1.30	0.00061
UBE2C	ubiquitin-conjugating enzyme E2C	506962	1.30	0.00075
MALL	mal, T-cell differentiation protein-like	512289	1.30	0.00164
RAD51AP1	RAD51 associated protein 1	615937	1.29	0.00123
ANLN	anillin, actin binding protein	518274	1.28	0.00054
CENPN	centromere protein N	513551	1.27	0.00084
OIP5	Opa interacting protein 5	511100	1.27	0.00098
MIR221	microRNA mir-221	790983	1.26	0.00293
PODXL	podocalyxin-like	616366	1.25	0.00133
E2F8	E2F transcription factor 8	786629	1.25	0.00047
CCNB1	cyclin B1	327679	1.25	0.00142
DCK	deoxycytidine kinase	530642	1.24	0.00088

ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	540722	1.24	0.00285
HJURP	Holliday junction recognition protein	617456	1.23	0.00093
ITGA6	integrin, alpha 6	535043	1.23	0.00041
HSPA12A	heat shock 70kDa protein 12A	540050	1.22	0.00054
AURKB	aurora kinase B	360192	1.21	0.00076
ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	782916	1.21	0.00107
LOC100335204	mCG141481-like	100335204	1.21	0.00521
AKAP12	A kinase (PRKA) anchor protein 12	513774	1.20	0.00050
FOS	FBJ murine osteosarcoma viral oncogene homolog	280795	1.20	0.00535
SPRY2	sprouty homolog 2 (Drosophila)	539090	1.20	0.00161
FANCI	Fanconi anemia, complementation group I	522442	1.20	0.00072
AURKA	aurora kinase A	504437	1.19	0.00490
NUSAP1	nucleolar and spindle associated protein 1	616028	1.19	0.00121
KLF4	Kruppel-like factor 4 (gut)	520842	1.19	0.00106
LOC540455	hypothetical protein LOC540455	540455	1.19	0.00119
PAF	KIAA0101 protein	540737	1.18	0.00397
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	514777	1.17	0.00059
NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	506867	1.17	0.00093
SMC2	structural maintenance of chromosomes 2	539217	1.16	0.00076
SPAG5	sperm associated antigen 5	504585	1.15	0.00072
CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	540641	1.15	0.00047
SPP1	secreted phosphoprotein 1	281499	1.15	0.00374
FBXO5	F-box protein 5	515080	1.14	0.00098
KIF2C	kinesin family member 2C	533161	1.14	0.00173
ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	510538	1.14	0.00041
CDCA8	cell division cycle associated 8	508022	1.14	0.00088
NPPC	natriuretic peptide C	281356	1.13	0.00137

MRAS	muscle RAS oncogene homolog	540803	1.13	0.00075
UHRF1	ubiquitin-like with PHD and ring finger domains 1	530411	1.12	0.00107
NCAPG2	non-SMC condensin II complex, subunit G2	516644	1.10	0.00148
PTPRB	protein tyrosine phosphatase, receptor type, B	505696	1.09	0.00041
BIRC5	baculoviral IAP repeat containing 5	414925	1.08	0.00110
KNTC1	kinetochore associated 1	506353	1.08	0.00238
CKAP2	cytoskeleton associated protein 2	515249	1.08	0.01720
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	537027	1.08	0.00223
LMO7	LIM domain 7	539359	1.07	0.02176
ARF4	ADP-ribosylation factor 4	282601	1.07	0.00103
CKS2	CDC28 protein kinase regulatory subunit 2	767985	1.06	0.00047
ATAD5	ATPase family, AAA domain containing 5	513059	1.06	0.00231
PRC1	protein regulator of cytokinesis 1	767818	1.06	0.00146
NCAPH	non-SMC condensin I complex, subunit H	504477	1.05	0.00075
SPC24	SPC24, NDC80 kinetochore complex component, homolog ( <i>S. cerevisiae</i> )	509117	1.05	0.00141
TSC22D3	TSC22 domain family, member 3	100125309	1.04	0.00164
TFRC	transferrin receptor (p90, CD71)	504698	1.04	0.00437
TCF19	transcription factor 19	514216	1.04	0.00301
KIF23	kinesin family member 23	515748	1.03	0.00093
TIMP3	TIMP metalloproteinase inhibitor 3	282094	1.03	0.00235
SGOL1	shugoshin-like 1 ( <i>S. pombe</i> )	614056	1.02	0.00161
KIFC1	kinesin family member C1	510995	1.02	0.00734
EPB42	erythrocyte membrane protein band 4.2	281754	1.02	0.00230
KIF22	kinesin family member 22	506294	1.02	0.00216
RRM2	ribonucleotide reductase M2	508167	1.02	0.00449
CKAP2L	cytoskeleton associated protein 2-like	507498	1.01	0.00047
CENPF	centromere protein F, 350/400kDa (mitosin)	533089	1.01	0.00131
SKA3	spindle and kinetochore associated complex subunit 3	509921	1.01	0.00058
LOC520939	similar to Krueppel-like factor 2 ( <i>Lung krueppel</i> - like factor)	520939	1.01	0.00080

DSN1	DSN1, MIND kinetochore complex component, homolog ( <i>S. cerevisiae</i> )	508271	1.00	0.00107
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	510420	1.00	0.00202
CKS1B	CDC28 protein kinase regulatory subunit 1B	615827	1.00	0.00144
TTR	transthyretin	280948	-2.28	0.00041
CLCA3P	chloride channel accessory 3 (pseudogene)	281694	-2.21	0.00041
FABP4	fatty acid binding protein 4, adipocyte	281759	-2.21	0.00041
SCARA5	scavenger receptor class A, member 5 (putative)	516087	-2.19	0.00113
CSF2	colony stimulating factor 2 (granulocyte-macrophage)	281095	-2.15	0.00041
MGC127538	hypothetical protein MGC127538	767920	-2.07	0.00109
CXCL5	chemokine (C-X-C motif) ligand 5	281735	-1.92	0.01093
GAS2	growth arrest-specific 2	614840	-1.87	0.00135
CCL26	chemokine (C-C motif) ligand 26	508387	-1.81	0.00137
IL8	interleukin 8	280828	-1.77	0.00861
FABP5	fatty acid binding protein 5 (psoriasis-associated)	281760	-1.70	0.00078
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	505824	-1.69	0.00041
DHRS3	dehydrogenase/reductase (SDR family) member 3	281482	-1.68	0.00103
HAS2	hyaluronan synthase 2	281220	-1.68	0.01012
RTP4	receptor (chemosensory) transporter protein 4	532442	-1.66	0.00076
FBXO32	F-box protein 32	513776	-1.65	0.00047
LOC539374	similar to Family with sequence similarity 43, member A	539374	-1.64	0.00041
NR2F1	nuclear receptor subfamily 2, group F, member 1	327684	-1.54	0.00041
ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	511220	-1.53	0.00288
MYLIP	myosin regulatory light chain interacting protein	541070	-1.49	0.00041
CSF1	colony stimulating factor 1 (macrophage)	281094	-1.48	0.00093
SEPP1	selenoprotein P, plasma, 1	282066	-1.46	0.00041
RPRM	reprimin, TP53 dependent G2 arrest mediator candidate	614739	-1.43	0.00041
ADM	adrenomedullin	280713	-1.41	0.00027
CCL5	chemokine (C-C motif) ligand 5	327712	-1.40	0.01443

CYB561	cytochrome b-561	317663	-1.39	0.00047
XAF1	XIAP associated factor 1	509740	-1.37	0.00053
LOC507696	G-protein coupled receptor-associated sorting protein 1-like	507696	-1.35	0.00061
LRIG3	leucine-rich repeats and immunoglobulin-like domains 3	506574	-1.35	0.00124
MMP1	matrix metalloproteinase 1 (interstitial collagenase)	281308	-1.35	0.02384
DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	538778	-1.32	0.00718
FST	follistatin	327681	-1.32	0.00521
PDLIM4	PDZ and LIM domain 4	515410	-1.30	0.00047
TCP11L2	t-complex 11 (mouse)-like 2	541012	-1.28	0.00041
LRRC33	leucine rich repeat containing 33	510688	-1.28	0.00098
PRUNE2	prune homolog 2 (Drosophila)	518308	-1.25	0.00137
RND3	Rho family GTPase 3	540224	-1.25	0.00041
BACE2	beta-site APP-cleaving enzyme 2	534774	-1.25	0.00076
H4	histone H4	280691	-1.23	0.00086
CD14	CD14 molecule	281048	-1.22	0.00923
VCAM1	vascular cell adhesion molecule 1	282118	-1.22	0.00103
IFI6	interferon, alpha-inducible protein 6	512913	-1.20	0.01195
CXCL2	chemokine (C-X-C motif) ligand 2	613667	-1.17	0.00156
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	493710	-1.17	0.03811
SLCO2A1	solute carrier organic anion transporter family, member 2A1	282468	-1.17	0.00076
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	282713	-1.15	0.00068
CXCL2	chemokine (C-X-C motif) ligand 2	281214	-1.15	0.00917
C10H5orf13	neuronal protein 3.1	1E+08	-1.15	0.00107
TAGLN	transgelin	513463	-1.13	0.00303
EEF2K	eukaryotic elongation factor-2 kinase	521730	-1.13	0.00047
BMP4	bone morphogenetic protein 4	407216	-1.12	0.00663
TMEM37	transmembrane protein 37	613815	-1.11	0.00263
LOC515042	similar to leucine-rich-domain inter-acting protein	515042	-1.10	0.00050

	1; LeR inter-acting protein 1; LEAP1			
LOC539690	CD93 molecule-like	539690	-1.08	0.00075
MEIS1	Meis homeobox 1	613877	-1.07	0.00251
FLRT2	KIAA0405-like	539905	-1.06	0.00088
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	280832	-1.05	0.00329
LOC539596	similar to Transforming growth factor-beta induced protein IG-H3 precursor (Beta IG-H3) (Kerato-epithelin) (RGD-containing collagen associated protein) (RGD-CAP)	539596	-1.05	0.00058
WISP2	WNT1 inducible signaling pathway protein 2	534658	-1.03	0.00147
TRPM6	transient receptor potential cation channel, subfamily M, member 6	527597	-1.03	0.00119
GHR	growth hormone receptor	280805	-1.03	0.01498
LOC100295656	rCG34432-like	100295656	-1.03	0.00283
LOC528994	similar to transmembrane protein 166	528994	-1.03	0.00041
LOC535353	pleckstrin homology domain-containing family G member 6	535353	-1.02	0.00072
PARM1	prostate androgen-regulated mucin-like protein 1	518368	-1.02	0.00054
GNG11	guanine nucleotide binding protein (G protein), gamma 11	511812	-1.02	0.00059
GCA	granalcin, EF-hand calcium binding protein	507139	-1.01	0.01947
CCL2	chemokine (C-C motif) ligand 2	281043	-1.01	0.00202
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	615342	-1.01	0.00357

\* Significantly enriched or depleted genes were identified between ECs exposed to uniform high WSS of 28.4 Pa and uniform WSS of 3.5 Pa by a linear model approach employing an empirical Bayes method at 5% FDR and more than two-fold change between groups. The ratio of the log<sub>2</sub> fold change along with the adjusted FDR p-value are indicated.