

Human Herpesvirus-8 Infection of Primary Pulmonary Microvascular Endothelial Cells

Todd M. Bull¹, Christina A. Meadows¹, Christopher D. Coldren¹, Mark Moore¹, Sylk M. Sotto-Santiago¹, Serge P. Nana-Sinkam², Thomas B. Campbell³, and Mark W. Geraci¹

¹Division of Pulmonary Sciences and Critical Care Medicine, and ³Division of Infectious Diseases, University of Colorado Health Sciences Center, Denver, Colorado; and ²Division of Pulmonary, Allergy, Critical Care and Sleep Medicine, The Ohio State University, Columbus, Ohio

Online Data Supplement

Corresponding author:

Todd M. Bull, MD
University of Colorado, Denver Health Sciences Center
Division of Pulmonary Sciences and Critical Care Medicine C-272
4200 E 9th Avenue
Denver, CO 80207
Todd.Bull@uchsc.edu

Expanded Materials and Methods

Preparation of RNA

Total RNA was extracted from HMVEC-L cells with the RNeasy Mini Kit (Qiagen, Valencia, CA). The concentration of each RNA sample was determined based on the absorbance at 260 nm (A₂₆₀). The purity of each sample was determined based on the ratio of A₂₆₀ to A₂₈₀. A range of 1.9-2.0 was considered adequately pure. Five micrograms of total RNA was converted to double-stranded cDNA (ds-cDNA) by using Superscript Choice System (Life Technologies, Rockville, MD). An oligo-dT primer containing a T7 RNA polymerase promoter (Promega Corporation, Madison, WI) was utilized. After second strand synthesis, the reaction product was isolated using GeneChip Sample Cleanup Module (Affymetrix, Santa Clara, CA).

In Vitro Transcription

In vitro transcription, to generate biotin-labeled cRNA, was performed using a BioArray High Yield RNA Transcript labeling Kit from Enzo (Farmingdale, NY). The double-stranded cDNA template was transcribed in the presence of a mixture of unlabeled ATP, CTP, GTP and UTP, plus biotin-labeled CTP and UTP (bio-11-CTP and bio-16-UTP). Biotin-labeled cRNA was purified using GeneChip Sample Cleanup Module (Affymetrix, Santa Clara, CA). To ensure optimal hybridization to the oligonucleotide array, the cRNA was fragmented. Fragmentation was performed by incubating the cRNA at 94° C for 35 minutes to produce cRNA fragments between 35-200 bases in length. The sample was then added to a hybridization solution containing 100 mM MES, 1 M Na⁺, and 20

mM EDTA in the presence of 0.01% Tween 20 to a final cRNA concentration of 0.05 micrograms/microliter.

Hybridization of the GeneChip

Hybridization was performed for 18-20 hours by incubating 200 ml of the sample on the Affymetrix GeneChip[®] (Affymetrix, Santa Clara, CA). After hybridization, the hybridization solutions were removed and the GeneChips were washed and stained with Streptavidin-phycoerythrin. Chips were read at a resolution of 1.53 microns with an Affymetrix GeneChip 3000 scanner (Affymetrix, Santa Clara, CA).

A MIAME checklist (see below) was used for array generation. Hybridization signals and detection calls were generated in BioConductor, using the *germa* and *affy* packages⁵⁰, and has been deposited in the NCBI GEO database, accession number GSE6489.

Fluorescence intensities were quantified using the Affymetrix Microarray Suite 5.0 statistical algorithm with default parameters for the array type used in this study (Affymetrix, Santa Clara, CA).

MIAME Checklist

This section contains the experimental details for this study, as recommended by the Microarray Gene Expression Data society.

Experimental Design:

- Direct comparison of HHV8-infected and mock-infected human pulmonary microvascular endothelial cells.
- Triplicate infection and mock infection samples were prepared. One hybridization per sample, 6 total hybridizations
- Single channel hybridization (no reference).
- Internal quality control for each hybridization includes comparison of overall intensity across all arrays (intensity varied within 2 standard deviations of the median intensity) and the integrity of the labeled target as determined by the ratio of hybridization intensity to 3' and 5' regions of GAPD and β -Actin (3'/5' ratios were less than 3 for all arrays).

Samples used, extract preparation and labeling:

- Human pulmonary microvascular endothelial cells (HMVEC-L, Clonetics, Walkersville MD), mock-infected or infected with Human herpesvirus-8.
- RNA extracted separately from each of three biological replicates.
- RNA extraction described above. RNA quality assessed by spectrophotometry ($A_{260}/A_{280} > 1.8$) and Agilent Bioanalyzer (28S/18S rRNA intensity > 1.5).
- Target labeling described above.
- Affymetrix Eukaryotic Hybridization Control mixture employed as external control.

Hybridization procedures and parameters: as described above

Measurement data and specifications:

- The complete set of gene expression data has been deposited in the GEO database (www.ncbi.nlm.nih.gov/geo/, we are awaiting final accession number and will forward this information to the editors upon receipt.). Image acquisition, signal quantification and normalization are described above.
- Data selection and transformation are described above.

Array Design:

- Affymetrix Hu133 Plus 2.0 arrays (part # 900469) were used in this study. This array design is described on the manufacturer's web site, and is described in GEO, as platform GPL 570.

Primer sequences for q-PCR:

LANA-1: Forward 5'-GCCGGTGGAGGTAAAGGTG-3' and Reverse 5'-GTCTAGTCCTACTTTACCGGTGGC-3';

ORF50: Forward 5'-GACAACCCGAGCTCTTTCCTG-3' and Reverse 5'-GCTGGGCCACTATAACCGTG-3';

K8.1A/B: Forward 5'-CCTGTGGCGCTCCTAATCC-3' and Reverse 5'-CGATACGTGGGACAATTGGC-3';

vGPCR: Forward 5'-CATTTTGGTGTGCGTTTTG-3' and Reverse 5'-CGGGAAAGAATATGATCCACG-3';

T1.1: Forward 5'-GCCGCTTCTGGTTTTTCATTG-3' and Reverse 5'-GTATATTGCCAAAAGCGACGC-3'; and

HPRT: Forward 5'-TGCTTTCCTTGGTCAGGCAG-3' and Reverse 5'-
AGCTTGCGACCTTGACCATC-3'

Protein Immunoblot Assay:

Samples were diluted to 10 μ g in 300 μ l PBS final volume, and then entire sample was applied to PVDF membrane (Osmonics, Inc., Minnetonka, MN) within a Minifold II slot blot manifold system (Schleicher & Schuell, Whatman plc, Middlesex, UK), following blotting protocol for Minifold II system by Schleicher & Schuell. Positive control cell lysate DU 145 (Santa Cruz Biotechnology Inc., Santa Cruz, CA) was diluted to 10 μ g in 300 μ l PBS and applied to membrane. Bovine Serum Albumin (Fisher Scientific, Fair Lawn, NJ) was diluted to 20 μ g, 10 μ g, and 5 μ g in 300 μ l each and applied to membrane for an irrelevant protein negative control, (data not shown). After samples were drawn into the membrane by vacuum, the membrane was blocked for 12 hours in 5% nonfat dry milk in Tris-buffered saline (TBS) at 4°C with continuous rocking. The membrane was incubated with primary α -BMPRIa antibody (Santa Cruz Biotechnology Inc., Santa Cruz, CA) at 1:200 or with α -BMP4 antibody (abCam, Cambridge MA) and then with secondary α -goat antibody or α -mouse antibody conjugated to alkaline phosphatase (Promega Corp, Madison, WI) at 1:5000. The membrane was then developed with Western Blue substrate (Promega Corp, Madison, WI) for 5 minutes. All incubations were for 2 hours at room temperature with continuous rocking. The membrane was washed between stains 3 times, 5 minutes each in TBS with 0.05% Tween-20 (TBST). All antibodies were diluted with 3% BSA in TBST. The membrane was imaged using a

Kodak imager and analyzed with Kodak software; density of the immunoblot was determined in relative units.

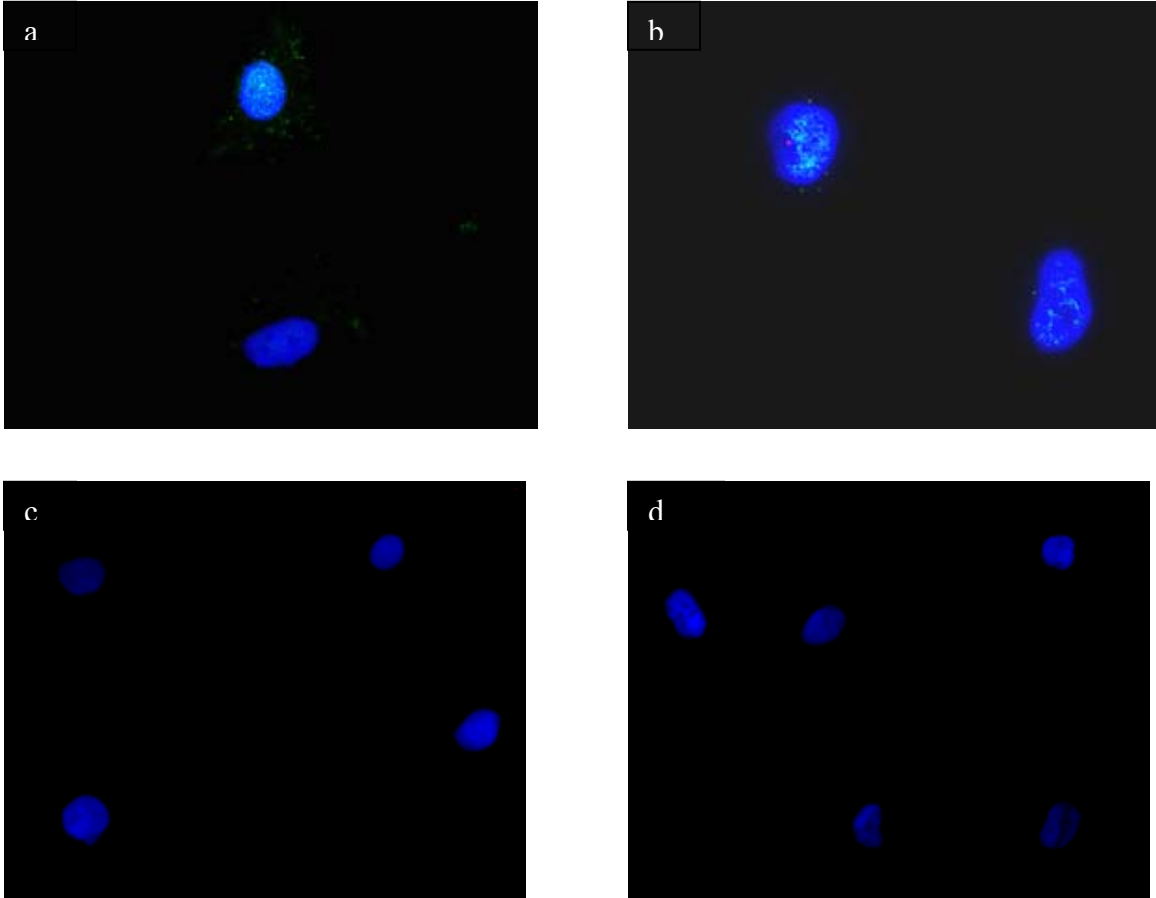


Figure E1: Co-culture infection of HMVEC-L. Representative LANA-1 staining of HMVEC-L exposed to BCBL-1 cells and then assayed by IFA at days 10, 15 and 20. a) and b) demonstrate LANA-1 positive staining of HMVEC-L at day 15 and 20 (similar findings at day 10 not shown). c) There were no LANA-1 positive cells in HMVEC-L exposed to conditioned media (media collected from infected cells but without infectious virus). d) There were no LANA-1 positive HMVEC-L in untreated cells (negative control). 40x magnification. Green indicates positive LANA-1 staining. Blue represents Hoechst nuclear staining.

Comparison of HHV-8 infection between time points and techniques

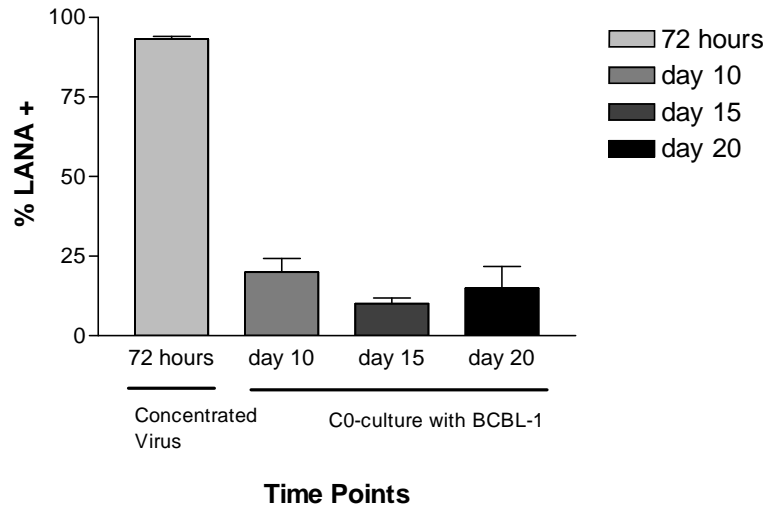


Figure E2: Comparison of percent of HMVEC-L infected with HHV-8 at different time points and two different infection techniques. The first column represents the % of LANA-1 positive cells at 72 hours following exposure to concentrated virus, (the infection technique used to generate the microarrays). The remaining columns represent the % of LANA-1 positive cells at the 3 time points assayed after initial co-culture and then removal of BCBL-1 cells (the infection technique used for the apoptosis experiments).

Supplemental Tables

Table E1: Transcripts increased in HMVEC-L cells upon infection with HHV-8. Genes listed in this table meet the stringent criteria ($p < 0.001$) for differential expression in a two sample t-test between HHV-8 infected and mock-infected cells ($n=3$ per group). Columns 1 and 2 report the mean signal intensity in the HHV-8 Infected and Mock Infected groups.

Infected	Mock	Fold chg	Probe set	symbol	name
4510.6	61.4	73.5	204475_at	MMP1	matrix metalloproteinase 1 (interstitial collagenase)
770.8	11.5	67.0	203477_at	COL15A1	collagen, type XV, alpha 1
385.1	15.9	24.2	204994_at	MX2	myxovirus (influenza virus) resistance 2 (mouse)
194.6	8.6	22.6	204439_at	IFI44L	interferon-induced protein 44-like
169.2	7.5	22.6	231798_at	NOG	Noggin
104.2	5.3	19.7	212909_at	LYPD1	LY6/PLAUR domain containing 1
2818.8	144.5	19.5	217757_at	A2M	alpha-2-macroglobulin
135.6	7.8	17.4	211122_s_at	CXCL11	chemokine (C-X-C motif) ligand 11
3291.3	202.2	16.3	203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1
1667.6	116.1	14.4	226702_at	LOC129607	hypothetical protein LOC129607
185.8	13.5	13.8	213797_at	RSAD2	radical S-adenosyl methionine domain containing 2
280.4	20.6	13.6	242625_at	RSAD2	radical S-adenosyl methionine domain containing 2
5004.8	384.3	13.0	202086_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78
242.4	19.5	12.4	203498_at	DSCR1L1	Down syndrome critical region gene 1-like 1
103.4	8.6	12.0	230112_at	MARCH4	membrane-associated ring finger (C3HC4) 4
268.9	25.3	10.6	230746_s_at	STC1	Stanniocalcin 1
311.9	30.2	10.3	219352_at	HERC6	hect domain and RLD 6
4897.9	499.2	9.8	222856_at	APLN	apelin, AGTRL1 ligand
130.6	14.1	9.3	210163_at	CXCL11	chemokine (C-X-C motif) ligand 11
122	13.4	9.1	201641_at	BST2	bone marrow stromal cell antigen 2
313.9	35.3	8.9	219872_at	DKFZp434L142	hypothetical protein DKFZp434L142
392.6	48	8.2	1559221_at	5583725	Homo sapiens, clone IMAGE:5583725, mRNA
180.3	22.2	8.1	227289_at	LOC144997	hypothetical protein LOC144997
414.1	51.6	8.0	228863_at	PCDH17	Protocadherin 17
949.4	118.5	8.0	221371_at	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18
1039.4	130.7	8.0	223204_at	DKFZp434L142	hypothetical protein DKFZp434L142
367.6	46.6	7.9	1556314_a_at	1NIB-4	(clone 1NIB-4) normalized cDNA library sequence
295.9	38.3	7.7	220037_s_at	XLKD1	extracellular link domain containing 1
690.7	94.2	7.3	204747_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
493.2	68.3	7.2	220116_at	KCNN2	potassium conductance calcium-activated channel, subfamily N, member 2
66.1	9.2	7.2	213415_at	CLIC2	chloride intracellular channel 2
978.5	140.3	7.0	226498_at	FLT1	Fms-related tyrosine kinase 1 (vascular endothelial growth factor receptor)
180.8	26.1	6.9	244280_at	ZC30H06	Full length insert cDNA clone ZC30H06
110.2	16.1	6.8	205656_at	PCDH17	protocadherin 17
2267.8	335.4	6.8	237261_at	MCPH1	Microcephaly, primary autosomal recessive 1
2628	398.3	6.6	229450_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3

Infected	Mock	Fold chg	Probe set	symbol	name
215.3	33	6.5	223454_at	CXCL16	chemokine (C-X-C motif) ligand 16
1409.6	216.9	6.5	204972_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
1163.9	184.6	6.3	222033_s_at	FLT1	Fms-related tyrosine kinase 1 (vascular endothelial growth factor receptor)
318.1	51.8	6.1	206786_at	HTN3	histatin 3
65.5	10.7	6.1	206715_at	TFEC	transcription factor EC
46.3	7.6	6.1	232099_at	PCDHB16	protocadherin beta 16
65	10.7	6.1	205660_at	OASL	2'-5'-oligoadenylate synthetase-like
6113.2	1024.5	6.0	205572_at	ANGPT2	angiopoietin 2
106.1	17.8	6.0	219655_at	C7orf10	chromosome 7 open reading frame 10
53	8.9	6.0	207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4
3490.6	591.8	5.9	236034_at	ANGPT2	Angiopoietin 2
666.1	113.7	5.9	226757_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2
93.3	16.1	5.8	214059_at	IFI44	Interferon-induced protein 44
69.1	12.1	5.7	205207_at	IL6	interleukin 6 (interferon, beta 2)
665.7	119.8	5.6	219211_at	USP18	ubiquitin specific peptidase 18
42.6	7.7	5.5	204595_s_at	STC1	stanniocalcin 1
418.3	78	5.4	205680_at	MMP10	matrix metalloproteinase 10 (stromelysin 2)
1022.9	192.9	5.3	214453_s_at	IFI44	interferon-induced protein 44
339.2	65.5	5.2	227677_at	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
829.8	161.8	5.1	226497_s_at	FLT1	Fms-related tyrosine kinase 1 (vascular endothelial growth factor receptor)
98.7	19.3	5.1	214022_s_at	IFITM1	interferon induced transmembrane protein 1 (9-27)
438.3	85.9	5.1	221489_s_at	SPRY4	sprouty homolog 4 (Drosophila)
11174.6	2194.3	5.1	205483_s_at	G1P2	interferon, alpha-inducible protein (clone IFI-15K)
7387.2	1460.8	5.1	211148_s_at	ANGPT2	angiopoietin 2
338.4	67.3	5.0	206553_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
322.9	64.4	5.0	219059_s_at	XLKD1	extracellular link domain containing 1
27.2	5.5	4.9	209031_at	IGSF4	Immunoglobulin superfamily, member 4
135.9	28.1	4.8	210797_s_at	OASL	2'-5'-oligoadenylate synthetase-like
475.3	99.4	4.8	214438_at	HLX1	H2.0-like homeo box 1 (Drosophila)
669.7	145.3	4.6	202411_at	IFI27	interferon, alpha-inducible protein 27
315.2	71.9	4.4	223657_at	C1orf90	chromosome 1 open reading frame 90
188.5	44.4	4.2	210287_s_at	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor receptor)
39.6	9.5	4.2	215033_at	TM4SF1	transmembrane 4 L six family member 1
220.2	53	4.2	230968_at		Full-length cDNA clone CS0DF032YA11 of Fetal brain of Homo sapiens (human)
143.2	34.7	4.1	222868_s_at	IL18BP	interleukin 18 binding protein
292.2	73	4.0	1559883_s_at	SAMHD1	SAM domain and HD domain 1
1061.6	265.6	4.0	223220_s_at	PARP9	poly (ADP-ribose) polymerase family, member 9
64.4	16.3	4.0	236570_at	ZNF366	zinc finger protein 366
1368.3	347.1	3.9	234987_at	C20orf118	Chromosome 20 open reading frame 118
293.4	75.1	3.9	205466_s_at	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
101.2	26.2	3.9	219863_at	HERC5	hect domain and RLD 5
86.1	22.4	3.8	1552489_s_at	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
703.1	184.2	3.8	227609_at	EPSTI1	epithelial stromal interaction 1 (breast)
689.3	189.9	3.6	209417_s_at	IFI35	interferon-induced protein 35

Infected	Mock	Fold chg	Probe set	symbol	name
57.5	15.9	3.6	235061_at	PPM1K	protein phosphatase 1K (PP2C domain containing)
1006.2	282.2	3.6	235529_x_at	C20orf118	Chromosome 20 open reading frame 118
448	126.6	3.5	207414_s_at	PCSK6	proprotein convertase subtilisin/kexin type 6
31.6	9	3.5	1552760_at	HDAC9	histone deacetylase 9
112.6	32.3	3.5	204533_at	CXCL10	chemokine (C-X-C motif) ligand 10
1303.2	382.9	3.4	222911_s_at	CXorf36	chromosome X open reading frame 36
1776.6	530.7	3.3	226302_at		Transcribed locus
788.6	240.8	3.3	227697_at	SOCS3	suppressor of cytokine signaling 3
875.7	267.5	3.3	235964_x_at	C20orf118	Chromosome 20 open reading frame 118
93.1	28.7	3.2	235643_at	SAMD9L	sterile alpha motif domain containing 9-like
760.7	234.8	3.2	204415_at	G1P3	interferon, alpha-inducible protein (clone IFI-6-16)
213.8	66	3.2	205366_s_at	HOXB6	homeo box B6
168.7	52.1	3.2	228167_at	KLHL6	kelch-like 6 (Drosophila)
6573.8	2052.4	3.2	218723_s_at	RGC32	response gene to complement 32
311.3	97.2	3.2	220334_at	RGS17	regulator of G-protein signalling 17
250.8	78.4	3.2	228230_at	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285
640.2	200.6	3.2	208436_s_at	IRF7	interferon regulatory factor 7
180.3	56.7	3.2	226301_at	C6orf192	chromosome 6 open reading frame 192
682.4	215.7	3.2	226603_at	SAMD9L	sterile alpha motif domain containing 9-like
1115.4	354.9	3.1	201387_s_at	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
551.1	175.4	3.1	211368_s_at	CASP1	caspace 1, apoptosis-related cysteine peptidase
1004	324	3.1	205659_at	HDAC9	histone deacetylase 9
443.2	143.1	3.1	205567_at	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
146.4	47.5	3.1	204779_s_at	HOXB7	homeo box B7
436.3	142.5	3.1	223125_s_at	C1orf21	chromosome 1 open reading frame 21
3014.7	984.8	3.1	202672_s_at	ATF3	activating transcription factor 3
58.6	19.2	3.1	206211_at	SELE	selectin E (endothelial adhesion molecule 1)
1092.9	358.8	3.0	201329_s_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
389	128.5	3.0	230036_at	SAMD9L	sterile alpha motif domain containing 9-like
93.4	31	3.0	207117_at	H-plk	Krüppel-related zinc finger protein
937.2	312.5	3.0	218943_s_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
100.8	34.1	3.0	218935_at	EHD3	EH-domain containing 3
468.7	158.7	3.0	209762_x_at	SP110	SP110 nuclear body protein
1118.9	384.9	2.9	1562367_at	FLJ39531	FLJ39531 protein
595	205	2.9	203148_s_at	TRIM14	tripartite motif-containing 14
342.8	120	2.9	215446_s_at	LOX	lysyl oxidase
616	217.2	2.8	213222_at	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)
790.7	283.1	2.8	219209_at	IFIH1	interferon induced with helicase C domain 1
805.8	289	2.8	201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
822.3	296.4	2.8	1554980_a_at	ATF3	activating transcription factor 3
1114.4	401.9	2.8	218400_at	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa
496.5	180.2	2.8	206639_x_at	HTN1	histatin 1
346.5	126	2.8	204279_at	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9
255.3	92.9	2.7	238733_at	CPM	Carboxypeptidase M
853.8	315.6	2.7	202869_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa
43	15.9	2.7	210174_at	NR5A2	nuclear receptor subfamily 5, group A, member 2

Infected	Mock	Fold chg	Probe set	symbol	name
295.7	110.7	2.7	211367_s_at	CASP1	caspace 1, apoptosis-related cysteine peptidase
149.9	56.6	2.6	204836_at	GLDC	glycine dehydrogenase
580.9	219.5	2.6	209301_at	CA2	carbonic anhydrase II
239.1	90.7	2.6	218468_s_at	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)
690.4	262.4	2.6	224558_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1
1419.7	540.5	2.6	209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2
151.9	57.9	2.6	209074_s_at	TU3A	TU3A protein
609.3	233.3	2.6	236099_at		Transcribed locus
82	31.6	2.6	224964_s_at	GNG2	guanine nucleotide binding protein (G protein), gamma 2
934.1	361	2.6	204502_at	SAMHD1	SAM domain and HD domain 1
975.9	377.2	2.6	209761_s_at	SP110	SP110 nuclear body protein
1002.4	388.2	2.6	222793_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
1993.3	772.8	2.6	201649_at	UBE2L6	ubiquitin-conjugating enzyme E2L 6
1412	550	2.6	223422_s_at	ARHGAP24	Rho GTPase activating protein 24
155	60.4	2.6	223980_s_at	SP110	SP110 nuclear body protein
27.2	10.6	2.6	225056_at	SIPA1L2	signal-induced proliferation-associated 1 like 2
312.6	122	2.6	213001_at	ANGPTL2	angiopoietin-like 2
101.2	39.5	2.6	213716_s_at	SECTM1	secreted and transmembrane 1
22	8.6	2.6	1554256_a_at	PCNXL2	pecanex-like 2 (Drosophila)
229.4	89.8	2.6	217373_x_at	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)
144.4	56.6	2.6	218469_at	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)
1412.9	555.1	2.5	208012_x_at	SP110	SP110 nuclear body protein
150	59.3	2.5	221030_s_at	ARHGAP24	Rho GTPase activating protein 24
33.5	13.3	2.5	232383_at	TFEC	transcription factor EC
146.2	58.2	2.5	242907_at	GBP2	guanylate binding protein 2, interferon-inducible
146.9	58.6	2.5	219593_at	SLC15A3	solute carrier family 15, member 3
2161	863.7	2.5	243610_at	LOC138255	OTTHUMP00000021439
448.4	179.6	2.5	204298_s_at	LOX	lysyl oxidase
1189.2	479.1	2.5	227006_at	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A
119.9	48.6	2.5	205934_at	PLCL1	phospholipase C-like 1
239.6	97.3	2.5	228109_at	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2
70.9	28.8	2.5	205386_s_at	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein
120	48.8	2.5	219497_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)
313.1	127.5	2.5	225540_at	MAP2	Microtubule-associated protein 2
1332.1	542.6	2.5	205552_s_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa
188.4	76.9	2.5	226814_at	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
3720.2	1518.8	2.4	204589_at	NUAK1	NUAK family, SNF1-like kinase, 1
469.7	191.8	2.4	215785_s_at	CYFIP2	cytoplasmic FMR1 interacting protein 2
808.2	331.5	2.4	203595_s_at	IFIT5	interferon-induced protein with tetratricopeptide repeats 5
91.3	37.6	2.4	211124_s_at	KITLG	KIT ligand
133.8	55.1	2.4	228132_at	ABLIM2	actin binding LIM protein family, member 2
545.2	224.8	2.4	241381_at	CXorf36	chromosome X open reading frame 36
96.5	40	2.4	227306_at		CDNA: FLJ21245 fis, clone COL01184
105.9	43.9	2.4	227807_at	PARP9	poly (ADP-ribose) polymerase family, member 9
138.2	57.3	2.4	218353_at	RGS5	regulator of G-protein signalling 5
447.7	187.8	2.4	203140_at	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)

Infected	Mock	Fold chg	Probe set	symbol	name
362	152	2.4	228347_at	SIX1	Sine oculis homeobox homolog 1 (Drosophila)
3915.7	1644.1	2.4	232080_at	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
19.7	8.3	2.4	208343_s_at	NR5A2	nuclear receptor subfamily 5, group A, member 2
1329.6	561.3	2.4	202307_s_at	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
1579.1	666.9	2.4	205801_s_at	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
146.8	62.2	2.4	210675_s_at	PTPRR	protein tyrosine phosphatase, receptor type, R
1758.3	754.1	2.3	204030_s_at	SCHIP1	schwannomin interacting protein 1
1519.2	651.7	2.3	205554_s_at	DNASE1L3	deoxyribonuclease I-like 3
2278.4	986.7	2.3	219837_s_at	CYTL1	cytokine-like 1
968.7	419.8	2.3	242961_x_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
1115.6	485.1	2.3	212328_at	KIAA1102	KIAA1102 protein
388.5	169.3	2.3	211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase
187	82.3	2.3	1556128_a_at	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2
292.2	129.2	2.3	221766_s_at	FAM46A	family with sequence similarity 46, member A
108.6	48	2.3	230425_at	EPHB1	EPH receptor B1
1005.1	445.8	2.3	212327_at	KIAA1102	KIAA1102 protein
286.4	127.7	2.2	207605_x_at	ZNF117	zinc finger protein 117 (HPF9)
49.6	22.2	2.2	1554717_a_at	PDE4D	phosphodiesterase 4D, cAMP-specific
64.6	29	2.2	230433_at	LOC400764	hypothetical gene supported by AK094796
176.7	79.6	2.2	226474_at	NOD27	nucleotide-binding oligomerization domains 27
1232.5	557.8	2.2	226534_at	KITLG	KIT ligand
133.5	60.5	2.2	207029_at	KITLG	KIT ligand
1491.3	676.6	2.2	205726_at	DIAPH2	diaphanous homolog 2 (Drosophila)
4016.6	1824.1	2.2	201926_s_at	DAF	decay accelerating factor for complement
3721.6	1690	2.2	225415_at	DTX3L	deltex 3-like (Drosophila)
87	39.6	2.2	238127_at	GAS6	Growth arrest-specific 6
502.1	230.4	2.2	218854_at	SART2	squamous cell carcinoma antigen recognized by T cells 2
395.2	181.6	2.2	216252_x_at	FAS	Fas (TNF receptor superfamily, member 6)
595.3	273.7	2.2	210510_s_at	NRP1	neuropilin 1
107.5	49.5	2.2	1554697_at	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
3808.8	1756.3	2.2	1555950_a_at	DAF	decay accelerating factor for complement
1780.5	828.5	2.1	218729_at	LXN	latexin
74	34.5	2.1	205543_at	HSPA4L	heat shock 70kDa protein 4-like
402.6	187.8	2.1	203596_s_at	IFIT5	interferon-induced protein with tetratricopeptide repeats 5
863.6	403.2	2.1	226725_at		Transcribed locus
438.3	204.8	2.1	227966_s_at	LOC90557	hypothetical protein BC016861
441.9	207	2.1	219656_at	PCDH12	protocadherin 12
101.6	48.1	2.1	222891_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)
1585.9	752	2.1	203236_s_at	LGALS9	lectin, galactoside-binding, soluble, 9 (galectin 9)
29.9	14.2	2.1	221874_at	KIAA1324	KIAA1324
4521.3	2147.8	2.1	204114_at	NID2	nidogen 2 (osteonidogen)
1161.9	554.6	2.1	205603_s_at	DIAPH2	diaphanous homolog 2 (Drosophila)
140.5	67.1	2.1	209030_s_at	IGSF4	immunoglobulin superfamily, member 4
129.3	61.8	2.1	213478_at	KIAA1026	kazrin
231.4	111.1	2.1	211919_s_at	CXCR4	chemokine (C-X-C motif) receptor 4
617.8	296.7	2.1	212325_at	KIAA1102	KIAA1102 protein

Infected	Mock	Fold chg	Probe set	symbol	name
433.3	208.8	2.1	227463_at	ACE	angiotensin I converting enzyme 1
303.4	146.5	2.1	213004_at	ANGPTL2	angiopoietin-like 2
192.9	93.3	2.1	232517_s_at	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285
216.7	105	2.1	217246_s_at	DIAPH2	diaphanous homolog 2 (Drosophila)
1444.8	700.6	2.1	204396_s_at	GRK5	G protein-coupled receptor kinase 5
613	297.6	2.1	217028_at	CXCR4	chemokine (C-X-C motif) receptor 4
3724.9	1814.5	2.1	228885_at	MAMDC2	MAM domain containing 2
2444.3	1192.1	2.1	208965_s_at	IFI16	interferon, gamma-inducible protein 16
144.8	70.7	2.0	202756_s_at	GPC1	glypican 1
1270.6	621.1	2.0	227522_at	LOC134147	similar to mouse 2310016A09Rik gene
203.4	99.5	2.0	202342_s_at	TRIM2	tripartite motif-containing 2
700.5	342.8	2.0	209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase
41.1	20.2	2.0	215101_s_at	CXCL5	chemokine (C-X-C motif) ligand 5
93.5	46	2.0	209550_at	NDN	necdin homolog (mouse)
140.8	69.3	2.0	1556325_at	FILIP1	filamin A interacting protein 1
1301.2	641.1	2.0	202269_x_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
941.2	463.6	2.0	224701_at	PARP14	poly (ADP-ribose) polymerase family, member 14
2698.2	1331.2	2.0	209652_s_at	PGF	placental growth factor, vascular endothelial growth factor-related protein
245.6	121.2	2.0	235276_at		
376.4	185.9	2.0	202838_at	FUCA1	fucosidase, alpha-L- 1, tissue
684.6	338.2	2.0	204527_at	MYO5A	myosin VA (heavy polypeptide 12, myosin)
367.3	181.6	2.0	206359_at	SOCS3	suppressor of cytokine signaling 3
815.7	406.5	2.0	219691_at	SAMD9	sterile alpha motif domain containing 9
429.5	214.2	2.0	225293_at	COL27A1	collagen, type XXVII, alpha 1
419.6	209.4	2.0	203329_at	PTPRM	protein tyrosine phosphatase, receptor type, M
413.3	206.2	2.0	223510_at	NRP2	neuropilin 2
7591.8	3809.6	2.0	208966_x_at	IFI16	interferon, gamma-inducible protein 16
664.8	335.6	2.0	230803_s_at	ARHGAP24	Rho GTPase activating protein 24
882.9	447.8	2.0	203882_at	ISGF3G	interferon-stimulated transcription factor 3, gamma 48kDa
329	167.1	2.0	225973_at	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
439.3	223.2	2.0	204681_s_at	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5
72.8	37	2.0	1555564_a_at	IF	I factor (complement)
117	59.7	2.0	1554937_x_at	LOC283849	hypothetical protein LOC283849
150	76.6	2.0	212978_at	TA-LRRP	Leucine rich repeat containing 8 family, member B
522.9	267.3	2.0	205885_s_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
657.7	337.3	2.0	225929_s_at	C17orf27	chromosome 17 open reading frame 27
14.6	7.5	1.9	1561254_at	LOC340340	hypothetical protein LOC340340
1405.7	723.1	1.9	228152_s_at	FLJ31033	hypothetical protein FLJ31033
1099.8	571.6	1.9	208370_s_at	DSCR1	Down syndrome critical region gene 1
1146.6	597.6	1.9	215719_x_at	FAS	Fas (TNF receptor superfamily, member 6)
699	365.4	1.9	207808_s_at	PROS1	protein S (alpha)
308	161.1	1.9	217542_at	CPM	Carboxypeptidase M
1181.5	620.2	1.9	202241_at	TRIB1	tribbles homolog 1 (Drosophila)
437.6	230.9	1.9	236089_at		Transcribed locus
272.5	143.9	1.9	203779_s_at	EVA1	epithelial V-like antigen 1
194	102.5	1.9	220092_s_at	ANTXR1	anthrax toxin receptor 1

Infected	Mock	Fold chg	Probe set	symbol	name
6425.7	3398.5	1.9	206332_s_at	IFI16	interferon, gamma-inducible protein 16
162	85.9	1.9	1566342_at		Transcribed locus
472.3	250.9	1.9	229350_x_at	PARP10	poly (ADP-ribose) polymerase family, member 10
729.1	387.6	1.9	228531_at	SAMD9	sterile alpha motif domain containing 9
782.4	416.4	1.9	218429_s_at	FLJ11286	hypothetical protein FLJ11286
584.6	311.8	1.9	204781_s_at	FAS	Fas (TNF receptor superfamily, member 6)
1239.4	666.5	1.9	224916_at	LOC340061	hypothetical protein LOC340061
308.6	166	1.9	217553_at	MGC87042	similar to Six transmembrane epithelial antigen of prostate
5945.9	3200.3	1.9	210815_s_at	CALCRL	calcitonin receptor-like
280.7	151.1	1.9	229507_at	LOC389119	similar to RIKEN cDNA 6530418L21
265.4	143.4	1.9	231720_s_at	JAM3	junctional adhesion molecule 3
256.8	139.8	1.8	242957_at	FLJ32009	hypothetical protein FLJ32009
4335	2361	1.8	206331_at	CALCRL	calcitonin receptor-like
426.1	232.8	1.8	1555491_a_at	FLJ11286	hypothetical protein FLJ11286
385.4	210.7	1.8	231721_at	JAM3	junctional adhesion molecule 3
1195.6	654.4	1.8	207813_s_at	FDXR	ferredoxin reductase
201.4	110.4	1.8	206360_s_at	SOCS3	suppressor of cytokine signaling 3
329.5	180.6	1.8	243999_at	MGC19764	likely ortholog of mouse schlafen 5
919.4	505.9	1.8	53720_at	FLJ11286	hypothetical protein FLJ11286
201.1	110.8	1.8	220104_at	ZC3HAV1	zinc finger CCCH-type, antiviral 1
1267.5	700.5	1.8	203037_s_at	MTSS1	metastasis suppressor 1
383.3	212.1	1.8	218642_s_at	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7
46.3	25.7	1.8	239229_at		Transcribed locus
705.8	392	1.8	203657_s_at	CTSF	cathepsin F
281.8	157.1	1.8	230254_at		Transcribed locus
590.7	330	1.8	221563_at	DUSP10	dual specificity phosphatase 10
5310.4	2967.7	1.8	202446_s_at	PLSCR1	phospholipid scramblase 1
1434.1	802	1.8	1552611_a_at	JAK1	Janus kinase 1 (a protein tyrosine kinase)
616	344.8	1.8	202145_at	LY6E	lymphocyte antigen 6 complex, locus E
938.4	525	1.8	219367_s_at	NRP2	Neuropilin 2
2005.9	1122.8	1.8	209684_at	RIN2	Ras and Rab interactor 2
1717.3	964.9	1.8	204780_s_at	FAS	Fas (TNF receptor superfamily, member 6)
765.7	431.2	1.8	213416_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
443	249.9	1.8	209182_s_at	C10orf10	chromosome 10 open reading frame 10
634.2	357.9	1.8	212240_s_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)
2394.4	1356.6	1.8	226244_at	CLEC14A	C-type lectin domain family 14, member A
3207.2	1820	1.8	1552610_a_at	JAK1	Janus kinase 1 (a protein tyrosine kinase)
1033.2	586.5	1.8	209040_s_at	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8
3557.7	2022.5	1.8	212190_at	SERPINE2	serpin peptidase inhibitor, clade E, member 2
851	484	1.8	218113_at	TMEM2	transmembrane protein 2
6067.7	3452.3	1.8	201648_at	JAK1	Janus kinase 1 (a protein tyrosine kinase)
929.1	529	1.8	212445_s_at	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like
2950.4	1686.4	1.8	227628_at	LOC493869	similar to RIKEN cDNA 2310016C16
3937.4	2263.3	1.7	203725_at	GADD45A	growth arrest and DNA-damage-inducible, alpha
177.5	102.1	1.7	226625_at	TGFBR3	Transforming growth factor, beta receptor III (betaglycan, 300kDa)
459.7	265.5	1.7	204491_at	PDE4D	Phosphodiesterase 4D, cAMP-specific

Infected	Mock	Fold chg	Probe set	symbol	name
458.4	265.5	1.7	205932_s_at	MSX1	msh homeo box homolog 1 (Drosophila)
1363.6	789.6	1.7	209183_s_at	C10orf10	chromosome 10 open reading frame 10
703.6	407.7	1.7	227964_at	FKSG44	FKSG44 gene
1280.7	743.8	1.7	214632_at	NRP2	neuropilin 2
840.3	489.3	1.7	211844_s_at	NRP2	neuropilin 2
105	61.2	1.7	201431_s_at	DPYSL3	dihydropyrimidinase-like 3
2050.1	1198.6	1.7	210089_s_at	LAMA4	laminin, alpha 4
1213.8	710.4	1.7	204992_s_at	PFN2	profilin 2
1742.5	1020.3	1.7	213294_at	FLJ38348	Hypothetical protein FLJ38348
354.1	207.6	1.7	222125_s_at	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase
1544.7	906.5	1.7	225566_at	NRP2	neuropilin 2
237.7	139.7	1.7	212249_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)
1258.2	739.5	1.7	224929_at	LOC340061	hypothetical protein LOC340061
916.9	539.4	1.7	201860_s_at	PLAT	plasminogen activator, tissue
16.1	9.5	1.7	212560_at	C11orf32	chromosome 11 open reading frame 32
1531.3	904.5	1.7	209457_at	DUSP5	dual specificity phosphatase 5
1565	924.7	1.7	212813_at	JAM3	junctional adhesion molecule 3
503.2	298.1	1.7	223195_s_at	SESN2	sestrin 2
45.5	27	1.7	206271_at	TLR3	toll-like receptor 3
1848.3	1097.2	1.7	201531_at	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)
358.9	213.3	1.7	202363_at	SPOCK	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)
615.3	367	1.7	213509_x_at	CES2	carboxylesterase 2 (intestine, liver)
113.7	67.8	1.7	218750_at	MGC5306	hypothetical protein MGC5306
608.4	363.5	1.7	210841_s_at	NRP2	neuropilin 2
1534.1	919.9	1.7	202565_s_at	SVIL	supervillin
1240.1	746.3	1.7	225076_s_at	KIAA1404	KIAA1404 protein
9075.1	5476	1.7	224724_at	SULF2	sulfatase 2
21.2	12.8	1.7	238168_at	TM4SF1	transmembrane 4 L six family member 1
575.2	347.8	1.7	213115_at	ATG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)
946.6	575	1.6	217983_s_at	RNASSET2	ribonuclease T2
1396.6	850.1	1.6	211163_s_at	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
1623.3	988.7	1.6	223533_at	LRRC8C	leucine rich repeat containing 8 family, member C
472.4	288.3	1.6	230645_at	FRMD3	FERM domain containing 3
1547.5	946.3	1.6	223631_s_at	C19orf33	chromosome 19 open reading frame 33
539	330.5	1.6	202902_s_at	CTSS	cathepsin S
1064.3	652.9	1.6	229900_at	CD109	CD109 antigen (Gov platelet alloantigens)
4815.7	2957.4	1.6	1558397_at		CDNA FLJ34100 fis, clone FCBBF3007597
6818.2	4190.6	1.6	217933_s_at	LAP3	leucine aminopeptidase 3
111.4	68.7	1.6	203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing
486.3	300.1	1.6	225931_s_at	C17orf27	chromosome 17 open reading frame 27
462.3	285.6	1.6	219686_at	STK32B	serine/threonine kinase 32B
140.9	87.1	1.6	210689_at	CLDN14	claudin 14
2884.9	1786.4	1.6	1553995_a_at	NT5E	5'-nucleotidase, ecto (CD73)
1320.5	818.1	1.6	229225_at	NRP2	neuropilin 2
221	137.4	1.6	239952_at		
63.2	39.3	1.6	1555725_a_at	RGS5	regulator of G-protein signalling 5

Infected	Mock	Fold chg	Probe set	symbol	name
375.3	233.4	1.6	213419_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
785.3	489.3	1.6	214765_s_at	ASAHL	N-acylsphingosine amidohydrolase (acid ceramidase)-like
913.8	570.3	1.6	202566_s_at	SVIL	supervillin
2466.1	1539.5	1.6	212558_at	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
273.8	171.4	1.6	210886_x_at	TP53AP1	TP53 activated protein 1
272.9	170.9	1.6	232617_at	CTSS	cathepsin S
706.5	443.1	1.6	209806_at	HIST1H2BK	histone 1, H2bk
628.3	394.7	1.6	203568_s_at	TRIM38	tripartite motif-containing 38
4332.5	2723.3	1.6	233555_s_at	SULF2	sulfatase 2
3632.4	2290.3	1.6	226545_at	CD109	CD109 antigen (Gov platelet alloantigens)
8693.6	5483.3	1.6	221898_at	PDPN	podoplanin
535.5	339	1.6	203567_s_at	TRIM38	tripartite motif-containing 38
166.3	105.3	1.6	230518_at	EVA1	epithelial V-like antigen 1
316.3	200.3	1.6	225803_at	FBXO32	F-box protein 32
751.2	476.4	1.6	203723_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B
198.1	125.8	1.6	217546_at	MT1M	metallothionein 1M
5256.7	3338.5	1.6	204048_s_at	PHACTR2	phosphatase and actin regulator 2
128.2	81.7	1.6	202755_s_at	GPC1	glypican 1
228.2	145.5	1.6	201601_x_at	IFITM1	interferon induced transmembrane protein 1 (9-27)
22.1	14.1	1.6	227810_at	ZNF558	zinc finger protein 558
2280.7	1458.5	1.6	202150_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9
1395.1	894.7	1.6	204134_at	PDE2A	phosphodiesterase 2A, cGMP-stimulated
174.1	112	1.6	227486_at	NT5E	5'-nucleotidase, ecto (CD73)
3946.9	2540.4	1.6	201695_s_at	NP	nucleoside phosphorylase
361.1	232.3	1.6	228977_at	IL17D	Interleukin 17D
159.5	102.7	1.6	226864_at	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha
1415	911.2	1.6	209667_at	CES2	carboxylesterase 2 (intestine, liver)
847	545.7	1.6	205032_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
3436	2216.8	1.6	204049_s_at	PHACTR2	phosphatase and actin regulator 2
2500.7	1614.7	1.5	225049_at	BLOC1S2	biogenesis of lysosome-related organelles complex-1, subunit 2
8.2	5.3	1.5	1564139_at	LOC144571	hypothetical protein LOC144571
481.7	311.5	1.5	230438_at	TBX15	T-box 15
6538.4	4232.9	1.5	202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
2983.7	1932.5	1.5	227530_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12
461.7	299.2	1.5	212985_at	APBB2	Amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
174	113	1.5	207571_x_at	C1orf38	chromosome 1 open reading frame 38
3282.3	2132.4	1.5	242277_at	PHACTR2	Phosphatase and actin regulator 2
1546.6	1005.2	1.5	203821_at	HBEGF	heparin-binding EGF-like growth factor
518.5	337.1	1.5	209917_s_at	TP53AP1	TP53 activated protein 1
5610.2	3649.5	1.5	228489_at	TM4SF18	transmembrane 4 L six family member 18
2422.4	1578	1.5	219099_at	C12orf5	chromosome 12 open reading frame 5
1153.1	755.9	1.5	227874_at	EMCN	Endomucin
4512.1	2960.5	1.5	204879_at	PDPN	podoplanin
361.1	237	1.5	219506_at	C1orf54	chromosome 1 open reading frame 54
2627.3	1726.2	1.5	212662_at	PVR	poliovirus receptor
763.8	502.1	1.5	227481_at	CNKSR3	CNKSR family member 3

Infected	Mock	Fold chg	Probe set	symbol	name
465.3	306.9	1.5	226824_at	CPXM2	carboxypeptidase X (M14 family), member 2
2466.4	1629.6	1.5	209124_at	MYD88	myeloid differentiation primary response gene (88)
1564.1	1033.2	1.5	225291_at	PNPT1	polyribonucleotide nucleotidyltransferase 1
614.9	406.1	1.5	218346_s_at	SESN1	sestrin 1
3615.8	2393.4	1.5	208991_at	STAT3	signal transducer and activator of transcription 3
497.3	329.1	1.5	218471_s_at	BBS1	Bardet-Biedl syndrome 1
1065.5	705.9	1.5	224690_at	C20orf108	chromosome 20 open reading frame 108
855.3	568.5	1.5	230333_at	SAT	Spermidine/spermine N1-acetyltransferase
574	383.2	1.5	204602_at	DKK1	dickkopf homolog 1 (Xenopus laevis)
1574.2	1053.1	1.5	226094_at	PIK3C2A	Phosphoinositide-3-kinase, class 2, alpha polypeptide
2878.4	1934.8	1.5	211799_x_at	HLA-C	major histocompatibility complex, class I, C
117.2	78.9	1.5	223577_x_at	PRO1073	PRO1073 protein
3199.9	2157.6	1.5	222885_at	EMCN	endomucin
5504.6	3725.1	1.5	218660_at	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
374	253.4	1.5	224693_at	C20orf108	chromosome 20 open reading frame 108
4704.9	3193.9	1.5	226658_at	PDPN	podoplanin
2260.4	1538.7	1.5	200974_at	ACTA2	actin, alpha 2, smooth muscle, aorta
13801.2	9419.1	1.5	201578_at	PODXL	podocalyxin-like
639.7	437.9	1.5	203367_at	DUSP14	dual specificity phosphatase 14
147.6	101.4	1.5	213974_at	ADAMTSL3	ADAMTS-like 3
392.8	269.8	1.5	226018_at	EIIs1	hypothetical protein EIIs1
1946	1337.3	1.5	229367_s_at	GIMAP6	GTPase, IMAP family member 6
285.8	196.6	1.5	207519_at	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
134.8	92.7	1.5	230722_at	BNC2	Basonuclin 2
751.3	519	1.4	32699_s_at	PVR	poliovirus receptor
425.4	294.7	1.4	204047_s_at	PHACTR2	phosphatase and actin regulator 2
321.2	222.8	1.4	225624_at	LOC92017	similar to RIKEN cDNA 4933437K13
620.9	430.6	1.4	226876_at	MGC45871	hypothetical protein MGC45871
1599.6	1110.6	1.4	227032_at	PLXNA2	Plexin A2
1580.5	1101.9	1.4	201069_at	MMP2	matrix metalloproteinase 2
12191.1	8511.6	1.4	208982_at	PECAM1	Platelet/endothelial cell adhesion molecule (CD31 antigen)
326.9	228.7	1.4	223402_at	DUSP23	dual specificity phosphatase 23
2033.4	1426.5	1.4	225369_at	ESAM	endothelial cell adhesion molecule
119.6	84.1	1.4	201250_s_at	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1
582.1	409.6	1.4	214443_at	PVR	poliovirus receptor
655.5	462.5	1.4	225698_at	TIGA1	TIGA1
418.2	295.5	1.4	205579_at	HRH1	histamine receptor H1
1660.7	1192.8	1.4	219243_at	GIMAP4	GTPase, IMAP family member 4
387.7	278.9	1.4	218407_x_at	NENF	neuron derived neurotrophic factor
66.3	47.8	1.4	226849_at	DENND1A	DENN/MADD domain containing 1A
45.2	32.7	1.4	1554205_s_at	ALS2CR15	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 15
646.3	468.8	1.4	221044_s_at	TRIM34	tripartite motif-containing 34
248.8	180.4	1.4	238063_at	FLJ32028	hypothetical protein FLJ32028
643.5	466.9	1.4	226113_at	ZNF436	zinc finger protein 436
265.2	192.4	1.4	238542_at	ULBP2	UL16 binding protein 2
11955.3	8680.3	1.4	211911_x_at	HLA-B	major histocompatibility complex, class I, B

Infected	Mock	Fold chg	Probe set	symbol	name
4959.6	3606.4	1.4	212387_at	TCF4	Transcription factor 4
878.3	641.2	1.4	223058_at	C10orf45	chromosome 10 open reading frame 45
206.2	150.7	1.4	227264_at	TRAF6	TNF receptor-associated factor 6
6129.5	4482.8	1.4	202878_s_at	C1QR1	complement component 1, q subcomponent, receptor 1
264.2	193.7	1.4	1555906_s_at	C3orf23	chromosome 3 open reading frame 23
12246.8	9137.8	1.3	209140_x_at	HLA-B	major histocompatibility complex, class I, B
929	700	1.3	65884_at	MAN1B1	mannosidase, alpha, class 1B, member 1
2358.7	1799	1.3	209086_x_at	MCAM	melanoma cell adhesion molecule

Table E2: Transcripts decreased in HMVEC-L cells upon infection with HHV-8. Genes listed in this table meet the stringent criteria ($p < 0.001$) for differential expression in a two sample t-test between HHV-8 infected and mock-infected cells ($n=3$ per group). Columns 1 and 2 report the mean signal intensity in the HHV-8 Infected and Mock Infected groups.

Infected	Mock	fold chg	Probe set	symbol	name
11.8	328.7	-27.8	212670_at	ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
24.7	201	-8.1	205523_at	HAPLN1	hyaluronan and proteoglycan link protein 1
11	83.9	-7.6	205524_s_at	HAPLN1	hyaluronan and proteoglycan link protein 1
25.4	188.6	-7.4	202016_at	MEST	mesoderm specific transcript homolog (mouse)
37.2	274	-7.4	230204_at	HAPLN1	Hyaluronan and proteoglycan link protein 1
114	820.3	-7.2	202404_s_at	COL1A2	collagen, type I, alpha 2
277	1967	-7.1	209283_at	CRYAB	crystallin, alpha B
79.1	548.1	-6.9	1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
15.5	103.6	-6.7	210121_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
186.3	1237.2	-6.6	213524_s_at	G0S2	G0/G1switch 2
28.5	178.9	-6.3	232336_at	ZSWIM5	zinc finger, SWIM-type containing 5
155	945	-6.1	222043_at	CLU	clusterin (apolipoprotein J)
202.9	1166.9	-5.7	205899_at	CCNA1	cyclin A1
9.1	49.9	-5.5	204614_at	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2
30.1	160.5	-5.3	221942_s_at	GUCY1A3	guanylate cyclase 1, soluble, alpha 3
25.5	135.4	-5.3	228608_at	VGCNL1	Voltage gated channel like 1
8.8	44.1	-5.0	206178_at	PLA2G5	phospholipase A2, group V
22.6	110.2	-4.9	229530_at	GUCY1A3	Guanylate cyclase 1, soluble, alpha 3
42.2	203.8	-4.8	214746_s_at	ZNF467	zinc finger protein 467
557.9	2627.8	-4.7	40687_at	GJA4	gap junction protein, alpha 4, 37kDa (connexin 37)
318.7	1500.2	-4.7	204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
14.4	67.3	-4.7	209990_s_at	GPR51	G protein-coupled receptor 51
353.7	1636.3	-4.6	202403_s_at	COL1A2	collagen, type I, alpha 2
111.7	501.7	-4.5	218211_s_at	MLPH	melanophilin
29.1	125.3	-4.3	213942_at	EGFL3	EGF-like-domain, multiple 3
244.5	1033.2	-4.2	226961_at	LOC222171	hypothetical protein LOC222171
95.3	398.5	-4.2	211959_at	IGFBP5	insulin-like growth factor binding protein 5
1556.2	6446.3	-4.1	208791_at	CLU	clusterin (apolipoprotein J)
179.4	725	-4.0	226869_at	EGFL3	EGF-like-domain, multiple 3
97	384.5	-4.0	209230_s_at	P8	p8 protein (candidate of metastasis 1)
1617.1	6335.6	-3.9	208792_s_at	CLU	clusterin (apolipoprotein J)
1509.9	5841.7	-3.9	204904_at	GJA4	gap junction protein, alpha 4, 37kDa (connexin 37)
202.8	753.1	-3.7	214238_at		Clone DT1P1B6 mRNA, CAG repeat region
59.7	218.6	-3.7	210619_s_at	HYAL1	hyaluronoglucosaminidase 1
23.2	84.8	-3.6	227235_at	GUCY1A3	Guanylate cyclase 1, soluble, alpha 3
210.2	747	-3.6	235050_at	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12
68.3	243.3	-3.6	227233_at	TSPAN2	tetraspanin 2
89.3	309.5	-3.5	231986_at	RIMS1	regulating synaptic membrane exocytosis 1
425	1471.5	-3.5	223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1

60	206.8	-3.4	225177_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)
6.3	21.6	-3.4	203729_at	EMP3	epithelial membrane protein 3
393.5	1330.6	-3.4	227058_at	FLJ14834	hypothetical protein FLJ14834
49.4	165.5	-3.4	209908_s_at	TGFB2	Transforming growth factor, beta 2
252.1	843	-3.3	227236_at	TSPAN2	tetraspanin 2
916.8	2984.1	-3.3	209159_s_at	NDRG4	NDRG family member 4
480	1554.7	-3.2	220108_at	GNA14	guanine nucleotide binding protein (G protein), alpha 14
148.2	472.1	-3.2	228245_s_at	OVOS2	ovostatin 2
316.2	994.6	-3.1	205581_s_at	NOS3	nitric oxide synthase 3 (endothelial cell)
78.7	244.3	-3.1	232227_at		HSPC324
691.6	2130.9	-3.1	244353_s_at	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12
112.1	343.2	-3.1	220407_s_at	TGFB2	transforming growth factor, beta 2
184.3	561.8	-3.0	203687_at	CX3CL1	chemokine (C-X3-C motif) ligand 1
170.8	520	-3.0	823_at	CX3CL1	chemokine (C-X3-C motif) ligand 1
178.9	541	-3.0	223313_s_at	MAGED4	melanoma antigen family D, 4
13.6	41	-3.0	208190_s_at	LISCH7	liver-specific bHLH-Zip transcription factor
93.3	280.1	-3.0	223842_s_at	SCARA3	scavenger receptor class A, member 3
44.6	133.5	-3.0	1556069_s_at	HIF3A	Hypoxia inducible factor 3, alpha subunit
40.9	121.2	-3.0	1560879_a_at	SYT15	synaptotagmin XV
14.1	41.7	-3.0	222549_at	CLDN1	claudin 1
80.1	236.6	-2.9	205921_s_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
300.5	884.1	-2.9	203423_at	RBP1	retinol binding protein 1, cellular
40.3	118.6	-2.9	203789_s_at	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
80	229.4	-2.9	213176_s_at	LTBP4	latent transforming growth factor beta binding protein 4
78.4	223.2	-2.8	203571_s_at	C10orf116	chromosome 10 open reading frame 116
13.6	38.6	-2.8	229004_at	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif, 15
316	895.2	-2.8	205529_s_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
67	188	-2.8	204989_s_at	ITGB4	integrin, beta 4
69.2	192.3	-2.8	202661_at	ITPR2	inositol 1,4,5-triphosphate receptor, type 2
84.3	229.7	-2.7	214520_at	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)
1404.6	3818.3	-2.7	201596_x_at	KRT18	keratin 18
70.1	190.6	-2.7	229029_at		Transcribed locus
711.8	1926.1	-2.7	210145_at	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)
114.8	310.2	-2.7	206805_at	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
383.5	1035.6	-2.7	223482_at	TMPIT	transmembrane protein induced by tumor necrosis factor alpha
170.2	456.8	-2.7	210082_at	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4
642.2	1702	-2.7	1552445_a_at	ESX1L	extraembryonic, spermatogenesis, homeobox 1-like
187.3	496.8	-2.7	221261_x_at	MAGED4	melanoma antigen family D, 4 /// melanoma antigen family D, 4
123.6	322.2	-2.6	229452_at	LOC92162	similar to RIKEN cDNA 2600017H02
475	1232.2	-2.6	210665_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
157.3	406	-2.6	1552309_a_at	NEXN	nexilin (F actin binding protein)
184.7	473.1	-2.6	204151_x_at	AKR1C1	aldo-keto reductase family 1, member C1
537.9	1370.8	-2.6	208510_s_at	PPARG	peroxisome proliferative activated receptor, gamma
86	219.1	-2.5	204149_s_at	GSTM4	glutathione S-transferase M4

119.3	303.3	-2.5	202036_s_at	SFRP1	secreted frizzled-related protein 1
775.1	1965.4	-2.5	214587_at	COL8A1	collagen, type VIII, alpha 1
53.8	136.6	-2.5	225381_at	LOC399959	hypothetical gene supported by BX647608
93.2	236.2	-2.5	219534_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2450	6207.3	-2.5	1555778_a_at	POSTN	periostin, osteoblast specific factor
67.6	169.9	-2.5	226303_at	PGM5	phosphoglucomutase 5
92.6	231.7	-2.5	202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa
548.4	1370.1	-2.5	222719_s_at	PDGFC	platelet derived growth factor C
179.6	445.5	-2.5	227337_at	ANKRD37	ankyrin repeat domain 37
84.8	210.3	-2.5	213182_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
122.2	303.5	-2.5	226980_at	DEPDC1B	DEP domain containing 1B
179.6	442.3	-2.5	218574_s_at	LMCD1	LIM and cysteine-rich domains 1
769.9	1880.1	-2.4	205547_s_at	TAGLN	transgelin
39.7	97	-2.4	235670_at	STX11	Syntaxin 11
131.4	320.8	-2.4	225817_at	CGNL1	cingulin-like 1
372	899.5	-2.4	204948_s_at	FST	follicle-stimulating hormone receptor-like 1
591.5	1429.5	-2.4	1555724_s_at	TAGLN	transgelin
186.1	448.3	-2.4	211653_x_at	AKR1C2	
76.1	182.9	-2.4	225777_at	C9orf140	chromosome 9 open reading frame 140
432.5	1039.1	-2.4	228121_at	TGFB2	Transforming growth factor, beta 2
381.6	910.8	-2.4	204339_s_at	RGS4	regulator of G-protein signalling 4
298.7	713.1	-2.4	204933_s_at	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
110.8	263.8	-2.4	219681_s_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)
161.9	384.5	-2.4	209642_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
169	400.8	-2.4	216594_x_at	AKR1C1	aldo-keto reductase family 1, member C1
331.7	784.5	-2.4	212611_at	DTX4	deltex 4 homolog (Drosophila)
76.3	179.9	-2.4	203210_s_at	RFC5	replication factor C (activator 1) 5, 36.5kDa
98.5	231.4	-2.3	201983_s_at	EGFR	epidermal growth factor receptor
310.5	725.8	-2.3	228568_at	Gcom1	GRINL1A combined protein
63.6	147.5	-2.3	208214_at	ADRB1	adrenergic, beta-1-, receptor
139.9	324.8	-2.3	204990_s_at	ITGB4	integrin, beta 4
54.9	127.5	-2.3	236295_s_at	NOD3	NOD3 protein
19.2	44.4	-2.3	206566_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
34.1	78.8	-2.3	1554539_a_at	RHOF	ras homolog gene family, member F (in filopodia)
775.8	1788.1	-2.3	203917_at	CXADR	coxsackie virus and adenovirus receptor
234.5	540.9	-2.3	202037_s_at	SFRP1	secreted frizzled-related protein 1
819.2	1883.5	-2.3	211354_s_at	LEPR	leptin receptor
92.3	211.5	-2.3	205141_at	ANG	angiogenin, ribonuclease, RNase A family, 5
86.6	198.6	-2.3	220295_x_at	DEPDC1	DEP domain containing 1
154.9	355.3	-2.3	215299_x_at	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1
266.6	605.5	-2.3	205279_s_at	GLRB	glycine receptor, beta
205.2	466.4	-2.3	227550_at	LOC143381	hypothetical protein LOC143381
149.4	338.2	-2.3	218559_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
313.6	707.2	-2.3	228827_at	RUNX1T1	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
230.1	518.7	-2.3	203968_s_at	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)

103.3	231.6	-2.2	205696_s_at	GFRA1	GDNF family receptor alpha 1
293.2	655.8	-2.2	232278_s_at	DEPDC1	DEP domain containing 1
425.7	952.6	-2.2	210580_x_at	SULT1A3	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3
305.9	683.2	-2.2	213348_at	CDKN1C	Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
830.8	1851.5	-2.2	218546_at	C1orf115	chromosome 1 open reading frame 115
53.4	118.8	-2.2	219306_at	KIF15	kinesin family member 15
3054.9	6784.7	-2.2	214701_s_at	FN1	fibronectin 1
2947	6456.8	-2.2	210809_s_at	POSTN	periostin, osteoblast specific factor
200.8	439.2	-2.2	238575_at	OSBPL6	oxysterol binding protein-like 6
10	21.9	-2.2	238013_at	PLEKHA2	pleckstrin homology domain containing, family A member 2
289.5	632.3	-2.2	205920_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
117.2	255.5	-2.2	207345_at	FST	follistatin
91.9	200.2	-2.2	225150_s_at	RTKN	rhotekin
73.2	158.7	-2.2	210205_at	B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
771.2	1674.7	-2.2	205715_at	BST1	bone marrow stromal cell antigen 1
2465.6	5330.3	-2.2	205923_at	RELN	reelin
3205	6888.5	-2.2	219689_at	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G
558.3	1199.2	-2.1	209356_x_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2
401.8	856.4	-2.1	228057_at	DDIT4L	DNA-damage-inducible transcript 4-like
926.1	1974.1	-2.1	211356_x_at	LEPR	leptin receptor
238.4	508.2	-2.1	203615_x_at	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1
6.2	13.2	-2.1	222123_s_at	HIF3A	hypoxia inducible factor 3, alpha subunit
143.2	305	-2.1	209506_s_at	NR2F1	nuclear receptor subfamily 2, group F, member 1
394.8	840.1	-2.1	209529_at	PPAP2C	phosphatidic acid phosphatase type 2C
374.8	793.6	-2.1	202479_s_at	TRIB2	tribbles homolog 2 (Drosophila)
341.4	721.2	-2.1	205158_at	RNASE4	ribonuclease, RNase A family, 4
371.1	782.6	-2.1	209160_at	AKR1C3	aldo-keto reductase family 1, member C3
871.5	1837.8	-2.1	211355_x_at	LEPR	leptin receptor
269.9	569.1	-2.1	209607_x_at	SULT1A3	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3
738.5	1550.1	-2.1	212154_at	SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
214.1	449.3	-2.1	204318_s_at	GTSE1	G-2 and S-phase expressed 1
398.9	834.7	-2.1	208534_s_at	RASA4	RAS p21 protein activator 4
209.4	437.5	-2.1	232596_at	DIAPH3	diaphanous homolog 3 (Drosophila)
555.4	1155.8	-2.1	204977_at	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
1238.2	2575.5	-2.1	202286_s_at	TACSTD2	tumor-associated calcium signal transducer 2
551	1142.2	-2.1	203418_at	CCNA2	cyclin A2
48.6	100.4	-2.1	211088_s_at	PLK4	polo-like kinase 4 (Drosophila)
257.5	530	-2.1	212021_s_at	MKI67	antigen identified by monoclonal antibody Ki-67
658.7	1351.2	-2.1	221019_s_at	COLEC12	collectin sub-family member 12
62.1	127.4	-2.1	238704_at		Homo sapiens, clone IMAGE:3866695, mRNA
255	522.8	-2.0	241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV
283.5	581.3	-2.0	222996_s_at	CXXC5	CXXC finger 5
281.7	576.6	-2.0	213342_at	YAP1	Yes-associated protein 1, 65kDa
100.8	205.7	-2.0	210115_at	RPL39L	ribosomal protein L39-like
793.4	1620.7	-2.0	207035_at	SLC30A3	solute carrier family 30 (zinc transporter), member 3

399.9	815.1	-2.0	1558143_a_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)
73.2	149	-2.0	227159_at	LGP1	homolog of mouse LGP1
155.7	317.3	-2.0	212020_s_at	MKI67	antigen identified by monoclonal antibody Ki-67
2982.9	6069.1	-2.0	201506_at	TGFBI	transforming growth factor, beta-induced, 68kDa
174.6	355.9	-2.0	228088_at		CDNA FLJ31513 fis, clone NT2RI1000127
95	192.9	-2.0	214591_at	KLHL4	kelch-like 4 (Drosophila)
996.4	2023.2	-2.0	204337_at	RGS4	regulator of G-protein signalling 4
295.1	598.6	-2.0	234863_x_at	FBXO5	F-box protein 5
429.8	871.3	-2.0	227717_at	FLJ41603	FLJ41603 protein
244	494.3	-2.0	224516_s_at	CXXC5	CXXC finger 5 /// CXXC finger 5
73	147.9	-2.0	229610_at	FLJ40629	hypothetical protein FLJ40629
109.9	221.8	-2.0	206655_s_at	GP1BB	glycoprotein Ib (platelet), beta polypeptide
37	74.6	-2.0	229671_s_at	C21orf45	Chromosome 21 open reading frame 45
66.4	133.8	-2.0	203851_at	IGFBP6	insulin-like growth factor binding protein 6
316.9	638.8	-2.0	209185_s_at	IRS2	insulin receptor substrate 2
18.3	36.9	-2.0	205214_at	STK17B	serine/threonine kinase 17b (apoptosis-inducing)
103.9	208.5	-2.0	227417_at	MOSC2	MOCO sulphurase C-terminal domain containing 2
305.1	612.4	-2.0	203962_s_at	NEBL	nebullette
2381.3	4779.7	-2.0	207469_s_at	PIR	pirin (iron-binding nuclear protein)
737.8	1482.2	-2.0	202478_at	TRIB2	tribbles homolog 2 (Drosophila)
586.9	1175.3	-2.0	226085_at	CBX5	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)
137	274.5	-2.0	200906_s_at	KIAA0992	palladin
603.2	1206.2	-2.0	233924_s_at	SEC15L1	SEC15-like 1 (<i>S. cerevisiae</i>)
1423.2	2843	-2.0	228754_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
83.4	166.3	-2.0	222343_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)
174.1	347	-2.0	212525_s_at	H2AFX	H2A histone family, member X
1171.2	2333.8	-2.0	212158_at	SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
150.9	300.1	-2.0	202948_at	IL1R1	interleukin 1 receptor, type I
369.1	734.5	-2.0	202662_s_at	ITPR2	inositol 1,4,5-triphosphate receptor, type 2
50.6	100.4	-2.0	226912_at	ZDHHC23	zinc finger, DHHC-type containing 23
174	344.8	-2.0	225627_s_at	CACHD1	cache domain containing 1
335.7	663.9	-2.0	228352_at	UNC13D	unc-13 homolog D (<i>C. elegans</i>)
79.6	156.9	-2.0	209347_s_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
188.9	372.6	-2.0	203961_at	NEBL	nebullette
687.5	1354.6	-2.0	219918_s_at	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)
80.6	158.4	-2.0	219304_s_at	PDGFD	platelet derived growth factor D
332.2	651.2	-2.0	218218_at	DIP13B	DIP13 beta
18.7	36.5	-2.0	1554783_s_at	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2
1047.4	2044.1	-2.0	209498_at	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1
154.3	300.9	-1.9	203967_at	CDC6	CDC6 cell division cycle 6 homolog (<i>S. cerevisiae</i>)
139.2	271.1	-1.9	207339_s_at	LTB	lymphotoxin beta (TNF superfamily, member 3)
443.7	863	-1.9	207761_s_at	DKFZP586A0522	DKFZP586A0522 protein
14.8	28.7	-1.9	204827_s_at	CCNF	cyclin F
182.5	353	-1.9	222881_at	HPSE	heparanase
125.6	243.1	-1.9	1552477_a_at	IRF6	interferon regulatory factor 6
32.4	62.6	-1.9	211141_s_at	CNOT3	CCR4-NOT transcription complex, subunit 3

105.9	203.9	-1.9	212157_at	SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
164.9	316.9	-1.9	213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
118.5	228.1	-1.9	201896_s_at	PSRC1	proline/serine-rich coiled-coil 1
141.3	271.4	-1.9	215509_s_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
28.9	55.5	-1.9	211679_x_at	GPR51	G protein-coupled receptor 51
359.8	689.5	-1.9	233955_x_at	CXXC5	CXXC finger 5
656.7	1257.5	-1.9	210983_s_at	MCM7	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
1223.6	2338.1	-1.9	218051_s_at	FLJ12442	hypothetical protein FLJ12442
565.5	1080.9	-1.9	219148_at	PBK	PDZ binding kinase
679.2	1299.6	-1.9	204519_s_at	PLLP	plasma membrane proteolipid (plasmolipin)
57.2	109.4	-1.9	206117_at	TPM1	tropomyosin 1 (alpha)
45.6	87	-1.9	230163_at	GFRA1	GDNF family receptor alpha 1
188.5	359.4	-1.9	205240_at	GPSM2	G-protein signalling modulator 2 (AGS3-like, C. elegans)
257.4	489.9	-1.9	212707_s_at	RASA4	RAS p21 protein activator 4 /// hypothetical protein FLJ21767
10.1	19.2	-1.9	239038_at	gm117	Chromosome 1 open reading frame 52
190.4	361.7	-1.9	232122_s_at	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)
107.2	203.6	-1.9	229233_at	NRG3	neuregulin 3
337.8	639.9	-1.9	222958_s_at	DEPDC1	DEP domain containing 1
71.3	134.7	-1.9	226844_at	MOBK12B	MOB1, Mps One Binder kinase activator-like 2B (yeast)
1758.6	3315	-1.9	206464_at	BMX	BMX non-receptor tyrosine kinase
131.1	247.3	-1.9	211519_s_at	KIF2C	kinesin family member 2C
482.7	909.7	-1.9	229097_at	DIAPH3	Diaphanous homolog 3 (Drosophila)
176.7	332.6	-1.9	225078_at	EMP2	epithelial membrane protein 2
1040.1	1959.5	-1.9	224895_at	YAP1	Yes-associated protein 1, 65kDa
372.8	700.9	-1.9	231862_at	CBX5	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)
4212.8	7922.5	-1.9	226237_at	COL8A1	Collagen, type VIII, alpha 1
136	255.7	-1.9	225526_at	MKLN1	muskelin 1, intracellular mediator containing kelch motifs
417	781.7	-1.9	1556051_a_at	BICD1	bicaudal D homolog 1 (Drosophila)
60	112.6	-1.9	206480_at	LTC4S	leukotriene C4 synthase
37.4	70.2	-1.9	203920_at	NR1H3	nuclear receptor subfamily 1, group H, member 3
29	54.4	-1.9	222812_s_at	RHOF	ras homolog gene family, member F (in filopodia)
311.6	583.6	-1.9	204962_s_at	CENPA	centromere protein A, 17kDa
140.4	262.8	-1.9	204442_x_at	LTBP4	latent transforming growth factor beta binding protein 4
4509.9	8446.2	-1.9	201785_at	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)
1347.3	2522.6	-1.9	201664_at	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)
516.9	967	-1.9	211883_x_at	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
116.4	217.1	-1.9	217640_x_at	C18orf24	chromosome 18 open reading frame 24
1657.1	3091.5	-1.9	209773_s_at	RRM2	ribonucleotide reductase M2 polypeptide
379.4	704.7	-1.9	205260_s_at	ACYP1	acylphosphatase 1, erythrocyte (common) type
489.1	907.2	-1.9	225606_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)
167.7	311.1	-1.9	204887_s_at	PLK4	polo-like kinase 4 (Drosophila)
39.7	73.5	-1.9	217287_s_at	TRPC6	transient receptor potential cation channel, subfamily C, member 6
31.1	57.5	-1.8	238858_at	TIFA	TRAF-interacting protein with a forkhead-associated domain
446.6	824.1	-1.8	211889_x_at	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
202.2	373.1	-1.8	235545_at	DEPDC1	DEP domain containing 1

80.5	148.6	-1.8	203592_s_at	FSTL3	follistatin-like 3 (secreted glycoprotein)
19.1	35.2	-1.8	228433_at	FLJ11236	hypothetical protein FLJ11236
111.8	205.8	-1.8	209184_s_at	IRS2	insulin receptor substrate 2
401.2	738.3	-1.8	211596_s_at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1
257	473.7	-1.8	226065_at	PRICKLE1	prickle-like 1 (Drosophila)
171.5	315.3	-1.8	221687_s_at	C9orf28	chromosome 9 open reading frame 28
2393.4	4400.7	-1.8	217317_s_at	D15F37	D15F37 gene
196.3	361.1	-1.8	235521_at	HOXA3	homeo box A3
169.3	311.4	-1.8	203508_at	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B
313	573.3	-1.8	225531_at	CABLES1	Cdk5 and Abl enzyme substrate 1
114.1	209.1	-1.8	203793_x_at	PCGF2	polycomb group ring finger 2
3570.7	6530.4	-1.8	201631_s_at	IER3	immediate early response 3
682.8	1246.5	-1.8	1552619_a_at	ANLN	anillin, actin binding protein (scraps homolog, Drosophila)
84.3	153.9	-1.8	221245_s_at	C2orf31	chromosome 2 open reading frame 31
82.2	150	-1.8	221258_s_at	KIF18A	kinesin family member 18A
438.7	800.3	-1.8	203636_at	MID1	midline 1 (Opitz/BBB syndrome)
779.1	1418.7	-1.8	225046_at	LOC389831	hypothetical gene supported by AL713796
138	250.8	-1.8	201690_s_at	TPD52	tumor protein D52
413.9	748.3	-1.8	225098_at	ABI2	Abl interactor 2
482.9	873.1	-1.8	209555_s_at	CD36	CD36 antigen (collagen type I receptor, thrombospondin receptor)
453.9	821.3	-1.8	212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67
532.5	960.4	-1.8	224657_at	ERRFI1	ERBB receptor feedback inhibitor 1
412.2	744.4	-1.8	209621_s_at	PDLIM3	PDZ and LIM domain 3
965.7	1743.5	-1.8	218009_s_at	PRC1	protein regulator of cytokinesis 1
141.5	255	-1.8	216894_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
193.3	348.4	-1.8	225303_at	KIRREL	kin of IRRE like (Drosophila)
741.6	1335.3	-1.8	212183_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4
88.1	158.5	-1.8	1557948_at	PHLDB3	pleckstrin homology-like domain, family B, member 3
160	287.6	-1.8	204128_s_at	RFC3	replication factor C (activator 1) 3, 38kDa
152	273.4	-1.8	219416_at	SCARA3	scavenger receptor class A, member 3
261	468.6	-1.8	41660_at	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
383.8	689.2	-1.8	209589_s_at	EPHB2	EPH receptor B2
664.8	1194	-1.8	44783_s_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1
176.5	316.1	-1.8	212776_s_at	OBSL1	obscurin-like 1
504.1	903.8	-1.8	218308_at	TACC3	transforming, acidic coiled-coil containing protein 3
595.6	1064.9	-1.8	222116_s_at	TBC1D16	TBC1 domain family, member 16
277	495.4	-1.8	225063_at	UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)
504.6	900.3	-1.8	227123_at	RAB3B	RAB3B, member RAS oncogene family
229.5	410	-1.8	219550_at	ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)
33.4	59.5	-1.8	222456_s_at	EPLIN	epithelial protein lost in neoplasm beta
82.1	146.4	-1.8	221335_x_at	FLJ12886	hypothetical protein FLJ12886
301	536.9	-1.8	210018_x_at	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1
1200	2140.9	-1.8	212741_at	MAOA	monoamine oxidase A
1951.7	3477.5	-1.8	218718_at	PDGFC	platelet derived growth factor C
140.6	250.2	-1.8	210821_x_at	CENPA	centromere protein A, 17kDa
283.7	504.4	-1.8	223921_s_at	GBA2	glucosidase, beta (bile acid) 2

126.9	225.6	-1.8	202240_at	PLK1	polo-like kinase 1 (Drosophila)
488.4	868.5	-1.8	205925_s_at	RAB3B	RAB3B, member RAS oncogene family
151.9	270.2	-1.8	240120_at	SORBS2	Sorbin and SH3 domain containing 2
203.6	360.7	-1.8	209464_at	AURKB	aurora kinase B
737.9	1308.9	-1.8	225687_at	C20orf129	chromosome 20 open reading frame 129
1865.3	3307.2	-1.8	204009_s_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
2190.5	3885.6	-1.8	219489_s_at	NXN	nucleoredoxin
11.7	20.7	-1.8	231223_at	CSMD1	CUB and Sushi multiple domains 1
471.8	835.5	-1.8	229800_at	DCAMKL1	Doublecortin and CaM kinase-like 1
104.1	184.3	-1.8	205232_s_at	PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa
262.9	465.5	-1.8	227041_at		CDNA FLJ31513 fis, clone NT2RI1000127
180.5	319.1	-1.8	218115_at	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)
282.2	498.9	-1.8	218500_at	C8orf55	chromosome 8 open reading frame 55
1120.1	1978.4	-1.8	219058_x_at	TINAGL1	tubulointerstitial nephritis antigen-like 1
399.8	704.7	-1.8	219527_at	MOSC2	MOCO sulphurase C-terminal domain containing 2
63.8	112.6	-1.8	226192_at		Transcribed locus
183.3	322.7	-1.8	226033_at	USP31	ubiquitin specific peptidase 31
64.8	113.8	-1.8	208806_at	CHD3	chromodomain helicase DNA binding protein 3
1635	2874.2	-1.8	212288_at	FBNP1	formin binding protein 1
209.8	368.6	-1.8	209052_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1
180.6	317.1	-1.8	1553613_s_at	FOXC1	forkhead box C1
259.2	454.7	-1.8	203988_s_at	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
216.8	380.2	-1.8	215942_s_at	GTSE1	G-2 and S-phase expressed 1
158.7	277.7	-1.8	205046_at	CENPE	centromere protein E, 312kDa
149.6	262.2	-1.8	209733_at	LOC286440	hypothetical protein LOC286440
194.9	341.2	-1.8	228171_s_at	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4
292	508.5	-1.7	223194_s_at	C6orf85	chromosome 6 open reading frame 85
114.9	200.3	-1.7	210059_s_at	MAPK13	mitogen-activated protein kinase 13
153.5	267.5	-1.7	212023_s_at	MKI67	antigen identified by monoclonal antibody Ki-67
233.7	406.1	-1.7	238323_at	TEAD2	TEA domain family member 2
42.1	73.1	-1.7	226201_at	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)
138.4	239.8	-1.7	203661_s_at	TMOD1	tropomodulin 1
163.4	282.7	-1.7	52975_at	C9orf28	chromosome 9 open reading frame 28
869.9	1505.6	-1.7	214710_s_at	CCNB1	cyclin B1
586.3	1013.9	-1.7	206576_s_at	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
176.3	305	-1.7	202156_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2
437.8	757.6	-1.7	205667_at	WRN	Werner syndrome
71.1	122.7	-1.7	214519_s_at	RLN2	relaxin 2
224.6	387.9	-1.7	222757_s_at	ZAK	sterile alpha motif and leucine zipper containing kinase AZK
366.7	631.6	-1.7	206932_at	CH25H	cholesterol 25-hydroxylase
246	423.2	-1.7	213164_at	SLC5A3	solute carrier family 5 (inositol transporters), member 3
275.8	474.7	-1.7	1555388_s_at	SNX25	sorting nexin 25
168.1	288.6	-1.7	204549_at	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
3194.4	5493.2	-1.7	212181_s_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4
812.6	1396.5	-1.7	205924_at	RAB3B	RAB3B, member RAS oncogene family
441.1	758.5	-1.7	209053_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1

262.3	447.3	-1.7	225136_at	PLEKHA2	Pleckstrin homology domain containing, family A member 2
1691.2	2887.4	-1.7	204341_at	TRIM16	tripartite motif-containing 16
539.2	918.6	-1.7	219588_s_at	LUZP5	leucine zipper protein 5
1364.4	2324.3	-1.7	211467_s_at	NFIB	nuclear factor I/B
211.5	360.2	-1.7	229549_at	OPN1SW	Opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)
291	495.1	-1.7	228323_at	CASC5	cancer susceptibility candidate 5
482.5	820	-1.7	211126_s_at	CSRP2	cysteine and glycine-rich protein 2
143.6	244.4	-1.7	1555483_x_at	FBLIM1	filamin binding LIM protein 1
203.6	346.4	-1.7	222037_at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)
254.9	433.1	-1.7	210651_s_at	EPHB2	EPH receptor B2
238.3	404.6	-1.7	209408_at	KIF2C	kinesin family member 2C
1012.8	1716.9	-1.7	205020_s_at	ARL4	ADP-ribosylation factor-like 4
2277.6	3859.3	-1.7	225604_s_at	C9orf19	chromosome 9 open reading frame 19
135.6	229.9	-1.7	236261_at	OSBPL6	Oxysterol binding protein-like 6
1162.2	1970.9	-1.7	201663_s_at	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)
253	428.4	-1.7	218726_at	DKFZp762E1312	hypothetical protein DKFZp762E1312
18.8	31.8	-1.7	203110_at	PTK2B	PTK2B protein tyrosine kinase 2 beta
340.2	575.9	-1.7	206036_s_at	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)
500.4	845.4	-1.7	207030_s_at	CSRP2	cysteine and glycine-rich protein 2
1409.4	2381	-1.7	222457_s_at	EPLIN	epithelial protein lost in neoplasm beta
369.2	624.1	-1.7	213940_s_at	FNBP1	formin binding protein 1
367.1	620	-1.7	218663_at	HCAP-G	chromosome condensation protein G
1164.4	1965.8	-1.7	213012_at	NEDD4	neural precursor cell expressed, developmentally down-regulated 4
133.2	225	-1.7	225935_at	CUTL1	Cut-like 1, CCAAT displacement protein (Drosophila)
110.1	185.5	-1.7	223595_at	AD031	AD031 protein
417.7	703.4	-1.7	205476_at	CCL20	chemokine (C-C motif) ligand 20
386.1	649.6	-1.7	208309_s_at	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1
1268	2134.1	-1.7	206303_s_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4
497.5	837.1	-1.7	224963_at	SLC26A2	solute carrier family 26 (sulfate transporter), member 2
337.1	567.5	-1.7	242931_at		
103.6	174	-1.7	220183_s_at	NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6
1781.4	2994	-1.7	239058_at	FOXC2	Forkhead box C2 (MFH-1, mesenchyme forkhead 1)
423.7	711	-1.7	221520_s_at	CDCA8	cell division cycle associated 8
249.6	418.9	-1.7	212142_at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)
50.4	84.5	-1.7	218833_at	ZAK	sterile alpha motif and leucine zipper containing kinase AZK
269.2	450.8	-1.7	219584_at	PLA1A	phospholipase A1 member A
739.6	1237.3	-1.7	206283_s_at	TAL1	T-cell acute lymphocytic leukemia 1
133.5	222.4	-1.7	204540_at	EEF1A2	eukaryotic translation elongation factor 1 alpha 2
665.4	1107.8	-1.7	201792_at	AEBP1	AE binding protein 1
1189.4	1978.3	-1.7	205097_at	SLC26A2	solute carrier family 26 (sulfate transporter), member 2
61.7	102.6	-1.7	1559840_s_at	TBX18	T-box 18
957.7	1591.7	-1.7	201853_s_at	CDC25B	cell division cycle 25B
952.2	1582.7	-1.7	1555758_a_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
186	309.1	-1.7	225816_at	PHF17	PHD finger protein 17
636.8	1058.4	-1.7	208079_s_at	STK6	serine/threonine kinase 6

33.6	55.8	-1.7	231296_at		
298.7	494.8	-1.7	218355_at	KIF4A	kinesin family member 4A
152.2	252.1	-1.7	220651_s_at	MCM10	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)
120.6	199.6	-1.7	204267_x_at	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1
602.4	994	-1.7	204767_s_at	FEN1	flap structure-specific endonuclease 1
227.6	375.5	-1.7	203158_s_at	GLS	glutaminase
471.8	778.6	-1.7	213346_at	LOC93081	hypothetical protein BC015148
150.5	248.1	-1.6	203976_s_at	CHAF1A	chromatin assembly factor 1, subunit A (p150)
72.7	119.8	-1.6	226611_s_at	PRR6	proline rich 6
9036.5	14879.8	-1.6	206116_s_at	TPM1	tropomyosin 1 (alpha)
97	159.5	-1.6	203304_at	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
218.4	359.5	-1.6	204431_at	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
628.7	1033.1	-1.6	213226_at	CCNA2	Cyclin A2
827.7	1360.1	-1.6	202017_at	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)
2423.7	3981.9	-1.6	224719_s_at	GRCC10	likely ortholog of mouse gene rich cluster, C10 gene
1717.4	2816.9	-1.6	221730_at	COL5A2	collagen, type V, alpha 2
404.1	661.9	-1.6	225062_at	LOC389831	hypothetical gene supported by AL713796
470.9	769.3	-1.6	203755_at	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
892.6	1459.1	-1.6	201058_s_at	MYL9	myosin, light polypeptide 9, regulatory
267.5	437.3	-1.6	1558117_s_at	USP31	ubiquitin specific peptidase 31
260.8	425.1	-1.6	227652_at	FAM69B	family with sequence similarity 69, member B
1333	2170.8	-1.6	226326_at	PCGF5	polycomb group ring finger 5
690.3	1121.8	-1.6	212126_at	CBX5	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)
3676.3	5978.3	-1.6	1555480_a_at	FBLIM1	filamin binding LIM protein 1
218.7	355.7	-1.6	201710_at	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
128.8	209	-1.6	1554930_a_at	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
1488.7	2417.6	-1.6	205436_s_at	H2AFX	H2A histone family, member X
1792	2902.8	-1.6	201539_s_at	FHL1	four and a half LIM domains 1
260.2	421.6	-1.6	225533_at	PHF19	PHD finger protein 19
386.3	624.9	-1.6	223307_at	CDCA3	cell division cycle associated 3
909.8	1473.2	-1.6	210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
46.7	75.5	-1.6	242652_at	EPB41L2	Erythrocyte membrane protein band 4.1-like 2
78.9	127.3	-1.6	242890_at	HELLS	Helicase, lymphoid-specific
99.2	159.9	-1.6	243529_at	MARS2	methionine-tRNA synthetase 2 (mitochondrial)
192.9	311.3	-1.6	220934_s_at	MGC3196	hypothetical protein MGC3196
463	746.6	-1.6	213221_s_at	SNF1LK2	SNF1-like kinase 2
3650.4	5885.2	-1.6	218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21
680.3	1093.9	-1.6	218350_s_at	GMNN	geminin, DNA replication inhibitor
675.5	1083.6	-1.6	203764_at	DLG7	discs, large homolog 7 (Drosophila)
121.1	194.5	-1.6	221591_s_at	FAM64A	family with sequence similarity 64, member A
157	252	-1.6	211080_s_at	NEK2	NIMA (never in mitosis gene a)-related kinase 2
285.7	458.7	-1.6	1558103_a_at	TM6SF1	Transmembrane 6 superfamily member 1
201.2	322.5	-1.6	222640_at	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha
490.4	785.8	-1.6	211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
915.7	1466.5	-1.6	204152_s_at	MFNG	manic fringe homolog (Drosophila)
666.9	1067.9	-1.6	203370_s_at	PDLIM7	PDZ and LIM domain 7 (enigma)

217.4	348	-1.6	210162_s_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
143.7	230.1	-1.6	207122_x_at	SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
48.5	77.4	-1.6	209832_s_at	CDT1	DNA replication factor
10.1	16.1	-1.6	1553120_at	CLSPN	claspin homolog (<i>Xenopus laevis</i>)
607.7	968.7	-1.6	238427_at	GRPEL2	GrpE-like 2, mitochondrial (<i>E. coli</i>)
341.8	544.8	-1.6	38918_at	SOX13	SRY (sex determining region Y)-box 13
147.7	235.1	-1.6	222809_x_at	C14orf65	chromosome 14 open reading frame 65
1907.7	3037.6	-1.6	202468_s_at	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1
1458.2	2321.1	-1.6	1554167_a_at	GOLGA7	golgi autoantigen, golgin subfamily a, 7
444.4	706.5	-1.6	218094_s_at	C20orf35	chromosome 20 open reading frame 35
430.1	684	-1.6	217838_s_at	EVL	Enah/Vasp-like
373.9	593.3	-1.6	201284_s_at	APEH	N-acylaminoacyl-peptide hydrolase
1713	2719	-1.6	202554_s_at	GSTM3	glutathione S-transferase M3 (brain)
957.5	1518.2	-1.6	205730_s_at	ABLIM3	actin binding LIM protein family, member 3
951.5	1508.5	-1.6	206580_s_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2
4931.7	7818.9	-1.6	209016_s_at	KRT7	keratin 7
341.8	540.9	-1.6	225108_at	AGPS	Alkylglycerone phosphate synthase
219.8	347.9	-1.6	208807_s_at	CHD3	chromodomain helicase DNA binding protein 3
118.3	186.9	-1.6	214847_s_at	GPSM3	G-protein signalling modulator 3 (AGS3-like, <i>C. elegans</i>)
699.3	1104.4	-1.6	208886_at	H1F0	H1 histone family, member 0
273.1	431.2	-1.6	206363_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
548.6	867	-1.6	209427_at	SMTN	smoothelin
1906.1	3005	-1.6	212501_at	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta
708.3	1117.6	-1.6	224013_s_at	SOX7	SRY (sex determining region Y)-box 7
473.4	745.7	-1.6	204975_at	EMP2	epithelial membrane protein 2
61.8	97.3	-1.6	232031_s_at	KIAA1632	KIAA1632
91.9	144.7	-1.6	225829_at	PDZK8	PDZ domain containing 8
251.9	396.4	-1.6	214110_s_at	LSP1	Lymphocyte-specific protein 1
1579.5	2481.4	-1.6	202856_s_at	SLC16A3	solute carrier family 16 (monocarboxylic acid transporters), member 3
244.8	384.3	-1.6	201195_s_at	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
361.9	568.2	-1.6	203432_at	TMPO	thymopoietin
130.6	204.8	-1.6	211165_x_at	EPHB2	EPH receptor B2
1256.3	1970.6	-1.6	201890_at	RRM2	ribonucleotide reductase M2 polypeptide
1313	2055.4	-1.6	211518_s_at	BMP4	bone morphogenetic protein 4
346.9	543	-1.6	225320_at	C10orf42	chromosome 10 open reading frame 42
643.1	1006.8	-1.6	203907_s_at	IQSEC1	IQ motif and Sec7 domain 1
158.6	248.2	-1.6	221004_s_at	ITM2C	integral membrane protein 2C /// integral membrane protein 2C
1892.1	2960.2	-1.6	204088_at	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4
180.3	282.1	-1.6	238587_at	STS-1	Cbl-interacting protein Sts-1
631	985.6	-1.6	1552476_s_at	PLCD3	phospholipase C, delta 3
342.4	535	-1.6	226408_at	TEAD2	TEA domain family member 2
1705.1	2659.2	-1.6	228266_s_at	HDFGRP3	hepatoma-derived growth factor, related protein 3
4606.7	7190.5	-1.6	202291_s_at	MGP	matrix Gla protein
2330.9	3633	-1.6	201262_s_at	BGN	biglycan
211.8	329.9	-1.6	227626_at	PAQR8	progesterone and adipoQ receptor family member VIII

397.5	619.1	-1.6	227776_at		Transcribed locus
149.9	233.2	-1.6	230259_at	C10orf125	chromosome 10 open reading frame 125
230.5	358.7	-1.6	237252_at	THBD	thrombomodulin
542.3	843.5	-1.6	224908_s_at	TTL	tubulin tyrosine ligase
1466.9	2273.4	-1.6	203404_at	ARMCX2	armadillo repeat containing, X-linked 2
507.7	787.4	-1.6	204162_at	KNTC2	kinetochore associated 2
489.8	758	-1.5	202459_s_at	LPIN2	lipin 2
287.5	444.1	-1.5	204241_at	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl
99.1	153.1	-1.5	227678_at	KUB3	Ku70-binding protein 3
613.6	948.3	-1.5	212658_at	LHFPL2	lipoma HMGIC fusion partner-like 2
1310.3	2026.3	-1.5	204153_s_at	MFNG	manic fringe homolog (Drosophila)
304.1	469.4	-1.5	224920_x_at	MYADM	myeloid-associated differentiation marker
650.5	1004.3	-1.5	213112_s_at	SQSTM1	sequestosome 1
1235.5	1902.6	-1.5	202161_at	PKN1	protein kinase N1
1128	1736.7	-1.5	226763_at	SESTD1	SEC14 and spectrin domains 1
198.8	306	-1.5	238720_at		
870.9	1338.5	-1.5	201906_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
230	353.1	-1.5	212045_at	GLG1	golgi apparatus protein 1
1466	2252.2	-1.5	212472_at	MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2
1993.6	3064	-1.5	213029_at	NFIB	Nuclear factor I/B
4337.3	6667.3	-1.5	200808_s_at	ZYX	zyxin
19.1	29.3	-1.5	230954_at	C20orf112	chromosome 20 open reading frame 112
207.4	317.7	-1.5	213352_at	TMCC1	transmembrane and coiled-coil domain family 1
750.6	1147.8	-1.5	217889_s_at	CYBRD1	cytochrome b reductase 1
56.4	86.2	-1.5	219189_at	FBXL6	F-box and leucine-rich repeat protein 6
606.6	927.8	-1.5	211599_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)
343.3	524.9	-1.5	221521_s_at	Pfs2	DNA replication complex GINS protein PSF2
421.5	641.2	-1.5	227100_at	B3GTL	beta 3-glycosyltransferase-like
24.3	37	-1.5	218182_s_at	CLDN1	claudin 1
486.5	740.4	-1.5	206102_at	PSF1	DNA replication complex GINS protein PSF1
308.7	470	-1.5	219131_at	UBIAD1	UbiA prenyltransferase domain containing 1
136.3	206.1	-1.5	227545_at	BARD1	BRCA1 associated RING domain 1
366.8	554.1	-1.5	222505_at	LMBR1	limb region 1 homolog (mouse)
1000.3	1509.6	-1.5	200907_s_at	KIAA0992	palladin
331.8	499.4	-1.5	226035_at	USP31	ubiquitin specific peptidase 31
1659.6	2496.5	-1.5	212724_at	RND3	Rho family GTPase 3
88.1	132.2	-1.5	232067_at	C6orf168	chromosome 6 open reading frame 168
195.8	294.1	-1.5	210567_s_at	SKP2	S-phase kinase-associated protein 2 (p45)
250.7	376.1	-1.5	202617_s_at	MECP2	methyl CpG binding protein 2 (Rett syndrome)
455	682.4	-1.5	220949_s_at	MGC5242	hypothetical protein MGC5242
763.5	1144.9	-1.5	224976_at	NFIA	nuclear factor I/A
384	575.9	-1.5	214121_x_at	PDLIM7	PDZ and LIM domain 7 (enigma)
611.1	915.7	-1.5	224718_at	YY1	YY1 transcription factor
488.5	730.8	-1.5	225079_at	EMP2	epithelial membrane protein 2
533.9	799.7	-1.5	214755_at	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1
120.3	180	-1.5	235232_at		Transcribed locus
492.6	736.7	-1.5	226287_at	NY-REN-41	NY-REN-41 antigen

202.1	301.9	-1.5	228006_at	PTEN	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
1514.9	2259.8	-1.5	206429_at	F2RL1	coagulation factor II (thrombin) receptor-like 1
1229.5	1831.6	-1.5	212614_at	ARID5B	AT rich interactive domain 5B (MRF1-like)
381.3	567.8	-1.5	208657_s_at	38969	septin 9
177.1	263.7	-1.5	213599_at	OIP5	Opa interacting protein 5
97.3	144.5	-1.5	223168_at	RHOU	ras homolog gene family, member U
546.6	811.4	-1.5	218755_at	KIF20A	kinesin family member 20A
345.8	513	-1.5	213807_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)
2375.3	3518	-1.5	223349_s_at	BOK	BCL2-related ovarian killer
1344.5	1991.5	-1.5	203510_at	MET	met proto-oncogene (hepatocyte growth factor receptor)
287.4	425.6	-1.5	203344_s_at	RBBP8	retinoblastoma binding protein 8
292.6	433.4	-1.5	223131_s_at	TRIM8	tripartite motif-containing 8
519.8	769.1	-1.5	211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3
1035.4	1529.1	-1.5	202855_s_at	SLC16A3	solute carrier family 16 (monocarboxylic acid transporters), member 3
261.5	385.6	-1.5	220009_at	LONRF3	LON peptidase N-terminal domain and ring finger 3
247.4	365.1	-1.5	226710_at	MGC70857	similar to RIKEN cDNA C030006K11 gene
276.4	407.8	-1.5	218290_at	PLEKHJ1	pleckstrin homology domain containing, family J member 1
3393.2	4994.1	-1.5	201261_x_at	BGN	biglycan
164.2	241.6	-1.5	238612_at	BRD4	Bromodomain containing 4
2529.2	3721.2	-1.5	225673_at	MYADM	myeloid-associated differentiation marker
227.9	335.3	-1.5	212880_at	WDR7	WD repeat domain 7
157.9	232	-1.5	213788_s_at	FLJ35348	FLJ35348
193.2	283.8	-1.5	225354_s_at	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2
250.8	368.5	-1.5	203046_s_at	TIMELESS	timeless homolog (Drosophila)
144.4	211.7	-1.5	203157_s_at	GLS	glutaminase
146.1	213.6	-1.5	206581_at	BNC1	basonuclin 1
783.5	1145.9	-1.5	214437_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
283.9	415.1	-1.5	230543_at		Similar to Chloride intracellular channel protein 4
1259.2	1837	-1.5	218031_s_at	CHES1	checkpoint suppressor 1
547.6	799.7	-1.5	204127_at	RFC3	replication factor C (activator 1) 3, 38kDa
763	1112.6	-1.5	214051_at	MGC39900	hypothetical protein MGC39900
168.4	245.5	-1.5	232331_at	PPARG	Peroxisome proliferative activated receptor, gamma
564.9	823.4	-1.5	216976_s_at	RYK	RYK receptor-like tyrosine kinase
446.2	650.1	-1.5	203234_at	UPP1	uridine phosphorylase 1
3201.3	4663.2	-1.5	209526_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3
442.3	644.2	-1.5	1563111_a_at	PIGX	phosphatidylinositol glycan, class X
3371.9	4909.3	-1.5	202779_s_at	UBE2S	ubiquitin-conjugating enzyme E2S
887.7	1290.6	-1.5	217992_s_at	EFHD2	EF-hand domain family, member D2
1246.1	1808.4	-1.5	201911_s_at	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
983.5	1426.9	-1.5	223622_s_at	HYI	hydroxypyruvate isomerase homolog (E. coli)
2458.5	3561.1	-1.4	204150_at	STAB1	stabilin 1
607.2	878.7	-1.4	227112_at	TMCC1	transmembrane and coiled-coil domain family 1
52.3	75.7	-1.4	231152_at		MRNA; cDNA DKFZp686D22106 (from clone DKFZp686D22106)
474	685.1	-1.4	231955_s_at	HIBADH	3-hydroxyisobutyrate dehydrogenase
283.2	409.5	-1.4	201357_s_at	SF3A1	splicing factor 3a, subunit 1, 120kDa
525.7	759.2	-1.4	223103_at	STARD10	START domain containing 10

956.7	1379.5	-1.4	226715_at	KIAA0415	Forkhead box K1
159.3	229.5	-1.4	242139_s_at	LOC113386	similar to envelope protein
140.4	202.4	-1.4	204772_s_at	TTF1	transcription termination factor, RNA polymerase I
788.3	1134.1	-1.4	201904_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
1417.9	2040.8	-1.4	223287_s_at	FOXP1	forkhead box P1
773.6	1112.5	-1.4	218099_at	HT008	uncharacterized hypothalamus protein HT008
142.4	204.6	-1.4	222238_s_at	POLM	polymerase (DNA directed), mu
177	253.8	-1.4	225642_at	KTI12	KTI12 homolog, chromatin associated (<i>S. cerevisiae</i>)
157.3	225.6	-1.4	204790_at	SMAD7	SMAD, mothers against DPP homolog 7 (<i>Drosophila</i>)
1811.7	2600.7	-1.4	209340_at	UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1
432.8	620.5	-1.4	224945_at	BTBD7	BTB (POZ) domain containing 7
143.3	205.2	-1.4	213008_at	FLJ10719	hypothetical protein FLJ10719
462.3	662.6	-1.4	230958_s_at		Transcribed locus
232.2	332.2	-1.4	203358_s_at	EZH2	enhancer of zeste homolog 2 (<i>Drosophila</i>)
123.8	177	-1.4	214095_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
128.7	184	-1.4	214908_s_at	TRRAP	transformation/transcription domain-associated protein
3295.4	4709.1	-1.4	200965_s_at	ABLIM1	actin binding LIM protein 1
711.8	1014.2	-1.4	225750_at	ERO1L	ERO1-like (<i>S. cerevisiae</i>)
411.8	586.9	-1.4	227584_at	NAV1	Neuron navigator 1
357.1	508.2	-1.4	205743_at	STAC	SH3 and cysteine rich domain
205.9	292.5	-1.4	209736_at	SOX13	SRY (sex determining region Y)-box 13
797.6	1133.5	-1.4	1552798_a_at	TLR4	toll-like receptor 4
72.3	102.5	-1.4	219036_at	Cep70	p10-binding protein
16	22.7	-1.4	202674_s_at	LMO7	LIM domain 7
192.4	272.9	-1.4	230329_s_at	NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6
120.4	170.6	-1.4	228257_at	FLJ34236	hypothetical protein FLJ34236
595.3	841.7	-1.4	230788_at	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
1046.8	1477.7	-1.4	212792_at	DPY19L1	dpy-19-like 1 (<i>C. elegans</i>)
1384.5	1956.5	-1.4	211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
779.8	1102	-1.4	225147_at	PSCD3	pleckstrin homology, Sec7 and coiled-coil domains 3
293.5	413.7	-1.4	222471_s_at	KCMF1	potassium channel modulatory factor 1
3559.6	5022.7	-1.4	221725_at	WASF2	WAS protein family, member 2
1167.1	1645.3	-1.4	204026_s_at	ZWINT	ZW10 interactor
1376.7	1937.9	-1.4	212124_at	RAI17	retinoic acid induced 17
135.8	190.2	-1.4	227470_at	ZNF553	zinc finger protein 553
2592.5	3628	-1.4	208817_at	COMT	catechol-O-methyltransferase
602.8	842	-1.4	210026_s_at	CARD10	caspase recruitment domain family, member 10
1628.4	2273.8	-1.4	225955_at	METRNL	meteorin, glial cell differentiation regulator-like
607.9	849.6	-1.4	210296_s_at	PXMP3	peroxisomal membrane protein 3, 35kDa (Zellweger syndrome)
2441.5	3399.9	-1.4	201668_x_at	MARCKS	myristoylated alanine-rich protein kinase C substrate
622.9	868.1	-1.4	221016_s_at	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)
204.1	283.5	-1.4	39817_s_at	C6orf108	chromosome 6 open reading frame 108
1227.4	1705.1	-1.4	218384_at	CARHSP1	calcium regulated heat stable protein 1, 24kDa
1204.6	1673.7	-1.4	208934_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)
222.2	308	-1.4	214831_at	MED28	Mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)
630.1	873.7	-1.4	209285_s_at	RAP140	retinoblastoma-associated protein 140

195.2	270.9	-1.4	226648_at		Full-length cDNA clone CS0DL007YI24
706.5	978.5	-1.4	204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma
1059	1467.3	-1.4	208398_s_at	TBPL1	TBP-like 1
1593.3	2203.8	-1.4	218039_at	NUSAP1	nucleolar and spindle associated protein 1
7050.1	9750.4	-1.4	1553962_s_at	RHOB	ras homolog gene family, member B
427	589.8	-1.4	202767_at	ACP2	acid phosphatase 2, lysosomal
2219.4	3064.8	-1.4	209108_at	TSPAN6	tetraspanin 6
420.1	579.5	-1.4	203859_s_at	PALM	paralemmin
41.3	56.9	-1.4	211538_s_at	HSPA2	heat shock 70kDa protein 2
182.1	250.5	-1.4	223083_s_at	EGLN2	egl nine homolog 2 (C. elegans)
1081.3	1488.2	-1.4	200671_s_at	SPTBN1	spectrin, beta, non-erythrocytic 1
327.1	449.1	-1.4	204222_s_at	GLIPR1	GLI pathogenesis-related 1 (glioma)
74.3	101.5	-1.4	202914_s_at	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11
364.2	497.7	-1.4	201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
1323.3	1808.8	-1.4	218915_at	NF2	neurofibromin 2 (bilateral acoustic neuroma)
294	400.3	-1.4	201182_s_at	CHD4	chromodomain helicase DNA binding protein 4
196.3	267.4	-1.4	203679_at	TMED1	transmembrane emp24 protein transport domain containing 1
609.3	829	-1.4	217781_s_at	ZFP106	zinc finger protein 106 homolog (mouse)
466.6	634.1	-1.4	211558_s_at	DHPS	deoxyhypusine synthase
1762.7	2394.1	-1.4	205890_s_at	UBD	ubiquitin D
550.5	746.8	-1.4	200849_s_at	AHCYL1	S-adenosylhomocysteine hydrolase-like 1
1108.5	1504	-1.4	223084_s_at	CCNDBP1	cyclin D-type binding-protein 1
2249.2	3047.2	-1.4	200621_at	CSRP1	cysteine and glycine-rich protein 1
437.4	591.9	-1.4	211113_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1
1902.5	2568.1	-1.3	200035_at	DULLARD	dullard homolog (Xenopus laevis)
2036.7	2741.2	-1.3	205022_s_at	CHES1	checkpoint suppressor 1
516.5	693.8	-1.3	238523_at	C16orf44	chromosome 16 open reading frame 44
69	92.6	-1.3	1555014_x_at	OK/SW-CL.92	OK/SW-CL.92
320.3	429.5	-1.3	205339_at	SIL	TAL1 (SCL) interrupting locus
1730.5	2313.8	-1.3	224918_x_at	MGST1	microsomal glutathione S-transferase 1
1056	1412.4	-1.3	201039_s_at	RAD23A	RAD23 homolog A (S. cerevisiae)
631.3	843.3	-1.3	212437_at	CENPB	centromere protein B, 80kDa
1671.3	2232.5	-1.3	218847_at	IMP-2	IGF-II mRNA-binding protein 2
1174.7	1567.2	-1.3	200922_at	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
1336.8	1783.2	-1.3	218368_s_at	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A
171.1	226.9	-1.3	209217_s_at	WDR45	WD repeat domain 45
1980.8	2621.5	-1.3	224748_at	WDR68	WD repeat domain 68
593	777.3	-1.3	228564_at	LOC375295	hypothetical gene supported by BC013438
266.9	349.3	-1.3	225091_at	ZCCHC3	zinc finger, CCHC domain containing 3
359.2	467	-1.3	205562_at	RPP38	ribonuclease P/MRP 38kDa subunit
203.7	261.6	-1.3	209998_at	PIGO	phosphatidylinositol glycan, class O