Supplemental Data

Supplemental Table 1. Genes differentially regulated by Ad-KLF2 vs. Ad-GFP infected EC. Three independent genome-wide transcriptional profiling experiments were performed, and significantly regulated genes were identified.

Color-coding scheme:	Up, $p < 1e-15$ Up, $1e-15 < p < 5e-10$ Up, $5e-10 < p < 5e-5$ Up, $5e-5 < p < .05$ Down, $p < 1e-15$ Down, $1e-15 < p < 5e-10$ Down, $5e-10 < p < 5e-5$ Down, $5e-5 < p < .05$ As determined by Zpool $p < .05$ as determined by Iterative Standard Deviation Algorithm as described in Supplemental Methods

Ratio	RefSeq Number	Gene Name
1,058.52		KRT13 - keratin 13
565.72	NM_007117.1	TRH - thyrotropin-releasing hormone
244.04	NM_001878.2	CRABP2 - cellular retinoic acid binding protein 2
118.90	NM_013279.1	C11orf9 - chromosome 11 open reading frame 9
109.68	NM_000517.3	HBA2;HBA1 - hemoglobin, alpha 2;hemoglobin, alpha 1
102.04	NM_001823.3	CKB - creatine kinase, brain
96.23		LYNX1
95.53	NM_002514.2	NOV - nephroblastoma overexpressed gene
75.82		CeleraFN113625
74.73	NM_000954.5	FLJ45224;PTGDS - FLJ45224 protein;prostaglandin D2 synthase 21kDa (brain)
68.53	NM_205545.1	UNQ430 - RGTR430
66.89	NM_005980.2	S100P - S100 calcium binding protein P
64.39	NM_153370.1	PI16 - protease inhibitor 16
58.24	NM_031918.1	KLF16 - Kruppel-like factor 16
46.45	NM_024409.1	NPPC - natriuretic peptide precursor C
45.48	NM_032470.2	TNXB - tenascin XB
34.92	NM_001264.2	CDSN - corneodesmosin
33.86	NM_017671.3	C20orf42 - chromosome 20 open reading frame 42
33.76	NM_024829.3	FLJ22662 - hypothetical protein FLJ22662
32.10	NM_003283.3	TNNT1 - troponin T1, skeletal, slow
31.45	AK095686.1	LOC388888 (LOC388888), mRNA according to UniGene - potential CONFLICT - LOC388888 (na) according to LocusLink.
28.73		PP2135 protein (PP2135)
28.20	NM_001803.1	CDW52 - CDW52 antigen (CAMPATH-1 antigen)
28.06	NM_031476.1	DKFZP434B044 - hypothetical protein DKFZp434B044
27.09	NM_002178.1	IGFBP6 - insulin-like growth factor binding protein 6
25.26	M32011.1	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2) (NCF2) neutrophil cytosolic factor 2
24.62	NM_005630.1	SLCO2A1 - solute carrier organic anion transporter family, member 2A1
24.56	NM_005978.3	S100A2 - S100 calcium binding protein A2
22.46	NM_000422.1	KRT17 - keratin 17
20.36	NM_198946.2	LCN10;LCN6 - lipocalin 10;lipocalin 6
19.27	NM_003278.1	TNA - tetranectin (plasminogen binding protein)
18.22	NM_019850.1	NGEF - neuronal guanine nucleotide exchange factor
16.74	NM_002776.3	KLK10 - kallikrein 10
16.69	NM_004669.2	CLIC3 - chloride intracellular channel 3
16.47	NM_014368.2	LHX6 - LIM homeobox 6
16.34	NM_002343.1	LTF - lactotransferrin
15.85	NM_002960.1	S100A3 - S100 calcium binding protein A3
15.01	NM_013279.1	C11orf9 - chromosome 11 open reading frame 9

14.74	BC046190.1	MRNA; cDNA DKFZp686A1124 (from clone DKFZp686A1124)
14.42	NM_014392.2	D4S234E - DNA segment on chromosome 4 (unique) 234 expressed sequence
14.41	NM_018414.2	SIAT7A - sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) A
14.14	NM_003665.2	FCN3 - ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)
13.49	AK123560.1	H19, imprinted maternally expressed untranslated mRNA (H19)
13.45	NM_000954.5	FLJ45224;PTGDS - FLJ45224 protein;prostaglandin D2 synthase 21kDa (brain)
13.45	NM_145899.1	HMGA1 - high mobility group AT-hook 1
13.29		Transcribed sequence with weak similarity to protein sp:P39191 (H.sapiens) ALU4_HUMAN Alu subfamily SB2 sequence contamination warning entry
12.76	NM_016816.1	OAS1 - 2',5'-oligoadenylate synthetase 1, 40/46kDa
11.88	NM_014715.2	RICS - Rho GTPase-activating protein
11.75	NM_198966.1	PTHLH - parathyroid hormone-like hormone
11.24	NM_019554.1	S100A4 - S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
11.20	NM_023004.5	RTN4R - reticulon 4 receptor
11.15	NM_003862.1	FGF18 - fibroblast growth factor 18
10.99	AJ426371.1_CDS_1	Partial mRNA for immunoglobulin lambda chain variable region (IGVL gene), sample GN20
10.92	NM_014070.1	C6orf15 - chromosome 6 open reading frame 15
10.57	NM_053044.2	HTRA3 - serine protease HTRA3
9.79	NM_007250.2	KLF8 - Kruppel-like factor 8
9.63	NM_182511.2	CBLN2 - cerebellin 2 precursor
9.55	NM_007177.1	TU3A - TU3A protein
9.32	NM_006477.2	RRP22 - RAS-related on chromosome 22
9.30	NM_017565.2	FAM20A - family with sequence similarity 20, member A
9.18	AK056490.1	Transcribed sequences (CeleraFN227268)
8.96	NM_033256.1	PPP1R14A - protein phosphatase 1, regulatory (inhibitor) subunit 14A
8.95	BC046190.1	ovostatin 2 (OVOS2)
8.89	NM_022965.1	FGFR3 - fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
8.75	NM_003670.1	BHLHB2 - basic helix-loop-helix domain containing, class B, 2
8.61	NM_001998.1	FBLN2 - fibulin 2
8.28	NM_000104.2	CYP1B1 - cytochrome P450, family 1, subfamily B, polypeptide 1
8.00	AF193048.1	PP2135 protein (PP2135)
7.93		CeleraFN216738
7.77	NM_000603.3	NOS3 - nitric oxide synthase 3 (endothelial cell)
7.62	NM_024979.2	MCF2L - MCF.2 cell line derived transforming sequence-like
7.39		argininosuccinate synthetase (ASS)
7.31		argininosuccinate synthetase (ASS)
7.30		argininosuccinate synthetase (ASS)
7.29	AK026560.1	KIAA0830 protein (KIAA0830)
7.26	NM_022772.2	EPS8L2 - EPS8-like 2
7.25		argininosuccinate synthetase (ASS)
7.07	BC039117.1	ovostatin 2 (OVOS2)
7.00	NM_033429.1	MGC4809 - serologically defined breast cancer antigen NY-BR-20
7.00		argininosuccinate synthetase (ASS)
7.00	NM_024786.1	ZDHHC11 - zinc finger, DHHC domain containing 11
6.86	NM_022664.1	ECM1 - extracellular matrix protein 1
6.82		Similar to Argininosuccinate synthase (Citrulline--aspartate ligase) (LOC402687), mRNA according to UniGene - potential CONFLICT - similar to Argininosuccinate synthase (Citrulline--aspartate ligase) (na) according to LocusLink.
6.81	NM_004695.2	SLC16A5 - solute carrier family 16 (monocarboxylic acid transporters), member 5
6.74	NM_006517.1	SLC16A2 - solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transporter)
6.34	NM_178557.2	FLJ37478 - hypothetical protein FLJ37478
6.32	NM_003773.2	HYAL2 - hyaluronoglucosaminidase 2
6.32	NM_023946.1	LYNX1 - Ly-6 neurotoxin-like protein 1

6.30	NM_000050.2	ASS - argininosuccinate synthetase
6.14	NM_004910.1	PITPNM1 - phosphatidylinositol transfer protein, membrane-associated 1
6.11	AB033063.2	HEG homolog (HEG)
6.08	NM_198391.1	FLRT3 - fibronectin leucine rich transmembrane protein 3
6.02	NM_004527.2	MEOX1 - mesenchyme homeo box 1
5.95		CeleraFN104748
5.91	NM_003965.3	CCRL2 - chemokine (C-C motif) receptor-like 2
5.90	AF022080.1	MRAS - muscle RAS oncogene homolog
5.85	NM_177457.1	LYNX1 - Ly-6 neurotoxin-like protein 1
5.73	NM_022664.1	ECM1 - extracellular matrix protein 1
5.72	NM_018421.1	TBC1D2 - TBC1 domain family, member 2
5.66	NM_015481.1	ZNF385 - zinc finger protein 385
5.65	NM_006291.2	TNFAIP2 - tumor necrosis factor, alpha-induced protein 2
5.55	NM_032717.3	MGC11324 - hypothetical protein MGC11324
5.52	NM_000962.2	PTGS1 - prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
5.43	NM_003155.1	STC1 - stanniocalcin 1
5.42	NM_002462.2	MX1 - myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
5.40		keratin 18 (KRT18)
5.39	AB033062.2	kinesin family member 26A (KIF26A)
5.38	NM_145637.1	APOL2 - apolipoprotein L, 2
5.33	NM_017842.1	FLJ20489 - hypothetical protein FLJ20489
5.32	NM_053032.2	MYLK - myosin, light polypeptide kinase
5.25	NM_018110.2	DOK4 - docking protein 4
5.20	NM_004585.2	RARRES3 - retinoic acid receptor responder (tazarotene induced) 3
5.19	NM_052854.1	CREB3L1 - cAMP responsive element binding protein 3-like 1
5.18		protein tyrosine phosphatase type IVA, member 3 (PTP4A3) protein tyrosine phosphatase type IVA, member 3 isoform 1
5.17	NM_002872.3	RAC2 - ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
5.06	NM_003456.1	ZNF205 - zinc finger protein 205
5.05		CeleraFN230454
5.04		CeleraFN165816
5.03		adenylate kinase 2 (AK2) adenylate kinase 2 isoform a
5.02	NM_005358.3	LMO7 - LIM domain only 7
5.01	NM_199054.1	MKNK2 - MAP kinase-interacting serine/threonine kinase 2
4.99		keratin 18 (KRT18)
4.98	NM_014725.2	STARD8 - START domain containing 8
4.96	Z84476.7_CDS_3	keratin 18 (KRT18)
4.94	NM_033520.1	C19orf33 - chromosome 19 open reading frame 33
4.94	NM_003661.2	APOL1 - apolipoprotein L, 1
4.94		CeleraFN162018
4.94		CeleraFN230618
4.93	NM_000591.1	CD14 - CD14 antigen
4.91		keratin 18 (KRT18)
4.87	NM_000224.2	KRT18 - keratin 18
4.86		CeleraFN232195
4.83		CeleraFN179564
4.82		CeleraFN184997
4.82		CeleraFN188718
4.82	NM_019858.1	GRCA - likely ortholog of mouse gene rich cluster, A gene
4.78		keratin 18 (KRT18)
4.77		CeleraFN236684
4.76		CeleraFN201278
4.75		CeleraFN182740
4.75	NM_006829.2	C10orf116 - chromosome 10 open reading frame 116
4.74	AL158175.7_CDS_1	keratin 18 (KRT18)
4.74	NM_004390.2	CTSH - cathepsin H
4.73		keratin 18 (KRT18)

4.73	NM_173465.2	COL23A1 - collagen, type XXIII, alpha 1
4.72	NM_002999.2	SDC4 - syndecan 4 (amphiglycan, ryudocan)
4.70		CeleraFN112215
4.69	NM_001848.1	COL6A1 - collagen, type VI, alpha 1
4.62	AL354915.5_CDS_2	Transcribed sequence with moderate similarity to protein sp:P05783 (H.sapiens) K1CR_HUMAN Keratin, type I cytoskeletal 18
4.55	NM_006340.1	BAIAP2 - BAI1-associated protein 2
4.53	NM_022124.2	CDH23 - cadherin-like 23
4.53		keratin 18 (KRT18)
4.51	NM_006278.1	SIAT4C - sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase)
4.51	NM_000213.2	ITGB4 - integrin, beta 4
4.50	NM_025214.1	SE57-1 - CTCL tumor antigen se57-1
4.45	NM_054033.1	FKBP1B - FK506 binding protein 1B, 12.6 kDa
4.44		CeleraFN228935
4.43	NM_004419.2	DUSP5 - dual specificity phosphatase 5
4.43	NM_199054.1	MKNK2 - MAP kinase-interacting serine/threonine kinase 2
4.43	NM_003741.2	CHRD - chordin
4.41		CeleraFN141172
4.38	AL022333.1_CDS_1	CeleraFN228862
4.33	NM_032369.1	MGC15619 - hypothetical protein MGC15619
4.26	NM_005099.3	ADAMTS4 - a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4
4.26	NM_014068.1	PSORS1C1 - psoriasis susceptibility 1 candidate 1
4.23		CeleraFN231137
4.20	NM_001425.1	EMP3 - epithelial membrane protein 3
4.10	BX537444.1	ATPase, Ca++ transporting, plasma membrane 4 (ATP2B4) plasma membrane calcium ATPase 4 isoform 4a
4.10	NM_198920.1	C6orf157 - chromosome 6 open reading frame 157
4.09	NM_033342.2	TRIM7 - tripartite motif-containing 7
4.08	NM_152494.1	FLJ32785;ADAM15 - hypothetical protein FLJ32785;a disintegrin and metalloproteinase domain 15 (metargidin)
4.07	NM_004252.1	SLC9A3R1 - solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1
4.00	NM_002201.4	ISG20 - interferon stimulated gene 20kDa
3.98	BC065221.1	hypothetical protein LOC124976 (LOC124976)
3.96	NM_003254.1	TIMP1 - tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
3.95	NM_004265.2	FADS2 - fatty acid desaturase 2
3.95	NM_139345.1	BIN1 - bridging integrator 1
3.92	NM_020467.2	LOC57228 - hypothetical protein from clone 643
3.91	NM_002135.3	NR4A1 - nuclear receptor subfamily 4, group A, member 1
3.91	NM_014279.2	OLFM1 - olfactomedin 1
3.90	NM_153321.1	PMP22 - peripheral myelin protein 22
3.89	NM_003060.2	SLC22A5 - solute carrier family 22 (organic cation transporter), member 5
3.87	NM_031426.1	C9orf58 - chromosome 9 open reading frame 58
3.83	NM_031430.1	RILP - Rab interacting lysosomal protein
3.83	NM_031946.3	CENTG3 - centaurin, gamma 3
3.82		argininosuccinate synthetase (ASS)
3.78	NM_018478.1	C20orf35 - chromosome 20 open reading frame 35
3.78	NM_019034.2	RHOF - ras homolog gene family, member F (in filopodia)
3.76	NM_002430.1	MN1 - meningioma (disrupted in balanced translocation) 1
3.74	NM_000201.1	ICAM1 - intercellular adhesion molecule 1 (CD54), human rhinovirus receptor
3.70	BX161387.1	fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8) fucosyltransferase 8 isoform a
3.69	NM_001505.1	GPR30 - G protein-coupled receptor 30
3.68	BC069216.1	LOC388610 (LOC388610), mRNA according to UniGene - potential CONFLICT - LOC388610 (na) according to LocusLink.
3.66	NM_020914.1	chromosome 17 open reading frame 27 (C17orf27)
3.65	NM_004429.3	EFNB1 - ephrin-B1

3.61		CeleraFN228381
3.60		CeleraFN230177
3.54	NM_139177.2	SLC39A11 - solute carrier family 39 (metal ion transporter), member 11
3.52	AK125329.1	FLJ43339 protein (FLJ43339)
3.51	U16811.1	BAK1 - BCL2-antagonist/killer 1
3.50	NM_148954.1	PSMB9 - proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)
3.50	NM_016428.2	ABI3 - ABI gene family, member 3
3.48	BC066348.1	placenta-specific 9 (PLAC9)
3.47	NM_000612.2	IGF2 - insulin-like growth factor 2 (somatomedin A)
3.46	NM_015516.2	E2IG4 - hypothetical protein, estradiol-induced
3.46	NM_030786.1	SYNCOILIN - intermediate filament protein syncoilin
3.44	NM_018478.1	C20orf35 - chromosome 20 open reading frame 35
3.41	NM_001975.2	ENO2 - enolase 2 (gamma, neuronal)
3.39	NM_003087.1	SNCG - synuclein, gamma (breast cancer-specific protein 1)
3.38	NM_023038.2	ADAM19 - a disintegrin and metalloproteinase domain 19 (meltrin beta)
3.37	NM_173608.1	CRIP1;C14orf80 - cysteine-rich protein 1 (intestinal);chromosome 14 open reading frame 80
3.37	NM_006730.1	DNASE1L1 - deoxyribonuclease I-like 1
3.33	NM_170697.1	ALDH1A2 - aldehyde dehydrogenase 1 family, member A2
3.32	NM_005655.1	TIEG - TGFB inducible early growth response
3.32	NM_032840.1	FLJ14800 - hypothetical protein FLJ14800
3.32	NM_005258.2	GCHFR - GTP cyclohydrolase I feedback regulator
3.31		NS5ATP13TP2 - NS5ATP13TP2 protein
3.30	NM_080625.2	C20orf160 - chromosome 20 open reading frame 160
3.29	AK025804.1	chromosome 9 open reading frame 88 (C9orf88)
3.29	NM_002599.1	PDE2A - phosphodiesterase 2A, cGMP-stimulated
3.29	NM_152832.1	SSSCA1;MTVR1 - Mouse Mammary Turmor Virus Receptor homolog 1;Sjogren's syndrome/scleroderma autoantigen 1
3.28	NM_001114.2	ADCY7 - adenylate cyclase 7
3.26	NM_004867.2	ITM2A - integral membrane protein 2A
3.26	NM_005655.1	TIEG - TGFB inducible early growth response
3.24	NM_000459.1	TEK - TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)
3.24	BX648726.1	TARSH - target of Nesh-SH3
3.23	NM_025224.1	BTBD4 - BTB (POZ) domain containing 4
3.20	NM_153634.2	CPNE8 - copine VIII
3.19	AK096673.1	phosphoinositol 3-phosphate-binding protein-3 (PEPP3)
3.19	NM_198232.1	RNASE1 - ribonuclease, RNase A family, 1 (pancreatic)
3.19	NM_025004.1	FLJ13215 - hypothetical protein FLJ13215
3.18	NM_000163.1	GHR - growth hormone receptor
3.16	NM_025081.1	KIAA1305 (KIAA1305)
3.15	NM_021805.1	SIGIRR - single Ig IL-1R-related molecule
3.14	NM_006105.3	RAPGEF3 - Rap guanine nucleotide exchange factor (GEF) 3
3.13		keratin 8 (KRT8)
3.09	NM_016557.2	CCRL1 - chemokine (C-C motif) receptor-like 1
3.07	NM_025201.3	pp9099 - PH domain-containing protein
3.06	BC003406.1	MRNA for CMP-N-acetylneuraminic acid hydroxylase, complete cds.
3.06	NM_024330.1	SLC27A3 - solute carrier family 27 (fatty acid transporter), member 3
3.05		TGFB inducible early growth response (TIEG)
3.04	AF178984.1	immediate early response 5 (IER5)
3.04	NM_015374.1	UNC84B - unc-84 homolog B (C. elegans)
3.02	NM_177528.1	SULT1A1;SULT1A2 - sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1;sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
3.02	NM_198925.1	SEMA4B - sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B
3.01	NM_000362.3	TIMP3 - tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)
3.01	NM_016531.3	KLF3 - Kruppel-like factor 3 (basic)
3.00	NM_177528.1	SULT1A1;SULT1A2 - sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1;sulfotransferase family, cytosolic, 1A, phenol-

		preferring, member 2
2.98	NM_002245.2	KCNK1 - potassium channel, subfamily K, member 1
2.98	AL833933.1	KIAA1522 protein (KIAA1522)
2.97		similar to prepro-Neuropeptide W polypeptide (PPL8)
2.97		TGFB inducible early growth response (TIEG)
2.96	NM_001760.2	CCND3 - cyclin D3
2.95	NM_144765.1	EVA1 - epithelial V-like antigen 1
2.91	NM_030882.2	APOL2 - apolipoprotein L, 2
2.91	NM_005629.1	FLJ43855;SLC6A8 - similar to sodium- and chloride-dependent creatine transporter;solute carrier family 6 (neurotransmitter transporter, creatine), member 8
2.91	NM_001752.1	CAT - catalase
2.89	NM_003595.2	TPST2 - tyrosylprotein sulfotransferase 2
2.87		Transcribed sequence (CeleraFN157952)
2.87	NM_004415.1	DSP - desmoplakin
2.86	NM_001424.3	EMP2 - epithelial membrane protein 2
2.86	NM_212530.1	CDC25B - cell division cycle 25B
2.86	NM_024668.2	MASK-BP3;EIF4EBP3;ANKHD1 - MASK-4E-BP3 alternate reading frame gene;eukaryotic translation initiation factor 4E binding protein 3;ankyrin repeat and KH domain containing 1
2.86	NM_178445.1	CCRL1 - chemokine (C-C motif) receptor-like 1
2.85	NM_177528.1	SULT1A1;SULT1A2 - sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1;sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
2.84	NM_006096.2	NDRG1 - N-myc downstream regulated gene 1
2.84	NM_002744.2	PRKCZ - protein kinase C, zeta
2.82	NM_001958.2	EEF1A2 - eukaryotic translation elongation factor 1 alpha 2
2.82	BX537506.1	Clone IMAGE:4401795, mRNA according to UniGene - potential CONFLICT - LOC389688 (na) according to LocusLink.
2.80	NM_003311.2	PHLDA2 - pleckstrin homology-like domain, family A, member 2
2.80	NM_003275.1	TMOD1 - tropomodulin 1
2.80	AK025783.1	neuralized-like (Drosophila) (NEURL) neuralized-like
2.79	AF161442.1	Similar to HSPC324 (LOC389811), mRNA according to UniGene - potential CONFLICT - similar to HSPC324 (na) according to LocusLink.
2.79	NM_138369.1	LOC91272 - hypothetical protein BC007436
2.78	NM_001779.1	CD58 - CD58 antigen, (lymphocyte function-associated antigen 3)
2.77	NM_015621.2	DKFZP434C171 - DKFZP434C171 protein
2.74	NM_033280.1	LOC90701 - similar to signal peptidase complex (18kD)
2.73	NM_032849.2	FLJ14834 - hypothetical protein FLJ14834
2.72	NM_181844.2	BCL6B - B-cell CLL/lymphoma 6, member B (zinc finger protein)
2.72	NM_015271.2	TRIM2 - tripartite motif-containing 2
2.72	AL110157.1	DUSP7 - dual specificity phosphatase 7
2.70		hypothetical protein FLJ33915 (FLJ33915)
2.70	NM_003166.2	SULT1A3;MGC5178 - sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3;hypothetical protein MGC5178
2.70	M25874.1	ATPase, Ca++ transporting, plasma membrane 4 (ATP2B4) plasma membrane calcium ATPase 4 isoform 4a
2.70	NM_007032.3	HRIHFB2122 - Tara-like protein
2.68	NM_182520.1	C22orf15 - chromosome 22 open reading frame 15
2.68	NM_004031.1	IRF7 - interferon regulatory factor 7
2.68	NM_003311.2	PHLDA2 - pleckstrin homology-like domain, family A, member 2
2.65		CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59) CD59 antigen p18-20
2.64	NM_172389.1	NFATC1 - nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
2.63	NM_003271.3	TM4SF7 - transmembrane 4 superfamily member 7
2.63	NM_018286.1	FLJ10970 - hypothetical protein FLJ10970
2.61	NM_006887.3	ZFP36L2 - zinc finger protein 36, C3H type-like 2
2.61	NM_003186.3	TAGLN - transgelin
2.60	NM_014328.2	RUSC1 - RUN and SH3 domain containing 1
2.58	NM_001549.2	IFIT4 - interferon-induced protein with tetratricopeptide repeats 4
2.58	NM_016307.3	PRRX2 - paired related homeobox 2

2.58		CeleraFN230120
2.58		CeleraFN163598
2.58	NM_014349.2	APOL3 - apolipoprotein L, 3
2.55	NM_005491.1	CXorf6 - chromosome X open reading frame 6
2.54	NM_015271.2	TRIM2 - tripartite motif-containing 2
2.54	NM_004356.2	CD81 - CD81 antigen (target of antiproliferative antibody 1)
2.54	NM_002194.2	INPP1 - inositol polyphosphate-1-phosphatase
2.53	NM_145247.3	C10orf78 - chromosome 10 open reading frame 78
2.53	NM_014824.1	FCHSD2 - FCH and double SH3 domains 2
2.51	NM_012244.2	SLC7A8 - solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
2.51	NM_005532.2	IFI27 - interferon, alpha-inducible protein 27
2.49	NM_021077.3	NMB - neuromedin B
2.49	NM_004735.1	LRRFIP1 - leucine rich repeat (in FLII) interacting protein 1
2.48	NM_005854.1	RAMP2 - receptor (calcitonin) activity modifying protein 2
2.47	NM_020448.2	DJ462O23.2 - hypothetical protein dJ462O23.2
2.47	NM_012100.1	DNPEP - aspartyl aminopeptidase
2.46	NM_032823.3	C9orf3 - chromosome 9 open reading frame 3
2.43	NM_182491.1	LOC90637 - hypothetical protein LOC90637
2.43		CeleraFN196112
2.42	NM_018125.2	FLJ10521 - hypothetical protein FLJ10521
2.42	NM_183243.1	IMPDH1 - IMP (inosine monophosphate) dehydrogenase 1
2.42	NM_024756.1	MMRN2 - multimerin 2
2.41	NM_003165.1	STXBP1 - syntaxin binding protein 1
2.41	NM_014216.3	ITPK1 - inositol 1,3,4-triphosphate 5/6 kinase
2.40	NM_003491.2	ARD1 - ARD1 homolog, N-acetyltransferase (S. cerevisiae)
2.39	AK095399.1	LOC196264 - hypothetical protein LOC196264
2.37	NM_014603.1	HUMPPA - paraneoplastic antigen
2.37	NM_005451.3	PDLIM7 - PDZ and LIM domain 7 (enigma)
2.36	NM_006887.3	ZFP36L2 - zinc finger protein 36, C3H type-like 2
2.36	NM_004613.2	TGM2 - transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
2.35	NM_033069.1	GFOD1;C6orf114 - glucose-fructose oxidoreductase domain containing 1;chromosome 6 open reading frame 114
2.35	NM_002727.2	PRG1 - proteoglycan 1, secretory granule
2.34	NM_024519.2	FLJ13725 - hypothetical protein FLJ13725
2.30	NM_001859.2	SLC31A1 - solute carrier family 31 (copper transporters), member 1
2.30	NM_001289.3	CLIC2 - chloride intracellular channel 2
2.29	NM_018431.2	DOK5 - docking protein 5
2.28	NM_020529.1	NFKBIA - nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
2.27		CeleraFN178315
2.27	NM_001547.3	IFIT2 - interferon-induced protein with tetratricopeptide repeats 2
2.27	NM_201554.1	DGKA - diacylglycerol kinase, alpha 80kDa
2.26	NM_017943.2	FBXO34 - F-box protein 34
2.26	NM_016579.1	8D6A;NDUFA7 - NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa;8D6 antigen
2.25	NM_006368.4	CREB3 - cAMP responsive element binding protein 3
2.24	NM_000169.1	GLA - galactosidase, alpha
2.24	NM_002224.1	ITPR3 - inositol 1,4,5-triphosphate receptor, type 3
2.24	NM_032227.1	FLJ22679 - hypothetical protein FLJ22679
2.24	NM_013974.1	DDAH2 - dimethylarginine dimethylaminohydrolase 2
2.24	NM_198252.1	GSN - gelsolin (amyloidosis, Finnish type)
2.24	NM_004287.2	GOSR2 - golgi SNAP receptor complex member 2
2.24	NM_002579.1	PALM - paralemmin
2.23	NM_139247.2	ADCY4 - adenylate cyclase 4
2.23	AF116571.1	SRY (sex determining region Y)-box 13 (SOX13) SRY-box 13
2.22	NM_032227.1	FLJ22679 - hypothetical protein FLJ22679
2.21		CeleraFN124964
2.21	NM_024709.2	FLJ14146 - hypothetical protein FLJ14146
2.21	NM_002541.1	OGDH - oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
2.20	NM_017585.2	SLC2A6 - solute carrier family 2 (facilitated glucose transporter),

		member 6
2.19	NM_147190.1	LASS5 - LAG1 longevity assurance homolog 5 (S. cerevisiae)
2.19	NM_002081.1	GPC1 - glypican 1
2.19	NM_203411.1	LOC92162 - similar to RIKEN cDNA 2600017H02
2.18	NM_017943.2	FBXO34 - F-box protein 34
2.18	NM_020728.1	KIAA1228 - KIAA1228 protein
2.18	NM_005271.1	GLUD2;GLUD1 - glutamate dehydrogenase 2;glutamate dehydrogenase 1
2.18	NM_000903.1	NQO1 - NAD(P)H dehydrogenase, quinone 1
2.17	BX647872.1	CDNA clone IMAGE:4822701, partial cds according to UniGene - potential CONFLICT - similar to RIKEN cDNA 8030451K01 (na) according to LocusLink.
2.17	BC015230.1	chromosome 9 open reading frame 115 (C9orf115)
2.17	NM_057158.2	DUSP4 - dual specificity phosphatase 4
2.17	BT009787.1	ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1) Na+/K+ -ATPase beta 1 subunit isoform a
2.17	NM_004735.1	LRRFIP1 - leucine rich repeat (in FLII) interacting protein 1
2.16	NM_024530.1	FOSL2 - FOS-like antigen 2
2.16	NM_019555.1	ARHGEF3 - Rho guanine nucleotide exchange factor (GEF) 3
2.16	NM_024071.2	ZFYVE21 - zinc finger, FYVE domain containing 21
2.14	NM_006634.2	VAMP8;VAMP5 - vesicle-associated membrane protein 8 (endobrevin);vesicle-associated membrane protein 5 (myobrevin)
2.14	NM_021732.1	AVPI1 - arginine vasopressin-induced 1
2.13	NM_002863.2	PYGL - phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
2.13	NM_006053.2	TCIRG1 - T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3
2.12	NM_012084.3	GLUD2;GLUD1 - glutamate dehydrogenase 2;glutamate dehydrogenase 1
2.12	NM_004735.1	LRRFIP1 - leucine rich repeat (in FLII) interacting protein 1
2.11	NM_024496.2	C14orf4 - chromosome 14 open reading frame 4
2.10		CeleraFN237035
2.09	NM_016463.5	CXXC5 - CXXC finger 5
2.09	AB002365.2	KIAA0367 (KIAA0367)
2.09	NM_181775.2	DKFZp434G0625 - hypothetical protein DKFZp434G0625
2.09	NM_000296.2	PKD1 - polycystic kidney disease 1 (autosomal dominant)
2.09	AK024480.1	hypothetical protein LOC126917 (LOC126917)
2.08	NM_033632.1	FBXW7 - F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)
2.08	NM_004287.2	GOSR2 - golgi SNAP receptor complex member 2
2.08	NM_005397.2	PODXL - podocalyxin-like
2.06		Similar to KIAA0563-related gene (LOC390845), mRNA according to UniGene - potential CONFLICT - similar to KIAA0563-related gene (na) according to LocusLink.
2.06	NM_000355.2	TCN2 - transcobalamin II; macrocytic anemia
2.05	NM_004041.2	ARRB1 - arrestin, beta 1
2.05	NM_002658.1	PLAU - plasminogen activator, urokinase
2.05		CeleraFN123356
2.05		natural killer cell transcript 4 (NK4)
2.04	NM_207336.1	EZI - likely ortholog of mouse zinc finger protein EZI
2.04	NM_006086.1	TUBB4 - tubulin, beta, 4
2.03	NM_004735.1	LRRFIP1 - leucine rich repeat (in FLII) interacting protein 1
2.03	NM_181785.1	LOC283537 - hypothetical protein LOC283537
2.03	NM_007150.1	ZNF185 - zinc finger protein 185 (LIM domain)
2.02	NM_002801.2	PSMB10;CTRL - proteasome (prosome, macropain) subunit, beta type, 10;chymotrypsin-like
2.02	NM_000877.2	IL1R1 - interleukin 1 receptor, type I
2.02	NM_005641.2	TAF6 - TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa
2.02	NM_005271.1	GLUD2;GLUD1 - glutamate dehydrogenase 2;glutamate dehydrogenase 1
2.02	NM_198857.1	FLJ43855;SLC6A8 - similar to sodium- and chloride-dependent creatine transporter;solute carrier family 6 (neurotransmitter transporter, creatine), member 8

2.02	NM_003012.2	SFRP1 - secreted frizzled-related protein 1
2.02	NM_006691.2	XLKD1 - extracellular link domain containing 1
2.01		natural killer cell transcript 4 (NK4)
2.01	NM_016081.2	KIAA0992 - palladin
2.01		CeleraFN101122
2.01	NM_020651.2	PELI1 - pellino homolog 1 (Drosophila)
2.00	NM_003567.1	BCAR3 - breast cancer anti-estrogen resistance 3
2.00	NM_001873.1	CPE - carboxypeptidase E
2.00	NM_007097.2	CLTB - clathrin, light polypeptide (Lcb)
1.99	NM_005114.1	HS3ST1 - heparan sulfate (glucosamine) 3-O-sulfotransferase 1
1.99	BC047724.1	chromosome 10 open reading frame 128 (C10orf128)
1.99	NM_004075.2	CRY1 - cryptochrome 1 (photolyase-like)
1.99	NM_022343.2	C9orf19 - chromosome 9 open reading frame 19
1.98	NM_015922.1	NSDHL - NAD(P) dependent steroid dehydrogenase-like
1.98	NM_001251.1	CD68 - CD68 antigen
1.98	NM_001859.2	SLC31A1 - solute carrier family 31 (copper transporters), member 1
1.98	NM_007274.2	BACH - brain acyl-CoA hydrolase
1.98	NM_001748.3	CAPN2 - calpain 2, (m/II) large subunit
1.97	NM_006795.2	EHD1 - EH-domain containing 1
1.97	NM_016619.1	PLAC8 - placenta-specific 8
1.97	NM_138809.2	LOC134147 - hypothetical protein BC001573
1.97	NM_004438.3	EPHA4 - EphA4
1.96	NM_002047.1	GARS - glycyl-tRNA synthetase
1.96	AB056106.1	TARSH - target of Nesh-SH3
1.96	NM_001458.1	FLNC - filamin C, gamma (actin binding protein 280)
1.96	NM_002222.1	ITPR1 - inositol 1,4,5-triphosphate receptor, type 1
1.96		synaptogyrin 2 (SYNGR2)
1.95	NM_024071.2	ZFYVE21 - zinc finger, FYVE domain containing 21
1.95	AK096056.1	MRNA; cDNA DKFZp566O134 (from clone DKFZp566O134)
1.95	NM_001001417.2	MGC44903;LOC414059;TBC1D3 - similar to TBC1 domain family, member 3, telomeric;similar to TBC1 domain family, member 3, centromeric;TBC1 domain family, member 3
1.95	NM_022343.2	C9orf19 - chromosome 9 open reading frame 19
1.94	NM_030666.2	SERPINB1 - serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1
1.94	NM_007274.2	BACH - brain acyl-CoA hydrolase
1.93	NM_003565.1	ULK1 - unc-51-like kinase 1 (C. elegans)
1.93	BC047069.1	KIAA1450 protein (KIAA1450)
1.93	NM_005346.3	HSPA1B;HSPA1A - heat shock 70kDa protein 1B;heat shock 70kDa protein 1A
1.92	NM_002837.2	PTPRB - protein tyrosine phosphatase, receptor type, B
1.92	NM_003641.2	IFITM1 - interferon induced transmembrane protein 1 (9-27)
1.92	NM_002841.2	PTPRG - protein tyrosine phosphatase, receptor type, G
1.92	NM_022168.2	MDA5 - melanoma differentiation associated protein-5
1.92		GLUD2
1.92	NM_022489.1	FLJ22056 - hypothetical protein FLJ22056
1.91	NM_172200.1	IL15RA - interleukin 15 receptor, alpha
1.91	L07772.1_CDS_1	Transcribed sequence with moderate similarity to protein sp:P07711 (H.sapiens) CATL_HUMAN Cathepsin L precursor
1.91	AL031963.40_CDS_7	tubulin, beta polypeptide paralog (MGC8685)
1.91	NM_002165.2	ID1 - inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
1.90	NM_016619.1	PLAC8 - placenta-specific 8
1.90	NM_003713.3	PPAP2B - phosphatidic acid phosphatase type 2B
1.90	NM_005863.2	NET1 - neuroepithelial cell transforming gene 1
1.89	NM_018837.2	SULF2 - sulfatase 2
1.88	AB051515.1	KIAA1728 protein (KIAA1728)
1.88	NM_003289.3	TPM2 - tropomyosin 2 (beta)
1.88	NM_001769.2	CD9 - CD9 antigen (p24)
1.88	AK095896.1	LOC340061 - hypothetical protein LOC340061
1.88	NM_152892.1	DKFZp434K1815 - hypothetical protein DKFZp434K1815
1.87	NM_004036.2	ADCY3 - adenylate cyclase 3

1.87	NM_006200.2	PCSK5 - proprotein convertase subtilisin/kexin type 5
1.87		Similar to Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS) (LOC341112), mRNA according to UniGene - potential CONFLICT - similar to Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS) (na) acco
1.87	NM_000081.1	CHS1 - Chediak-Higashi syndrome 1
1.87	NM_000611.4	CD59 - CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
1.87	NM_022566.1	MESDC1 - mesoderm development candidate 1
1.87	NM_020338.1	RAI17 - retinoic acid induced 17
1.86	NM_000396.2	CTSK - cathepsin K (pycnodysostosis)
1.86		Transcribed sequence with moderate similarity to protein sp:P00367 (H.sapiens) DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial precursor
1.86	NM_019594.1	LRRC8 - leucine rich repeat containing 8
1.86	NM_000138.2	FBN1 - fibrillin 1 (Marfan syndrome)
1.86	NM_006432.3	NPC2 - Niemann-Pick disease, type C2
1.85		CeleraFN228644
1.85	NM_005786.3	SDCCAG33 - serologically defined colon cancer antigen 33
1.85		CeleraFN224412
1.85	NM_024112.2	C9orf16 - chromosome 9 open reading frame 16
1.84	NM_201443.1	TEAD4 - TEA domain family member 4
1.84	NM_006867.1	RBPMS - RNA binding protein with multiple splicing
1.84	NM_032627.1	SSBP4 - single stranded DNA binding protein 4
1.83	NM_016357.1	EPLIN - epithelial protein lost in neoplasm beta
1.83	NM_198991.1	KCTD1 - potassium channel tetramerisation domain containing 1
1.83	NM_004079.3	CTSS - cathepsin S
1.83	NM_014624.2	S100A6 - S100 calcium binding protein A6 (calcyclin)
1.83	NM_003916.3	AP1S2 - adaptor-related protein complex 1, sigma 2 subunit
1.83	NM_130766.1	SKIP - skeletal muscle and kidney enriched inositol phosphatase
1.83	NM_007097.2	CLTB - clathrin, light polypeptide (Lcb)
1.82	AC004668.1_CDS_4	CeleraFN187317
1.82	NM_001769.2	CD9 - CD9 antigen (p24)
1.82	NM_016357.1	EPLIN - epithelial protein lost in neoplasm beta
1.82	NM_006310.2	NPEPPS - aminopeptidase puromycin sensitive
1.82	NM_194281.2	C18orf37 - chromosome 18 open reading frame 37
1.81	NM_024329.4	EFHD2 - EF hand domain containing 2
1.81	NM_197974.1	BTN3A3 - butyrophilin, subfamily 3, member A3
1.81	NM_012294.2	RAPGEF5 - Rap guanine nucleotide exchange factor (GEF) 5
1.80	NM_213646.1	WARS - tryptophanyl-tRNA synthetase
1.79	NM_014624.2	S100A6 - S100 calcium binding protein A6 (calcyclin)
1.79	NM_005620.1	S100A11 - S100 calcium binding protein A11 (calgizzarin)
1.79	NM_001195.2	BFSP1 - beaded filament structural protein 1, filensin
1.79	NM_182483.1	NSFL1C - NSFL1 (p97) cofactor (p47)
1.79	NM_016368.3	ISYNA1 - myo-inositol 1-phosphate synthase A1
1.78	NM_004221.3	NK4 - natural killer cell transcript 4
1.78	NM_004159.3	PSMB8 - proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)
1.78	NM_017805.2	RASIP1 - Ras interacting protein 1
1.78	NM_014164.4	FXYD5 - FXYD domain containing ion transport regulator 5
1.78	NM_000943.4	PPIC - peptidylprolyl isomerase C (cyclophilin C)
1.78	NM_006088.4	TUBB2 - tubulin, beta, 2
1.77	NM_178012.3	MGC8685 - tubulin, beta polypeptide paralog
1.77	NM_003916.3	AP1S2 - adaptor-related protein complex 1, sigma 2 subunit
1.77	NM_033252.1	B3GNT1 - UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
1.77		CeleraFN201686
1.77	NM_207369.1	FLJ00193 protein (FLJ00193)
1.76		CeleraFN236579
1.76	NM_001822.2	CHN1 - chimerin (chimaerin) 1
1.76	NM_006472.1	TXNIP - thioredoxin interacting protein
1.75	NM_012428.1	SDFR1 - stromal cell derived factor receptor 1

1.75	AK002100.1	PHCA - phytoceramidase, alkaline
1.75	NM_006084.3	ISGF3G - interferon-stimulated transcription factor 3, gamma 48kDa
1.75	NM_016081.2	KIAA0992 - palladin
1.74	NM_003359.1	UGDH - UDP-glucose dehydrogenase
1.74	NM_021034.1	IFITM3 - interferon induced transmembrane protein 3 (1-8U)
1.74	NM_021980.3	OPTN - optineurin
1.74	NM_021979.2	HSPA2 - heat shock 70kDa protein 2
1.74	NM_021056.1	TSC2 - tuberous sclerosis 2
1.73	NM_014164.4	FXYD5 - FXYD domain containing ion transport regulator 5
1.73	AC004668.1_CDS_4	CeleraFN144800
1.73	NM_152288.1	MGC13024 - hypothetical protein MGC13024
1.72	NM_030652.1	PPT2;EGFL8 - palmitoyl-protein thioesterase 2;EGF-like-domain, multiple 8
1.72	NM_032627.1	SSBP4 - single stranded DNA binding protein 4
1.72	NM_016131.2	RAB10 - RAB10, member RAS oncogene family
1.72	NM_024324.2	MGC11256 - hypothetical protein MGC11256
1.72	NM_025246.1	TMEM22 - transmembrane protein 22
1.71	NM_015524.2	C6orf4 - chromosome 6 open reading frame 4
1.71	NM_002053.1	GBP1 - guanylate binding protein 1, interferon-inducible, 67kDa
1.71	NM_014222.2	NDUFA8 - NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
1.70	NM_024728.1	C7orf10 - chromosome 7 open reading frame 10
1.70	NM_018837.2	SULF2 - sulfatase 2
1.70	NM_006232.2	POLR2H - polymerase (RNA) II (DNA directed) polypeptide H
1.70	AX884008.1_CDS_1	Clone DNA100312 VSSW1971 (UNQ1971) mRNA, complete cds
1.70	NM_145799.2	6-Sep - septin 6
1.69	NM_006164.2	NFE2L2 - nuclear factor (erythroid-derived 2)-like 2
1.69	NM_004615.2	TM4SF2 - transmembrane 4 superfamily member 2
1.69	NM_001748.3	CAPN2 - calpain 2, (m/II) large subunit
1.69	NM_021034.1	IFITM3 - interferon induced transmembrane protein 3 (1-8U)
1.67	NM_004827.1	ABCG2 - ATP-binding cassette, sub-family G (WHITE), member 2
1.67	NM_001797.2	CDH11 - cadherin 11, type 2, OB-cadherin (osteoblast)
1.66	NM_005552.3	KNS2 - kinesin 2 60/70kDa
1.66	NM_005013.1	NUCB2 - nucleobindin 2
1.66	NM_199144.1	Kua-UEV;Kua;UBE2V1 - ubiquitin-conjugating enzyme E2 variant 1;ubiquitin-conjugating enzyme variant Kua;ubiquitin-conjugating enzyme E2 variant 1
1.65	NM_016306.3	DNAJB11 - DnaJ (Hsp40) homolog, subfamily B, member 11
1.64	NM_198183.1	UBE2L6 - ubiquitin-conjugating enzyme E2L 6
1.64	NM_001329.1	CTBP2 - C-terminal binding protein 2
1.63	BC064948.1	MBC3205 (UNQ501)
1.63	NM_007048.3	BTN3A1 - butyrophilin, subfamily 3, member A1
1.62	NM_017958.1	PLEKHB2 - pleckstrin homology domain containing, family B (evectins) member 2
1.62	AB051437.1	SH3 and multiple ankyrin repeat domains 3 (SHANK3)
1.62	NM_002413.3	MGST2 - microsomal glutathione S-transferase 2
1.62	NM_080737.1	SYTL4 - synaptotagmin-like 4 (granuphilin-a)
1.62	NM_023009.4	MLP - MARCKS-like protein
1.61	NM_144712.2	FLJ12610;SLC23A3 - hypothetical protein FLJ12610;solute carrier family 23 (nucleobase transporters), member 3
1.61	NM_001776.3	ENTPD1 - ectonucleoside triphosphate diphosphohydrolase 1
1.61	NM_002149.2	HPCAL1 - hippocalcin-like 1
1.61	NM_019041.2	MTRF1L - mitochondrial translational release factor 1-like
1.60	NM_003134.2	SRP14 - signal recognition particle 14kDa (homologous Alu RNA binding protein)
1.60	NM_194279.1	HBLD1 - HESB like domain containing 1
1.60	NM_000688.4	ALAS1 - aminolevulinate, delta-, synthase 1
1.59	NM_001312.2	CRIP2 - cysteine-rich protein 2
1.59	AF086226.1	EGF-like-domain, multiple 3 (EGFL3)
1.58	BC011852.2	glutamate-ammonia ligase (glutamine synthase) (GLUL)
1.57	NM_004207.1	SLC16A3 - solute carrier family 16 (monocarboxylic acid transporters),

		member 3
1.57	BC016168.1	small nuclear ribonucleoprotein polypeptide N (SNRPN)
1.57		inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (ID2B)
1.56	NM_005979.1	S100 calcium binding protein A13 (S100A13)
1.56		CeleraFN121739
1.56		Clone IMAGE:4825049, mRNA, partial cds
1.56	AF466367.1	SH3BGRL3 - SH3 domain binding glutamic acid-rich protein like 3
1.56	NM_001329.1	CTBP2 - C-terminal binding protein 2
1.56	AL096879.1	C22orf5 - chromosome 22 open reading frame 5
1.55	AB033030.1	KIAA1204 protein (CDGAP)
1.55		interferon induced transmembrane protein 3 (1-8U) (IFITM3) interferon-induced transmembrane protein 3 (1-8U)
1.55	NM_003290.1	TPM4 - tropomyosin 4
1.54	NM_198590.1	BSG - basigin (OK blood group)
1.54	NM_004663.3	RAB11A - RAB11A, member RAS oncogene family
1.54	NM_015170.1	SULF1 - sulfatase 1
1.53	NM_003289.3	TPM2 - tropomyosin 2 (beta)
1.53	NM_000690.2	ALDH2 - aldehyde dehydrogenase 2 family (mitochondrial)
1.52	NM_147184.1	TP53I3 - tumor protein p53 inducible protein 3
1.52	NM_182471.1	PKM2 - pyruvate kinase, muscle
1.52	NM_183001.2	SHC1 - SHC (Src homology 2 domain containing) transforming protein 1
1.52	NM_003134.2	SRP14 - signal recognition particle 14kDa (homologous Alu RNA binding protein)
1.51	NM_007282.3	RNF13 - ring finger protein 13
1.51	NM_005101.1	G1P2 - interferon, alpha-inducible protein (clone IFI-15K)
1.51		interferon induced transmembrane protein 3 (1-8U) (IFITM3) interferon-induced transmembrane protein 3 (1-8U)
1.51		interferon induced transmembrane protein 3 (1-8U) (IFITM3) interferon-induced transmembrane protein 3 (1-8U)
1.51		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ) tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polypeptide
1.51	NM_002292.2	LAMB2 - laminin, beta 2 (laminin S)
1.50	NM_003127.1	SPTAN1 - spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
1.49		Similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U) (LOC144383), mRNA according to UniGene - potential CONFLICT - similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U) (na) ac
1.49	NM_002166.4	ID2 - inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
1.48		Transcribed sequence with strong similarity to protein sp:P00722 (E. coli) BGAL_ECOLI Beta-galactosidase
1.46		KIAA1005 protein (KIAA1005)
1.46	NM_003290.1	TPM4 - tropomyosin 4
1.45	NM_005347.2	HSPA5 - heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
1.45	NM_006870.2	DSTN - destrin (actin depolymerizing factor)
1.31	NM_001831.2	CLU - clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
-1.25	NM_182793.1	TMSL6;TMSL4;TMSL3;TMSL2;TMSB4X - thymosin-like 6;thymosin-like 4;thymosin-like 3;thymosin-like 2;thymosin, beta 4, X-linked
-1.29		CeleraFN124143
-1.44		nucleolin (NCL)
-1.45	NM_001540.2	HSPB1 - heat shock 27kDa protein 1
-1.45	NM_031157.1	HNRPA1 - heterogeneous nuclear ribonucleoprotein A1
-1.45	NM_030939.2	C6orf62 - chromosome 6 open reading frame 62
-1.47	AL035542.8_CDS_8	CeleraFN230865
-1.47	NM_006001.1	TUBA2 - tubulin, alpha 2
-1.47	NM_019007.2	FLJ20811 - hypothetical protein FLJ20811

-1.48	NM_002128.3	HMGB1 - high-mobility group box 1
-1.48	AL832297.1	hypothetical protein FLJ14959 (FLJ14959)
-1.48	NM_178335.1	C3orf6 - chromosome 3 open reading frame 6
-1.48		myosin regulatory light chain MRLC2 (MRLC2) myosin regulatory light chain MRCL2
-1.48	NM_001343.1	DAB2 - disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
-1.48		CDNA FLJ10131 fis, clone HEMBA1003041
-1.49		high-mobility group box 1 (HMGB1)
-1.49	AC007277.2_CDS_1	CeleraFN101692
-1.49		CeleraFN142255
-1.50		high-mobility group box 1 (HMGB1)
-1.50		CeleraFN232964
-1.50	BC007792.1	chromosome 14 open reading frame 170 (C14orf170) according to UniGene - potential CONFLICT - YLP motif containing 1 (YLPM1) according to LocusLink.
-1.50		MRCL3;MRLC2 - myosin regulatory light chain MRCL3;myosin regulatory light chain MRLC2
-1.51	NM_002128.3	HMGB1 - high-mobility group box 1
-1.51		CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2) nuclear LIM interactor-interacting factor 2
-1.51	BC014381.1	hypothetical protein LOC285346 (LOC285346)
-1.52	NM_138286.1	LOC148213 - hypothetical protein FLJ31526
-1.52	NM_032704.2	TUBA6 - tubulin alpha 6
-1.52	NM_002906.2	RDX - radixin
-1.52	NM_001483.1	GBAS - glioblastoma amplified sequence
-1.54	NM_145687.2	MAP4K4 - mitogen-activated protein kinase kinase kinase kinase 4
-1.54		CeleraFN230167
-1.54		cell division cycle 42 (GTP binding protein, 25kDa) (CDC42) cell division cycle 42 isoform 1
-1.55	NM_152400.1	FLJ39370 - hypothetical protein FLJ39370
-1.55	BC049823.1	similar to ribosomal protein L22 (LOC200916)
-1.55	NM_005463.2	HNRPDL - heterogeneous nuclear ribonucleoprotein D-like
-1.55	NM_016242.2	EMCN - endomucin
-1.55		HMG4L - high-mobility group (nonhistone chromosomal) protein 4-like
-1.56	NM_001753.3	CAV1 - caveolin 1, caveolae protein, 22kDa
-1.56		high-mobility group box 1 (HMGB1)
-1.56	NM_001233.3	CAV2 - caveolin 2
-1.56	NM_007034.3	DNAJB4 - DnaJ (Hsp40) homolog, subfamily B, member 4
-1.57	NM_006963.2	ZNF22 - zinc finger protein 22 (KOX 15)
-1.57		CeleraFN202399
-1.57	NM_006500.1	MCAM - melanoma cell adhesion molecule
-1.57	AK092012.1	zinc finger protein 37a (KOX 21) (ZNF37A)
-1.57	NM_005779.1	LHFPL2 - lipoma HMGIC fusion partner-like 2
-1.57	NM_001984.1	ESD - esterase D/formylglutathione hydrolase
-1.57	NM_014782.4	ARMCX2 - armadillo repeat containing, X-linked 2
-1.57		CeleraFN233375
-1.58	NM_182796.1	MAT2B - methionine adenosyltransferase II, beta
-1.58	NM_025019.1	TUBA4 - tubulin, alpha 4
-1.58	NM_133325.1	PHF10 - PHD finger protein 10
-1.59	NM_033546.2	MRCL3;MRLC2 - myosin regulatory light chain MRCL3;myosin regulatory light chain MRLC2
-1.59	NM_207292.1	MBNL1 - muscleblind-like (Drosophila)
-1.59		CeleraFN173570
-1.59	NM_016073.2	HDGFRP3 - hepatoma-derived growth factor, related protein 3
-1.59		CeleraFN177411
-1.60	NM_198902.1	TM4SF8 - transmembrane 4 superfamily member 8
-1.61	NM_014812.1	KAB - KARP-1-binding protein
-1.61		lysophospholipase I (LYPLA1)
-1.61	NM_020648.3	TWSG1 - twisted gastrulation homolog 1 (Drosophila)
-1.61	NM_012250.3	RRAS2 - related RAS viral (r-ras) oncogene homolog 2

-1.62	AF119663.1	GNG12 - guanine nucleotide binding protein (G protein), gamma 12
-1.62	NM_006547.2	IMP-3 - IGF-II mRNA-binding protein 3
-1.62	NM_182488.1	USP12 - ubiquitin specific protease 12
-1.62	NM_031442.2	TM4SF10 - transmembrane 4 superfamily member 10
-1.63	NM_014268.1	MAPRE2 - microtubule-associated protein, RP/EB family, member 2
-1.63	NM_018894.1	EFEMP1 - EGF-containing fibulin-like extracellular matrix protein 1
-1.63	NM_006330.2	LYPLA1 - lysophospholipase I
-1.63	NM_020169.2	LXN - latexin
-1.64	NM_015472.3	TAZ - transcriptional co-activator with PDZ-binding motif (TAZ)
-1.64	NM_006823.2	PKIA - protein kinase (cAMP-dependent, catalytic) inhibitor alpha
-1.64		CeleraFN181519
-1.64	NM_005156.3	ROD1 - ROD1 regulator of differentiation 1 (S. pombe)
-1.65	NM_001196.2	BID - BH3 interacting domain death agonist
-1.65	NM_012193.2	FZD4 - frizzled homolog 4 (Drosophila)
-1.65	NM_080655.1	MGC17337 - similar to RIKEN cDNA 5730528L13 gene
-1.65	NM_003074.2	SMARCC1 - SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
-1.65	NM_005596.1	NFIB - nuclear factor I/B
-1.66	NM_006330.2	LYPLA1 - lysophospholipase I
-1.67	NM_001718.2	BMP6 - bone morphogenetic protein 6
-1.67	NM_006317.3	BASP1 - brain abundant, membrane attached signal protein 1
-1.67	NM_182661.1	CERK - ceramide kinase
-1.68	AX746918.1	CDNA FLJ34013 fis, clone FCBBF2002111
-1.68	NM_080655.1	MGC17337 - similar to RIKEN cDNA 5730528L13 gene
-1.68	NM_003107.2	SOX4 - SRY (sex determining region Y)-box 4
-1.68	NM_001363.2	DKC1 - dyskeratosis congenita 1, dyskerin
-1.68	NM_145341.2	PDCD4 - programmed cell death 4 (neoplastic transformation inhibitor)
-1.68	NM_004124.2	GMFB - glia maturation factor, beta
-1.69	NM_020749.2	mitochondrial tumor suppressor 1 (MTUS1) mitochondrial tumor suppressor 1 isoform 1
-1.69	NM_006426.1	DPYSL4 - dihydropyrimidinase-like 4
-1.70	NM_207422.1	FLJ44635 - FLJ44635 protein
-1.70	NM_006287.3	TFPI - tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
-1.71	NM_001001323.1	ATP2B1 - ATPase, Ca++ transporting, plasma membrane 1
-1.71	NM_058172.1	ANTXR2 - anthrax toxin receptor 2
-1.71	NM_002210.2	ITGAV - integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
-1.72	AL451107.6_CDS_2	supervillin (SVIL) supervillin isoform 1
-1.73		CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2) nuclear LIM interactor-interacting factor 2
-1.73	NM_004342.5	CALD1 - caldesmon 1
-1.73	BC034790.1	CDNA FLJ26890 fis, clone PRS09675
-1.73	NM_018003.1	UACA - uveal autoantigen with coiled-coil domains and ankyrin repeats
-1.73	NM_018976.3	SLC38A2 - solute carrier family 38, member 2
-1.73		prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2) prostaglandin-endoperoxide synthase 2 precursor
-1.74	NM_005964.1	MYH10 - myosin, heavy polypeptide 10, non-muscle
-1.74	BC012493.1	LCHN protein (LCHN)
-1.74	NM_033515.2	ARHGAP18 - Rho GTPase activating protein 18
-1.75	NM_152264.2	SLC39A13 - solute carrier family 39 (zinc transporter), member 13
-1.75	NM_004126.2	GNG11 - guanine nucleotide binding protein (G protein), gamma 11
-1.75	AL136094.13_CDS_1	CeleraFN232864
-1.75	NM_058172.1	ANTXR2 - anthrax toxin receptor 2
-1.76	X77307.1	HTR2B - 5-hydroxytryptamine (serotonin) receptor 2B
-1.76	NM_004052.2	BNIP3 - BCL2/adenovirus E1B 19kDa interacting protein 3
-1.76	NM_004772.1	C5orf13 - chromosome 5 open reading frame 13
-1.76	NM_002317.3	LOX - lysyl oxidase
-1.76	NM_004815.2	PARG1 - PTPL1-associated RhoGAP 1

-1.77	NM_199512.1	URB - steroid sensitive gene 1
-1.77	NM_148170.1	CTSC - cathepsin C
-1.77	NM_003598.1	TEAD2 - TEA domain family member 2
-1.77	NM_182757.1	IBRDC2 - IBR domain containing 2
-1.77		chromosome 5 open reading frame 13 (C5orf13) neuronal protein 3.1
-1.77	NM_003633.1	ENC1 - ectodermal-neural cortex (with BTB-like domain)
-1.77	NM_001839.2	CNN3 - calponin 3, acidic
-1.78	NM_145687.2	MAP4K4 - mitogen-activated protein kinase kinase kinase kinase 4
-1.79	NM_012334.1	MYO10 - myosin X
-1.79	AK055620.1	CDNA FLJ31058 fis, clone HSYRA2000828
-1.79	AK054822.1	Hypothetical gene supported by AK054822 (LOC402632), mRNA according to UniGene - potential CONFLICT - hypothetical gene supported by AK054822 (na) according to LocusLink.
-1.79	NM_004772.1	C5orf13 - chromosome 5 open reading frame 13
-1.80	NM_006452.2	PAICS - phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
-1.80	BC023546.2	KIAA1102 protein (KIAA1102)
-1.80		gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1) connexin 43
-1.80	NM_004167.3	CCL15;CCL14 - chemokine (C-C motif) ligand 15;chemokine (C-C motif) ligand 14
-1.80	NM_002421.2	MMP1 - matrix metalloproteinase 1 (interstitial collagenase)
-1.81	NM_201280.1	MUTED - muted homolog (mouse)
-1.82	NM_012342.1	BAMBI - BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
-1.82	NM_002356.4	MARCKS - myristoylated alanine-rich protein kinase C substrate
-1.83	NM_006452.2	PAICS - phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
-1.84	NM_004280.2	EEF1E1 - eukaryotic translation elongation factor 1 epsilon 1
-1.84	NM_207578.1	PRKACB - protein kinase, cAMP-dependent, catalytic, beta
-1.84	NM_021631.1	FKSG2 - apoptosis inhibitor
-1.84	NM_175060.1	C14orf27 - chromosome 14 open reading frame 27
-1.85	NM_012334.1	MYO10 - myosin X
-1.86	NM_002069.4	GNAI1 - guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
-1.86	NM_033407.1	DOCK7 - dedicator of cytokinesis 7
-1.87	NM_005402.2	RALA - v-ral simian leukemia viral oncogene homolog A (ras related)
-1.87	U06715.1	CYB561 - cytochrome b-561
-1.87		Transcribed sequence with weak similarity to protein ref:NP_034081.1 (M.musculus) insulin-like growth factor 2, binding protein 1; coding region determinant binding protein; zipcode-binding protein 1; zipcode binding protein 1 [Mus musculus]
-1.87	BC062632.1	E3 ubiquitin ligase SMURF2 (SMURF2)
-1.88	NM_002467.2	MYC - v-myc myelocytomatosis viral oncogene homolog (avian)
-1.88	NM_181671.1	PITPNC1 - phosphatidylinositol transfer protein, cytoplasmic 1
-1.88	NM_005952.2	MT1X - metallothionein 1X
-1.89		myristoylated alanine-rich protein kinase C substrate (MARCKS)
-1.89	NM_052871.1	MGC4677 - hypothetical protein MGC4677
-1.89		CeleraFN133737
-1.90	NM_004095.2	EIF4EBP1 - eukaryotic translation initiation factor 4E binding protein 1
-1.91	NM_001724.3	BPGM - 2,3-bisphosphoglycerate mutase
-1.91		CeleraFN232983
-1.91	NM_007315.2	STAT1 - signal transducer and activator of transcription 1, 91kDa
-1.91	NM_006528.2	TFPI2 - tissue factor pathway inhibitor 2
-1.91	BC059410.1	hypothetical protein LOC285148 (LOC285148)
-1.92	NM_004177.3	STX3A - syntaxin 3A
-1.92	NM_018660.2	ZNF395 - zinc finger protein 395
-1.93	NM_173667.1	FLJ37543 - hypothetical protein FLJ37543
-1.93		Transcribed sequence with moderate similarity to protein sp:P09651 (H.sapiens) ROA1_HUMAN Heterogeneous nuclear ribonucleoprotein A1
-1.93	NM_001759.2	CCND2 - cyclin D2
-1.94	NM_016152.2	RARB - retinoic acid receptor, beta

-1.94	NM_014452.3	TNFRSF21 - tumor necrosis factor receptor superfamily, member 21
-1.94		tumor necrosis factor receptor superfamily, member 21 (TNFRSF21) tumor necrosis factor receptor superfamily, member 21 precursor
-1.95	NM_000689.3	ALDH1A1 - aldehyde dehydrogenase 1 family, member A1
-1.95	NM_001839.2	CNN3 - calponin 3, acidic
-1.95		CeleraFN233611
-1.96	NM_005556.2	KRT7 - keratin 7
-1.96	NM_007315.2	STAT1 - signal transducer and activator of transcription 1, 91kDa
-1.97	NM_003325.3	HIRA - HIR histone cell cycle regulation defective homolog A (S. cerevisiae)
-1.97	NM_006897.1	HOXC9 - homeo box C9
-1.97	NM_014399.2	TM4SF13 - transmembrane 4 superfamily member 13
-1.97	NM_005127.2	CLECSF2 - C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)
-1.97	NM_005102.1	FEZ2 - fasciculation and elongation protein zeta 2 (zygin II)
-1.97	NM_030810.2	TXNDC5 - thioredoxin domain containing 5
-1.98	NM_198225.1	RHOBTB1 - Rho-related BTB domain containing 1
-1.98	BC023546.2	KIAA1102 protein (KIAA1102)
-1.98	NM_000165.2	GJA1 - gap junction protein, alpha 1, 43kDa (connexin 43)
-1.98	NM_152243.1	CDC42EP1 - CDC42 effector protein (Rho GTPase binding) 1
-1.98	NM_207323.1	DKFZp667M2411;LOC114659 - hypothetical protein DKFZp667M2411;KIAA0563-related gene
-1.98	NM_004815.2	PARG1 - PTPL1-associated RhoGAP 1
-1.99	NM_019042.2	hypothetical protein FLJ20485 (FLJ20485)
-1.99	NM_002839.1	PTPRD - protein tyrosine phosphatase, receptor type, D
-2.00	NM_005402.2	RALA - v-ral simian leukemia viral oncogene homolog A (ras related)
-2.00		CeleraFN234359
-2.00	NM_024017.3	HOXB9 - homeo box B9
-2.00	NM_138373.2	MYADM - myeloid-associated differentiation marker
-2.01	NM_017515.3	SLC35F2 - solute carrier family 35, member F2
-2.01	NM_019042.2	hypothetical protein FLJ20485 (FLJ20485)
-2.02	NM_002971.2	SATB1 - special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)
-2.04		CeleraFN202664
-2.04	NM_004052.2	BNIP3 - BCL2/adenovirus E1B 19kDa interacting protein 3
-2.04	NM_152831.1	ACE - angiotensin I converting enzyme (peptidyl-dipeptidase A) 1
-2.04	NM_012329.1	MMD - monocyte to macrophage differentiation-associated
-2.04	NM_014391.2	ANKRD1 - ankyrin repeat domain 1 (cardiac muscle)
-2.06	NM_022908.1	FLJ12442 - hypothetical protein FLJ12442
-2.06	NM_022068.1	FAM38B;C18orf30 - chromosome 18 open reading frame 30;family with sequence similarity 38, member B
-2.06	NM_030797.1	DKFZP566A1524 - hypothetical protein DKFZp566A1524
-2.07	NM_002425.1	MMP10 - matrix metalloproteinase 10 (stromelysin 2)
-2.07		CeleraFN228051
-2.08	NM_031453.2	C10orf45 - chromosome 10 open reading frame 45
-2.08	NM_000259.1	MYO5A - myosin VA (heavy polypeptide 12, myoxin)
-2.08	NM_173674.1	DCBLD1 - discoidin, CUB and LCCL domain containing 1
-2.08		poly(A) binding protein interacting protein 2 (PAIP2)
-2.09	NM_020726.1	NLN - neurolysin (metallopeptidase M3 family)
-2.09	NM_031207.2	HT036 - hypothetical protein HT036
-2.09	NM_144586.3	MGC29643 - hypothetical protein MGC29643
-2.10	NM_018660.2	ZNF395 - zinc finger protein 395
-2.12	NM_138786.1	LOC116441 - hypothetical protein BC014339
-2.13	NM_012137.2	DDAH1 - dimethylarginine dimethylaminohydrolase 1
-2.13	NM_030648.1	SET7 - SET domain-containing protein 7
-2.14		CeleraFN127212
-2.15	NM_024717.2	FLJ22344 - hypothetical protein FLJ22344
-2.15	NM_022739.2	SMURF2 - E3 ubiquitin ligase SMURF2
-2.15	NM_016441.1	CRIM1 - cysteine-rich motor neuron 1
-2.17	NM_002970.1	SAT - spermidine/spermine N1-acetyltransferase
-2.17	NM_002353.1	TACSTD2 - tumor-associated calcium signal transducer 2
-2.17	BC071800.1	CDNA clone IMAGE:4666428, partial cds
-2.18	NM_019094.3	NUDT4 - nudix (nucleoside diphosphate linked moiety X)-type motif 4

-2.18	NM_000044.2	AR - androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
-2.22		CeleraFN233638
-2.22	NM_006033.1	LIPG - lipase, endothelial
-2.22	NM_014363.3	SACS - spastic ataxia of Charlevoix-Saguenay (sacsin)
-2.24		CeleraFN186558
-2.25	NM_138375.1	CABLES1 - Cdk5 and Abl enzyme substrate 1
-2.25	NM_001172.2	ARG2 - arginase, type II
-2.27	NM_003483.3	HMGA2 - high mobility group AT-hook 2
-2.28	NM_018371.3	ChGn - chondroitin beta1,4 N-acetylgalactosaminyltransferase
-2.28	NM_019117.3	KLHL4 - kelch-like 4 (Drosophila)
-2.33	NM_001124.1	ADM - adrenomedullin
-2.33	NM_001511.1	CXCL1 - chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
-2.34	AB028965.1	OIP106 - OGT(O-Glc-NAc transferase)-interacting protein 106 KDa
-2.34	NM_033516.2	NYD-SP25 - protein kinase NYD-SP25
-2.35	NM_002203.2	ITGA2 - integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
-2.36	NM_001300.3	COPEB - core promoter element binding protein
-2.37	NM_170773.1	RASSF2 - Ras association (RalGDS/AF-6) domain family 2
-2.37		Transcribed sequence with moderate similarity to protein sp:Q92503 (H.sapiens) SC14_HUMAN SEC14-like protein 1
-2.39		Similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC402628), mRNA according to UniGene - potential CONFLICT - similar to Fatty acid-binding protein, epidermal (E-FABP) (Ps
-2.39	NM_003003.1	SEC14L1 - SEC14-like 1 (S. cerevisiae)
-2.41	NM_005947.1	MT1B - metallothionein 1B (functional)
-2.42	M64936.1	CeleraFN151560
-2.44	NM_130851.1	BMP4 - bone morphogenetic protein 4
-2.45	NM_005952.2	MT1X - metallothionein 1X
-2.45	NM_003199.1	TCF4 - transcription factor 4
-2.47	NM_006009.2	TUBA3 - tubulin, alpha 3
-2.47	NM_003199.1	TCF4 - transcription factor 4
-2.50	NM_001635.2	AMPH - amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen)
-2.51	NM_001554.3	CYR61 - cysteine-rich, angiogenic inducer, 61
-2.54	NM_005946.1	MT2A;MT1K;MT1E;MT1A - metallothionein 2A;metallothionein 1K;metallothionein 1E (functional);metallothionein 1A (functional)
-2.59	BC033939.1	Clone IMAGE:5271452, mRNA
-2.59	NM_175856.2	chondroitin sulfate synthase 3 (CSS3)
-2.60	NM_175856.2	chondroitin sulfate synthase 3 (CSS3)
-2.60	NM_005946.1	MT2A;MT1K;MT1E;MT1A - metallothionein 2A;metallothionein 1K;metallothionein 1E (functional);metallothionein 1A (functional)
-2.62	NM_080760.2	DACH1 - dachshund homolog 1 (Drosophila)
-2.65	NM_138455.2	CTHRC1 - collagen triple helix repeat containing 1
-2.68	NM_198552.1	MGC15887 - hypothetical gene supported by BC009447
-2.68	NM_001444.1	FABP5 - fatty acid binding protein 5 (psoriasis-associated)
-2.69	NM_001444.1	FABP5 - fatty acid binding protein 5 (psoriasis-associated)
-2.70	NM_004309.3	ARHGDIA - Rho GDP dissociation inhibitor (GDI) alpha
-2.70	NM_022475.1	HHIP - hedgehog interacting protein
-2.71	AF333388.1	CeleraFN180868
-2.71	NM_003714.1	STC2 - stanniocalcin 2
-2.72	NM_005796.1	NUTF2 - nuclear transport factor 2
-2.73	NM_001444.1	FABP5 - fatty acid binding protein 5 (psoriasis-associated)
-2.73	NM_214461.1	MGC50273;C2orf27 - chromosome 2 open reading frame 27;MGC50273 protein
-2.74		CeleraFN217560
-2.76	NM_032181.1	FLJ13391 - hypothetical protein FLJ13391
-2.76		spermine synthase (SMS)
-2.76	NM_005946.1	MT1K;MT1E;MT1A;MT2A - metallothionein 2A;metallothionein 1K;metallothionein 1E (functional);metallothionein 1A (functional)
-2.76	NM_005946.1	MT2A;MT1K;MT1E;MT1A - metallothionein 2A;metallothionein 1K;metallothionein 1E (functional);metallothionein 1A (functional)

-2.77	NM_032935.1	MT4 - metallothionein IV
-2.78	NM_144497.1	AKAP12 - A kinase (PRKA) anchor protein (gravin) 12
-2.79	NM_080759.2	DACH1 - dachshund homolog 1 (Drosophila)
-2.81	NM_005952.2	MT1X - metallothionein 1X
-2.82		Similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC402628), mRNA according to UniGene - potential CONFLICT - similar to Fatty acid-binding protein, epidermal (E-FABP) (Ps
-2.83	NM_015068.2	paternally expressed 10 (PEG10)
-2.83		CeleraFN125490
-2.84		CeleraFN201473
-2.84	NM_001654.1	ARAF1 - v-raf murine sarcoma 3611 viral oncogene homolog 1
-2.85	NM_005824.1	LRRC17 - leucine rich repeat containing 17
-2.89	NM_005952.2	MT1X - metallothionein 1X
-2.90	NM_005951.1	MT1H - metallothionein 1H
-2.91		Similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC387934), mRNA according to UniGene - potential CONFLICT - similar to Fatty acid-binding protein, epidermal (E-FABP) (Ps
-2.98	NM_001964.2	EGR1 - early growth response 1
-3.00	NM_001955.2	EDN1 - endothelin 1
-3.04	AF086187.1	Full length insert cDNA clone ZC30H06
-3.11	NM_024607.1	PPP1R3B - protein phosphatase 1, regulatory (inhibitor) subunit 3B
-3.17	NM_014344.2	FJX1 - four jointed box 1 (Drosophila)
-3.18	NM_007036.2	ESM1 - endothelial cell-specific molecule 1
-3.19		metallothionein 2A (MT2A)
-3.23	NM_001792.2	CDH2 - cadherin 2, type 1, N-cadherin (neuronal)
-3.25	NM_001901.1	CTGF - connective tissue growth factor
-3.28	NM_000602.1	SERPINE1 - serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
-3.28		Transcribed sequence with moderate similarity to protein sp:Q93083 (H.sapiens) MT1R_HUMAN METALLOTHIONEIN-IR
-3.42	NM_003956.2	CH25H - cholesterol 25-hydroxylase
-3.48		CeleraFN234523
-3.48	NM_006653.3	FRS3 - fibroblast growth factor receptor substrate 3
-3.54	NM_005118.2	TNFSF15 - tumor necrosis factor (ligand) superfamily, member 15
-3.70	NM_002982.2	CCL2 - chemokine (C-C motif) ligand 2
-3.78	BC017966.1	CDNA FLJ16218 fis, clone CTONG3001501, highly similar to Mus musculus glucocorticoid-induced gene 1 mRNA
-3.78	NM_002852.2	PTX3 - pentaxin-related gene, rapidly induced by IL-1 beta
-3.85	NM_015687.2	FILIP1 - filamin A interacting protein 1
-3.96	NM_003246.2	THBS1 - thrombospondin 1
-4.01	NM_016270.1	KLF2 - Kruppel-like factor 2 (lung)
-4.11	M30640.1	selectin E (endothelial adhesion molecule 1) (SELE) selectin E precursor
-4.15	NM_001442.1	FABP4 - fatty acid binding protein 4, adipocyte
-4.22	NM_001147.1	ANGPT2 - angiopoietin 2
-4.32	NM_014059.1	RGC32 - response gene to complement 32
-5.00	NM_000584.2	IL8 - interleukin 8
-5.16	NM_178470.2	WDR40B - WD repeat domain 40B

Supplemental Table 2. Genes in which flow-mediated regulation is dependent on KLF2. Three independent genome-wide transcriptional profiling experiments were performed to identify genes in which regulation by athero-protective flow vs. static, no flow conditions is altered by KLF2 siRNA.

Color-coding scheme:	Up, p < 1e-15 Up, 1e-15 < p < 5e-10 Up, 5e-10 < p < 5e-5 Up, 5e-5 < p <.05 Down, p < 1e-15 Down, 1e-15 < p < 5e-10 Down, 5e-10 < p < 5e-5 Down, 5e-5 < p <.05	} As determined by Zpool
	p<.05 as determined by Iterative Standard Deviation Algorithm as described in Supplemental Methods	

Heading	Definition
Gene Name	name of gene probed
RefSeq Number	Reference Sequence number for the transcript probed
KLF2 siRNA Ratio:	fold-change in expression level between cells treated with KLF2 siRNA and cells treated with control siRNA, both in the presence of athero-protective waveform
KLF2 siRNA p Value:	p value for the KLF2 siRNA Ratio
Flow/Static Ratio:	fold-change in expression level between cells exposed to athero-protective waveform and cells cultured under static, no flow conditions, both in the presence of control siRNA
Flow/Static p Value:	p value for the Flow/Static Ratio

Gene Name	RefSeq Number	KLF2 siRNA Ratio	KLF2 siRNA p Value	Flow/ Static Ratio	Flow/ Static P Value
PI16 - protease inhibitor 16	NM_153370.1	-19.34	1E-15	25.35	1E-15
H19, imprinted maternally expressed untranslated mRNA (H19)	AK123560.1	-7.27	7E-05	4.06	1E-03
NOV - nephroblastoma overexpressed gene	NM_002514.2	-6.65	6E-05	22.29	1E-15
FLJ45224;PTGDS - FLJ45224 protein;prostaglandin D2 synthase 21kDa (brain)	NM_000954.5	-6.65	4E-02	10.65	4E-02
CCRL1 - chemokine (C-C motif) receptor-like 1	NM_178445.1	-6.55	4E-09	2.63	1E-04
SLCO2A1 - solute carrier organic anion transporter family, member 2A1	NM_005630.1	-5.25	1E-15	69.93	1E-15
Similar to Argininosuccinate synthase (Citrulline--aspartate ligase) (LOC402687), mRNA according to UniGene - potential CONFLICT - similar to Argininosuccinate synthase (Citrulline--aspartate ligase) (na) according to LocusLink.		-4.78	3E-02	8.1	6E-07
FBLN2 - fibulin 2	NM_001998.1	-4.48	2E-08	3.76	2E-03
S100A4 - S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	NM_019554.1	-4.47	6E-05	3.81	6E-03
GPR48 - G protein-coupled receptor 48	NM_018490.1	-4.47	3E-04	3.64	2E-03
argininosuccinate synthetase (ASS)		-4.41	7E-05	8.51	3E-10
NGEF - neuronal guanine nucleotide exchange factor	NM_019850.1	-4.11	2E-07	9.7	9E-06
argininosuccinate synthetase (ASS)		-3.97	1E-15	8.29	1E-15
CeleraFN233804		-3.76	1E-15	5.04	3E-02
C10orf10 - chromosome 10 open reading frame 10	NM_007021.2	-3.75	7E-07	-12.43	1E-15
CRIP1;C14orf80 - cysteine-rich protein 1 (intestinal);chromosome 14 open reading frame 80	NM_173608.1	-3.64	1E-15	12.57	2E-03

FLJ10970 - hypothetical protein FLJ10970	NM_018286.1	-3.57	2E-02	30.92	4E-03
SULF1 - sulfatase 1	NM_015170.1	-3.54	1E-02	4.87	2E-03
TOP2A - topoisomerase (DNA) II alpha 170kDa	NM_001067.2	-3.43	1E-05	-7.46	1E-15
argininosuccinate synthetase (ASS)		-3.4	2E-06	11.01	1E-06
argininosuccinate synthetase (ASS)		-3.34	1E-15	9.7	1E-15
FOXM1 - forkhead box M1	NM_021953.2	-3.34	8E-05	-2.56	1E-02
BIRC5 - baculoviral IAP repeat-containing 5 (survivin)	NM_001168.1	-3.32	8E-07	-7.74	3E-05
LCN10;LCN6 - lipocalin 10;lipocalin 6	NM_198946.2	-3.23	2E-05	14.2	5E-05
CENPF - centromere protein F, 350/400ka (mitosin)	NM_016343.2	-3.22	1E-03	-3.3	2E-05
CeleraFN229737		-3.21	1E-03	8.68	4E-02
argininosuccinate synthetase (ASS)		-3.14	2E-07	6.03	3E-10
PPAP2A - phosphatidic acid phosphatase type 2A	NM_176895.1	-3.12	7E-03	5.84	1E-15
Transcribed sequence with weak similarity to protein pir:OSHU7B (H.sapiens) OSHU7B cytochrome-c oxidase		-3.12	7E-03	2.85	3E-02
Transcribed sequences (CeleraFN186161)		-3.02	3E-04	4.26	2E-02
FCN3 - ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	NM_003665.2	-3	1E-09	42.9	2E-03
FBN1 - fibrillin 1 (Marfan syndrome)	NM_000138.2	-2.99	1E-15	2.04	5E-03
placenta-specific 9 (PLAC9)	BC066348.1	-2.93	1E-15	10.19	1E-15
S100P - S100 calcium binding protein P	NM_005980.2	-2.89	1E-15	65.15	1E-15
IL1R1 - interleukin 1 receptor, type I	NM_000877.2	-2.86	7E-07	3.45	2E-05
KIAA0101 - KIAA0101	NM_014736.3	-2.84	1E-04	-4.53	1E-15
ASS - argininosuccinate synthetase	NM_000050.2	-2.76	6E-03	5.9	3E-03
PLAC8 - placenta-specific 8	NM_016619.1	-2.7	4E-05	12.14	8E-03
RAMP3 - receptor (calcitonin) activity modifying protein 3	NM_005856.1	-2.65	1E-04	5.32	5E-07
COL23A1 - collagen, type XXIII, alpha 1	NM_173465.2	-2.63	1E-03	4.42	5E-03
CeleraFN701053	AK025151.1	-2.63	5E-03	3.42	3E-02
CeleraFN138145		-2.59	8E-06	3.14	4E-03
ZWINT - ZW10 interactor	NM_007057.2	-2.59	1E-02	-3.25	2E-07
CXCL12 - chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	NM_000609.3	-2.55	3E-03	11.73	5E-04
RAMP2 - receptor (calcitonin) activity modifying protein 2	NM_005854.1	-2.52	1E-15	3.94	1E-15
Similar to eukaryotic translation elongation factor 1 alpha 1; CTCL tumor antigen; translation elongation factor 1 alpha 1-like 14; prostate tumor-inducing protein 1; EF1a-like protein; glucocorticoid receptor AF-1 specific elongation fa ... accordi		-2.51	1E-06	5.33	4E-02
APOL2 - apolipoprotein L, 2	NM_145637.1	-2.51	1E-08	2.2	1E-02
TYMS - thymidylate synthetase	BC013919.1	-2.49	1E-05	-4.66	1E-15
FSTL1 - follistatin-like 1	NM_007085.3	-2.38	5E-11	2.38	7E-05
FGFR3 - fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	NM_022965.1	-2.36	8E-03	9.37	2E-03
APOL1 - apolipoprotein L, 1	NM_003661.2	-2.33	8E-03	3.43	5E-04
CeleraFN216738		-2.27	7E-09	7.26	1E-15
PRC1 - protein regulator of cytokinesis 1	NM_003981.2	-2.27	7E-03	-3.04	2E-07
DGKA - diacylglycerol kinase, alpha 80kDa	NM_201554.1	-2.24	1E-03	2.8	2E-03
SYNCOILIN - intermediate filament protein syncoilin	NM_030786.1	-2.19	9E-03	3.1	6E-03
PLCG2 - phospholipase C, gamma 2 (phosphatidylinositol-specific)	NM_002661.1	-2.19	2E-03	2.65	6E-03
DHFR - dihydrofolate reductase	NM_000791.2	-2.18	2E-02	-2.69	9E-04

PLAC8 - placenta-specific 8	NM_016619.1	-2.17	5E-03	6.97	2E-05
CYP1B1 - cytochrome P450, family 1, subfamily B, polypeptide 1	NM_000104.2	-2.16	2E-08	50.08	1E-15
Transcribed sequences (CeleraFN165327)		-2.15	2E-03	2.63	2E-02
CeleraFN232775		-2.14	1E-05	2.6	1E-04
PTTG1 - pituitary tumor-transforming 1	NM_004219.2	-2.11	1E-02	-4.14	9E-12
KLF2 - Kruppel-like factor 2 (lung)	NM_016270.1	-2.07	3E-10	12.69	1E-15
C9orf3 - chromosome 9 open reading frame 3	NM_032823.3	-2	5E-02	4.51	3E-04
CeleraFN228104		-1.94	7E-07	2.65	2E-07
PTTG3 - pituitary tumor-transforming 3	NM_021000.1	-1.91	3E-02	-5.17	1E-15
CADPS2 - Ca2+-dependent activator protein for secretion 2	NM_017954.7	-1.9	5E-02	2.55	3E-04
LMO7 - LIM domain only 7	NM_005358.3	-1.84	8E-03	5.45	1E-15
FLJ33915 - hypothetical protein FLJ33915	NM_182613.1	-1.84	3E-06	2.09	2E-04
KDELR2 - KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	NM_017756.1	-1.81	2E-02	-2.03	3E-02
CD58 - CD58 antigen, (lymphocyte function-associated antigen 3)	NM_001779.1	-1.8	1E-02	5.9	1E-15
CALCRL - calcitonin receptor-like	NM_005795.2	-1.8	4E-04	4.11	6E-03
SLC16A2 - solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transporter)	NM_006517.1	-1.8	4E-02	3.3	7E-05
C10orf116 - chromosome 10 open reading frame 116	NM_006829.2	-1.77	6E-03	4.34	1E-15
PTPRG - protein tyrosine phosphatase, receptor type, G	NM_002841.2	-1.74	4E-02	4.28	2E-03
EMP3 - epithelial membrane protein 3	NM_001425.1	-1.71	2E-03	7.16	1E-15
CeleraFN230384		-1.71	4E-03	2.13	2E-02
STOM - stomatin	NM_004099.4	-1.7	4E-02	2.53	8E-03
MN1 - meningioma (disrupted in balanced translocation) 1	NM_002430.1	-1.67	5E-03	7.61	1E-15
BMP-binding endothelial regulator precursor protein (BMPER)		-1.66	4E-02	11.27	1E-09
DSTN - destrin (actin depolymerizing factor)	NM_006870.2	-1.61	1E-05	3.4	1E-15
PRKCDBP - protein kinase C, delta binding protein	NM_145040.2	-1.58	3E-02	2.31	2E-06
CeleraFN230369		-1.57	2E-03	1.99	1E-03
SRP14 - signal recognition particle 14kDa (homologous Alu RNA binding protein)	NM_003134.2	-1.57	2E-04	1.7	3E-02
TPM4 - tropomyosin 4	NM_003290.1	-1.45	3E-02	1.77	7E-03
SERPINE1 - serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_000602.1	1.42	3E-04	1.57	1E-02
CTGF - connective tissue growth factor	NM_001901.1	1.47	2E-02	2.31	3E-07
GPX1 - glutathione peroxidase 1	M21304.1	1.63	2E-02	-3.4	1E-15
SCHIP1 - schwannomin interacting protein 1	NM_014575.1	1.68	3E-03	-2.12	2E-03
Similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC387934), mRNA according to UniGene - potential CONFLICT - similar to Fatty acid-binding protein, epidermal (E-FABP)		1.76	4E-05	-5.19	1E-15
SGK - serum/glucocorticoid regulated kinase	NM_005627.2	1.79	1E-04	9.29	1E-15
Similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC402628), mRNA according to UniGene - potential CONFLICT - similar to Fatty acid-binding protein, epidermal (E-FABP) (Ps		1.82	3E-04	-4.91	1E-15
TUBA3 - tubulin, alpha 3	NM_006009.2	1.84	2E-07	-2.02	1E-04
BCL6B - B-cell CLL/lymphoma 6, member B (zinc	NM_181844.2	1.9	9E-03	-2.96	3E-03

finger protein)					
FJX1 - four jointed box 1 (Drosophila)	NM_014344.2	1.98	2E-02	-3.13	6E-03
CLDN5 - claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	NM_003277.2	1.98	4E-02	-10.13	2E-07
SOX4 - SRY (sex determining region Y)-box 4	NM_003107.2	1.99	9E-06	-2.89	7E-09
FABP5 - fatty acid binding protein 5 (psoriasis-associated)	NM_001444.1	1.99	2E-07	-5.72	1E-15
FABP5 - fatty acid binding protein 5 (psoriasis-associated)	NM_001444.1	2.02	2E-08	-5.6	1E-15
SLC4A7 - solute carrier family 4, sodium bicarbonate cotransporter, member 7	NM_003615.2	2.03	8E-03	-3.57	9E-09
TCF4 - transcription factor 4	NM_003199.1	2.05	3E-07	-3.61	1E-15
FABP5 - fatty acid binding protein 5 (psoriasis-associated)	NM_001444.1	2.06	9E-10	-5.88	1E-15
CLECSF2 - C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	NM_005127.2	2.07	9E-04	-3.47	1E-08
TGIF - TGFB-induced factor (TALE family homeobox)	NM_173211.1	2.16	3E-07	-2.63	4E-05
CXCR4 - chemokine (C-X-C motif) receptor 4	NM_003467.1	2.21	4E-05	-22.06	1E-15
KITLG - KIT ligand	NM_003994.3	2.25	1E-05	3.28	2E-02
PHLDA1 - pleckstrin homology-like domain, family A, member 1	NM_007350.1	2.25	1E-03	-2.62	8E-03
Similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC402628), mRNA according to UniGene - potential CONFLICT - similar to Fatty acid-binding protein, epidermal (E-FABP) (Ps		2.25	2E-09	-6.01	1E-15
ADM - adrenomedullin	NM_001124.1	2.35	2E-02	-5.1	1E-10
CYR61 - cysteine-rich, angiogenic inducer, 61	NM_001554.3	2.54	1E-15	-2.12	2E-03
KIAA0040 gene product (KIAA0040)	D25539.1	2.81	8E-04	-3.27	3E-03
CHST1 - carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	NM_003654.2	2.86	1E-06	-26.03	1E-15
PDE4B - phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_002600.2	3.35	3E-10	-5.08	2E-09
CDNA clone IMAGE:5092935, partial cds	BC052239.1	3.65	3E-03	-10.51	4E-08
RGC32 - response gene to complement 32	NM_014059.1	3.99	7E-05	-10.98	1E-15
TNFSF15 - tumor necrosis factor (ligand) superfamily, member 15	NM_005118.2	4.36	8E-04	-16.92	1E-15
ANGPT2 - angiopoietin 2	NM_001147.1	6.13	7E-05	-26.18	1E-15

Supplemental Methods

Microarray processing and statistics

Array images were processed using the Applied Biosystems 1700 Array Scanner software, to generate spot quantifications and exclude poor quality spots. Genes differentially regulated between any two conditions (X and Y) were detected based on three pairs of replicate arrays for condition X and condition Y. Spot measurements between paired arrays for each comparison were normalized between conditions using Lowess (1). Regulated genes are comprised of the statistically significant ($p<.05$) genes selected from either of two methods. The first method involved using a minimum intensity variance estimation-based Z-test, a method termed Zpool (2). The second method involved calculating p values based on a standard deviation which was determined through an iterative process. Through each iteration, a recalculation of the standard deviation was performed after the removal of genes regulated more than 2.5 standard deviations from the mean. Iterations were performed until the standard deviation converged (<.001).

GEDI Clustering

Self-organizing maps were generated from transcriptional profiling data using software described elsewhere (3). Only genes that were regulated an average of at least twofold in at least one condition relative to control (Ad-GFP) were included in map generation. Cluster regions were designated based on the following criteria:

	Ad-KLF2	**Ad-GFP+IL-1**	**Ad-KLF2+IL-1**
I	< 0.5 * Ad-GFP+IL-1	> 0.5 & < 2	< 0.5 * Ad-GFP+IL-1
II	> 2	> 0.5 & < 2	> 2
III	< 2	$> 2^{1.5}$	< 0.5 * Ad-GFP+IL-1
IV	> 0.5 * Ad-GFP+IL-1 & < 2 * Ad-GFP+IL-1	> 0.5 * Ad-KLF2 & < 2 * Ad-KLF2	> 2 * Ad-KLF2 & > 2 * Ad-GFP+IL-1

Ad-KLF2, Ad-GFP+IL-1, and Ad-KLF2+IL-1 denote the non-logged expression of genes in each experimental condition relative to Ad-GFP.

Prostaglandin extraction for 15d-PGJ2 ELISA

Prior to analysis, prostaglandin was acid extracted on a reverse phase column from 2 mL supernatant. Samples were acidified to ~pH 3.0 by addition of 100 µL 2N HCl followed by incubation at 4 degrees for 15 minutes. Samples were cleared by centrifugation at RT for 2 minutes. Amprep C-18 500 µg minicolumns (Amersham Biosciences) were equilibrated by washing with 10 volumes (28 mL) of ethanol followed by 10 volumes of water. Samples were then applied using slight positive pressure (flow rate ~0.5 mL/min), and the columns were washed with 28 mL of water, 28 mL 15% ethanol, and 28 mL hexane. Prostaglandins were then eluted with 20 mL ethyl acetate. The samples were then evaporated under a stream of nitrogen; 50 µl was added to the dried samples, followed by reconstitution with 200 µL of assay buffer provided in the kit.

Zebrafish probes and in situ hybridization

RT-PCR was used to amplify zebrafish KLF2a from total embryo RNA with the following primers (1) 5'-ATGCATCTCAGCTGCATAGCTGACCTATCT-3' and (2) 5'-TAATACGACTCACTATAGGGCTACATATGACGTTTCATATGAAGG-3'. KLF2a probe was transcribed using T7 polymerase and digoxin labelled using a kit (Roche). Flk probe was transcribed from a clone described previously (4). In situ hybridization of pooled embryos was performed as described previously (5), after which silent heart mutants were scored by visualizing the yolk sac indentation due to pericardial edema.

Transfection of siRNA Duplexes into HUVEC

HUVEC were plated 16 hours prior to transfection at a density of 40,000 cells/cm^2 in HUVEC growth medium without antibiotics. At the time of transfection with siRNA, the cells were 85-95% confluent. Individual siRNAs (KLF2 siRNA a & b, 6 nmol each, or negative control siRNA, 12 nmol) were mixed with Oligofectamine (80 μl) and Opti-MEM (Invitrogen) in a final volume of 2 ml and incubated at room temperature for 15 min for the lipid-siRNA complex to form. Cells were washed once and 8ml Opti-MEM was added. The 2 ml Oligofectamine-siRNA complex solution was then added dropwise to the cells. The cells were then incubated for 6 hours at 37°C, and then 5 ml HUVEC growth medium was added. Flow experiments were performed 24 hours after the siRNA transfection. Interferon response was monitored in every sample for each siRNA experiment by RT-PCR of the dsRNA-responsive genes 2'-5'-oligoadenylate synthetase (OAS2) and interferon-induced transmembrane protein 1 (IFITM1). 10 µg/mL Poly(I)·Poly(C) dsRNA (Sigma) was used as a positive control for induction of the interferon response. No upregulation of the two genes tested was found in any of the siRNA transfection experiments.

References (for Supplemental Methods)

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3. Eichler, G.S., Huang, S., and Ingber, D.E. 2003. Gene Expression Dynamics Inspector (GEDI): for integrative analysis of expression profiles. *Bioinformatics* 19:2321-2322.

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