Supplemental Data

Table S1. Differentially expressed genes between high WSS and static control treated cells*

Symbol	Description	Gene ID	Ratio	Adjusted *p* value
IL1F6	interleukin 1 family, member 6 (epsilon)	523429	5.23	0.0000018
AQP1	aquaporin 1 (Colton blood group)	282653	4.30	0.0000025
AFF1	AF4/FMR2 family, member 1	781149	4.24	0.0000004
SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	521920	4.19	0.0000038
NQO1	NAD(P)H dehydrogenase, quinone 1	519632	3.96	0.0000001
PI3	peptidase inhibitor 3, skin-derived (SKALP)	407165	3.89	0.0000060
ANO1	anoctamin 1, calcium activated chloride channel	532126	3.88	0.0000034
SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	531606	3.79	0.0000002
SELP	selectin P	281486	3.68	0.0000014
CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	613811	3.67	0.0000051
SLC39A8	solute carrier family 39 (zinc transporter), member 8	508193	3.40	0.0000018
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	512171	3.40	0.0000048
NPPC	natriuretic peptide precursor C	281356	3.39	0.0000008
PTPRR	protein tyrosine phosphatase, receptor type, R	536337	3.19	0.0000003
ISG20	interferon stimulated exonuclease gene 20kDa	506604	3.18	0.0000020
HES1	hairy and enhancer of split 1, (Drosophila)	539547	3.14	0.0000027
AIF1L	allograft inflammatory factor 1-like	617493	2.99	0.0000004
MALL	mal, T-cell differentiation protein-like	512289	2.95	0.0000004
PLEK2	pleckstrin 2	784941	2.87	0.0000001
SELE	selectin E	281484	2.87	0.0000324
LOC520939	similar to Krueppel-like factor 2 (Lung krueppel-like factor)	520939	2.78	0.0000005
CCDC80	coiled-coil domain containing 80	515235	2.75	0.0000004
MTMR11	myotubularin related protein 11	506122	2.72	0.0000005
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	615535	2.72	0.0000017
SKIL	SKI-like oncogene	527910	2.71	0.0000010
SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	768005	2.70	0.0000008

NCEH1	neutral cholesterol ester hydrolase 1	534212	2.68	0.0000027
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	509952	2.66	0.0000399
CAMK1D	calcium/calmodulin-dependent protein kinase ID	526873	2.65	0.0000048
PODXL	podocalyxin-like	616366	2.49	0.0000048
EXOC3L2	exocyst complex component 3-like 2	539328	2.48	0.0000123
EID3	EP300 interacting inhibitor of differentiation 3	507232	2.47	0.0000062
PLAT	plasminogen activator, tissue	281407	2.41	0.0000004
TXNRD1	thioredoxin reductase 1	282388	2.41	0.0000017
PMP22	peripheral myelin protein 22	534497	2.37	0.0000015
NOS3	nitric oxide synthase 3 (endothelial cell)	287024	2.35	0.0000196
AKAP12	A kinase (PRKA) anchor protein 12	513774	2.35	0.0000099
CSRP2	cysteine and glycine-rich protein 2	539381	2.34	0.0000006
MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	539519	2.31	0.0001108
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	281375	2.26	0.0000082
NCAPG	non-SMC condensin I complex, subunit G	531234	2.24	0.0000012
MGC165862	hypothetical LOC614805	614805	2.23	0.0000037
CYB561	cytochrome b-561	317663	2.22	0.0000202
STBD1	starch binding domain 1	513376	2.18	0.0000061
LOC537017	similar to cytidine monophosphate-N-acetylneuraminic acid hydroxylase	537017	2.16	0.0000137
ARF4	ADP-ribosylation factor 4	282601	2.15	0.0000004
GFPT2	glutamine-fructose-6-phosphate transaminase 2	530101	2.13	0.0000072
MYADM	myeloid-associated differentiation marker	506295	2.12	0.0000014
DCK	deoxycytidine kinase	530642	2.05	0.0000040
ABHD5	abhydrolase domain containing 5	535588	2.05	0.0000011
ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	497011	2.03	0.0000041
PLK3	polo-like kinase 3 (Drosophila)	504282	2.03	0.0000008
FAM134B	family with sequence similarity 134, member B	540068	2.03	0.0000027
SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	281376	2.02	0.0031435
PMEPA1	prostate transmembrane protein, androgen induced 1	617469	1.99	0.0000085
TMC6	transmembrane channel-like 6	505575	1.98	0.0000085

FHL2	four and a half LIM domains 2	510008	1.95	0.0000091
GCLM	glutamate-cysteine ligase, modifier subunit	525659	1.93	0.0000016
PLVAP	plasmalemma vesicle associated protein	524990	1.91	0.0000991
MYOZ2	myozenin 2	540487	1.88	0.0000014
GPR116	G protein-coupled receptor 116	532674	1.84	0.0000048
ENG	endoglin	615844	1.81	0.0000166
SPAG9	sperm associated antigen 9	540689	1.77	0.0000061
CRYAB	crystallin, alpha B	281719	1.77	0.0000460
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	540722	1.77	0.0000070
PTPRB	protein tyrosine phosphatase, receptor type, B	505696	1.77	0.0000041
ALAS1	aminolevulinate, delta-, synthase 1	534286	1.76	0.0000030
LOC529423	similar to family with sequence similarity 40, member B	529423	1.73	0.0002436
LAP3	leucine aminopeptidase 3	781648	1.72	0.0000032
SQRDL	sulfide quinone reductase-like (yeast)	507858	1.72	0.0000038
MFAP5	microfibrillar associated protein 5	281908	1.72	0.0000048
ENDOD1	endonuclease domain containing 1	538618	1.71	0.0000085
GATA2	GATA binding protein 2	506809	1.70	0.0000039
RBP4	retinol binding protein 4, plasma	281444	1.69	0.0000166
LOC781772	similar to RIKEN cDNA 2200001I15	781772	1.69	0.0000300
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	281650	1.69	0.0000021
ANLN	anillin, actin binding protein	518274	1.69	0.0000541
TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	282704	1.67	0.0000354
NR4A2	nuclear receptor subfamily 4, group A, member 2	540245	1.66	0.0000650
LOC511659	similar to phospholipase C, gamma 2	511659	1.66	0.0000540
CBR1	carbonyl reductase 1	515946	1.65	0.0000160
OIP5	Opa interacting protein 5	511100	1.65	0.0000166
LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	404179	1.64	0.0002816
ABHD2	abhydrolase domain containing 2	508717	1.63	0.0000063
LOC615685	UPF0452 protein C7orf41 homolog	615685	1.63	0.0000093
SLC41A2	solute carrier family 41, member 2	524417	1.62	0.0000043
HMCN1	hemicentin 1	521326	1.62	0.0009112
CLIC2	chloride intracellular channel 2	532777	1.62	0.0000034
ENC1	ectodermal-neural cortex (with BTB-like domain)	617091	1.61	0.0000068

HEY1	hairy/enhancer-of-split related with YRPW motif 1	408005	1.61	0.0001367
MELK	maternal embryonic leucine zipper kinase	520088	1.61	0.0000093
PDLIM2	PDZ and LIM domain 2 (mystique)	512907	1.59	0.0000046
NUP160	nucleoporin 160kDa	540111	1.59	0.0000065
PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	282299	1.58	0.0000039
LBH	limb bud and heart development homolog (mouse)	616148	1.58	0.0000333
NCAPG2	non-SMC condensin II complex, subunit G2	516644	1.58	0.0000059
FOXM1	forkhead box M1	513643	1.56	0.0000069
LOC787330	similar to Intersectin-2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP-associated protein)	787330	1.55	0.0000054
PTGIS	prostaglandin I2 (prostacyclin) synthase	282021	1.53	0.0000040
ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	281873	1.53	0.0000165
ZDHHC23	zinc finger, DHHC-type containing 23	512177	1.53	0.0000750
SIRPA	signal-regulatory protein alpha	327666	1.52	0.0000051
RRM2	ribonucleotide reductase M2 polypeptide	508167	1.52	0.0000103
ECT2	epithelial cell transforming sequence 2 oncogene	504746	1.51	0.0000052
ANXA8	annexin A8	281627	1.51	0.0049042
KLF4	Kruppel-like factor 4 (gut)	520842	1.50	0.0001074
FGF2	fibroblast growth factor 2 (basic)	281161	1.50	0.0000172
TALDO1	transaldolase 1	513453	1.49	0.0000106
TRIB1	tribbles homolog 1 (Drosophila)	521857	1.48	0.0000263
LOC100270684	hypothetical protein LOC100270684	100270684	1.47	0.0001030
H4	histone H4	280691	1.47	0.0000521
CDC2	cell division cycle 2, G1 to S and G2 to M	281061	1.46	0.0000061
DOK4	docking protein 4	618756	1.46	0.0000389
HYAL1	hyaluronoglucosaminidase 1	515397	1.46	0.0000072
TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	507226	1.46	0.0000034
FXYD5	FXYD domain containing ion transport regulator 5	505584	1.45	0.0000085
ABHD3	abhydrolase domain containing 3	539795	1.45	0.0002699
ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	782916	1.45	0.0000462
RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	533908	1.44	0.0000219
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	509328	1.44	0.0000048

ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	532015	1.44	0.0000521
LOC506746	similar to thyroid hormone receptor interactor 13	506746	1.44	0.0000089
IL1R1	interleukin 1 receptor, type I	515640	1.44	0.0000407
CD46	CD46 molecule, complement regulatory protein	280851	1.43	0.0000211
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	514777	1.43	0.0000159
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	506740	1.43	0.0000204
TEK	TEK tyrosine kinase, endothelial	280939	1.42	0.0000040
TACC1	transforming, acidic coiled-coil containing protein 1	507012	1.42	0.0000041
CD200	CD200 molecule	534910	1.42	0.0000790
RAD51AP1	RAD51 associated protein 1	615937	1.42	0.0000065
PLIN2	perilipin 2	280981	1.39	0.0000204
CDCA8	cell division cycle associated 8	508022	1.39	0.0000048
PDK4	pyruvate dehydrogenase kinase, isozyme 4	507367	1.38	0.0007245
STEAP3	STEAP family member 3	504235	1.38	0.0000090
SNTA1	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	527488	1.37	0.0000082
KLF11	Kruppel-like factor 11	616730	1.37	0.0000114
HSPA12B	heat shock 70kD protein 12B	515590	1.36	0.0000242
ELN	elastin	280781	1.36	0.0000760
LOC788353	similar to Uncharacterized protein KIAA1522 homolog	788353	1.36	0.0000196
GJC1	gap junction protein, gamma 1, 45kDa	511119	1.36	0.0000163
EMP3	epithelial membrane protein 3	535273	1.36	0.0000183
AURKA	aurora kinase A	504437	1.36	0.0000185
RSBN1	round spermatid basic protein 1	508231	1.35	0.0000466
ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	510538	1.35	0.0000066
CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	540641	1.34	0.0000165
SHCBP1	SHC SH2-domain binding protein 1	523367	1.34	0.0000152
CCDC99	coiled-coil domain containing 99	515158	1.33	0.0000167
PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	533527	1.33	0.0000049
SERINC2	serine incorporator 2	513593	1.33	0.0000200
SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	504407	1.33	0.0000199
TUBB2A	tubulin, beta 2A	281555	1.33	0.0000095

HMOX1	heme oxygenase (decycling) 1	513221	1.32	0.0000399
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	282642	1.32	0.0000461
DNASE1L1	deoxyribonuclease I-like 1	515176	1.32	0.0000052
SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	518758	1.32	0.0000126
TIMP1	TIMP metallopeptidase inhibitor 1	282092	1.31	0.0000052
LOC533350	similar to KIAA1451 protein	533350	1.31	0.0000167
C22H3ORF64	chromosome 3 open reading frame 64 ortholog	508782	1.31	0.0000551
EIF2C2	eukaryotic translation initiation factor 2C, 2	404130	1.31	0.0000072
DYRK3	ual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	505149	1.31	0.0000156
MYOZ3	myozenin 3	613741	1.31	0.0011007
AURKB	aurora kinase B	360192	1.30	0.0000082
SMC4	structural maintenance of chromosomes 4	353350	1.30	0.0000043
MYO6	myosin VI	535127	1.29	0.0002149
SMC2	structural maintenance of chromosomes 2	539217	1.29	0.0000397
TCF7	transcription factor 7 (T-cell specific, HMG-box)	782690	1.28	0.0006445
CRTAC1	cartilage acidic protein 1	100139581	1.28	0.0000112
CKS1B	CDC28 protein kinase regulatory subunit 1B	615827	1.28	0.0000066
TUBD1	tubulin, delta 1	510838	1.28	0.0000096
CENP-N	centromere protein N	513551	1.27	0.0000493
NPHP1	nephronophthisis 1 (juvenile)	505421	1.27	0.0000229
CTSH	cathepsin H	510524	1.26	0.0000722
PPAP2B	phosphatidic acid phosphatase type 2B	617707	1.26	0.0000376
PCP4L1	Purkinje cell protein 4 like 1	100126444	1.26	0.0000586
TMEM54	transmembrane protein 54	509773	1.26	0.0000083
EZR	ezrin	281574	1.26	0.0000421
RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	511190	1.26	0.0000496
STK38L	serine/threonine kinase 38 like	514787	1.26	0.0000650
COTL1	coactosin-like 1 (Dictyostelium)	617165	1.26	0.0000915
TRAF3IP2	TRAF3 interacting protein 2	616801	1.26	0.0000393
ACSL6	acyl-CoA synthetase long-chain family member 6	506059	1.26	0.0000087
AMD1	adenosylmethionine decarboxylase 1	280997	1.25	0.0000110
CCNB1	cyclin B1	327679	1.25	0.0000294

KIAA0101	KIAA0101 protein	540737	1.25	0.0001082
MAP9	microtubule-associated protein 9	613821	1.24	0.0001261
SKA3	spindle and kinetochore associated complex subunit 3	509921	1.24	0.0000253
GSPT1	G1 to S phase transition 1	532337	1.24	0.0000147
HYAL2	hyaluronoglucosaminidase 2	281838	1.24	0.0000150
FANCI	Fanconi anemia, complementation group I	522442	1.24	0.0000205
POP5	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	507410	1.23	0.0000338
PDLIM7	PDZ and LIM domain 7 (enigma)	533851	1.23	0.0000217
PARVB	parvin, beta	616294	1.23	0.0000106
EHBP1L1	EH domain binding protein 1-like 1	788760	1.23	0.0000953
SSFA2	sperm specific antigen 2	538826	1.22	0.0002601
SGOL1	shugoshin-like 1 (S. pombe)	614056	1.22	0.0000167
IL8	interleukin 8	280828	1.22	0.0002920
UGDH	UDP-glucose dehydrogenase	281564	1.22	0.0000569
APOL3	apolipoprotein L, 3	512905	1.21	0.0000086
KIF2C	kinesin family member 2C	533161	1.21	0.0000227
JUP	junction plakoglobin	445543	1.21	0.0000333
LOC518821	similar to Centromeric protein E (CENP-E)	518821	1.21	0.0000851
PRC1	protein regulator of cytokinesis 1	767818	1.21	0.0000095
DEPDC7	DEP domain containing 7	532586	1.20	0.0001096
FBXO5	F-box protein 5	515080	1.20	0.0000171
SGK1	serum/glucocorticoid regulated kinase 1	515854	1.19	0.0000180
LMO7	LIM domain 7	539359	1.19	0.0000326
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	519739	1.19	0.0005852
GATA4	GATA binding protein 4	327716	1.19	0.0001326
DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	508271	1.19	0.0000177
STX17	syntaxin 17	534304	1.19	0.0000143
ORAI1	ORAI calcium release-activated calcium modulator 1	517688	1.18	0.0000419
F2RL1	coagulation factor II (thrombin) receptor-like 1	526525	1.18	0.0001894
NUSAP1	nucleolar and spindle associated protein 1	616028	1.18	0.0000354
CENPI	centromere protein I	512877	1.18	0.0000165
MCM10	minichromosome maintenance complex component 10	527595	1.18	0.0000169

KIF9	kinesin family member 9	508574	1.18	0.0004305
RHOBTB1	Rho-related BTB domain containing 1	540513	1.17	0.0000072
VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	511223	1.17	0.0001147
PRKCI	protein kinase C, iota	528478	1.17	0.0000121
MGC148992	similar to RGC-32	614348	1.17	0.0001239
BRCA1	breast cancer 1, early onset	353120	1.16	0.0000354
IRF6	interferon regulatory factor 6	614253	1.16	0.0000247
POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	518653	1.16	0.0000674
CDCA2	cell division cycle associated 2	515287	1.16	0.0000234
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	281872	1.15	0.0000395
CRIP2	cysteine-rich protein 2	780821	1.15	0.0000466
KIF4A	kinesin family member 4A	537127	1.15	0.0000074
PLAUR	plasminogen activator, urokinase receptor	281983	1.15	0.0000163
LOC510012	similar to SCL/TAL1 interrupting locus	510012	1.15	0.0000238
SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	513825	1.15	0.0000541
NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	538789	1.15	0.0000218
LOC615263	hypothetical protein LOC615263	615263	1.15	0.0000148
CSTB	cystatin B (stefin B)	514170	1.15	0.0000281
CHMP4C	chromatin modifying protein 4C	507572	1.14	0.0001095
SYNPO	synaptopodin	533531	1.14	0.0000604
TMEM131	transmembrane protein 131	540861	1.13	0.0000533
POGK	pogo transposable element with KRAB domain	539790	1.13	0.0000238
SASH1	SAM and SH3 domain containing 1	539603	1.13	0.0000637
LOC618360	similar to Nitric oxide-inducible gene protein	618360	1.13	0.0000245
FAM48A	family with sequence similarity 48, member A	534126	1.13	0.0000631
RAD18	RAD18 homolog (S. cerevisiae)	514440	1.13	0.0000408
TK1	thymidine kinase 1, soluble	504652	1.13	0.0000144
NR4A1	nuclear receptor subfamily 4, group A, member 1	528390	1.13	0.0001069
PLN	phospholamban	100125240	1.13	0.0002132
JUNB	jun B proto-oncogene	514246	1.13	0.0000376
PRDX1	peroxiredoxin 1	281997	1.13	0.0000099
ATAD5	ATPase family, AAA domain containing 5	513059	1.12	0.0000257

HAT1	histone acetyltransferase 1	509329	1.12	0.0000166
CDC6	cell division cycle 6 homolog (S. cerevisiae)	515301	1.12	0.0001595
IQGAP3	IQ motif containing GTPase activating protein 3	505886	1.12	0.0000175
HSPA12A	heat shock 70kDa protein 12A	540050	1.12	0.0001331
CCNB2	cyclin B2	281668	1.12	0.0000408
KIF20A	kinesin family member 20A	527854	1.12	0.0000190
MECOM	MDS1 and EVI1 complex locus	532209	1.12	0.0000444
FEN1	flap structure-specific endonuclease 1	616242	1.11	0.0000254
FXYD3	FXYD domain containing ion transport regulator 3	780807	1.11	0.0002234
PRKCD	protein kinase C, delta	505708	1.11	0.0000619
PRICKLE1	prickle homolog 1 (Drosophila)	785152	1.11	0.0000735
MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	534041	1.11	0.0000378
DPH3	DPH3, KTI11 homolog (S. cerevisiae)	511579	1.10	0.0000649
RBBP8	retinoblastoma binding protein 8	512977	1.10	0.0000167
THEX1	three prime histone mRNA exonuclease 1	540728	1.10	0.0002351
LOC540455	hypothetical protein LOC540455	540455	1.10	0.0000650
MEGF9	similar to multiple EGF-like-domains 9	533820	1.10	0.0000321
IER5	immediate early response 5	523618	1.10	0.0000342
TACC3	transforming, acidic coiled-coil containing protein 3	506194	1.09	0.0000352
UHRF1	ubiquitin-like with PHD and ring finger domains 1	530411	1.09	0.0000257
LOC618459	similar to Protein FAM101B	618459	1.09	0.0000120
NCAPH	non-SMC condensin I complex, subunit H	504477	1.09	0.0000284
SPTLC2	serine palmitoyltransferase, long chain base subunit 2	537972	1.09	0.0000135
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	539378	1.09	0.0000609
SRPX2	sushi-repeat-containing protein, X-linked 2	514742	1.08	0.0030843
TMBIM1	transmembrane BAX inhibitor motif containing 1	404134	1.08	0.0000481
TMEM45A	transmembrane protein 45A	509461	1.08	0.0000483
ANKH	ankylosis, progressive homolog (mouse)	511800	1.08	0.0001368
LIG1	ligase I, DNA, ATP-dependent	100124507	1.08	0.0000204
UNC93A	unc-93 homolog A (C. elegans)	613535	1.07	0.0002772
CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	505144	1.07	0.0001214
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	537027	1.07	0.0000155

MAP3K8	mitogen-activated protein kinase kinase kinase 8	535622	1.07	0.0000790
UBE2C	ubiquitin-conjugating enzyme E2C	506962	1.07	0.0000199
GLO1	glyoxalase I	540335	1.07	0.0000462
TXN	thioredoxin	280950	1.07	0.0000107
LOC782395	similar to malignant fibrous histiocytoma amplified sequence 1	782395	1.06	0.0000460
DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	528615	1.06	0.0000193
LMNA	lamin A/C	404144	1.06	0.0000259
CD47	CD47 molecule	282661	1.06	0.0000111
ENO2	enolase 2 (gamma, neuronal)	526006	1.06	0.0001765
MLEC	malectin	515309	1.06	0.0000887
KLF10	Kruppel-like factor 10	522795	1.06	0.0000460
SLPI	secretory leukocyte peptidase inhibitor	504598	1.06	0.0076782
SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	614128	1.05	0.0002651
SBDS	Shwachman-Bodian-Diamond syndrome	513237	1.05	0.0000399
AIDA	axin interactor, dorsalization associated	508353	1.05	0.0001169
LOC100138230	similar to Huntingtin interacting protein K	100138230	1.05	0.0000276
ACTR6	ARP6 actin-related protein 6 homolog (yeast)	613596	1.04	0.0000393
RCC2	regulator of chromosome condensation 2	509120	1.04	0.0000601
CENPF	centromere protein F, 350/400ka (mitosin)	533089	1.04	0.0001898
LGTN	ligatin	511844	1.04	0.0000720
FGF1	fibroblast growth factor 1 (acidic)	281160	1.04	0.0001186
TOP2A	topoisomerase (DNA) II alpha 170kDa	787696	1.04	0.0001090
MAP2K1	mitogen-activated protein kinase kinase 1	533199	1.04	0.0000339
RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	514943	1.04	0.0000156
CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	504742	1.04	0.0000848
LOC619120	similar to Protein FAM65A	619120	1.03	0.0000441
PHLDA1	pleckstrin homology-like domain, family A, member 1	540135	1.03	0.0000275
RFC4	replication factor C (activator 1) 4, 37kDa	504637	1.03	0.0000827
MCM3	minichromosome maintenance complex component 3	281302	1.03	0.0000598
KPNA4	karyopherin alpha 4 (importin alpha 3)	535090	1.02	0.0001229
PKM2	pyruvate kinase, muscle	512571	1.02	0.0000474
AVL9	AVL9 homolog (S. cerevisiase)	534141	1.02	0.0000358

SAR1B	SAR1 homolog B (S. cerevisiae)	515999	1.02	0.0000349
FBP2	fructose-1,6-bisphosphatase 2	514066	1.01	0.0003098
LIMS2	LIM and senescent cell antigen-like domains 2	515401	1.01	0.0000276
GINS3	GINS complex subunit 3 (Psf3 homolog)	538943	1.01	0.0007958
MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	282276	1.01	0.0000883
RPA2	replication protein A2, 32kDa	507912	1.01	0.0002582
ACOT2	acyl-CoA thioesterase 2	511033	1.00	0.0001468
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	540985	1.00	0.0000417
ACSL5	acyl-CoA synthetase long-chain family member 5	514159	1.00	0.0000272
AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	282138	1.00	0.0006018
PIGW	phosphatidylinositol glycan anchor biosynthesis, class W	768052	1.00	0.0000407
FABP4	fatty acid binding protein 4, adipocyte	281759	-5.11	0.0000010
MGC127538	hypothetical protein MGC127538	767920	-4.77	0.0000008
FABP5	fatty acid binding protein 5 (psoriasis-associated)	281760	-3.48	0.0000002
OLFML3	olfactomedin-like 3	505318	-3.23	0.0000061
SDC2	syndecan 2	615785	-3.18	0.0000009
COL6A3	collagen, type VI, alpha 3	530657	-3.14	0.0000388
DHRS3	dehydrogenase/reductase (SDR family) member 3	281482	-3.08	0.0000005
PRUNE2	prune homolog 2 (Drosophila)	518308	-3.07	0.0000001
SCARA5	scavenger receptor class A, member 5 (putative)	516087	-2.86	0.0000127
RBM3	RNA binding motif (RNP1, RRM) protein 3	509771	-2.82	0.0000014
SDPR	serum deprivation response (phosphatidylserine binding protein)	532333	-2.77	0.0000215
SNN	stannin	615361	-2.73	0.0000014
EMCN	endomucin	616367	-2.73	0.0000009
LOC539690	similar to Complement component C1q receptor precursor (Complement component 1 q subcomponent receptor 1) (C1qR) (C1qRp) (C1qR(p)) (C1q/MBL/SPA receptor) (Matrix-remodeling-associated protein 4) (CD93 antigen) (CDw93)	539690	-2.56	0.0000074
LOC509972	similar to C-type lectin domain family 2, member d11	509972	-2.55	0.0000085

LOC614047	hypothetical protein LOC614047	614047	-2.51	0.0000010
SST	somatostatin	280932	-2.48	0.0000257
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	535379	-2.41	0.0000094
CXCL5	chemokine (C-X-C motif) ligand 5	281735	-2.40	0.0029137
BMP4	bone morphogenetic protein 4	407216	-2.38	0.0000021
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	505824	-2.37	0.0000069
TTR	transthyretin	280948	-2.30	0.0000286
PGF	placental growth factor	280894	-2.27	0.0000009
PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	282091	-2.25	0.0000039
EGR1	early growth response 1	407125	-2.24	0.0001157
WNT11	wingless-type MMTV integration site family, member 11	613288	-2.24	0.0000006
CCL26	chemokine (C-C motif) ligand 26	508387	-2.19	0.0000223
ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	511220	-2.13	0.0001917
RGL1	ral guanine nucleotide dissociation stimulator-like 1	522344	-2.13	0.0000008
GSTT1	glutathione S-transferase theta 1	517724	-2.06	0.0000009
KLF15	Kruppel-like factor 15	407241	-2.00	0.0000018
ZNF608	zinc finger protein 608	509992	-1.99	0.0000072
AFAP1L1	actin filament associated protein 1-like 1	510738	-1.98	0.0000009
IL20RA	interleukin 20 receptor, alpha	509038	-1.98	0.0000069
PLXDC2	plexin domain containing 2	515731	-1.98	0.0000021
LDOC1	leucine zipper, down-regulated in cancer 1	616591	-1.98	0.0000012
NOV	nephroblastoma overexpressed	505727	-1.96	0.0000124
CIRBP	cold inducible RNA binding protein	507120	-1.95	0.0000180
GAMT	guanidinoacetate N-methyltransferase	515270	-1.94	0.0000008
MXRA5	matrix-remodelling associated 5	786844	-1.94	0.0000291
NRG1	neuregulin 1	281361	-1.93	0.0000039
ASCL1	achaete-scute complex homolog 1 (Drosophila)	540473	-1.93	0.0017583
ADM	adrenomedullin	280713	-1.93	0.0000234
LRRC33	leucine rich repeat containing 33	510688	-1.92	0.0000061
LOC524694	similar to Paladin	524694	-1.91	0.0000607
LOC534839	similar to high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha; putative GAP protein alpha	534839	-1.90	0.0000059
FADS2	fatty acid desaturase 2	521822	-1.88	0.0000215

RNF183	ring finger protein 183	539200	-1.85	0.0000041
MT1E	metallothionein 1E	613358	-1.84	0.0028373
MARCKS	myristoylated alanine-rich protein kinase C substrate	613548	-1.83	0.0000048
RCSD1	RCSD domain containing 1	512205	-1.79	0.0000120
SH3KBP1	SH3-domain kinase binding protein 1	510489	-1.79	0.0000095
NRBP2	nuclear receptor binding protein 2	504664	-1.79	0.0000085
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	540357	-1.77	0.0000079
TXNIP	thioredoxin interacting protein	506790	-1.76	0.0000854
KBTBD6	kelch repeat and BTB (POZ) domain containing 6	538461	-1.76	0.0001095
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	414732	-1.76	0.0001244
FAM129A	family with sequence similarity 129, member A	614787	-1.75	0.0000019
CFH	complement factor H	280816	-1.74	0.0000167
VCAM1	vascular cell adhesion molecule 1	282118	-1.74	0.0027898
THBD	thrombomodulin	281529	-1.73	0.0000040
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	615342	-1.73	0.0000062
TCP11L2	t-complex 11 (mouse)-like 2	541012	-1.72	0.0000152
CAV1	caveolin 1, caveolae protein, 22kDa	281040	-1.71	0.0000061
CSF2	colony stimulating factor 2 (granulocyte-macrophage)	281095	-1.70	0.0000526
HAS2	hyaluronan synthase 2	281220	-1.70	0.0005234
ZFP36L1	zinc finger protein 36, C3H type-like 1	614773	-1.69	0.0000584
SEPP1	selenoprotein P, plasma, 1	282066	-1.68	0.0000185
MT1E	metallothionein 1E	404071	-1.68	0.0035607
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	281002	-1.68	0.0000850
PDLIM4	PDZ and LIM domain 4	515410	-1.67	0.0000043
APOA1	apolipoprotein A-I	281631	-1.65	0.0000090
IL7	interleukin 7	280827	-1.65	0.0000328
VEGFA	vascular endothelial growth factor A	281572	-1.64	0.0000074
NEIL2	nei like 2 (E. coli)	444987	-1.64	0.0000020
LOC511229	similar to mCG142710	511229	-1.63	0.0000167
TRPM6	transient receptor potential cation channel, subfamily M, member 6	527597	-1.62	0.0000735
MMP11	matrix metallopeptidase 11 (stromelysin 3)	539109	-1.61	0.0000039

SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	507095	-1.60	0.0000112
SLAMF8	SLAM family member 8	514609	-1.60	0.0000042
SLITRK2	SLIT and NTRK-like family, member 2	540117	-1.60	0.0002827
UBA7	ubiquitin-like modifier activating enzyme 7	497204	-1.59	0.0000171
CBX6	chromobox homolog 6	513830	-1.59	0.0000076
LOC100125763	neuronal protein 3.1	100125763	-1.59	0.0000094
WISP2	WNT1 inducible signaling pathway protein 2	534658	-1.58	0.0000069
LOC781004	hypothetical LOC781004	781004	-1.57	0.0000062
LOC515042	similar to leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1	515042	-1.57	0.0000018
WDFY2	WD repeat and FYVE domain containing 2	523432	-1.56	0.0000043
VEGFB	vascular endothelial growth factor B	282121	-1.56	0.0000167
RSF1	remodeling and spacing factor 1	541248	-1.56	0.0002105
LGALS9	lectin, galactoside-binding, soluble, 9	510813	-1.55	0.0000155
MGC128424	hypothetical protein MGC128424	767924	-1.54	0.0000115
ICAM3	intercellular adhesion molecule 3	281840	-1.54	0.0000778
CNRIP1	cannabinoid receptor interacting protein 1	539715	-1.53	0.0000052
SRL	sarcalumenin	513912	-1.51	0.0000054
VAMP5	vesicle-associated membrane protein 5 (myobrevin)	540406	-1.50	0.0000063
DDAH1	dimethylarginine dimethylaminohydrolase 1	537391	-1.49	0.0000046
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	282223	-1.48	0.0000609
TNC	tenascin C	540664	-1.48	0.0000862
PHLDB2	pleckstrin homology-like domain, family B, member 2	509784	-1.47	0.0000048
RNPEP	arginyl aminopeptidase (aminopeptidase B)	282040	-1.46	0.0000064
ISG12(B)	similar to TLH29 protein precursor	617420	-1.46	0.0000287
TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	527162	-1.46	0.0000085
MDK	midkine (neurite growth-promoting factor 2)	280852	-1.46	0.0000150
RND3	Rho family GTPase 3	540224	-1.46	0.0000063
N4BP2L1	NEDD4 binding protein 2-like 1	616069	-1.45	0.0000702
PDIA5	protein disulfide isomerase family A, member 5	511603	-1.45	0.0000092
CXCL2	chemokine (C-X-C motif) ligand 2	613667	-1.44	0.0021504
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	280924	-1.44	0.0002694
COL15A1	collagen, type XV, alpha 1	100139730	-1.44	0.0017955
MGST3	microsomal glutathione S-transferase 3	507346	-1.44	0.0000095

SCML1	sex comb on midleg-like 1 (Drosophila)	786670	-1.43	0.0000048
HOXA5	homeobox A5	768039	-1.43	0.0000063
CCDC85B	coiled-coil domain containing 85B	540332	-1.43	0.0000044
NTS	neurotensin	280881	-1.42	0.0018248
AMIGO2	adhesion molecule with Ig-like domain 2	514273	-1.42	0.0000076
TSPYL4	TSPY-like 4	508104	-1.41	0.0000089
GPR125	G protein-coupled receptor 125	541147	-1.41	0.0000041
AGFG2	ArfGAP with FG repeats 2	510361	-1.40	0.0000350
COL12A1	collagen, type XII, alpha 1	359712	-1.40	0.0000149
RGS7	regulator of G-protein signaling 7	281452	-1.38	0.0000155
RP2	retinitis pigmentosa 2 (X-linked recessive)	534054	-1.38	0.0001391
LOC616969	Rho-guanine nucleotide exchange factor	616969	-1.37	0.0000065
MCF2L	MCF.2 cell line derived transforming sequence-like	505595	-1.37	0.0000477
ASPH	aspartate beta-hydroxylase	286771	-1.37	0.0000227
LOC538778	similar to dapper 1	538778	-1.37	0.0000631
ECHDC2	enoyl Coenzyme A hydratase domain containing 2	513795	-1.36	0.0000057
BMPER	BMP binding endothelial regulator	534101	-1.34	0.0000514
LOC784007	similar to LOC496253 protein	784007	-1.34	0.0000642
LOC526200	similar to Absent in melanoma 1 protein	526200	-1.33	0.0000709
LOC100196901	hypothetical LOC100196901	100196901	-1.33	0.0000517
SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	338050	-1.33	0.0000700
GAB1	GRB2-associated binding protein 1	540085	-1.33	0.0000936
LOC535166	similar to mKIAA1077 protein	535166	-1.32	0.0005091
JAM3	junctional adhesion molecule 3	513412	-1.32	0.0000095
TIFA	TRAF-interacting protein with forkhead-associated domain	783855	-1.32	0.0000521
UNC119	unc-119 homolog (C. elegans)	538501	-1.32	0.0000061
LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	505750	-1.32	0.0000393
SGSH	N-sulfoglucosamine sulfohydrolase	535442	-1.31	0.0000051
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	504531	-1.30	0.0000165
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	510972	-1.30	0.0001811
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	507477	-1.29	0.0002366
NME4	non-metastatic cells 4, protein expressed in	789324	-1.29	0.0000068
MAP2K6	mitogen-activated protein kinase kinase 6	286883	-1.28	0.0000194

SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	540904	-1.28	0.0000098
PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	514428	-1.27	0.0000180
HMGA1	high mobility group AT-hook 1	618849	-1.27	0.0000324
LOC529052	similar to F55A4.8a	529052	-1.27	0.0000123
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	506264	-1.27	0.0000157
COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	338086	-1.27	0.0000082
SYTL2	synaptotagmin-like 2	614406	-1.26	0.0001722
YPEL3	yippee-like 3 (Drosophila)	787498	-1.26	0.0000103
LIX1L	Lix1 homolog (mouse)-like	788858	-1.26	0.0000308
CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	282179	-1.26	0.0000072
VEGFC	vascular endothelial growth factor C	282122	-1.26	0.0000167
ZNF462	zinc finger protein 462	515561	-1.26	0.0001176
COMMD1	copper metabolism (Murr1) domain containing 1	534683	-1.25	0.0000089
C19H17ORF28	chromosome 17 open reading frame 28 ortholog	540436	-1.25	0.0000748
TPPP3	tubulin polymerization-promoting protein family member 3	614988	-1.25	0.0000184
LOC507141	CE5 protein-like	507141	-1.25	0.0000080
PTGDS	prostaglandin D2 synthase 21kDa (brain)	286858	-1.25	0.0000171
SLC22A17	solute carrier family 22, member 17	539848	-1.25	0.0003853
LOC535439	similar to Probable global transcription activator SNF2L1 (Nucleosome-remodeling factor subunit SNF2L) (ATP-dependent helicase SMARCA1) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1)	535439	-1.24	0.0000661
NTHL1	nth endonuclease III-like 1 (E. coli)	535203	-1.24	0.0000093
PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	506485	-1.24	0.0000070
LOC540312	similar to Protein DDX26B	540312	-1.24	0.0000994
CXCR4	chemokine (C-X-C motif) receptor 4	281736	-1.23	0.0022377
RSPRY1	ring finger and SPRY domain containing 1	538571	-1.23	0.0000135
PIK3IP1	phosphoinositide-3-kinase interacting protein 1	512082	-1.23	0.0000405
SEPT4	septin 4	538801	-1.22	0.0000095
CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	521378	-1.22	0.0003377
METTL12	methyltransferase like 12	512401	-1.22	0.0000483

ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	404164	-1.22	0.0000143
EIF4E3	eukaryotic translation initiation factor 4E family member 3	616906	-1.21	0.0002595
WASF1	WAS protein family, member 1	531488	-1.21	0.0000317
SLCO2A1	solute carrier organic anion transporter family, member 2A1	282468	-1.21	0.0000947
NFIL3	nuclear factor, interleukin 3 regulated	506097	-1.20	0.0000461
S100A16	S100 calcium binding protein A16	505679	-1.20	0.0000298
MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	514547	-1.20	0.0000316
PSAT1	phosphoserine aminotransferase 1	533044	-1.20	0.0007964
FASN	fatty acid synthase	281152	-1.20	0.0001350
TMOD1	tropomodulin 1	780784	-1.20	0.0001894
DDT	D-dopachrome tautomerase	615999	-1.20	0.0000122
KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	281883	-1.19	0.0039708
LOC512304	similar to ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	512304	-1.19	0.0000208
CLEC2D	C-type lectin domain family 2, member D	617565	-1.19	0.0001097
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	529115	-1.19	0.0000112
CRYBA4	crystallin, beta A4	282204	-1.19	0.0000159
IFI6	interferon, alpha-inducible protein 6	512913	-1.18	0.0000196
IGFBP4	insulin-like growth factor binding protein 4	282262	-1.17	0.0000936
TC2N	tandem C2 domains, nuclear	534419	-1.17	0.0000352
LOC534672	similar to family with sequence similarity 20, member C	534672	-1.17	0.0000242
LOC539374	similar to Family with sequence similarity 43, member A	539374	-1.16	0.0000169
ANXA11	annexin A11	282142	-1.16	0.0000309
LOC507983	similar to KIAA1728 protein	507983	-1.16	0.0000325
ACOX2	acyl-Coenzyme A oxidase 2, branched chain	514969	-1.16	0.0000215
GNG11	guanine nucleotide binding protein (G protein), gamma 11	511812	-1.15	0.0000165
LOC615936	similar to autism susceptibility candidate 2	615936	-1.15	0.0001084
EEF2K	eukaryotic elongation factor-2 kinase	521730	-1.15	0.0000103
TIMP2	TIMP metallopeptidase inhibitor 2	282093	-1.15	0.0001159
MGC128008	hypothetical LOC510399	510399	-1.15	0.0000460
LOC784866	hypothetical LOC784866	784866	-1.14	0.0000121

SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	523846	-1.14	0.0003339
CADM1	cell adhesion molecule 1	529873	-1.14	0.0000953
RTP4	receptor (chemosensory) transporter protein 4	532442	-1.14	0.0009939
OSBPL11	oxysterol binding protein-like 11	538576	-1.14	0.0000521
ZNF503	zinc finger protein 503	789846	-1.14	0.0000416
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	532663	-1.14	0.0000462
HINT2	histidine triad nucleotide binding protein 2	281816	-1.14	0.0000165
PEAR1	platelet endothelial aggregation receptor 1	787112	-1.14	0.0000120
CMTM3	CKLF-like MARVEL transmembrane domain containing 3	787512	-1.13	0.0000394
FBXL20	F-box and leucine-rich repeat protein 20	511007	-1.13	0.0000131
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	527528	-1.13	0.0021501
ERO1L	ERO1-like (S. cerevisiae)	100125317	-1.13	0.0047819
WARS	tryptophanyl-tRNA synthetase	281576	-1.12	0.0000183
LMCD1	LIM and cysteine-rich domains 1	540474	-1.12	0.0025153
ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	538583	-1.11	0.0001786
PXMP2	peroxisomal membrane protein 2, 22kDa	508609	-1.11	0.0001982
EFNA5	ephrin-A5	616742	-1.10	0.0000326
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	516209	-1.10	0.0000625
AVPR1A	arginine vasopressin receptor 1A	538439	-1.10	0.0004043
ABLIM1	actin binding LIM protein 1	504968	-1.10	0.0000112
VCAN	versican	282662	-1.10	0.0000393
LOC535887	similar to pantothenate kinase 1	535887	-1.10	0.0055952
MIPEP	mitochondrial intermediate peptidase	517531	-1.10	0.0000179
GALM	galactose mutarotase (aldose 1-epimerase)	616676	-1.09	0.0000247
RHOT1	ras homolog gene family, member T1	511257	-1.09	0.0000156
PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	508045	-1.09	0.0000138
PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	510041	-1.08	0.0000337
KLHL23	kelch-like 23 (Drosophila)	100140861	-1.08	0.0001317
FIG4	FIG4 homolog (S. cerevisiae)	534118	-1.08	0.0000200

MOCOS	molybdenum cofactor sulfurase	281226	-1.07	0.0000700
ZNF292	zinc finger protein 292	541264	-1.07	0.0000551
IPO11	importin 11	538236	-1.06	0.0000858
IGFBP3	insulin-like growth factor binding protein 3	282261	-1.06	0.0006117
DPYD	dihydropyrimidine dehydrogenase	281124	-1.06	0.0000666
TBC1D12	TBC1 domain family, member 12	509093	-1.06	0.0000280
SYNGR1	synaptogyrin 1	534995	-1.06	0.0000183
CPEB1	cytoplasmic polyadenylation element binding protein 1	514174	-1.06	0.0000428
SYNM	synemin, intermediate filament protein	514186	-1.06	0.0001060
FHL1	four and a half LIM domains 1	509056	-1.06	0.0000169
ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	538427	-1.05	0.0000667
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	614834	-1.05	0.0000243
CCRL1	chemokine (C-C motif) receptor-like 1	281672	-1.05	0.0035105
AHNAK2	AHNAK nucleoprotein 2	527701	-1.05	0.0000167
GRAMD1C	GRAM domain containing 1C	505581	-1.05	0.0000779
NFIB	nuclear factor I/B	538474	-1.05	0.0000771
IDUA	iduronidase, alpha-L-	511050	-1.05	0.0000461
PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	510593	-1.05	0.0001498
CADM4	cell adhesion molecule 4	523277	-1.04	0.0000907
NT5E	5'-nucleotidase, ecto (CD73)	281363	-1.04	0.0001074
STX10	syntaxin 10	525379	-1.04	0.0000168
BDH2	3-hydroxybutyrate dehydrogenase, type 2	515321	-1.04	0.0000947
RELL1	RELT-like 1	768210	-1.03	0.0000339
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	281308	-1.03	0.0015825
BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	530147	-1.03	0.0002098
GSN	gelsolin (amyloidosis, Finnish type)	535077	-1.03	0.0000535
RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	100139484	-1.03	0.0000155
GCSH	glycine cleavage system protein H (aminomethyl carrier)	317723	-1.03	0.0000987
GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	614203	-1.03	0.0000340

PAGE4	P antigen family, member 4 (prostate associated)	505725	-1.03	0.0001979
FST	follistatin	327681	-1.03	0.0009974
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	520056	-1.02	0.0000336
MYLIP	myosin regulatory light chain interacting protein	541070	-1.02	0.0005559
SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	510932	-1.02	0.0002318
ICA1	islet cell autoantigen 1, 69kDa	535346	-1.02	0.0000387
NRP1	neuropilin 1	539369	-1.02	0.0006813
IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	614320	-1.02	0.0000601
MEIS1	Meis homeobox 1	613877	-1.01	0.0000925
SLC38A9	solute carrier family 38, member 9	534045	-1.01	0.0000308
UNC13B	unc-13 homolog B (C. elegans)	530692	-1.01	0.0000216
PDGFRL	platelet-derived growth factor receptor-like	515017	-1.01	0.0000449
APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	505734	-1.01	0.0000980
FRMD6	FERM domain containing 6	530910	-1.01	0.0003716
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	535136	-1.01	0.0000127
RPS6KL1	ribosomal protein S6 kinase-like 1	530047	-1.01	0.0000336
UPK1B	uroplakin 1B	282113	-1.01	0.0009277
CST3	cystatin C	281102	-1.00	0.0000179
LOC783163	similar to protein phosphatase 4, regulatory subunit 1	783163	-1.00	0.0000609
PATZ1	POZ (BTB) and AT hook containing zinc finger 1	532416	-1.00	0.0000486
SSLP-1	secreted seminal vesicle Ly-6 protein 1	100125878	-1.00	0.0001040

*****Significantly enriched or depleted genes were identified between ECs exposed to high WSS (10 Pa) and no flow static cultures (0 Pa) by a linear model approach employing an empirical Bayes method at 1% FDR and more than two-fold change between groups. The ratio of the $\log_2$ fold change along with the adjusted FDR p-value are indicated.

Table S2. Differentially expressed genes between normal WSS and static control treated cells*

Symbol	Description	Gene ID	Ratio	Adjusted *p* value
CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	613811	4.20	0.0000121
SELP	selectin P	281486	3.25	0.0000121
CYB561	cytochrome b-561	317663	3.24	0.0000151
IL1F6	interleukin 1 family, member 6 (epsilon)	523429	3.06	0.0001047
SELE	selectin E	281484	3.02	0.0001047
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	281375	2.94	0.0000121
HES1	hairy and enhancer of split 1, (Drosophila)	539547	2.67	0.0000251
IL8	interleukin 8	280828	2.62	0.0000251
SRPX2	sushi-repeat-containing protein, X-linked 2	514742	2.48	0.0001307
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	509952	2.48	0.0002166
CCDC80	coiled-coil domain containing 80	515235	2.47	0.0000033
NQO1	NAD(P)H dehydrogenase, quinone 1	519632	2.46	0.0000033
ANO1	anoctamin 1, calcium activated chloride channel	532126	2.45	0.0001195
ISG20	interferon stimulated exonuclease gene 20kDa	506604	2.38	0.0000378
CSRP2	cysteine and glycine-rich protein 2	539381	2.33	0.0000033
CAMK1D	calcium/calmodulin-dependent protein kinase ID	526873	2.30	0.0000416
SKIL	SKI-like oncogene	527910	2.20	0.0000126
PLEK2	pleckstrin 2	784941	2.16	0.0000033
SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	531606	2.12	0.0000151
SLC39A8	solute carrier family 39 (zinc transporter), member 8	508193	2.12	0.0000783
TAGLN	transgelin	513463	2.02	0.0000556
MGC148992	similar to RGC-32	614348	2.00	0.0000377
ENG	endoglin	615844	1.93	0.0000571
FAT1	FAT tumor suppressor homolog 1 (Drosophila)	508251	1.86	0.0000393
PI3	peptidase inhibitor 3, skin-derived (SKALP)	407165	1.85	0.0008737
LOC615685	UPF0452 protein C7orf41 homolog	615685	1.82	0.0000259
ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	532015	1.81	0.0000756

TXNRD1	thioredoxin reductase 1	282388	1.80	0.0000324
NCAPG	non-SMC condensin I complex, subunit G	531234	1.76	0.0000179
PLVAP	plasmalemma vesicle associated protein	524990	1.74	0.0005784
LAP3	leucine aminopeptidase 3	781648	1.73	0.0000126
NCEH1	neutral cholesterol ester hydrolase 1	534212	1.73	0.0000927
PDK4	pyruvate dehydrogenase kinase, isozyme 4	507367	1.72	0.0006777
FLRT2	similar to KIAA0405	539905	1.72	0.0000121
PMEPA1	prostate transmembrane protein, androgen induced 1	617469	1.69	0.0000783
CXCL2	chemokine (C-X-C motif) ligand 2	281212	1.69	0.0005255
STBD1	starch binding domain 1	513376	1.69	0.0000918
MGC165862	hypothetical LOC614805	614805	1.68	0.0000571
RPRM	reprimo, TP53 dependent G2 arrest mediator candidate	614739	1.66	0.0006152
LOC100270684	hypothetical protein LOC100270684	100270684	1.66	0.0002068
EXOC3L2	exocyst complex component 3-like 2	539328	1.60	0.0004446
CTSH	cathepsin H	510524	1.60	0.0000930
AXL	AXL receptor tyrosine kinase	516598	1.59	0.0000930
ALAS1	aminolevulinate, delta-, synthase 1	534286	1.58	0.0000204
SGK1	serum/glucocorticoid regulated kinase 1	515854	1.58	0.0000220
PHLDA1	pleckstrin homology-like domain, family A, member 1	540135	1.56	0.0000173
NOS3	nitric oxide synthase 3 (endothelial cell)	287024	1.55	0.0006201
TACC1	transforming, acidic coiled-coil containing protein 1	507012	1.53	0.0000121
LOC520939	similar to Krueppel-like factor 2 (Lung krueppel-like factor)	520939	1.52	0.0000388
ENC1	ectodermal-neural cortex (with BTB-like domain)	617091	1.51	0.0000393
TCF7	transcription factor 7 (T-cell specific, HMG-box)	782690	1.51	0.0008156
PRM1	protamine 1	281423	1.50	0.0003217
GATA2	GATA binding protein 2	506809	1.47	0.0000316
CSTB	cystatin B (stefin B)	514170	1.46	0.0000386
FBXO32	F-box protein 32	513776	1.45	0.0000121
PLK3	polo-like kinase 3 (Drosophila)	504282	1.44	0.0000204
STEAP3	STEAP family member 3	504235	1.42	0.0000378
CLCA3P	chloride channel accessory 3 (pseudogene)	281694	1.42	0.0001470
LBH	limb bud and heart development homolog (mouse)	616148	1.41	0.0002255
HMOX1	heme oxygenase (decycling) 1	513221	1.39	0.0001283
ANLN	anillin, actin binding protein	518274	1.39	0.0005665

COL18A1	collagen, type XVIII, alpha 1	508076	1.37	0.0000769
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	282713	1.35	0.0005622
EID3	EP300 interacting inhibitor of differentiation 3	507232	1.35	0.0004883
AFF1	AF4/FMR2 family, member 1	781149	1.34	0.0004036
PMP22	peripheral myelin protein 22	534497	1.33	0.0001065
NPPC	natriuretic peptide precursor C	281356	1.33	0.0002966
UGDH	UDP-glucose dehydrogenase	281564	1.33	0.0001504
TRAF3IP2	TRAF3 interacting protein 2	616801	1.33	0.0001231
TMC6	transmembrane channel-like 6	505575	1.32	0.0002664
IL18R1	interleukin 18 receptor 1	407221	1.31	0.0017451
FHL2	four and a half LIM domains 2	510008	1.30	0.0002825
MYADM	myeloid-associated differentiation marker	506295	1.30	0.0000744
AQP1	aquaporin 1 (Colton blood group)	282653	1.29	0.0032938
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	509328	1.29	0.0000381
DEPDC7	DEP domain containing 7	532586	1.27	0.0003056
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	281650	1.27	0.0000386
LOC615263	hypothetical protein LOC615263	615263	1.25	0.0000427
HEY1	hairy/enhancer-of-split related with YRPW motif 1	408005	1.25	0.0016835
PRSS23	protease, serine, 23	538575	1.24	0.0000393
ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	497011	1.24	0.0001739
ANKH	ankylosis, progressive homolog (mouse)	511800	1.24	0.0000783
FBN1	fibrillin 1	281154	1.24	0.0000571
PODXL	podocalyxin-like	616366	1.23	0.0005840
SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	518758	1.23	0.0000796
ATF3	activating transcription factor 3	515266	1.23	0.0000586
FAM48A	family with sequence similarity 48, member A	534126	1.22	0.0001739
COTL1	coactosin-like 1 (Dictyostelium)	617165	1.21	0.0004055
DNASE1L1	deoxyribonuclease I-like 1	515176	1.21	0.0000378
IL1R1	interleukin 1 receptor, type I	515640	1.19	0.0003989
SLC41A2	solute carrier family 41, member 2	524417	1.19	0.0000796
GCLM	glutamate-cysteine ligase, modifier subunit	525659	1.18	0.0000783

MALL	mal, T-cell differentiation protein-like	512289	1.17	0.0001448
SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	768005	1.17	0.0001944
LOC507627	similar to SLAM family member 9	507627	1.17	0.0001456
SNTA1	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	527488	1.17	0.0000796
TMEM45A	transmembrane protein 45A	509461	1.15	0.0001469
RBP4	retinol binding protein 4, plasma	281444	1.15	0.0004649
LOC532244	similar to microtubule associated monoxygenase, calponin and LIM domain containing 3	532244	1.15	0.0001992
NQO2	NAD(P)H dehydrogenase, quinone 2	508566	1.15	0.0002903
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	539378	1.14	0.0001919
SQRDL	sulfide quinone reductase-like (yeast)	507858	1.14	0.0001052
NUDT22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	533578	1.13	0.0001210
ABHD5	abhydrolase domain containing 5	535588	1.13	0.0000869
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	282642	1.13	0.0003972
SASH1	SAM and SH3 domain containing 1	539603	1.13	0.0002567
PRICKLE1	prickle homolog 1 (Drosophila)	785152	1.13	0.0001470
CD200	CD200 molecule	534910	1.12	0.0009257
RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	514943	1.12	0.0000481
MYO6	myosin VI	535127	1.12	0.0014408
PLIN2	perilipin 2	280981	1.11	0.0002651
PCP4L1	Purkinje cell protein 4 like 1	100126444	1.09	0.0004682
SYNPO	synaptopodin	533531	1.09	0.0002883
THBS1	thrombospondin 1	281530	1.09	0.0073629
H4	histone H4	280691	1.09	0.0008893
NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	788119	1.08	0.0003309
SCFD2	sec1 family domain containing 2	535130	1.08	0.0002255
SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	521920	1.08	0.0096442
LOC787330	similar to Intersectin-2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP-associated protein)	787330	1.08	0.0001327
APOL3	apolipoprotein L, 3	512905	1.07	0.0000769
RSBN1	round spermatid basic protein 1	508231	1.07	0.0005681

PPAP2B	phosphatidic acid phosphatase type 2B	617707	1.07	0.0004898
OIP5	Opa interacting protein 5	511100	1.07	0.0005784
ABHD2	abhydrolase domain containing 2	508717	1.06	0.0002114
NCAPG2	non-SMC condensin II complex, subunit G2	516644	1.05	0.0001703
FGF2	fibroblast growth factor 2 (basic)	281161	1.05	0.0004233
ARF4	ADP-ribosylation factor 4	282601	1.05	0.0000581
TUBD1	tubulin, delta 1	510838	1.05	0.0001141
CBR1	carbonyl reductase 1	515946	1.04	0.0006201
NET1	neuroepithelial cell transforming gene 1	507365	1.04	0.0000975
FOXM1	forkhead box M1	513643	1.04	0.0002034
LOC100196898	hypothetical LOC100196898	100196898	1.04	0.0006915
PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	533527	1.04	0.0000744
MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	534041	1.04	0.0002034
GPR116	G protein-coupled receptor 116	532674	1.04	0.0003127
CHMP4C	chromatin modifying protein 4C	507572	1.03	0.0001068
TEK	TEK tyrosine kinase, endothelial	280939	1.03	0.0000783
TSPAN6	tetraspanin 6	514741	1.03	0.0002966
CRYAB	crystallin, alpha B	281719	1.02	0.0026049
TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	507226	1.02	0.0000780
MTMR11	myotubularin related protein 11	506122	1.01	0.0002616
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	505025	1.01	0.0000878
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	506740	1.00	0.0004871
ECT2	epithelial cell transforming sequence 2 oncogene	504746	1.00	0.0001601
SERINC2	serine incorporator 2	513593	1.00	0.0003426
FABP4	fatty acid binding protein 4, adipocyte	281759	-3.42	0.0000324
EMCN	endomucin	616367	-2.94	0.0000033
OLFML3	olfactomedin-like 3	505318	-2.61	0.0000769
SDPR	serum deprivation response (phosphatidylserine binding protein)	532333	-2.57	0.0001364
RBM3	RNA binding motif (RNP1, RRM) protein 3	509771	-2.56	0.0000121
PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	282091	-2.43	0.0000121

LOC509972	similar to C-type lectin domain family 2, member d11	509972	-2.43	0.0000516
EGR1	early growth response 1	407125	-2.42	0.0002903
LOC512304	similar to ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	512304	-2.40	0.0000215
SNN	stannin	615361	-2.37	0.0000121
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	535379	-2.33	0.0000524
MGC127538	hypothetical protein MGC127538	767920	-2.31	0.0001172
LDOC1	leucine zipper, down-regulated in cancer 1	616591	-2.26	0.0000033
KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	281883	-2.21	0.0004442
LOC614047	hypothetical protein LOC614047	614047	-2.21	0.0000111
FADS2	fatty acid desaturase 2	521822	-2.20	0.0000454
FABP5	fatty acid binding protein 5 (psoriasis-associated)	281760	-2.15	0.0000097
WNT11	wingless-type MMTV integration site family, member 11	613288	-2.15	0.0000033
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	414732	-2.09	0.0001968
TXNIP	thioredoxin interacting protein	506790	-2.04	0.0001601
PGF	placental growth factor	280894	-2.02	0.0000090
LOC524694	similar to Paladin	524694	-2.01	0.0001839
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	280924	-2.01	0.0001739
MARCKS	myristoylated alanine-rich protein kinase C substrate	613548	-2.00	0.0000138
IL20RA	interleukin 20 receptor, alpha	509038	-1.93	0.0000378
SLITRK2	SLIT and NTRK-like family, member 2	540117	-1.92	0.0003735
ISG12(B)	similar to TLH29 protein precursor	617420	-1.88	0.0000381
LDB2	LIM domain binding 2	617976	-1.84	0.0000246
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	281002	-1.84	0.0002034
DHRS3	dehydrogenase/reductase (SDR family) member 3	281482	-1.80	0.0000314
CIRBP	cold inducible RNA binding protein	507120	-1.74	0.0001390
LOC539690	similar to Complement component C1q receptor precursor (Complement component 1 q subcomponent receptor 1) (C1qR) (C1qRp) (C1qR(p)) (C1q/MBL/SPA receptor) (Matrix-remodeling-associated protein 4) (CD93 antigen)	539690	-1.74	0.0002034
ICAM3	intercellular adhesion molecule 3	281840	-1.72	0.0001739
NTS	neurotensin	280881	-1.72	0.0017820

PSAT1	phosphoserine aminotransferase 1	533044	-1.70	0.0004026
ZNF608	zinc finger protein 608	509992	-1.70	0.0000744
COL15A1	collagen, type XV, alpha 1	100139730	-1.69	0.0019927
LRRC33	leucine rich repeat containing 33	510688	-1.68	0.0000523
LOC535166	similar to mKIAA1077 protein	535166	-1.66	0.0004890
PLAU	plasminogen activator, urokinase	281408	-1.63	0.0000571
FAM129A	family with sequence similarity 129, member A	614787	-1.63	0.0000121
BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	530147	-1.60	0.0000888
COL6A3	collagen, type VI, alpha 3	530657	-1.58	0.0042244
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	540357	-1.56	0.0000674
UPK1B	uroplakin 1B	282113	-1.56	0.0002940
RGL1	ral guanine nucleotide dissociation stimulator-like 1	522344	-1.55	0.0000151
LOC532409	similar to high-mobility group box 3	532409	-1.55	0.0008584
EPAS1	endothelial PAS domain protein 1	282711	-1.52	0.0001778
INSIG1	insulin induced gene 1	511899	-1.52	0.0012556
MGST3	microsomal glutathione S-transferase 3	507346	-1.51	0.0000372
SDC2	syndecan 2	615785	-1.51	0.0001365
CFH	complement factor H	280816	-1.51	0.0001508
SOCS2	suppressor of cytokine signaling 2	338437	-1.47	0.0026654
GSTT1	glutathione S-transferase theta 1	517724	-1.47	0.0000209
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	404164	-1.46	0.0000280
LOC535439	similar to Probable global transcription activator SNF2L1 (Nucleosome-remodeling factor subunit SNF2L) (ATP-dependent helicase SMARCA1) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1)	535439	-1.44	0.0001283
LGALS9	lectin, galactoside-binding, soluble, 9	510813	-1.44	0.0000975
VAMP5	vesicle-associated membrane protein 5 (myobrevin)	540406	-1.42	0.0000380
IDI1	isopentenyl-diphosphate delta isomerase 1	514293	-1.37	0.0008488
VEGFA	vascular endothelial growth factor A	281572	-1.37	0.0000825
ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	538583	-1.36	0.0002241
SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	507095	-1.35	0.0001132

LOC781004	hypothetical LOC781004	781004	-1.35	0.0000577
CAV1	caveolin 1, caveolae protein, 22kDa	281040	-1.34	0.0000852
NOV	nephroblastoma overexpressed	505727	-1.34	0.0003372
MMP11	matrix metallopeptidase 11 (stromelysin 3)	539109	-1.31	0.0000393
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	282223	-1.31	0.0004387
IL4R	interleukin 4 receptor	404154	-1.29	0.0000904
NEIL2	nei like 2 (E. coli)	444987	-1.29	0.0000289
SRL	sarcalumenin	513912	-1.29	0.0000511
SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	338050	-1.28	0.0003224
MAP2K6	mitogen-activated protein kinase kinase 6	286883	-1.26	0.0000930
PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	404169	-1.25	0.0000975
FDFT1	farnesyl-diphosphate farnesyltransferase 1	281767	-1.25	0.0000874
C1H21ORF63	chromosome 21 open reading frame 63 ortholog	516536	-1.24	0.0016137
NFIB	nuclear factor I/B	538474	-1.23	0.0001361
CNRIP1	cannabinoid receptor interacting protein 1	539715	-1.22	0.0000706
CPEB1	cytoplasmic polyadenylation element binding protein 1	514174	-1.22	0.0000925
IL7	interleukin 7	280827	-1.22	0.0005784
IPO11	importin 11	538236	-1.22	0.0001703
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	516209	-1.21	0.0001601
BMPER	BMP binding endothelial regulator	534101	-1.20	0.0003447
FASN	fatty acid synthase	281152	-1.20	0.0004872
KLF15	Kruppel-like factor 15	407241	-1.20	0.0000975
EHD3	EH-domain containing 3	510183	-1.19	0.0001021
ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	538427	-1.19	0.0001470
MARCKSL1	MARCKS-like 1	539555	-1.19	0.0001565
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	535136	-1.19	0.0000276
PRUNE2	prune homolog 2 (Drosophila)	518308	-1.18	0.0000393
PLXDC2	plexin domain containing 2	515731	-1.18	0.0001087
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	527528	-1.18	0.0040681
ZFP36L1	zinc finger protein 36, C3H type-like 1	614773	-1.18	0.0013203
GPR125	G protein-coupled receptor 125	541147	-1.18	0.0000388

MGST1	microsomal glutathione S-transferase 1	493719	-1.17	0.0018042
AFAP1L1	actin filament associated protein 1-like 1	510738	-1.17	0.0000542
ISG12(A)	similar to putative ISG12(a) protein	507138	-1.16	0.0006495
PIK3IP1	phosphoinositide-3-kinase interacting protein 1	512082	-1.16	0.0002068
UBA7	ubiquitin-like modifier activating enzyme 7	497204	-1.16	0.0003489
EIF4E3	eukaryotic translation initiation factor 4E family member 3	616906	-1.16	0.0010510
TNIK	TRAF2 and NCK interacting kinase	539627	-1.15	0.0012557
LMO2	LIM domain only 2 (rhombotin-like 1)	614876	-1.15	0.0005784
SSLP-1	secreted seminal vesicle Ly-6 protein 1	100125878	-1.15	0.0001949
PRCP	prolylcarboxypeptidase (angiotensinase C)	534927	-1.15	0.0017019
LOC100125763	neuronal protein 3.1	100125763	-1.14	0.0002034
FAR2	fatty acyl CoA reductase 2	534380	-1.14	0.0001104
CALCRL	calcitonin receptor-like	527140	-1.14	0.0036428
TCP11L2	t-complex 11 (mouse)-like 2	541012	-1.13	0.0004916
GAMT	guanidinoacetate N-methyltransferase	515270	-1.13	0.0000427
CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	404118	-1.12	0.0000702
MAOA	monoamine oxidase A	281293	-1.12	0.0000381
SPP1	secreted phosphoprotein 1	281499	-1.12	0.0004398
LOC540312	similar to Protein DDX26B	540312	-1.12	0.0005949
MGC128424	hypothetical protein MGC128424	767924	-1.12	0.0002387
LOC618444	hypothetical LOC618444	618444	-1.11	0.0004423
CADM4	cell adhesion molecule 4	523277	-1.10	0.0002518
NDRG2	NDRG family member 2	515063	-1.10	0.0003372
APOA1	apolipoprotein A-I	281631	-1.10	0.0002895
TSPYL4	TSPY-like 4	508104	-1.09	0.0001361
ECHDC2	enoyl Coenzyme A hydratase domain containing 2	513795	-1.09	0.0000744
PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	508045	-1.09	0.0000616
SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	523846	-1.09	0.0013050
SH3KBP1	SH3-domain kinase binding protein 1	510489	-1.09	0.0004764
SLCO2A1	solute carrier organic anion transporter family, member 2A1	282468	-1.08	0.0005892
LOC536909	similar to SNF related kinase	536909	-1.08	0.0001141
EXTL3	exostoses (multiple)-like 3	783970	-1.08	0.0001800

ZNF503	zinc finger protein 503	789846	-1.08	0.0002082
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	520056	-1.07	0.0001087
RELL1	RELT-like 1	768210	-1.07	0.0001174
MGC128008	hypothetical LOC510399	510399	-1.07	0.0002582
THBD	thrombomodulin	281529	-1.07	0.0001610
HMGA1	high mobility group AT-hook 1	618849	-1.07	0.0003056
SYTL2	synaptotagmin-like 2	614406	-1.07	0.0013559
NFIL3	nuclear factor, interleukin 3 regulated	506097	-1.06	0.0003372
AMIGO2	adhesion molecule with Ig-like domain 2	514273	-1.06	0.0001448
LOC511229	similar to mCG142710	511229	-1.05	0.0006046
RHOBTB1	Rho-related BTB domain containing 1	540513	-1.05	0.0001506
LOC515042	similar to leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1	515042	-1.05	0.0000571
N4BP2L1	NEDD4 binding protein 2-like 1	616069	-1.05	0.0013200
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	510972	-1.04	0.0018083
TPPP3	tubulin polymerization-promoting protein family member 3	614988	-1.04	0.0001954
PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	539466	-1.04	0.0017820
SLC20A2	solute carrier family 20 (phosphate transporter), member 2	518905	-1.04	0.0002953
ABLIM1	actin binding LIM protein 1	504968	-1.04	0.0000717
TRIB2	tribbles homolog 2 (Drosophila)	352960	-1.03	0.0018458
IFNAR2	interferon (alpha, beta and omega) receptor 2	282258	-1.03	0.0008470
OSBPL11	oxysterol binding protein-like 11	538576	-1.02	0.0003414
JAM2	junctional adhesion molecule 2	538846	-1.02	0.0051204
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	507215	-1.02	0.0005997
TCEAL4	transcription elongation factor A (SII)-like 4	513987	-1.02	0.0001558
CLEC14A	C-type lectin domain family 14, member A	509367	-1.02	0.0004423
COMMD1	copper metabolism (Murr1) domain containing 1	534683	-1.01	0.0001141
AGFG2	ArfGAP with FG repeats 2	510361	-1.01	0.0006903
RAMP3	receptor (G protein-coupled) activity modifying protein 3	613547	-1.01	0.0001919
SQLE	squalene epoxidase	526535	-1.00	0.0019354
MIPEP	mitochondrial intermediate peptidase	517531	-1.00	0.0001210
GRAMD1A	GRAM domain containing 1A	507027	-1.00	0.0003626
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	615342	-1.00	0.0003564
PDIA5	protein disulfide isomerase family A, member 5	511603	-1.00	0.0002353

***** Significantly enriched or depleted genes were identified between ECs exposed to normal WSS (2 Pa) and no flow static cultures (0 Pa) by a linear model approach employing an empirical Bayes method at 1% FDR and more than two-fold change between groups. The ratio of the $\log_2$ fold change along with the adjusted FDR p-value are indicated.

Table S3: Differentially expressed genes between high WSS and normal WSS treated cells*

Symbol	Description	GeneID	Ratio	Adjusted *p* value
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	512171	3.87	0.0000108
SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	521920	3.11	0.0000476
AQP1	aquaporin 1 (Colton blood group)	282653	3.00	0.0000443
AFF1	AF4/FMR2 family, member 1	781149	2.90	0.0000108
PTPRR	protein tyrosine phosphatase, receptor type, R	536337	2.64	0.0000051
IL1F6	interleukin 1 family, member 6 (epsilon)	523429	2.17	0.0003745
AIF1L	allograft inflammatory factor 1-like	617493	2.16	0.0000108
NPPC	natriuretic peptide precursor C	281356	2.06	0.0000307
PI3	peptidase inhibitor 3, skin-derived (SKALP)	407165	2.04	0.0003830
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	615535	1.90	0.0000320
MALL	mal, T-cell differentiation protein-like	512289	1.78	0.0000182
PROCR	protein C receptor, endothelial (EPCR)	282005	1.75	0.0000163
MTMR11	myotubularin related protein 11	506122	1.72	0.0000182
PLAT	plasminogen activator, tissue	281407	1.67	0.0000108
SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	531606	1.67	0.0000330
AKAP12	A kinase (PRKA) anchor protein 12	513774	1.67	0.0001672
PTPRB	protein tyrosine phosphatase, receptor type, B	505696	1.54	0.0000283
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	540722	1.53	0.0000476
SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	768005	1.53	0.0000422
NQO1	NAD(P)H dehydrogenase, quinone 1	519632	1.51	0.0000296
LOC511659	similar to phospholipase C, gamma 2	511659	1.49	0.0002466
ANO1	anoctamin 1, calcium activated chloride channel	532126	1.43	0.0010611
HYAL2	hyaluronoglucosaminidase 2	281838	1.40	0.0000300
LOC538402	similar to Protein FAM81A	538402	1.39	0.0004365
GFPT2	glutamine-fructose-6-phosphate transaminase 2	530101	1.38	0.0001799
BHLHB2	basic helix-loop-helix domain containing, class B, 2	506945	1.34	0.0002369
RCAN3	RCAN family member 3	506601	1.33	0.0013940
LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	404179	1.33	0.0017793
NPHP1	nephronophthisis 1 (juvenile)	505421	1.32	0.0000614

MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	539519	1.32	0.0041838
MYOZ2	myozenin 2	540487	1.30	0.0000300
TIMP3	TIMP metallopeptidase inhibitor 3	282094	1.30	0.0000633
SLC39A8	solute carrier family 39 (zinc transporter), member 8	508193	1.28	0.0005603
LOC520939	similar to Krueppel-like factor 2 (Lung krueppel-like factor)	520939	1.26	0.0000640
RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	511190	1.26	0.0001539
PODXL	podocalyxin-like	616366	1.26	0.0003699
LOC537017	similar to cytidine monophosphate-N-acetylneuraminic acid hydroxylase	537017	1.22	0.0006263
LOC529423	similar to family with sequence similarity 40, member B	529423	1.21	0.0031118
TMEM131	transmembrane protein 131	540861	1.20	0.0001191
DCK	deoxycytidine kinase	530642	1.18	0.0001663
SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	513825	1.16	0.0001542
HSPA12B	heat shock 70kD protein 12B	515590	1.15	0.0001715
HMCN1	hemicentin 1	521326	1.14	0.0085866
RGS2	regulator of G-protein signaling 2, 24kDa	513055	1.14	0.0001909
CLIC2	chloride intracellular channel 2	532777	1.13	0.0000556
PLAUR	plasminogen activator, urokinase receptor	281983	1.13	0.0000606
DPYSL5	dihydropyrimidinase-like 5	100126171	1.13	0.0003949
EID3	EP300 interacting inhibitor of differentiation 3	507232	1.12	0.0007921
FAM134B	family with sequence similarity 134, member B	540068	1.12	0.0001361
MRAS	muscle RAS oncogene homolog	540803	1.12	0.0000661
FXYD3	FXYD domain containing ion transport regulator 3	780807	1.10	0.0005319
ARF4	ADP-ribosylation factor 4	282601	1.10	0.0000333
PLAU	plasminogen activator, urokinase	281408	1.08	0.0002676
ZDHHC23	zinc finger, DHHC-type containing 23	512177	1.06	0.0011463
LOC788353	similar to Uncharacterized protein KIAA1522 homolog	788353	1.05	0.0002121
KLF4	Kruppel-like factor 4 (gut)	520842	1.04	0.0015850
PLN	phospholamban	100125240	1.04	0.0007232
PMP22	peripheral myelin protein 22	534497	1.03	0.0002466
JUP	junction plakoglobin	445543	1.03	0.0002106
ARHGEF15	Rho guanine nucleotide exchange factor (GEF) 15	512021	1.02	0.0001417

LOC512304	similar to ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	512304	1.02	0.0008623
HSPA12A	heat shock 70kDa protein 12A	540050	1.02	0.0005250
ORAI1	ORAI calcium release-activated calcium modulator 1	517688	1.02	0.0002447
SIRPA	signal-regulatory protein alpha	327666	1.01	0.0001140
CLEC14A	C-type lectin domain family 14, member A	509367	1.01	0.0003043
INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	534793	1.01	0.0028228
DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing 2	507590	1.01	0.0009296
HOPX	HOP homeobox	281270	1.00	0.0024787
CXCL5	chemokine (C-X-C motif) ligand 5	281735	-3.03	0.0015045
ASCL1	achaete-scute complex homolog 1 (Drosophila)	540473	-2.83	0.0004663
TTR	transthyretin	280948	-2.69	0.0000444
SCARA5	scavenger receptor class A, member 5 (putative)	516087	-2.66	0.0000614
MGC127538	hypothetical protein MGC127538	767920	-2.45	0.0000633
CSF2	colony stimulating factor 2 (granulocyte-macrophage)	281095	-2.05	0.0000633
CXCL2	chemokine (C-X-C motif) ligand 2	613667	-2.01	0.0007065
RSF1	remodeling and spacing factor 1	541248	-1.98	0.0001638
ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	511220	-1.90	0.0007677
PRUNE2	prune homolog 2 (Drosophila)	518308	-1.88	0.0000067
THBS1	thrombospondin 1	281530	-1.74	0.0005344
FABP4	fatty acid binding protein 4, adipocyte	281759	-1.69	0.0006002
SDC2	syndecan 2	615785	-1.68	0.0000614
ADM	adrenomedullin	280713	-1.61	0.0001724
GHR	growth hormone receptor	280805	-1.60	0.0001062
RPRM	reprimo, TP53 dependent G2 arrest mediator candidate	614739	-1.60	0.0005265
BMP4	bone morphogenetic protein 4	407216	-1.59	0.0000476
COL6A3	collagen, type VI, alpha 3	530657	-1.55	0.0032122
LOC538778	similar to dapper 1	538778	-1.53	0.0001095
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	505824	-1.53	0.0001786
SST	somatostatin	280932	-1.50	0.0008444
CCL26	chemokine (C-C motif) ligand 26	508387	-1.47	0.0004624
CXCL2	chemokine (C-X-C motif) ligand 2	281212	-1.46	0.0007382
LOC539374	similar to Family with sequence similarity 43, member A	539374	-1.42	0.0000243

IL8	interleukin 8	280828	-1.40	0.0003217
SRPX2	sushi-repeat-containing protein, X-linked 2	514742	-1.40	0.0014159
COL12A1	collagen, type XII, alpha 1	359712	-1.39	0.0000508
CLCA3P	chloride channel accessory 3 (pseudogene)	281694	-1.38	0.0001262
FABP5	fatty acid binding protein 5 (psoriasis-associated)	281760	-1.33	0.0000559
PAH	phenylalanine hydroxylase	510583	-1.30	0.0014388
LOC783538	similar to AT rich interactive domain 5B (MRF1-like)	783538	-1.28	0.0000680
DHRS3	dehydrogenase/reductase (SDR family) member 3	281482	-1.28	0.0001140
FBXO32	F-box protein 32	513776	-1.27	0.0000188
MYLIP	myosin regulatory light chain interacting protein	541070	-1.26	0.0004078
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	529115	-1.24	0.0000320
WISP2	WNT1 inducible signaling pathway protein 2	534658	-1.23	0.0000673
RBM3	RNA binding motif (RNP1, RRM) protein 3	509771	-1.22	0.0019053
RNF183	ring finger protein 183	539200	-1.22	0.0000919
THUMPD3	THUMP domain containing 3	508940	-1.20	0.0000735
ZRANB2	zinc finger, RAN-binding domain containing 2	508905	-1.20	0.0001140
TSC1	tuberous sclerosis 1	533440	-1.17	0.0005250
SEPP1	selenoprotein P, plasma, 1	282066	-1.16	0.0003388
RND3	Rho family GTPase 3	540224	-1.13	0.0000640
CCRL1	chemokine (C-C motif) receptor-like 1	281672	-1.13	0.0038837
FAT1	FAT tumor suppressor homolog 1 (Drosophila)	508251	-1.12	0.0001525
KBTBD6	kelch repeat and BTB (POZ) domain containing 6	538461	-1.12	0.0024534
TAGLN	transgelin	513463	-1.12	0.0006028
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	282713	-1.12	0.0009440
PDLIM4	PDZ and LIM domain 4	515410	-1.12	0.0000865
NRBP2	nuclear receptor binding protein 2	504664	-1.10	0.0002676
AXL	AXL receptor tyrosine kinase	516598	-1.07	0.0004190
LOC534839	similar to high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha; putative GAP protein alpha	534839	-1.06	0.0002676
LOC781795	similar to hCG1779312	781795	-1.06	0.0000640
NQO2	NAD(P)H dehydrogenase, quinone 2	508566	-1.04	0.0003217

CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	521378	-1.04	0.0015850
RNPC3	RNA-binding region (RNP1, RRM) containing 3	768060	-1.03	0.0001542
CYB561	cytochrome b-561	317663	-1.02	0.0025320
CXCR4	chemokine (C-X-C motif) receptor 4	281736	-1.02	0.0088926
NRG1	neuregulin 1	281361	-1.01	0.0002328
CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	525906	-1.01	0.0018281
PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	100124505	-1.00	0.0004658
FRMD6	FERM domain containing 6	530910	-1.00	0.0007921
SLC17A9	solute carrier family 17, member 9	518062	-1.00	0.0003699
MXRA5	matrix-remodelling associated 5	786844	-1.00	0.0019897

*****Significantly enriched or depleted genes were identified between ECs exposed to high WSS (10 Pa) and normal WSS (2 Pa) by a linear model approach employing an empirical Bayes method at 1% FDR and more than two-fold change between groups. The ratio of the $\log_2$ fold change along with the adjusted FDR p-value are indicated.

Table S4. Genes regulated in opposite directions when high WSS and static control treated cells are compared to normal WSS treated cells

			Normal WSS vs. Static Control		High WSS vs. Normal WSS	
Symbol	Description	Gene ID	Ratio	Adjusted *p* value	Ratio	Adjusted *p* value
FBXO32	F-box protein 32	513776	1.45	0.0000121	-1.27	0.0000188
CYB561	cytochrome b-561	317663	3.24	0.0000151	-1.38	0.0001262
IL8	interleukin 8	280828	2.62	0.0000251	-1.12	0.0001525
FAT1	FAT tumor suppressor homolog 1 (Drosophila)	508251	1.86	0.0000393	-1.04	0.0003217
TAGLN	transgelin	513463	2.02	0.0000556	-1.40	0.0003217
AXL	AXL receptor tyrosine kinase	516598	1.59	0.0000930	-1.07	0.0004190
SRPX2	sushi-repeat-containing protein, X-linked 2	514742	2.48	0.0001307	-1.60	0.0005265
CLCA3P	chloride channel accessory 3 (pseudogene)	281694	1.42	0.0001470	-1.74	0.0005344
NQO2	NAD(P)H dehydrogenase, quinone 2	508566	1.15	0.0002903	-1.12	0.0006028
CXCL2	chemokine (C-X-C motif) ligand 2	281212	1.69	0.0005255	-1.46	0.0007382
RPRM	reprimo, TP53 dependent G2 arrest mediator candidate	614739	1.66	0.0005622	-1.12	0.0009440
THBS1	thrombospondin 1	281530	1.09	0.0006152	-1.40	0.0014159
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	282713	1.35	0.0073629	-1.02	0.0025320
PLAU	plasminogen activator, urokinase	281408	-1.63	0.0000571	1.08	0.0002676
LOC512304	similar to ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	512304	-2.40	0.0000215	1.02	0.0008623
CLEC14A	C-type lectin domain family 14, member A	509367	-1.02	0.0004423	1.01	0.0003043

*Significantly enriched or depleted genes were identified by Venn Analysis between ECs exposed to high WSS (10 Pa) and normal WSS (2 Pa) compared to those genes enriched or depleted between normal WSS (2 Pa) and no flow static cultures (0 Pa). Genes overlapping between but having opposite directions of regulation are listed with their ratio of the $\log_2$ fold change and adjusted FDR p-value.

Table S5. Complete list of significantly enriched or depleted gene categories between high WSS and normal WSS treated cells determined by GO-based GSEA*

Gene Ontology Term	Ratio	Adjusted *p* value
GO:0005694 chromosome	9.98	0.011
GO:0022403 cell cycle phase	9.70	0.012
GO:0000279 M phase	9.70	0.012
GO:0004222 metalloendopeptidase activity	9.24	0.009
GO:0044427 chromosomal part	9.18	0.009
GO:0000278 mitotic cell cycle	8.53	0.012
GO:0015630 microtubule cytoskeleton	8.25	0.043
GO:0000087 M phase of mitotic cell cycle	8.24	0.011
GO:0007067 mitosis	8.14	0.011
GO:0031404 chloride ion binding	7.89	0.011
GO:0043168 anion binding	7.89	0.011
GO:0051301 cell division	7.18	0.011
GO:0018958 phenol metabolic process	7.15	0.011
GO:0008237 metallopeptidase activity	7.11	0.009
GO:0000775 chromosome, centromeric region	6.92	0.019
GO:0000793 condensed chromosome	6.60	0.030
GO:0014704 intercalated disc	6.50	0.009
GO:0005254 chloride channel activity	6.36	0.011
GO:0006066 alcohol metabolic process	6.18	0.013
GO:0005819 spindle	6.09	0.012
GO:0001664 G-protein-coupled receptor binding	-10.86	0.043
GO:0006817 phosphate transport	-8.64	0.013
GO:0007389 pattern specification process	-8.23	0.011
GO:0001764 neuron migration	-8.06	0.025
GO:0005179 hormone activity	-7.84	0.012
GO:0007507 heart development	-7.58	0.011
GO:0002274 myeloid leukocyte activation	-7.42	0.009
GO:0007420 brain development	-7.15	0.011
GO:0001655 urogenital system development	-6.94	0.011

GO:0030900 forebrain development	-6.77	0.015
GO:0001822 kidney development	-6.63	0.011
GO:0002573 myeloid leukocyte differentiation	-6.56	0.011
GO:0031983 vesicle lumen	-6.48	0.023
GO:0060205 cytoplasmic membrane-bounded vesicle lumen	-6.48	0.023
GO:0042446 hormone biosynthetic process	-6.46	0.009
GO:0051046 regulation of secretion	-6.46	0.015
GO:0031093 platelet alpha granule lumen	-6.12	0.031
GO:0006941 striated muscle contraction	-6.05	0.015

***** Gene set enrichment analysis (GSEA) was performed using parametric GSEA to the gene ontology (GO) database. A linear model approach employing an empirical Bayes method was used to generate a moderated t-test statistic and FDR corrected p-values associated with specific gene set enrichment were calculated. GO categories were identified at a 5% FDR and more than six- $\log_2$ fold change between high WSS and normal WSS profiles.

Table S6. Complete list of significantly enriched or depleted gene categories between high WSS and normal WSS treated cells determined by KEGG-based GSEA*

KEGG Pathway	KEGG ID	Ratio	Adjusted *p* value
Cell cycle	04110	4.74	0.021
MAPK signaling pathway	04010	4.39	0.021
Glutamate metabolism	00251	4.39	0.034
Biosynthesis of steroids	00100	4.26	0.037
Long-term potentiation	04720	4.08	0.038
DNA replication	03030	3.21	0.030
Nicotinate and nicotinamide metabolism	00760	2.91	0.030
B cell receptor signaling pathway	04662	2.88	0.050
Pentose phosphate pathway	00030	2.68	0.041
Calcium signaling pathway	04020	2.66	0.038
Phosphatidylinositol signaling system	04070	2.56	0.039
Pyrimidine metabolism	00240	2.47	0.038
Pathogenic Escherichia coli infection - EHEC	05130	2.35	0.041
Pathogenic Escherichia coli infection - EPEC	05131	2.35	0.041
Ether lipid metabolism	00565	2.26	0.041
Cytokine-cytokine receptor interaction	04060	-11.50	0.037
Jak-STAT signaling pathway	04630	-6.93	0.023
TGF-beta signaling pathway	04350	-5.07	0.021
Ribosome	03010	-3.41	0.034
Bladder cancer	05219	-2.94	0.041

*****Gene set enrichment analysis (GSEA) was performed using parametric GSEA to the KEGG pathway database. A linear model approach employing an empirical Bayes method was used to generate a moderated t-test statistic and FDR corrected p-values associated with specific gene set enrichment were calculated. Categories were identified at a 5% FDR and are represented as the $\log_2$ fold change between high WSS and normal WSS profiles