

Supplementary Information

Table S1. Details of 1236 probes selected from ADE-treated TK6 cells.

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
200049_at	MYST histone acetyltransferase 2	<i>MYST2</i>	0.4269
200050_at	zinc finger protein 146	<i>ZNF146</i>	0.3454
200664_s_at	DnaJ (Hsp40) homolog, subfamily B, member 1	<i>DNAJB1</i>	0.3713
200666_s_at	DnaJ (Hsp40) homolog, subfamily B, member 1	<i>DNAJB1</i>	0.3927
200670_at	X-box binding protein 1	<i>XBPI</i>	0.4811
200676_s_at	ubiquitin-conjugating enzyme E2L 3	<i>UBE2L3</i>	1.7951
200684_s_at	ubiquitin-conjugating enzyme E2L 3	<i>UBE2L3</i>	1.7688
200685_at	splicing factor, arginine/serine-rich 11	<i>SFRS11</i>	1.9781
200703_at	dynein, light chain, LC8-type 1	<i>DYNLL1</i>	0.4769
200768_s_at	methionine adenosyltransferase II, alpha	<i>MAT2A</i>	0.3680
200769_s_at	methionine adenosyltransferase II, alpha	<i>MAT2A</i>	0.3544
200798_x_at	myeloid cell leukemia sequence 1 (BCL2-related)	<i>MCL1</i>	0.4781
200800_s_at	heat shock 70 kDa protein 1A///heat shock 70 kDa protein 1B	<i>HSPA1A/HSPA1B</i>	0.1884
200815_s_at	platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45 kDa)	<i>PAFAH1B1</i>	0.2655
200868_s_at	ring finger protein 114	<i>RNF114</i>	0.4707
200874_s_at	NOP56 ribonucleoprotein homolog (yeast)	<i>NOP56</i>	0.4369
200961_at	selenophosphate synthetase 2	<i>SEPHS2</i>	0.2579
200992_at	importin 7	<i>IPO7</i>	0.4390
200993_at	importin 7	<i>IPO7</i>	0.4836
200994_at	importin 7	<i>IPO7</i>	0.4067
201041_s_at	dual specificity phosphatase 1	<i>DUSP1</i>	0.3398
201155_s_at	mitofusin 2	<i>MFN2</i>	0.4877
201196_s_at	adenosylmethionine decarboxylase 1	<i>AMD1</i>	0.3825
201197_at	adenosylmethionine decarboxylase 1	<i>AMD1</i>	0.3849
201207_at	tumor necrosis factor, alpha-induced protein 1 (endothelial)	<i>TNFAIP1</i>	0.3662
201228_s_at	ariadne homolog 2 (Drosophila)	<i>ARIH2</i>	1.5010
201243_s_at	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	<i>ATP1B1</i>	0.4407
201329_s_at	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	<i>ETS2</i>	0.3591
201336_at	vesicle-associated membrane protein 3 (cellubrevin)	<i>VAMP3</i>	0.4950
201368_at	zinc finger protein 36, C3H type-like 2	<i>ZFP36L2</i>	0.2133
201384_s_at	neighbor of BRCA1 gene 1	<i>NBR1</i>	0.4572

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
201394_s_at	RNA binding motif protein 5	<i>RBM5</i>	0.4499
201395_at	RNA binding motif protein 5	<i>RBM5</i>	0.3968
201417_at	SRY (sex determining region Y)-box 4	<i>SOX4</i>	0.2860
201471_s_at	sequestosome 1	<i>SQSTM1</i>	0.3927
201473_at	jun B proto-oncogene	<i>JUNB</i>	0.3375
201520_s_at	G-rich RNA sequence binding factor 1	<i>GRSF1</i>	0.3644
201531_at	zinc finger protein 36, C3H type, homolog (mouse)	<i>ZFP36</i>	0.2445
201566_x_at	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	<i>ID2</i>	0.4164
201585_s_at	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	<i>SFPQ</i>	0.3827
201586_s_at	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	<i>SFPQ</i>	0.4774
201602_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	<i>PPP1R12A</i>	0.3687
201603_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	<i>PPP1R12A</i>	0.3490
201604_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	<i>PPP1R12A</i>	0.3714
201631_s_at	immediate early response 3	<i>IER3</i>	0.1905
201644_at	tissue specific transplantation antigen P35B	<i>TSTA3</i>	1.5005
201685_s_at	TOX high mobility group box family member 4	<i>TOX4</i>	0.4846
201715_s_at	apoptotic chromatin condensation inducer 1	<i>ACIN1</i>	0.4405
201734_at	Chloride channel 3	<i>CLCN3</i>	0.4467
201735_s_at	chloride channel 3	<i>CLCN3</i>	0.4351
201758_at	tumor susceptibility gene 101	<i>TSG101</i>	0.4766
201773_at	activity-dependent neuroprotector homeobox	<i>ADNP</i>	0.3386
201783_s_at	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	<i>RELA</i>	0.2338
201788_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	<i>DDX42</i>	0.4994
201823_s_at	ring finger protein 14	<i>RNF14</i>	0.3915
201841_s_at	heat shock 27 kDa protein 1	<i>HSPB1</i>	1.5951
201850_at	capping protein (actin filament), gelsolin-like	<i>CAPG</i>	1.6171
201877_s_at	protein phosphatase 2, regulatory subunit B', gamma isoform	<i>PPP2R5C</i>	0.4798

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
201881_s_at	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	<i>ARIH1</i>	0.4508
201896_s_at	proline/serine-rich coiled-coil 1	<i>PSRC1</i>	0.4186
201924_at	AF4/FMR2 family, member 1	<i>AFF1</i>	0.3314
201948_at	guanine nucleotide binding protein-like 2 (nucleolar)	<i>GNL2</i>	0.4355
201964_at	senataxin	<i>SETX</i>	0.4075
201965_s_at	senataxin	<i>SETX</i>	0.4586
201987_at	mediator complex subunit 13	<i>MED13</i>	0.4943
201992_s_at	kinesin family member 5B	<i>KIF5B</i>	0.4833
201993_x_at	heterogeneous nuclear ribonucleoprotein D-like	<i>HNRPDL</i>	1.6963
201999_s_at	dynein, light chain, Tctex-type 1	<i>DYNLT1</i>	0.4985
202006_at	protein tyrosine phosphatase, non-receptor type 12	<i>PTPN12</i>	0.3970
202033_s_at	RB1-inducible coiled-coil 1	<i>RB1CC1</i>	0.4034
202034_x_at	RB1-inducible coiled-coil 1	<i>RB1CC1</i>	0.4239
202049_s_at	zinc finger, MYM-type 4	<i>ZMYM4</i>	0.3908
202066_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	<i>PPFIA1</i>	0.3380
202081_at	immediate early response 2	<i>IER2</i>	0.2585
202094_at	baculoviral IAP repeat-containing 5	<i>BIRC5</i>	1.7418
202096_s_at	translocator protein (18 kDa)	<i>TSPO</i>	1.5257
202097_at	nucleoporin 153 kDa	<i>NUP153</i>	0.4282
202113_s_at	sorting nexin 2	<i>SNX2</i>	0.4194
202114_at	sorting nexin 2	<i>SNX2</i>	0.3759
202116_at	D4, zinc and double PHD fingers family 2	<i>DPF2</i>	0.2467
202124_s_at	trafficking protein, kinesin binding 2	<i>TRAK2</i>	0.4927
202136_at	zinc finger, MYND domain containing 11	<i>ZMYND11</i>	0.4497
202153_s_at	nucleoporin 62 kDa	<i>NUP62</i>	0.3135
202155_s_at	nucleoporin 214 kDa	<i>NUP214</i>	0.4488
202159_at	phenylalanyl-tRNA synthetase, alpha subunit	<i>FARSA</i>	0.4497
202160_at	CREB binding protein	<i>CREBBP</i>	0.3249
202176_at	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	<i>ERCC3</i>	0.3918
202190_at	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50 kDa	<i>CSTF1</i>	0.3357

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
202215_s_at	nuclear transcription factor Y, gamma	<i>NFYC</i>	0.4856
202218_s_at	fatty acid desaturase 2	<i>FADS2</i>	1.5531
202226_s_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	<i>CRK</i>	0.4647
202241_at	tribbles homolog 1 (Drosophila)	<i>TRIB1</i>	0.2160
202258_s_at	NEDD4 binding protein 2-like 2	<i>N4BP2L2</i>	0.4758
202260_s_at	syntaxin binding protein 1	<i>STXBP1</i>	0.4521
202266_at	TRAF and TNF receptor associated protein	<i>TTRAP</i>	0.3915
202272_s_at	F-box protein 28	<i>FBXO28</i>	0.2530
202293_at	stromal antigen 1	<i>STAG1</i>	0.4698
202301_s_at	arginine/serine-rich coiled-coil 2	<i>RSRC2</i>	1.7114
202302_s_at	arginine/serine-rich coiled-coil 2	<i>RSRC2</i>	1.7024
202333_s_at	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	<i>UBE2B</i>	0.4683
202348_s_at	torsin family 1, member A (torsin A)	<i>TORIA</i>	0.3966
202349_at	torsin family 1, member A (torsin A)	<i>TORIA</i>	0.4713
202351_at	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	<i>ITGAV</i>	0.4170
202375_at	SEC24 family, member D (S. cerevisiae)	<i>SEC24D</i>	0.4291
202393_s_at	Kruppel-like factor 10	<i>KLF10</i>	3.2931
202417_at	kelch-like ECH-associated protein 1	<i>KEAP1</i>	0.4212
202431_s_at	v-myc myelocytomatosis viral oncogene homolog (avian)	<i>MYC</i>	0.1103
202495_at	tubulin folding cofactor C	<i>TBCC</i>	0.4629
202506_at	sperm specific antigen 2	<i>SSFA2</i>	0.4723
202535_at	Fas (TNFRSF6)-associated via death domain	<i>FADD</i>	0.1025
202547_s_at	Rho guanine nucleotide exchange factor (GEF) 7	<i>ARHGEF7</i>	0.3125
202548_s_at	Rho guanine nucleotide exchange factor (GEF) 7	<i>ARHGEF7</i>	0.4518
202553_s_at	SYF2 homolog, RNA splicing factor (S. cerevisiae)	<i>SYF2</i>	1.5262
202581_at	heat shock 70 kDa protein 1A/heat shock 70 kDa protein 1B	<i>HSPA1A/HSPA1B</i>	0.2554
202582_s_at	RAN binding protein 9	<i>RANBP9</i>	0.3393
202583_s_at	RAN binding protein 9	<i>RANBP9</i>	0.3233
202599_s_at	nuclear receptor interacting protein 1	<i>NRIP1</i>	0.4146
202613_at	CTP synthase	<i>CTPS</i>	0.4702
202615_at	Guanine nucleotide binding protein (G protein), q polypeptide	<i>GNAQ</i>	1.7111

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
202629_at	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	<i>APPBP2</i>	0.3407
202637_s_at	intercellular adhesion molecule 1	<i>ICAM1</i>	0.4681
202638_s_at	intercellular adhesion molecule 1	<i>ICAM1</i>	0.4104
202640_s_at	RAN binding protein 3	<i>RANBP3</i>	0.4790
202644_s_at	tumor necrosis factor, alpha-induced protein 3	<i>TNFAIP3</i>	0.4757
202648_at	–	–	0.4621
202653_s_at	membrane-associated ring finger (C3HC4) 7	<i>MARCH7</i>	0.4225
202654_x_at	membrane-associated ring finger (C3HC4) 7	<i>MARCH7</i>	0.4290
202679_at	Niemann-Pick disease, type C1	<i>NPC1</i>	0.3191
202689_at	RNA binding motif protein 15B	<i>RBM15B</i>	0.3662
202693_s_at	serine/threonine kinase 17a	<i>STK17A</i>	0.4783
202702_at	tripartite motif-containing 26	<i>TRIM26</i>	0.2855
202703_at	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	<i>DUSP11</i>	0.3392
202704_at	transducer of ERBB2, 1	<i>TOB1</i>	0.3794
202706_s_at	uridine monophosphate synthetase	<i>UMPS</i>	0.3140
202717_s_at	cell division cycle 16 homolog (S. cerevisiae)	<i>CDC16</i>	0.4932
202750_s_at	tuftelin interacting protein 11	<i>TFIP11</i>	0.4394
202769_at	cyclin G2	<i>CCNG2</i>	1.9691
202776_at	deoxynucleotidyltransferase, terminal, interacting protein 2	<i>DNTTIP2</i>	0.4339
202777_at	soc-2 suppressor of clear homolog (C. elegans)	<i>SHOC2</i>	0.4641
202798_at	SEC24 family, member B (S. cerevisiae)	<i>SEC24B</i>	0.3143
202814_s_at	hexamethylene bis-acetamide inducible 1	<i>HEXIM1</i>	0.1837
202816_s_at	synovial sarcoma translocation, chromosome 18	<i>SS18</i>	0.4143
202817_s_at	synovial sarcoma translocation, chromosome 18	<i>SS18</i>	0.4078
202832_at	GRIP and coiled-coil domain containing 2	<i>GCC2</i>	0.4888
202841_x_at	opioid growth factor receptor	<i>OGFR</i>	0.4351
202866_at	DnaJ (Hsp40) homolog, subfamily B, member 12	<i>DNAJB12</i>	0.4760
202871_at	TNF receptor-associated factor 4	<i>TRAF4</i>	0.4461
202872_at	ATPase, H ⁺ transporting, lysosomal 42 kDa, V1 subunit C1	<i>ATP6V1C1</i>	0.4570
202887_s_at	DNA-damage-inducible transcript 4	<i>DDIT4</i>	0.3705
202915_s_at	family with sequence similarity 20, member B	<i>FAM20B</i>	0.4922
202916_s_at	family with sequence similarity 20, member B	<i>FAM20B</i>	0.4940
202918_s_at	MOB1, Mps One Binder kinase activator-like 3 (yeast)	<i>MOBKL3</i>	0.2046

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
202919_at	MOB1, Mps One Binder kinase activator-like 3 (yeast)	<i>MOBKL3</i>	0.4753
202922_at	glutamate-cysteine ligase, catalytic subunit	<i>GCLC</i>	0.4884
202923_s_at	glutamate-cysteine ligase, catalytic subunit	<i>GCLC</i>	0.3841
202947_s_at	glycophorin C (Gerbich blood group)	<i>GYPE</i>	1.5039
202949_s_at	four and a half LIM domains 2	<i>FHL2</i>	0.3901
202951_at	serine/threonine kinase 38	<i>STK38</i>	0.3901
202955_s_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	<i>ARFGEF1</i>	0.4811
202956_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	<i>ARFGEF1</i>	0.4340
202968_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	<i>DYRK2</i>	0.3474
202969_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	<i>DYRK2</i>	0.3440
202979_s_at	CREB/ATF bZIP transcription factor	<i>CREBZF</i>	1.5614
202984_s_at	BCL2-associated athanogene 5	<i>BAG5</i>	0.4437
202985_s_at	BCL2-associated athanogene 5	<i>BAG5</i>	0.3705
203026_at	zinc finger and BTB domain containing 5	<i>ZBTB5</i>	0.4976
203043_at	zinc finger, BED-type containing 1	<i>ZBED1</i>	0.3960
203044_at	chondroitin sulfate synthase 1	<i>CHSY1</i>	0.3372
203051_at	bromo adjacent homology domain containing 1	<i>BAHD1</i>	0.4627
203053_at	breast carcinoma amplified sequence 2	<i>BCAS2</i>	0.3350
203063_at	protein phosphatase 1F (PP2C domain containing)	<i>PPM1F</i>	1.5867
203064_s_at	forkhead box K2	<i>FOXK2</i>	0.4265
203065_s_at	caveolin 1, caveolae protein, 22 kDa	<i>CAV1</i>	1.5817
203073_at	component of oligomeric golgi complex 2	<i>COG2</i>	0.4563
203077_s_at	SMAD family member 2	<i>SMAD2</i>	0.4545
203087_s_at	kinesin heavy chain member 2A	<i>KIF2A</i>	0.4665
203102_s_at	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	<i>MGAT2</i>	0.1396
203112_s_at	Wolf-Hirschhorn syndrome candidate 2	<i>WHSC2</i>	0.4796
203135_at	TATA box binding protein	<i>TBP</i>	0.2283
203137_at	Wilms tumor 1 associated protein	<i>WTAP</i>	0.4961
203156_at	A kinase (PRKA) anchor protein 11	<i>AKAP11</i>	0.3887
203164_at	solute carrier family 33 (acetyl-CoA transporter), member 1	<i>SLC33A1</i>	0.3449

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
203165_s_at	solute carrier family 33 (acetyl-CoA transporter), member 1	<i>SLC33A1</i>	0.3493
203182_s_at	SFRS protein kinase 2	<i>SRPK2</i>	0.3499
203194_s_at	nucleoporin 98 kDa	<i>NUP98</i>	0.4604
203195_s_at	nucleoporin 98 kDa	<i>NUP98</i>	0.3578
203205_at	lysine (K)-specific demethylase 4A	<i>KDM4A</i>	0.3473
203214_x_at	cell division cycle 2, G1 to S and G2 to M	<i>CDC2</i>	0.4866
203231_s_at	ataxin 1	<i>ATXN1</i>	2.3701
203232_s_at	ataxin 1	<i>ATXN1</i>	2.0669
203239_s_at	CCR4-NOT transcription complex, subunit 3	<i>CNOT3</i>	0.4708
203250_at	RNA binding motif protein 16	<i>RBM16</i>	0.3761
203265_s_at	mitogen-activated protein kinase 4	<i>MAP2K4</i>	0.4888
203266_s_at	mitogen-activated protein kinase 4	<i>MAP2K4</i>	0.4330
203274_at	coagulation factor VIII-associated (intronic transcript) 1/coagulation factor VIII-associated (intronic transcript) 2/coagulation factor VIII-associated (intronic transcript) 3	<i>F8A1/F8A2/F8A3</i>	0.2433
203291_at	CCR4-NOT transcription complex, subunit 4	<i>CNOT4</i>	0.3175
203293_s_at	lectin, mannose-binding, 1	<i>LMAN1</i>	1.6687
203310_at	syntaxin binding protein 3	<i>STXBP3</i>	0.4179
203311_s_at	ADP-ribosylation factor 6	<i>ARF6</i>	0.4786
203317_at	pleckstrin and Sec7 domain containing 4	<i>PSD4</i>	0.4269
203318_s_at	zinc finger protein 148	<i>ZNF148</i>	0.4724
203319_s_at	zinc finger protein 148	<i>ZNF148</i>	0.4333
203341_at	CCAAT/enhancer binding protein (C/EBP), zeta	<i>CEBPZ</i>	0.1951
203345_s_at	metal response element binding transcription factor 2	<i>MTF2</i>	0.4779
203347_s_at	metal response element binding transcription factor 2	<i>MTF2</i>	0.4256
203351_s_at	origin recognition complex, subunit 4-like (yeast)	<i>ORC4L</i>	0.3239
203356_at	calpain 7	<i>CAPN7</i>	0.3266
203373_at	suppressor of cytokine signaling 2	<i>SOCS2</i>	0.3872
203377_s_at	cell division cycle 40 homolog (S. cerevisiae)	<i>CDC40</i>	0.3825
203391_at	FK506 binding protein 2, 13 kDa	<i>FKBP2</i>	1.5554
203403_s_at	ring finger protein (C3H2C3 type) 6	<i>RNF6</i>	0.4043
203420_at	family with sequence similarity 8, member A1	<i>FAM8A1</i>	0.3459
203427_at	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	<i>ASF1A</i>	0.3697
203428_s_at	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	<i>ASF1A</i>	0.2908

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
203429_s_at	chromosome 1 open reading frame 9	<i>C1orf9</i>	0.3497
203447_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	<i>PSMD5</i>	0.4588
203455_s_at	spermidine/spermine N1-acetyltransferase 1	<i>SAT1</i>	1.5004
203481_at	family with sequence similarity 178, member A	<i>FAM178A</i>	0.4434
203486_s_at	armadillo repeat containing 8	<i>ARMC8</i>	0.3010
203487_s_at	armadillo repeat containing 8	<i>ARMC8</i>	0.3237
203496_s_at	mediator complex subunit 1	<i>MED1</i>	0.4900
203521_s_at	zinc finger protein 318	<i>ZNF318</i>	0.2566
203531_at	cullin 5	<i>CUL5</i>	0.4862
203544_s_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	<i>STAM</i>	0.3966
203552_at	mitogen-activated protein kinase 5	<i>MAP4K5</i>	0.4153
203553_s_at	mitogen-activated protein kinase 5	<i>MAP4K5</i>	0.3291
203556_at	zinc fingers and homeoboxes 2	<i>ZHX2</i>	0.3502
203565_s_at	menage a trois homolog 1, cyclin H assembly factor (<i>Xenopus laevis</i>)	<i>MNAT1</i>	0.4492
203567_s_at	tripartite motif-containing 38	<i>TRIM38</i>	0.4804
203569_s_at	oral-facial-digital syndrome 1	<i>OFD1</i>	0.4891
203583_at	unc-50 homolog (<i>C. elegans</i>)	<i>UNC50</i>	0.3815
203584_at	tetratricopeptide repeat domain 35	<i>TTC35</i>	0.3693
203597_s_at	WW domain binding protein 4 (formin binding protein 21)	<i>WBP4</i>	0.3340
203598_s_at	WW domain binding protein 4 (formin binding protein 21)	<i>WBP4</i>	0.3515
203599_s_at	WW domain binding protein 4 (formin binding protein 21)	<i>WBP4</i>	0.3025
203600_s_at	chromosome 4 open reading frame 8	<i>C4orf8</i>	0.4198
203611_at	telomeric repeat binding factor 2	<i>TERF2</i>	0.3710
203612_at	bystin-like	<i>BYSL</i>	0.4392
203614_at	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	<i>UTP14C</i>	0.3345
203622_s_at	partner of NOB1 homolog (<i>S. cerevisiae</i>)	<i>PNO1</i>	0.4730
203635_at	Down syndrome critical region gene 3	<i>DSCR3</i>	0.4796
203659_s_at	tripartite motif-containing 13	<i>TRIM13</i>	0.2809
203660_s_at	pericentrin	<i>PCNT</i>	0.4972
203665_at	heme oxygenase (decycling) 1	<i>HMOX1</i>	0.4421
203688_at	polycystic kidney disease 2 (autosomal dominant)	<i>PKD2</i>	0.4598

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
203690_at	tubulin, gamma complex associated protein 3	<i>TUBGCP3</i>	0.2094
203694_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 16	<i>DHX16</i>	0.4642
203732_at	thyroid hormone receptor interactor 4	<i>TRIP4</i>	0.3633
203734_at	forkhead box J2	<i>FOXJ2</i>	0.4950
203737_s_at	peroxisome proliferator-activated receptor γ , coactivator-related 1	<i>PPRC1</i>	0.3377
203739_at	zinc finger protein 217	<i>ZNF217</i>	0.1756
203751_x_at	jun D proto-oncogene	<i>JUND</i>	0.4293
203752_s_at	jun D proto-oncogene	<i>JUND</i>	0.3675
203755_at	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	<i>BUB1B</i>	0.4048
203769_s_at	steroid sulfatase (microsomal), isozyme S	<i>STS</i>	1.9268
203828_s_at	interleukin 32	<i>IL32</i>	1.5638
203829_at	elongation protein 4 homolog (S. cerevisiae)	<i>ELP4</i>	0.4226
203836_s_at	mitogen-activated protein kinase 5	<i>MAP3K5</i>	0.4018
203837_at	mitogen-activated protein kinase 5	<i>MAP3K5</i>	0.4427
203846_at	tripartite motif-containing 32	<i>TRIM32</i>	0.2318
203881_s_at	dystrophin	<i>DMD</i>	1.8377
203893_at	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kDa	<i>TAF9</i>	0.3663
203909_at	solute carrier family 9 (sodium/hydrogen exchanger), member 6	<i>SLC9A6</i>	0.4960
203916_at	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	<i>NDST2</i>	0.2485
203925_at	glutamate-cysteine ligase, modifier subunit	<i>GCLM</i>	0.3640
203927_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	<i>NFKBIE</i>	0.3363
203944_x_at	butyrophilin, subfamily 2, member A1	<i>BTN2A1</i>	0.3412
203947_at	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77 kDa	<i>CSTF3</i>	0.2995
203966_s_at	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	<i>PPM1A</i>	0.4284
203967_at	cell division cycle 6 homolog (S. cerevisiae)	<i>CDC6</i>	0.2992
203968_s_at	cell division cycle 6 homolog (S. cerevisiae)	<i>CDC6</i>	0.3440
203975_s_at	chromatin assembly factor 1, subunit A (p150)	<i>CHAF1A</i>	0.3548
203976_s_at	chromatin assembly factor 1, subunit A (p150)	<i>CHAF1A</i>	0.1815
203978_at	nucleotide binding protein 1 (MinD homolog, E. coli)	<i>NUBP1</i>	0.4403
203984_s_at	caspase 9, apoptosis-related cysteine peptidase	<i>CASP9</i>	0.3815
204003_s_at	nucleoporin like 2	<i>NUPL2</i>	0.3678

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
204011_at	sprouty homolog 2 (Drosophila)	<i>SPRY2</i>	0.4025
204023_at	replication factor C (activator 1) 4, 37 kDa	<i>RFC4</i>	0.3455
204033_at	thyroid hormone receptor interactor 13	<i>TRIP13</i>	0.3302
204065_at	carbohydrate sulfotransferase 10	<i>CHST10</i>	0.3135
204067_at	sulfite oxidase	<i>SUOX</i>	0.4240
204080_at	target of EGR1, member 1 (nuclear)	<i>TOE1</i>	0.3750
204089_x_at	mitogen-activated protein kinase 4	<i>MAP3K4</i>	0.2911
204092_s_at	aurora kinase A	<i>AURKA</i>	0.2974
204094_s_at	TSC22 domain family, member 2	<i>TSC22D2</i>	0.1922
204118_at	CD48 molecule	<i>CD48</i>	1.5169
204159_at	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	<i>CDKN2C</i>	0.3561
204162_at	NDC80 homolog, kinetochore complex component (S. cerevisiae)	<i>NDC80</i>	0.2141
204173_at	myosin, light chain 6B, alkali, smooth muscle and non-muscle	<i>MYL6B</i>	1.6219
204175_at	zinc finger protein 593	<i>ZNF593</i>	0.3686
204194_at	BTB and CNC homology 1, basic leucine zipper transcription factor 1	<i>BACH1</i>	2.0975
204197_s_at	runt-related transcription factor 3	<i>RUNX3</i>	0.2983
204198_s_at	runt-related transcription factor 3	<i>RUNX3</i>	0.3713
204203_at	CCAAT/enhancer binding protein (C/EBP), γ	<i>CEBPG</i>	0.3157
204216_s_at	zinc finger CCCH-type containing 14	<i>ZC3H14</i>	0.3409
204224_s_at	GTP cyclohydrolase 1	<i>GCH1</i>	0.4439
204233_s_at	choline kinase alpha	<i>CHKA</i>	0.4624
204244_s_at	DBF4 homolog (S. cerevisiae)	<i>DBF4</i>	0.4184
204245_s_at	ribonuclease P/MRP 14 kDa subunit	<i>RPP14</i>	0.3637
204258_at	chromodomain helicase DNA binding protein 1	<i>CHD1</i>	0.4922
204263_s_at	carnitine palmitoyltransferase 2	<i>CPT2</i>	0.4473
204264_at	carnitine palmitoyltransferase 2	<i>CPT2</i>	0.4480
204265_s_at	G-protein signaling modulator 3 (AGS3-like, C. elegans)	<i>GPSM3</i>	1.7744
204266_s_at	choline kinase alpha	<i>CHKA</i>	0.4463
204291_at	zinc finger protein 518A	<i>ZNF518A</i>	0.3049
204317_at	G-2 and S-phase expressed 1	<i>GTSE1</i>	0.4979
204318_s_at	G-2 and S-phase expressed 1	<i>GTSE1</i>	0.4962
204335_at	coiled-coil domain containing 94	<i>CCDC94</i>	0.3634
204336_s_at	regulator of G-protein signaling 19	<i>RGS19</i>	0.4863
204350_s_at	mediator complex subunit 7	<i>MED7</i>	0.2429
204355_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	<i>DHX30</i>	0.4984

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
204383_at	DiGeorge syndrome critical region gene 14	<i>DGCR14</i>	0.4738
204391_x_at	tripartite motif-containing 24	<i>TRIM24</i>	0.3053
204396_s_at	G protein-coupled receptor kinase 5	<i>GRK5</i>	0.4897
204407_at	transcription termination factor, RNA polymerase II	<i>TTF2</i>	0.4629
204434_at	spermatogenesis associated 2	<i>SPATA2</i>	1.5021
204435_at	nucleoporin like 1	<i>NUPL1</i>	1.7656
204474_at	zinc finger protein 142	<i>ZNF142</i>	0.4552
204478_s_at	RAB interacting factor	<i>RABIF</i>	0.4396
204489_s_at	CD44 molecule (Indian blood group)	<i>CD44</i>	1.5509
204494_s_at	chromosome 15 open reading frame 39	<i>C15orf39</i>	0.2663
204495_s_at	chromosome 15 open reading frame 39	<i>C15orf39</i>	0.2546
204496_at	striatin, calmodulin binding protein 3	<i>STRN3</i>	0.3717
204507_s_at	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	<i>PPP3R1</i>	0.4845
204516_at	ataxin 7	<i>ATXN7</i>	0.4740
204523_at	zinc finger protein 140	<i>ZNF140</i>	0.4399
204544_at	Hermansky-Pudlak syndrome 5	<i>HPS5</i>	0.3939
204562_at	interferon regulatory factor 4	<i>IRF4</i>	0.4713
204563_at	selectin L	<i>SELL</i>	1.7303
204605_at	cell growth regulator with ring finger domain 1	<i>CGRRF1</i>	0.3236
204618_s_at	GA binding protein transcription factor, β subunit 1	<i>GABPB1</i>	0.4782
204630_s_at	golgi SNAP receptor complex member 1	<i>GOSR1</i>	0.4274
204674_at	lymphoid-restricted membrane protein	<i>LRMP</i>	1.5645
204676_at	transmembrane protein 186	<i>TMEM186</i>	0.2083
204689_at	hematopoietically expressed homeobox	<i>HHEX</i>	0.3754
204695_at	cell division cycle 25 homolog A (S. pombe)	<i>CDC25A</i>	0.2856
204699_s_at	chromosome 1 open reading frame 107	<i>C1orf107</i>	0.3324
204700_x_at	chromosome 1 open reading frame 107	<i>C1orf107</i>	0.3693
204702_s_at	nuclear factor (erythroid-derived 2)-like 3	<i>NFE2L3</i>	0.4741
204709_s_at	kinesin family member 23	<i>KIF23</i>	0.4891
204715_at	pannexin 1	<i>PANX1</i>	0.3630
204747_at	interferon-induced protein with tetratricopeptide repeats 3	<i>IFIT3</i>	0.4178
204775_at	chromatin assembly factor 1, subunit B (p60)	<i>CHAF1B</i>	0.4739
204794_at	dual specificity phosphatase 2	<i>DUSP2</i>	0.3054
204799_at	zinc finger, BED-type containing 4	<i>ZBED4</i>	0.3342
204826_at	cyclin F	<i>CCNF</i>	0.1492
204832_s_at	bone morphogenetic protein receptor, type IA	<i>BMPRIA</i>	0.4660

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
204853_at	origin recognition complex, subunit 2-like (yeast)	<i>ORC2L</i>	0.4717
204859_s_at	apoptotic peptidase activating factor 1	<i>APAF1</i>	0.4443
204868_at	immature colon carcinoma transcript 1	<i>ICT1</i>	0.3463
204899_s_at	Sin3A-associated protein, 30 kDa	<i>SAP30</i>	0.3918
204900_x_at	Sin3A-associated protein, 30 kDa	<i>SAP30</i>	0.3936
204928_s_at	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	<i>SLC10A3</i>	0.3722
204962_s_at	centromere protein A	<i>CENPA</i>	0.4072
204995_at	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	<i>CDK5R1</i>	0.4531
205027_s_at	mitogen-activated protein kinase 8	<i>MAP3K8</i>	2.2556
205034_at	cyclin E2	<i>CCNE2</i>	0.3293
205042_at	glucosamine UDP- <i>N</i> -acetyl)-2-epimerase/ <i>N</i> -acetylmannosamine kinase	<i>GNE</i>	0.3959
205046_at	centromere protein E, 312 kDa	<i>CENPE</i>	0.3278
205063_at	survival of motor neuron protein interacting protein 1	<i>SIP1</i>	0.2996
205071_x_at	X-ray repair complementing defective repair in Chinese hamster cells 4	<i>XRCC4</i>	0.4442
205089_at	zinc finger protein 7	<i>ZNF7</i>	0.3153
205097_at	solute carrier family 26 (sulfate transporter), member 2	<i>SLC26A2</i>	0.4198
205114_s_at	chemokine (C-C motif) ligand 3/chemokine (C-C motif) ligand 3-like 1 /chemokine (C-C motif) ligand 3-like 3	<i>CCL3/CCL3L1/ CCL3L3</i>	0.0650
205126_at	vaccinia related kinase 2	<i>VRK2</i>	0.4551
205134_s_at	nuclear fragile X mental retardation protein interacting protein 1	<i>NUFIP1</i>	0.2150
205135_s_at	nuclear fragile X mental retardation protein interacting protein 1	<i>NUFIP1</i>	0.3208
205136_s_at	nuclear fragile X mental retardation protein interacting protein 1	<i>NUFIP1</i>	0.4554
205153_s_at	CD40 molecule, TNF receptor superfamily member 5	<i>CD40</i>	0.4922
205173_x_at	CD58 molecule	<i>CD58</i>	0.4356
205178_s_at	retinoblastoma binding protein 6	<i>RBBP6</i>	0.2679
205191_at	retinitis pigmentosa 2 (X-linked recessive)	<i>RP2</i>	0.4516
205218_at	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	<i>POLR3F</i>	0.3990

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
205231_s_at	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	<i>EPM2A</i>	0.4948
205235_s_at	kinesin family member 20B	<i>KIF20B</i>	0.3276
205241_at	SCO cytochrome oxidase deficient homolog 2 (yeast)	<i>SCO2</i>	0.2972
205251_at	period homolog 2 (Drosophila)	<i>PER2</i>	0.3907
205264_at	CD3e molecule, epsilon associated protein	<i>CD3EAP</i>	0.3621
205296_at	retinoblastoma-like 1 (p107)	<i>RBL1</i>	0.3843
205335_s_at	signal recognition particle 19 kDa	<i>SRP19</i>	0.3209
205340_at	zinc finger and BTB domain containing 24	<i>ZBTB24</i>	0.3528
205345_at	BRCA1 associated RING domain 1	<i>BARD1</i>	0.4616
205419_at	G protein-coupled receptor 183	<i>GPR183</i>	0.1704
205429_s_at	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	<i>MPP6</i>	0.3866
205443_at	small nuclear RNA activating complex, polypeptide 1, 43 kDa	<i>SNAPC1</i>	0.2233
205519_at	WD repeat domain 76	<i>WDR76</i>	0.2430
205526_s_at	katanin p60 (ATPase-containing) subunit A 1	<i>KATNA1</i>	0.3454
205527_s_at	gem (nuclear organelle) associated protein 4	<i>GEMIN4</i>	0.0927
205548_s_at	BTG family, member 3	<i>BTG3</i>	0.4853
205562_at	ribonuclease P/MRP 38 kDa subunit	<i>RPP38</i>	0.4032
205596_s_at	SMAD specific E3 ubiquitin protein ligase 2	<i>SMURF2</i>	0.4844
205599_at	TNF receptor-associated factor 1	<i>TRAF1</i>	0.2434
205621_at	alkB, alkylation repair homolog 1 (E. coli)	<i>ALKBH1</i>	0.4517
205633_s_at	aminolevulinate, delta-, synthase 1	<i>ALAS1</i>	0.2504
205661_s_at	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	<i>FLAD1</i>	0.4569
205664_at	KIN, antigenic determinant of recA protein homolog (mouse)	<i>KIN</i>	0.2606
205667_at	Werner syndrome, RecQ helicase-like	<i>WRN</i>	0.4692
205707_at	interleukin 17 receptor A	<i>IL17RA</i>	0.4173
205733_at	Bloom syndrome, RecQ helicase-like	<i>BLM</i>	0.3418
205739_x_at	zinc finger protein 107	<i>ZNF107</i>	0.2381
205748_s_at	ring finger protein 126	<i>RNF126</i>	0.4356
205750_at	biphenyl hydrolase-like (serine hydrolase)	<i>BPHL</i>	1.5994
205811_at	polymerase (DNA directed), gamma 2, accessory subunit	<i>POLG2</i>	0.3510
205854_at	tubby like protein 3	<i>TULP3</i>	0.3663
205875_s_at	three prime repair exonuclease 1	<i>TREX1</i>	0.3701

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
205909_at	polymerase (DNA directed), epsilon 2 (p59 subunit)	<i>POLE2</i>	0.4623
205928_at	zinc finger protein 443	<i>ZNF443</i>	0.4204
205930_at	general transcription factor IIE, polypeptide 1, alpha 56 kDa	<i>GTF2E1</i>	0.4764
205981_s_at	inhibitor of growth family, member 2	<i>ING2</i>	0.4386
206003_at	centrosomal protein 135 kDa	<i>CEP135</i>	0.4687
206015_s_at	forkhead box J3	<i>FOXJ3</i>	0.4180
206052_s_at	stem-loop binding protein	<i>SLBP</i>	0.4968
206096_at	zinc finger protein 35	<i>ZNF35</i>	0.4270
206140_at	LIM homeobox 2	<i>LHX2</i>	0.4788
206173_x_at	GA binding protein transcription factor, beta subunit 1	<i>GABPB1</i>	0.3343
206219_s_at	vav 1 guanine nucleotide exchange factor	<i>VAV1</i>	0.4337
206245_s_at	influenza virus NS1A binding protein	<i>IVNS1ABP</i>	1.5584
206337_at	chemokine (C-C motif) receptor 7	<i>CCR7</i>	0.3956
206364_at	kinesin family member 14	<i>KIF14</i>	0.3452
206451_at	TBCC domain containing 1	<i>TBCCD1</i>	0.3240
206468_s_at	methyltransferase like 13	<i>METTL13</i>	0.3090
206472_s_at	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	<i>TLE3</i>	0.4974
206715_at	transcription factor EC	<i>TFEC</i>	2.8486
206723_s_at	lysophosphatidic acid receptor 2	<i>LPAR2</i>	1.7424
206809_s_at	heterogeneous nuclear ribonucleoprotein A3/ heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	<i>HNRNPA3/HNRNP A3P1</i>	1.8673
206845_s_at	ring finger protein 40	<i>RNF40</i>	0.4356
206860_s_at	missing oocyte, meiosis regulator, homolog (Drosophila)	<i>MIOS</i>	0.3871
206875_s_at	STE20-like kinase (yeast)	<i>SLK</i>	0.3724
206928_at	zinc finger protein 124	<i>ZNF124</i>	0.3201
206934_at	signal-regulatory protein beta 1	<i>SIRPB1</i>	2.0646
207000_s_at	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	<i>PPP3CC</i>	0.4052
207098_s_at	mitofusin 1	<i>MFN1</i>	0.3193
207131_x_at	gamma-glutamyltransferase 1	<i>GGT1</i>	1.5684
207153_s_at	glomulin, FKBP associated protein	<i>GLMN</i>	0.4633
207318_s_at	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	<i>CDC2L5</i>	0.2190
207338_s_at	zinc finger protein 200	<i>ZNF200</i>	0.2695

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
207390_s_at	smoothelin	<i>SMTN</i>	0.3577
207391_s_at	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	<i>PIP5K1A</i>	0.3147
207405_s_at	RAD17 homolog (S. pombe)	<i>RAD17</i>	0.4737
207480_s_at	Meis homeobox 2	<i>MEIS2</i>	0.4632
207513_s_at	zinc finger protein 189	<i>ZNF189</i>	0.4484
207564_x_at	O-linked N-acetylglucosamine (GlcNAc) transferase	<i>OGT</i>	1.5844
207574_s_at	growth arrest and DNA-damage-inducible, beta	<i>GADD45B</i>	1.6085
207614_s_at	cullin 1	<i>CUL1</i>	0.3848
207719_x_at	centrosomal protein 170 kDa	<i>CEP170</i>	0.4877
207730_x_at	—	—	1.5112
207738_s_at	NCK-associated protein 1	<i>NCKAPI</i>	0.2958
207740_s_at	nucleoporin 62 kDa	<i>NUP62</i>	0.4599
207826_s_at	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	<i>ID3</i>	0.3906
207830_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 8	<i>PPP1R8</i>	0.3388
207842_s_at	cancer susceptibility candidate 3	<i>CASC3</i>	0.4487
207845_s_at	anaphase promoting complex subunit 10	<i>ANAPC10</i>	0.4598
207861_at	chemokine (C-C motif) ligand 22	<i>CCL22</i>	1.5772
207877_s_at	nuclear VCP-like	<i>NVL</i>	0.4605
207922_s_at	macrophage erythroblast attacher	<i>MAEA</i>	0.4022
207945_s_at	casein kinase 1, delta	<i>CSNK1D</i>	0.4897
207980_s_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	<i>CITED2</i>	0.4785
208042_at	angiogenic factor with G patch and FHA domains 1	<i>AGGF1</i>	0.3896
208079_s_at	aurora kinase A	<i>AURKA</i>	0.2976
208089_s_at	tudor domain containing 3	<i>TDRD3</i>	0.4068
208238_x_at	—	—	1.9098
208284_x_at	gamma-glutamyltransferase 1	<i>GGT1</i>	1.5608
208290_s_at	eukaryotic translation initiation factor 5	<i>EIF5</i>	0.4803
208309_s_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	<i>MALT1</i>	0.4632
208398_s_at	TBP-like 1	<i>TBPL1</i>	0.4336
208406_s_at	GRB2-related adaptor protein 2	<i>GRAP2</i>	0.4985
208523_x_at	histone cluster 1, H2bi	<i>HIST1H2BI</i>	1.8311
208687_x_at	heat shock 70 kDa protein 8	<i>HSPA8</i>	0.4837
208708_x_at	eukaryotic translation initiation factor 5	<i>EIF5</i>	0.4742

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
208725_at	eukaryotic translation initiation factor 2, subunit 2 beta, 38 kDa	<i>EIF2S2</i>	1.8373
208763_s_at	TSC22 domain family, member 3	<i>TSC22D3</i>	1.6888
208773_s_at	ankyrin repeat and KH domain containing 1 /ANKHD1-EIF4EBP3 readthrough transcript	<i>ANKHD1/ANKHD1-EIF4EBP3</i>	0.4969
208878_s_at	p21 protein (Cdc42/Rac)-activated kinase 2	<i>PAK2</i>	0.3237
208903_at	ribosomal protein S28	<i>RPS28</i>	3.0867
208916_at	solute carrier family 1 (neutral amino acid transporter), member 5	<i>SLC1A5</i>	0.3943
208922_s_at	nuclear RNA export factor 1	<i>NXF1</i>	0.4596
208924_at	ring finger protein 11	<i>RNF11</i>	0.4535
208925_at	claudin domain containing 1	<i>CLDND1</i>	0.4431
208952_s_at	La ribonucleoprotein domain family, member 4B	<i>LARP4B</i>	0.3382
208954_s_at	La ribonucleoprotein domain family, member 4B	<i>LARP4B</i>	0.4007
208961_s_at	Kruppel-like factor 6	<i>KLF6</i>	2.5039
208962_s_at	fatty acid desaturase 1	<i>FADS1</i>	1.7655
208963_x_at	fatty acid desaturase 1	<i>FADS1</i>	1.5331
208964_s_at	fatty acid desaturase 1	<i>FADS1</i>	1.5261
208979_at	nuclear receptor coactivator 6	<i>NCOA6</i>	0.4422
208995_s_at	peptidylprolyl isomerase G (cyclophilin G)	<i>PPIG</i>	0.4280
209004_s_at	F-box and leucine-rich repeat protein 5	<i>FBXL5</i>	0.3434
209007_s_at	chromosome 1 open reading frame 63	<i>C1orf63</i>	3.3283
209027_s_at	abl-interactor 1	<i>ABI1</i>	0.3906
209034_at	proline-rich nuclear receptor coactivator 1	<i>PNRC1</i>	0.4925
209055_s_at	CDC5 cell division cycle 5-like (S. pombe)	<i>CDC5L</i>	0.4796
209067_s_at	heterogeneous nuclear ribonucleoprotein D-like	<i>HNRPDL</i>	1.5012
209068_at	heterogeneous nuclear ribonucleoprotein D-like	<i>HNRPDL</i>	2.7055
209085_x_at	replication factor C (activator 1) 1, 145 kDa	<i>RFC1</i>	0.4968
209091_s_at	SH3-domain GRB2-like endophilin B1	<i>SH3GLB1</i>	0.4253
209099_x_at	jagged 1 (Alagille syndrome)	<i>JAG1</i>	0.3782
209102_s_at	HMG-box transcription factor 1	<i>HBPI</i>	1.8251
209112_at	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	<i>CDKN1B</i>	0.4690
209115_at	ubiquitin-like modifier activating enzyme 3	<i>UBA3</i>	0.4756
209122_at	perilipin 2	<i>PLIN2</i>	0.4135
209124_at	myeloid differentiation primary response gene (88)	<i>MYD88</i>	0.3917

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
209136_s_at	ubiquitin specific peptidase 10	<i>USP10</i>	0.3886
209137_s_at	ubiquitin specific peptidase 10	<i>USP10</i>	0.3893
209161_at	PRP4 pre-mRNA processing factor 4 homolog (yeast)	<i>PRPF4</i>	0.2924
209162_s_at	PRP4 pre-mRNA processing factor 4 homolog (yeast)	<i>PRPF4</i>	0.3220
209174_s_at	glutamine-rich 1	<i>QRICH1</i>	0.4915
209199_s_at	myocyte enhancer factor 2C	<i>MEF2C</i>	1.5226
209222_s_at	oxysterol binding protein-like 2	<i>OSBPL2</i>	0.3415
209240_at	O-linked N-acetylglucosamine (GlcNAc) transferase	<i>OGT</i>	1.7389
209257_s_at	structural maintenance of chromosomes 3	<i>SMC3</i>	0.4894
209258_s_at	structural maintenance of chromosomes 3	<i>SMC3</i>	0.4500
209259_s_at	structural maintenance of chromosomes 3	<i>SMC3</i>	0.4724
209262_s_at	nuclear receptor subfamily 2, group F, member 6	<i>NR2F6</i>	0.3666
209271_at	bromodomain PHD finger transcription factor	<i>BPTF</i>	0.2290
209273_s_at	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	<i>ISCA1</i>	0.4803
209274_s_at	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	<i>ISCA1</i>	0.4763
209282_at	protein kinase D2	<i>PRKD2</i>	0.4624
209284_s_at	chromosome 3 open reading frame 63	<i>C3orf63</i>	0.4958
209287_s_at	CDC42 effector protein (Rho GTPase binding) 3	<i>CDC42EP3</i>	0.4343
209296_at	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	<i>PPM1B</i>	0.1153
209304_x_at	growth arrest and DNA-damage-inducible, beta	<i>GADD45B</i>	1.7149
209305_s_at	growth arrest and DNA-damage-inducible, beta	<i>GADD45B</i>	1.6447
209336_at	PWP2 periodic tryptophan protein homolog (yeast)	<i>PWP2</i>	0.3520
209357_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	<i>CITED2</i>	0.4512
209358_at	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28 kDa	<i>TAF11</i>	0.3282
209375_at	xeroderma pigmentosum, complementation group C	<i>XPC</i>	0.3108
209382_at	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	<i>POLR3C</i>	0.3286
209398_at	histone cluster 1, H1c	<i>HIST1H1C</i>	1.6145
209406_at	BCL2-associated athanogene 2	<i>BAG2</i>	0.3574

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
209427_at	smoothelin	<i>SMTN</i>	0.3869
209428_s_at	zinc finger protein-like 1	<i>ZFPL1</i>	0.4666
209431_s_at	POZ (BTB) and AT hook containing zinc finger 1	<i>PATZ1</i>	0.4365
209435_s_at	Rho/Rac guanine nucleotide exchange factor (GEF) 2	<i>ARHGEF2</i>	0.2864
209446_s_at	chromosome 7 open reading frame 44	<i>C7orf44</i>	1.8668
209451_at	TRAF family member-associated NFKB activator	<i>TANK</i>	0.4850
209457_at	dual specificity phosphatase 5	<i>DUSP5</i>	0.4543
209473_at	ectonucleoside triphosphate diphosphohydrolase 1	<i>ENTPD1</i>	1.6226
209474_s_at	ectonucleoside triphosphate diphosphohydrolase 1	<i>ENTPD1</i>	1.5613
209484_s_at	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	<i>NSL1</i>	0.3850
209486_at	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	<i>UTP3</i>	0.3700
209494_s_at	POZ (BTB) and AT hook containing zinc finger 1	<i>PATZ1</i>	0.3433
209517_s_at	ash2 (absent, small, or homeotic)-like (Drosophila)	<i>ASH2L</i>	0.4114
209527_at	exosome component 2	<i>EXOSC2</i>	0.4954
209533_s_at	phospholipase A2-activating protein	<i>PLAA</i>	0.3745
209565_at	ring finger protein 113A	<i>RNF113A</i>	0.4636
209567_at	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	<i>RRS1</i>	0.3010
209572_s_at	embryonic ectoderm development	<i>EED</i>	0.3066
209579_s_at	methyl-CpG binding domain protein 4	<i>MBD4</i>	0.4907
209580_s_at	methyl-CpG binding domain protein 4	<i>MBD4</i>	0.2772
209585_s_at	multiple inositol polyphosphate histidine phosphatase, 1	<i>MINPP1</i>	0.4431
209586_s_at	prune homolog (Drosophila)	<i>PRUNE</i>	0.3012
209593_s_at	torsin family 1, member B (torsin B)	<i>TOR1B</i>	0.3745
209606_at	cytohesin 1 interacting protein	<i>CYTIP</i>	0.3968
209636_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	<i>NFKB2</i>	0.3945
209642_at	budding uninhibited by benzimidazoles 1 homolog (yeast)	<i>BUB1</i>	0.3996

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
209644_x_at	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	<i>CDKN2A</i>	1.5256
209654_at	KIAA0947	<i>KIAA0947</i>	0.4461
209658_at	cell division cycle 16 homolog (S. cerevisiae)	<i>CDC16</i>	0.4877
209659_s_at	cell division cycle 16 homolog (S. cerevisiae)	<i>CDC16</i>	0.4903
209662_at	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	<i>CETN3</i>	0.4078
209670_at	T cell receptor alpha constant	<i>TRAC</i>	1.7473
209671_x_at	T cell receptor alpha locus/T cell receptor alpha constant	<i>TRA@/TRAC</i>	2.1949
209680_s_at	kinesin family member C1	<i>KIFC1</i>	0.2191
209688_s_at	coiled-coil domain containing 93	<i>CCDC93</i>	0.4408
209695_at	protein tyrosine phosphatase type IVA, member 3	<i>PTP4A3</i>	1.6314
209748_at	spastin	<i>SPAST</i>	0.3865
209760_at	KIAA0922	<i>KIAA0922</i>	0.4269
209798_at	nuclear protein, ataxia-telangiectasia locus	<i>NPAT</i>	0.2526
209799_at	protein kinase, AMP-activated, alpha 1 catalytic subunit	<i>PRKAA1</i>	0.4050
209814_at	zinc finger protein 330	<i>ZNF330</i>	0.4020
209824_s_at	aryl hydrocarbon receptor nuclear translocator-like	<i>ARNTL</i>	0.4255
209827_s_at	interleukin 16 (lymphocyte chemoattractant factor)	<i>IL16</i>	0.4482
209845_at	makorin ring finger protein 1	<i>MKRNI</i>	1.6318
209849_s_at	RAD51 homolog C (S. cerevisiae)	<i>RAD51C</i>	0.3555
209863_s_at	tumor protein p63	<i>TP63</i>	1.6137
209891_at	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	<i>SPC25</i>	0.4729
209892_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	<i>FUT4</i>	0.2444
209893_s_at	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	<i>FUT4</i>	0.3789
209916_at	dehydrogenase E1 and transketolase domain containing 1	<i>DHTKD1</i>	1.5910
209919_x_at	gamma-glutamyltransferase 1	<i>GGT1</i>	1.6504
209921_at	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	<i>SLC7A11</i>	0.4482
209928_s_at	musculin (activated B-cell factor-1)	<i>MSC</i>	0.1415
210001_s_at	suppressor of cytokine signaling 1	<i>SOCS1</i>	0.2655

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
210017_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	<i>MALT1</i>	0.3405
210018_x_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	<i>MALT1</i>	0.4941
210101_x_at	SH3-domain GRB2-like endophilin B1	<i>SH3GLB1</i>	0.4023
210212_x_at	mature T-cell proliferation 1 neighbor	<i>MTCP1NB</i>	1.7215
210235_s_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	<i>PPFIA1</i>	0.4411
210252_s_at	MAP-kinase activating death domain	<i>MADD</i>	0.4554
210266_s_at	tripartite motif-containing 33	<i>TRIM33</i>	0.4851
210279_at	G protein-coupled receptor 18	<i>GPR18</i>	0.2244
210356_x_at	membrane-spanning 4-domains, subfamily A, member 1	<i>MS4A1</i>	1.5324
210387_at	histone cluster 1, H2bg	<i>HIST1H2BG</i>	2.8097
210449_x_at	mitogen-activated protein kinase 14	<i>MAPK14</i>	0.4828
210538_s_at	baculoviral IAP repeat-containing 3	<i>BIRC3</i>	0.3136
210541_s_at	tripartite motif-containing 27	<i>TRIM27</i>	0.2068
210573_s_at	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	<i>POLR3C</i>	0.3491
210592_s_at	spermidine/spermine N1-acetyltransferase 1	<i>SAT1</i>	1.5579
210621_s_at	RAS p21 protein activator (GTPase activating protein) 1	<i>RASA1</i>	0.4747
210649_s_at	AT rich interactive domain 1A (SWI-like)	<i>ARID1A</i>	0.3646
210681_s_at	ubiquitin specific peptidase 15	<i>USP15</i>	0.4692
210779_x_at	survival of motor neuron protein interacting protein 1	<i>SIP1</i>	0.4046
210827_s_at	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	<i>ELF3</i>	0.3493
210946_at	phosphatidic acid phosphatase type 2A	<i>PPAP2A</i>	0.4977
210962_s_at	A kinase (PRKA) anchor protein (yotiao) 9	<i>AKAP9</i>	0.3219
210971_s_at	aryl hydrocarbon receptor nuclear translocator-like	<i>ARNTL</i>	0.3425
210972_x_at	T cell receptor alpha locus/T cell receptor alpha constant/T cell receptor alpha joining 17/T cell receptor alpha variable 20	<i>TRA@/TRAC /TRAJ17/TRAV20</i>	2.0916
210993_s_at	SMAD family member 1	<i>SMAD1</i>	0.4584
211061_s_at	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	<i>MGAT2</i>	0.1679

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
211080_s_at	NIMA (never in mitosis gene a)-related kinase 2	<i>NEK2</i>	0.3147
211090_s_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	<i>PRPF4B</i>	0.3853
211114_x_at	survival of motor neuron protein interacting protein 1	<i>SIP1</i>	0.4022
211115_x_at	survival of motor neuron protein interacting protein 1	<i>SIP1</i>	0.3523
211257_x_at	zinc finger protein 638	<i>ZNF638</i>	0.2377
211285_s_at	ubiquitin protein ligase E3A	<i>UBE3A</i>	0.4439
211336_x_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	<i>LILRB1</i>	1.7621
211383_s_at	WD repeat domain 37	<i>WDR37</i>	0.3785
211392_s_at	POZ (BTB) and AT hook containing zinc finger 1	<i>PATZ1</i>	0.3865
211423_s_at	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, <i>S. cerevisiae</i>)-like	<i>SC5DL</i>	0.3897
211450_s_at	mutS homolog 6 (<i>E. coli</i>)	<i>MSH6</i>	0.4394
211454_x_at	FKSG49	<i>FKSG49</i>	1.5925
211530_x_at	major histocompatibility complex, class I, G	<i>HLA-G</i>	1.5550
211575_s_at	ubiquitin protein ligase E3A	<i>UBE3A</i>	0.3116
211600_at	protein tyrosine phosphatase, receptor type, O	<i>PTPRO</i>	1.7699
211654_x_at	major histocompatibility complex, class II, DQ beta 1	<i>HLA-DQB1</i>	1.6637
211686_s_at	MAK16 homolog (<i>S. cerevisiae</i>)	<i>MAK16</i>	0.2894
211692_s_at	BCL2 binding component 3	<i>BBC3</i>	1.6744
211724_x_at	missing oocyte, meiosis regulator, homolog (<i>Drosophila</i>)	<i>MIOS</i>	0.3674
211792_s_at	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	<i>CDKN2C</i>	0.4478
211801_x_at	mitofusin 1	<i>MFN1</i>	0.4884
211929_at	heterogeneous nuclear ribonucleoprotein A3	<i>HNRNPA3</i>	1.5334
211962_s_at	zinc finger protein 36, C3H type-like 1	<i>ZFP36L1</i>	0.3687
212000_at	splicing factor, arginine/serine-rich 14	<i>SFRS14</i>	1.6157
212001_at	splicing factor, arginine/serine-rich 14	<i>SFRS14</i>	2.0654
212020_s_at	antigen identified by monoclonal antibody Ki-67	<i>MKI67</i>	0.4805
212022_s_at	antigen identified by monoclonal antibody Ki-67	<i>MKI67</i>	0.4600
212023_s_at	antigen identified by monoclonal antibody Ki-67	<i>MKI67</i>	0.4016
212056_at	KIAA0182	<i>KIAA0182</i>	0.4777
212108_at	Fas associated factor family member 2	<i>FAF2</i>	0.4493

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
212111_at	syntaxin 12	<i>STX12</i>	0.3622
212112_s_at	syntaxin 12	<i>STX12</i>	0.4096
212116_at	tripartite motif-containing 27	<i>TRIM27</i>	0.2156
212132_at	LSM14A, SCD6 homolog A (S. cerevisiae)	<i>LSM14A</i>	0.4884
212152_x_at	AT rich interactive domain 1A (SWI-like)	<i>ARID1A</i>	0.4672
212168_at	RNA binding motif protein 12	<i>RBM12</i>	0.3406
212173_at	adenylate kinase 2	<i>AK2</i>	1.5220
212177_at	splicing factor, arginine/serine-rich 18	<i>SFRS18</i>	1.7773
212195_at	interleukin 6 signal transducer (gp130, oncostatin M receptor)	<i>IL6ST</i>	0.4749
212201_at	ankyrin repeat and LEM domain containing 2	<i>ANKLE2</i>	0.4277
212211_at	ankyrin repeat domain 17	<i>ANKRD17</i>	0.4645
212222_at	proteasome (prosome, macropain) activator subunit 4	<i>PSME4</i>	0.4318
212260_at	GRB10 interacting GYF protein 2	<i>GIGYF2</i>	0.3778
212261_at	GRB10 interacting GYF protein 2	<i>GIGYF2</i>	0.4736
212264_s_at	wings apart-like homolog (Drosophila)	<i>WAPAL</i>	0.3564
212267_at	wings apart-like homolog (Drosophila)	<i>WAPAL</i>	0.2625
212269_s_at	minichromosome maintenance complex component 3 associated protein	<i>MCM3AP</i>	0.4783
212306_at	cytoplasmic linker associated protein 2	<i>CLASP2</i>	0.3299
212313_at	CHMP family, member 7	<i>CHMP7</i>	0.4588
212356_at	KIAA0323	<i>KIAA0323</i>	0.4439
212361_s_at	ATPase, Ca ²⁺ transporting, cardiac muscle, slow twitch 2	<i>ATP2A2</i>	0.2242
212373_at	fem-1 homolog b (C. elegans)	<i>FEM1B</i>	0.4563
212375_at	E1A binding protein p400	<i>EP400</i>	0.4769
212397_at	radixin	<i>RDX</i>	0.3813
212398_at	radixin	<i>RDX</i>	0.4406
212402_at	zinc finger CCCH-type containing 13	<i>ZC3H13</i>	0.4035
212405_s_at	methyltransferase like 13	<i>METTL13</i>	0.3179
212407_at	methyltransferase like 13	<i>METTL13</i>	0.3783
212418_at	E74-like factor 1 (ets domain transcription factor)	<i>ELF1</i>	0.4405
212420_at	E74-like factor 1 (ets domain transcription factor)	<i>ELF1</i>	0.4518
212429_s_at	general transcription factor IIIC, polypeptide 2, beta 110 kDa	<i>GTF3C2</i>	0.4755
212434_at	GrpE-like 1, mitochondrial (E. coli)	<i>GRPEL1</i>	0.4070
212436_at	tripartite motif-containing 33	<i>TRIM33</i>	0.3059

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
212439_at	inositol hexakisphosphate kinase 1	<i>IP6K1</i>	0.4803
212441_at	KIAA0232	<i>KIAA0232</i>	0.4777
212445_s_at	neural precursor cell expressed, developmentally down-regulated 4-like	<i>NEDD4L</i>	0.4875
212453_at	KIAA1279	<i>KIAA1279</i>	0.4204
212454_x_at	heterogeneous nuclear ribonucleoprotein D-like	<i>HNRPDL</i>	3.7212
212458_at	sprouty-related, EVH1 domain containing 2	<i>SPRED2</i>	0.3361
212465_at	SET domain containing 3	<i>SETD3</i>	0.4942
212480_at	cytospin A	<i>CY TSA</i>	0.4937
212485_at	G patch domain containing 8	<i>GPATCH8</i>	0.4150
212496_s_at	lysine (K)-specific demethylase 4B	<i>KDM4B</i>	0.4208
212500_at	2-aminoethanethiol (cysteamine) dioxygenase	<i>ADO</i>	0.2550
212501_at	CCAAT/enhancer binding protein (C/EBP), beta	<i>CEBPB</i>	0.1776
212502_at	2-aminoethanethiol (cysteamine) dioxygenase	<i>ADO</i>	0.2663
212506_at	phosphatidylinositol binding clathrin assembly protein	<i>PICALM</i>	0.3364
212513_s_at	ubiquitin specific peptidase 33	<i>USP33</i>	0.4842
212548_s_at	FRY-like	<i>FRYL</i>	0.4100
212557_at	zinc finger protein 451	<i>ZNF451</i>	0.4658
212564_at	potassium channel tetramerisation domain containing 2	<i>KCTD2</i>	0.4564
212571_at	chromodomain helicase DNA binding protein 8	<i>CHD8</i>	0.4755
212589_at	related RAS viral (r-ras) oncogene homolog 2	<i>RRAS2</i>	0.4826
212591_at	RNA binding motif protein 34	<i>RBM34</i>	0.2913
212596_s_at	HMG box domain containing 4	<i>HMGXB4</i>	0.3414
212597_s_at	HMG box domain containing 4	<i>HMGXB4</i>	0.2234
212612_at	REST corepressor 1	<i>RCOR1</i>	0.3815
212638_s_at	WW domain containing E3 ubiquitin protein ligase 1	<i>WWP1</i>	0.4695
212648_at	DEAH (Asp-Glu-Ala-His) box polypeptide 29	<i>DHX29</i>	0.4786
212653_s_at	EH domain binding protein 1	<i>EHBP1</i>	0.2513
212663_at	FK506 binding protein 15, 133 kDa	<i>FKBP15</i>	0.4222
212674_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	<i>DHX30</i>	0.3638
212675_s_at	centrosomal protein 68 kDa	<i>CEP68</i>	0.3111
212685_s_at	transducin (beta)-like 2	<i>TBL2</i>	0.3378
212688_at	phosphoinositide-3-kinase, catalytic, beta polypeptide	<i>PIK3CB</i>	0.3653
212711_at	calmodulin regulated spectrin-associated protein 1	<i>CAMSAP1</i>	0.4125
212724_at	Rho family GTPase 3	<i>RND3</i>	0.4222

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
212731_at	ankyrin repeat domain 46	<i>ANKRD46</i>	0.4150
212740_at	phosphoinositide-3-kinase, regulatory subunit 4	<i>PIK3R4</i>	0.4867
212747_at	ankyrin repeat and sterile alpha motif domain containing 1A	<i>ANKS1A</i>	0.3838
212749_s_at	ring finger and CHY zinc finger domain containing 1	<i>RCHY1</i>	0.4495
212754_s_at	MON2 homolog (S. cerevisiae)	<i>MON2</i>	0.4307
212756_s_at	ubiquitin protein ligase E3 component n-recognin 2	<i>UBR2</i>	0.4668
212765_at	calmodulin regulated spectrin-associated protein 1-like 1	<i>CAMSAP1L1</i>	0.4191
212766_s_at	interferon stimulated exonuclease gene 20 kDa-like 2	<i>ISG20L2</i>	0.3768
212781_at	retinoblastoma binding protein 6	<i>RBBP6</i>	0.2168
212783_at	retinoblastoma binding protein 6	<i>RBBP6</i>	0.3023
212787_at	YLP motif containing 1	<i>YLPM1</i>	0.3377
212804_s_at	GTPase activating protein and VPS9 domains 1	<i>GAPVD1</i>	0.4425
212812_at	—	—	0.4984
212825_at	PAX interacting (with transcription-activation domain) protein 1	<i>PAXIP1</i>	0.3755
212835_at	family with sequence similarity 175, member B	<i>FAM175B</i>	0.2857
212837_at	family with sequence similarity 175, member B	<i>FAM175B</i>	0.3052
212841_s_at	PTPRF interacting protein, binding protein 2 (liprin beta 2)	<i>PPFIBP2</i>	0.4164
212855_at	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	<i>DCUN1D4</i>	0.4196
212861_at	major facilitator superfamily domain containing 5	<i>MFSD5</i>	0.3677
212875_s_at	C2 calcium-dependent domain containing 2	<i>C2CD2</i>	0.4438
212880_at	WD repeat domain 7	<i>WDR7</i>	0.4969
212881_at	protein inhibitor of activated STAT, 4	<i>PIAS4</i>	0.2652
212885_at	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	<i>MPHOSPH10</i>	0.4549
212893_at	zinc finger, ZZ-type containing 3	<i>ZZZ3</i>	0.3506
212894_at	suppressor of var1, 3-like 1 (S. cerevisiae)	<i>SUPV3L1</i>	0.4928
212898_at	KIAA0406	<i>KIAA0406</i>	0.2954
212899_at	cell division cycle 2-like 6 (CDK8-like)	<i>CDC2L6</i>	0.4584
212900_at	SEC24 family, member A (S. cerevisiae)	<i>SEC24A</i>	0.4193
212904_at	leucine rich repeat containing 47	<i>LRRC47</i>	0.4482

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
212905_at	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64 kDa, tau variant	<i>CSTF2T</i>	0.4776
212910_at	THAP domain containing 11	<i>THAP11</i>	0.1698
212920_at	—	—	0.3823
212949_at	non-SMC condensin I complex, subunit H	<i>NCAPH</i>	0.3579
212964_at	hypermethylated in cancer 2	<i>HIC2</i>	0.4615
212978_at	leucine rich repeat containing 8 family, member B	<i>LRRC8B</i>	0.4537
213017_at	abhydrolase domain containing 3	<i>ABHD3</i>	0.4260
213019_at	RAN binding protein 6	<i>RANBP6</i>	0.1697
213021_at	golgi SNAP receptor complex member 1	<i>GOSR1</i>	0.3880
213035_at	ankyrin repeat domain 28	<i>ANKRD28</i>	1.8091
213046_at	poly(A) binding protein, nuclear 1	<i>PABPN1</i>	3.6114
213049_at	GTPase activating Rap/RanGAP domain-like 1	<i>GARNL1</i>	0.2914
213063_at	zinc finger CCCH-type containing 14	<i>ZC3H14</i>	0.4465
213064_at	zinc finger CCCH-type containing 14	<i>ZC3H14</i>	0.4431
213069_at	HEG homolog 1 (zebrafish)	<i>HEG1</i>	0.4326
213070_at	phosphoinositide-3-kinase, class 2, alpha polypeptide	<i>PIK3C2A</i>	0.4948
213090_s_at	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135 kDa	<i>TAF4</i>	0.3134
213117_at	kelch-like 9 (Drosophila)	<i>KLHL9</i>	0.3089
213123_at	microfibrillar-associated protein 3	<i>MFAP3</i>	0.4469
213126_at	mediator complex subunit 8	<i>MED8</i>	0.3017
213127_s_at	mediator complex subunit 8	<i>MED8</i>	0.3692
213128_s_at	ubiquitin protein ligase E3A	<i>UBE3A</i>	0.3072
213145_at	F-box and leucine-rich repeat protein 14	<i>FBXL14</i>	0.4408
213153_at	SET domain containing 1B	<i>SETD1B</i>	0.3378
213184_at	SUMO1/sentrin specific peptidase 5	<i>SEN5</i>	0.4881
213189_at	MYC induced nuclear antigen	<i>MINA</i>	0.4423
213233_s_at	kelch-like 9 (Drosophila)	<i>KLHL9</i>	0.4332
213262_at	spastic ataxia of Charlevoix-Saguenay (sacsin)	<i>SACS</i>	0.3587
213286_at	zinc finger RNA binding protein	<i>ZFR</i>	0.4637
213291_s_at	ubiquitin protein ligase E3A	<i>UBE3A</i>	0.2897
213301_x_at	tripartite motif-containing 24	<i>TRIM24</i>	0.3631
213309_at	phospholipase C-like 2	<i>PLCL2</i>	0.4622
213346_at	chromosome 13 open reading frame 27	<i>C13orf27</i>	0.3533

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
213359_at	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37 kDa)	<i>HNRNPD</i>	4.0092
213365_at	exoribonuclease 2	<i>ERI2</i>	0.3947
213372_at	progesterone and adiponectin receptor family member III	<i>PAQR3</i>	0.3985
213373_s_at	caspase 8, apoptosis-related cysteine peptidase	<i>CASP8</i>	0.3860
213390_at	zinc finger CCCH-type containing 4	<i>ZC3H4</i>	0.3865
213391_at	dpy-19-like 4 (C. elegans)	<i>DPY19L4</i>	0.4492
213405_at	RAB22A, member RAS oncogene family	<i>RAB22A</i>	0.4772
213407_at	PH domain and leucine rich repeat protein phosphatase 2	<i>PHLPP2</i>	0.4240
213452_at	zinc finger protein 184	<i>ZNF184</i>	0.4168
213459_at	ribosomal protein L37a	<i>RPL37A</i>	1.5011
213517_at	poly(rC) binding protein 2	<i>PCBP2</i>	2.6367
213532_at	ADAM metalloproteinase domain 17	<i>ADAM17</i>	0.4871
213546_at	hypothetical protein DKFZp586I1420	<i>DKFZP586I1420</i>	1.5110
213578_at	bone morphogenetic protein receptor, type IA	<i>BMPRIA</i>	0.4611
213593_s_at	transformer 2 alpha homolog (Drosophila)	<i>TRA2A</i>	2.3280
213599_at	Opa interacting protein 5	<i>OIP5</i>	0.4042
213608_s_at	SRR1 domain containing	<i>SRRD</i>	0.2799
213610_s_at	kelch-like 23 (Drosophila)	<i>KLHL23</i>	0.4151
213618_at	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	<i>ARAP2</i>	0.3856
213620_s_at	intercellular adhesion molecule 2	<i>ICAM2</i>	0.4823
213643_s_at	inositol polyphosphate-5-phosphatase, 75 kDa	<i>INPP5B</i>	1.6177
213653_at	methyltransferase like 3	<i>METTL3</i>	2.2853
213670_x_at	NOL1/NOP2/Sun domain family, member 5B	<i>NSUN5B</i>	1.6390
213696_s_at	mediator complex subunit 8	<i>MED8</i>	0.3191
213708_s_at	MAX-like protein X	<i>MLX</i>	0.2927
213743_at	cyclin T2	<i>CCNT2</i>	1.5741
213761_at	Mdm1 nuclear protein homolog (mouse)	<i>MDM1</i>	0.4802
213775_x_at	zinc finger protein 638	<i>ZNF638</i>	0.3009
213838_at	nucleolar protein 7, 27 kDa	<i>NOL7</i>	0.4690
213848_at	dual specificity phosphatase 7	<i>DUSP7</i>	0.2787
213872_at	Chromosome 6 open reading frame 62	<i>C6orf62</i>	0.4525
213875_x_at	chromosome 6 open reading frame 62	<i>C6orf62</i>	0.4804
213918_s_at	Nipped-B homolog (Drosophila)	<i>NIPBL</i>	0.2508
213923_at	RAP2B, member of RAS oncogene family	<i>RAP2B</i>	0.4947
213926_s_at	ArfGAP with FG repeats 1	<i>AGFG1</i>	0.4162

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
213931_at	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein/inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)	<i>ID2/ID2B</i>	1.8545
213988_s_at	spermidine/spermine N1-acetyltransferase 1 splicing factor proline/glutamine-rich	<i>SAT1</i>	1.7034
214016_s_at	(polypyrimidine tract binding protein associated)	<i>SFPQ</i>	2.2671
214047_s_at	methyl-CpG binding domain protein 4	<i>MBD4</i>	0.3636
214061_at	WD repeat domain 67	<i>WDR67</i>	0.2582
214085_x_at	GLI pathogenesis-related 1	<i>GLIPR1</i>	1.9128
214126_at	–	–	0.4304
214129_at	phosphodiesterase 4D interacting protein	<i>PDE4DIP</i>	0.3771
214194_at	DIS3 mitotic control homolog (S. cerevisiae)	<i>DIS3</i>	1.9357
214280_x_at	heterogeneous nuclear ribonucleoprotein A1	<i>HNRNPA1</i>	2.1966
214281_s_at	ring finger and CHY zinc finger domain containing 1	<i>RCHY1</i>	0.4488
214290_s_at	histone cluster 2, H2aa3///histone cluster 2, H2aa4	<i>HIST2H2AA3/HIST2H2AA4</i>	1.5993
214291_at	similar to ribosomal protein L17///ribosomal protein L17	<i>LOC729046/RPL17</i>	10.8583
214299_at	topoisomerase (DNA) III alpha	<i>TOP3A</i>	0.4494
214426_x_at	chromatin assembly factor 1, subunit A (p150)	<i>CHAF1A</i>	0.3272
214427_at	NOP2 nucleolar protein homolog (yeast)	<i>NOP2</i>	0.4167
214429_at	myotubularin related protein 6	<i>MTMR6</i>	0.3674
214440_at	N-acetyltransferase 1 (arylamine N-acetyltransferase)	<i>NAT1</i>	0.2942
214507_s_at	exosome component 2	<i>EXOSC2</i>	0.4270
214659_x_at	YLP motif containing 1	<i>YLPM1</i>	0.3164
214662_at	WD repeat domain 43	<i>WDR43</i>	0.4733
214683_s_at	CDC-like kinase 1///peptidylprolyl isomerase (cyclophilin)-like 3	<i>CLK1/PPIL3</i>	2.9074
214700_x_at	RAP1 interacting factor homolog (yeast)	<i>RIF1</i>	0.2826
214710_s_at	cyclin B1	<i>CCNB1</i>	0.4785
214722_at	Notch homolog 2 (Drosophila) N-terminal like	<i>NOTCH2NL</i>	2.5367
214751_at	zinc finger protein 468	<i>ZNF468</i>	0.4612
214766_s_at	AT hook containing transcription factor 1	<i>AHCTF1</i>	0.3638
214787_at	DENN/MADD domain containing 4A	<i>DENND4A</i>	0.4388
214877_at	CDK5 regulatory subunit associated protein 1-like 1	<i>CDKAL1</i>	1.5166

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
214919_s_at	ANKHD1-EIF4EBP3 readthrough transcript/ eukaryotic translation initiation factor 4E binding protein 3	<i>ANKHD1-EIF4EBP3</i>	0.4981
214943_s_at	RNA binding motif protein 34 family with sequence similarity 21, member A/family with sequence similarity 21,	<i>RBM34</i>	0.2778
214946_x_at	member B/family with sequence similarity 21, member C/family with sequence similarity 21, member D	<i>FAM21A/FAM21B/ FAM21C/FAM21D</i>	0.4293
214989_x_at	—	—	1.5969
215009_s_at	SEC31 homolog A (S. cerevisiae)	<i>SEC31A</i>	1.6306
215031_x_at	ring finger protein 126	<i>RNF126</i>	0.4688
215073_s_at	nuclear receptor subfamily 2, group F, member 2	<i>NR2F2</i>	0.4837
215084_s_at	leucine rich repeat containing 42	<i>LRRC42</i>	0.3423
215158_s_at	death effector domain containing	<i>DEDD</i>	0.4523
215165_x_at	uridine monophosphate synthetase	<i>UMPS</i>	0.3126
215236_s_at	phosphatidylinositol binding clathrin assembly protein	<i>PICALM</i>	0.2604
215239_x_at	zinc finger protein 273	<i>ZNF273</i>	0.4167
215346_at	CD40 molecule, TNF receptor superfamily member 5	<i>CD40</i>	0.4600
215373_x_at	—	—	1.5963
215411_s_at	TRAF3 interacting protein 2	<i>TRAF3IP2</i>	0.3487
215493_x_at	butyrophilin, subfamily 2, member A1	<i>BTN2A1</i>	0.3577
215504_x_at	—	—	1.7256
215933_s_at	hematopoietically expressed homeobox	<i>HHEX</i>	0.2860
215942_s_at	G-2 and S-phase expressed 1	<i>GTSE1</i>	0.4005
215948_x_at	zinc finger, MYM-type 5	<i>ZMYM5</i>	0.3795
216125_s_at	RAN binding protein 9	<i>RANBP9</i>	0.4389
216199_s_at	mitogen-activated protein kinase 4	<i>MAP3K4</i>	0.2732
216253_s_at	parvin, beta	<i>PARVB</i>	1.5066
216267_s_at	transmembrane protein 115	<i>TMEM115</i>	0.3509
216348_at	ribosomal protein S17 pseudogene 5	<i>RPS17P5</i>	1.5444
216602_s_at	phenylalanyl-tRNA synthetase, alpha subunit	<i>FARSA</i>	0.3805
216713_at	KRIT1, ankyrin repeat containing	<i>KRIT1</i>	0.4350
216996_s_at	FAST kinase domains 2	<i>FASTKD2</i>	0.3203
217043_s_at	mitofusin 1	<i>MFN1</i>	0.4022
217078_s_at	CD300a molecule	<i>CD300A</i>	0.3757
217099_s_at	gem (nuclear organelle) associated protein 4	<i>GEMIN4</i>	0.1145

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
217196_s_at	calmodulin regulated spectrin-associated protein 1-like 1	<i>CAMSAP1L1</i>	0.3384
217329_x_at	–	–	1.6237
217336_at	ribosomal protein S10/ribosomal protein S10 pseudogene 5/ribosomal protein S10 pseudogene 7	<i>RPS10/RPS10P5/RPS10P7</i>	1.5694
217363_x_at	–	–	1.6752
217418_x_at	membrane-spanning 4-domains, subfamily A, member 1	<i>MS4A1</i>	1.5110
217448_s_at	TOX high mobility group box family member 4	<i>TOX4</i>	0.4637
217619_x_at	–	–	1.8777
217640_x_at	spindle and kinetochore associated complex subunit 1	<i>SKA1</i>	0.3733
217672_x_at	eukaryotic translation initiation factor 1	<i>EIF1</i>	1.8972
217678_at	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	<i>SLC7A11</i>	0.4204
217730_at	transmembrane BAX inhibitor motif containing 1	<i>TMBIM1</i>	1.9169
217742_s_at	WW domain containing adaptor with coiled-coil	<i>WAC</i>	0.4326
217781_s_at	zinc finger protein 106 homolog (mouse)	<i>ZFP106</i>	0.4536
217798_at	CCR4-NOT transcription complex, subunit 2	<i>CNOT2</i>	0.3794
217843_s_at	mediator complex subunit 4	<i>MED4</i>	0.4780
217879_at	cell division cycle 27 homolog (S. cerevisiae)	<i>CDC27</i>	0.4841
217880_at	cell division cycle 27 homolog (S. cerevisiae)	<i>CDC27</i>	0.4623
217881_s_at	cell division cycle 27 homolog (S. cerevisiae)	<i>CDC27</i>	0.4953
217893_s_at	akirin 1	<i>AKIRIN1</i>	0.4342
217894_at	potassium channel tetramerisation domain containing 3	<i>KCTD3</i>	0.4993
217905_at	chromosome 10 open reading frame 119	<i>C10orf119</i>	1.5025
217906_at	kelch domain containing 2	<i>KLHDC2</i>	0.4352
217909_s_at	MAX-like protein X	<i>MLX</i>	0.4728
217910_x_at	MAX-like protein X	<i>MLX</i>	0.2775
217911_s_at	BCL2-associated athanogene 3	<i>BAG3</i>	0.3311
217912_at	dihydrouridine synthase 1-like (S. cerevisiae)	<i>DUS1L</i>	1.5629
217936_at	Rho GTPase activating protein 5	<i>ARHGAP5</i>	0.4830
217941_s_at	erbb2 interacting protein	<i>ERBB2IP</i>	0.4582
217950_at	nitric oxide synthase interacting protein	<i>NOSIP</i>	0.4658
217954_s_at	PHD finger protein 3	<i>PHF3</i>	0.4947
217965_s_at	SAP30 binding protein	<i>SAP30BP</i>	0.4323
217976_s_at	dynein, cytoplasmic 1, light intermediate chain 1	<i>DYNC1L1I</i>	0.2763

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
217986_s_at	bromodomain adjacent to zinc finger domain, 1A	<i>BAZ1A</i>	0.4687
217995_at	sulfide quinone reductase-like (yeast)	<i>SQRDL</i>	1.6723
218013_x_at	dynactin 4 (p62)	<i>DCTN4</i>	0.4960
218016_s_at	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	<i>POLR3E</i>	0.3873
218023_s_at	family with sequence similarity 53, member C	<i>FAM53C</i>	0.3802
218041_x_at	solute carrier family 38, member 2	<i>SLC38A2</i>	0.3741
218071_s_at	makorin ring finger protein 2	<i>MKRN2</i>	0.4800
218088_s_at	Ras-related GTP binding C	<i>RRAGC</i>	0.4705
218089_at	chromosome 20 open reading frame 4	<i>C20orf4</i>	0.4941
218092_s_at	ArfGAP with FG repeats 1	<i>AGFG1</i>	0.4154
218103_at	FtsJ homolog 3 (E. coli)	<i>FTSJ3</i>	0.4789
218104_at	testis expressed 10	<i>TEX10</i>	0.3662
218107_at	WD repeat domain 26	<i>WDR26</i>	0.2617
218129_s_at	nuclear transcription factor Y, beta	<i>NFYB</i>	0.4593
218133_s_at	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	<i>NIF3L1</i>	0.4896
218141_at	ubiquitin-conjugating enzyme E2O	<i>UBE2O</i>	0.4432
218145_at	tribbles homolog 3 (Drosophila)	<i>TRIB3</i>	0.4837
218191_s_at	LMBR1 domain containing 1	<i>LMBRD1</i>	0.4775
218196_at	osteopetrosis associated transmembrane protein 1	<i>OSTM1</i>	0.4822
218214_at	chromosome 12 open reading frame 44	<i>C12orf44</i>	0.3834
218228_s_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	<i>TNKS2</i>	0.3640
218229_s_at	pogo transposable element with KRAB domain	<i>POGK</i>	0.4650
218231_at	N-acetylglucosamine kinase	<i>NAGK</i>	0.3121
218238_at	GTP binding protein 4	<i>GTPBP4</i>	0.2757
218239_s_at	GTP binding protein 4	<i>GTPBP4</i>	0.3568
218241_at	golgi autoantigen, golgin subfamily a, 5	<i>GOLGA5</i>	0.2441
218244_at	nucleolar protein 8	<i>NOL8</i>	0.4821
218246_at	mitochondrial E3 ubiquitin ligase 1	<i>MUL1</i>	0.4581
218251_at	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	<i>MID1IP1</i>	0.3554
218252_at	cytoskeleton associated protein 2	<i>CKAP2</i>	0.3209
218259_at	MKL/myocardin-like 2	<i>MKL2</i>	0.4512
218263_s_at	zinc finger, BED-type containing 5	<i>ZBED5</i>	0.1549
218276_s_at	salvador homolog 1 (Drosophila)	<i>SAV1</i>	0.4930
218304_s_at	oxysterol binding protein-like 11	<i>OSBPL11</i>	0.3958

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
218308_at	transforming, acidic coiled-coil containing protein 3	<i>TACC3</i>	0.2966
218325_s_at	death inducer-obliterator 1	<i>DIDO1</i>	0.4547
218329_at	PR domain containing 4	<i>PRDM4</i>	0.4698
218331_s_at	chromosome 10 open reading frame 18	<i>C10orf18</i>	0.3095
218341_at	phosphopantothenoylcysteine synthetase	<i>PPCS</i>	0.4582
218344_s_at	REST corepressor 3	<i>RCOR3</i>	0.3927
218350_s_at	geminin, DNA replication inhibitor	<i>GMNN</i>	0.4145
218355_at	kinesin family member 4A	<i>KIF4A</i>	0.3521
218356_at	FtsJ homolog 2 (E. coli)	<i>FTSJ2</i>	0.3746
218360_at	RAB22A, member RAS oncogene family	<i>RAB22A</i>	0.3187
218376_s_at	microtubule associated monooxygenase, calponin and LIM domain containing 1	<i>MICAL1</i>	1.6456
218398_at	mitochondrial ribosomal protein S30	<i>MRPS30</i>	0.4106
218401_s_at	zinc finger protein 281	<i>ZNF281</i>	0.4002
218405_at	activator of basal transcription 1	<i>ABT1</i>	0.4140
218411_s_at	MAP3K12 binding inhibitory protein 1	<i>MBIP</i>	0.3698
218423_x_at	vacuolar protein sorting 54 homolog (S. cerevisiae)	<i>VPS54</i>	0.4577
218437_s_at	leucine zipper transcription factor-like 1	<i>LZTFL1</i>	2.2652
218442_at	tetratricopeptide repeat domain 4	<i>TTC4</i>	0.2102
218452_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	<i>SMARCA1</i>	0.3988
218458_at	germ cell-less homolog 1 (Drosophila)	<i>GMCL1</i>	0.4651
218462_at	brix domain containing 5	<i>BXDC5</i>	0.4344
218464_s_at	chromosome 17 open reading frame 63	<i>C17orf63</i>	0.3523
218470_at	tyrosyl-tRNA synthetase 2, mitochondrial	<i>YARS2</i>	0.4315
218472_s_at	pelota homolog (Drosophila)	<i>PELO</i>	0.3577
218474_s_at	potassium channel tetramerisation domain containing 5	<i>KCTD5</i>	0.4958
218492_s_at	THAP domain containing 7	<i>THAP7</i>	0.4930
218512_at	WD repeat domain 12	<i>WDR12</i>	0.4531
218514_at	chromosome 17 open reading frame 71	<i>C17orf71</i>	0.3984
218519_at	solute carrier family 35, member A5	<i>SLC35A5</i>	0.4027
218520_at	TANK-binding kinase 1	<i>TBK1</i>	0.3940
218528_s_at	ring finger protein 38	<i>RNF38</i>	0.4026
218534_s_at	angiogenic factor with G patch and FHA domains 1	<i>AGGF1</i>	0.3497
218539_at	F-box protein 34	<i>FBXO34</i>	0.4859

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
218542_at	centrosomal protein 55 kDa	<i>CEP55</i>	0.4127
218547_at	dehydrodolichyl diphosphate synthase	<i>DHDDS</i>	0.4310
218564_at	ring finger and WD repeat domain 3	<i>RFWD3</i>	0.4036
218565_at	chromosome 9 open reading frame 114	<i>C9orf114</i>	0.2507
218578_at	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	<i>CDC73</i>	0.3109
218601_at	up-regulated gene 4	<i>URG4</i>	0.2741
218602_s_at	HAUS augmin-like complex, subunit 6	<i>HAUS6</i>	0.3327
218604_at	LEM domain containing 3	<i>LEMD3</i>	0.3044
218612_s_at	tumor suppressing subtransferable candidate 4	<i>TSSC4</i>	0.4161
218614_at	chromosome 12 open reading frame 35	<i>C12orf35</i>	0.2489
218619_s_at	suppressor of variegation 3-9 homolog 1 (Drosophila)	<i>SUV39H1</i>	0.4161
218626_at	eukaryotic translation initiation factor 4E nuclear import factor 1	<i>EIF4ENIF1</i>	0.2853
218646_at	chromosome 4 open reading frame 27	<i>C4orf27</i>	0.4743
218647_s_at	yrdC domain containing (E. coli)	<i>YRDC</i>	1.5458
218648_at	CREB regulated transcription coactivator 3	<i>CRTC3</i>	0.4322
218662_s_at	non-SMC condensin I complex, subunit G	<i>NCAPG</i>	0.2763
218663_at	non-SMC condensin I complex, subunit G	<i>NCAPG</i>	0.2437
218682_s_at	solute carrier family 4 (anion exchanger), member 1, adaptor protein	<i>SLC4A1AP</i>	0.3496
218687_s_at	mucin 13, cell surface associated	<i>MUC13</i>	0.4745
218695_at	exosome component 4	<i>EXOSC4</i>	0.2496
218708_at	NTF2-like export factor 1	<i>NXT1</i>	0.4485
218715_at	UTP6, small subunit (SSU) processome component, homolog (yeast)	<i>UTP6</i>	0.4574
218722_s_at	coiled-coil domain containing 51	<i>CCDC51</i>	0.4059
218726_at	Holliday junction recognition protein	<i>HJURP</i>	0.2644
218728_s_at	cornichon homolog 4 (Drosophila)	<i>CNIH4</i>	0.4981
218732_at	peptidyl-tRNA hydrolase 2	<i>PTRH2</i>	0.4607
218735_s_at	zinc finger protein 544	<i>ZNF544</i>	0.4155
218750_at	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41 kDa	<i>TAF1D</i>	6.8154
218758_s_at	ribosomal RNA processing 1 homolog (S. cerevisiae)	<i>RRP1</i>	0.4605
218763_at	syntxin 18	<i>STX18</i>	0.2798
218776_s_at	transmembrane protein 62	<i>TMEM62</i>	0.3526
218777_at	receptor accessory protein 4	<i>REEP4</i>	0.4156

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
218782_s_at	ATPase family, AAA domain containing 2	<i>ATAD2</i>	0.3425
218793_s_at	sex comb on midleg-like 1 (Drosophila)	<i>SCML1</i>	1.5424
218819_at	integrator complex subunit 6	<i>INTS6</i>	0.2475
218823_s_at	potassium channel tetramerisation domain containing 9	<i>KCTD9</i>	0.2941
218837_s_at	ubiquitin-conjugating enzyme E2D 4 (putative)	<i>UBE2D4</i>	0.4999
218842_at	RNA polymerase II associated protein 3	<i>RPAP3</i>	0.4491
218846_at	mediator complex subunit 23	<i>MED23</i>	0.4627
218850_s_at	LIM domains containing 1	<i>LIMD1</i>	0.4978
218853_s_at	motile sperm domain containing 1	<i>MOSPD1</i>	0.4160
218859_s_at	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	<i>ESF1</i>	0.3903
218873_at	gon-4-like (C. elegans)	<i>GON4L</i>	0.4599
218882_s_at	WD repeat domain 3	<i>WDR3</i>	0.2898
218887_at	mitochondrial ribosomal protein L2	<i>MRPL2</i>	0.4729
218889_at	nucleolar complex associated 3 homolog (S. cerevisiae)	<i>NOC3L</i>	0.4819
218898_at	family with sequence similarity 57, member A	<i>FAM57A</i>	0.4145
218912_at	GRIP and coiled-coil domain containing 1	<i>GCCI</i>	0.2433
218917_s_at	AT rich interactive domain 1A (SWI-like)	<i>ARID1A</i>	0.3374
218929_at	CDKN2A interacting protein	<i>CDKN2AIP</i>	1.9541
218932_at	zinc finger, HIT type 6	<i>ZNHIT6</i>	0.4880
218933_at	spermatogenesis associated 5-like 1	<i>SPATA5L1</i>	0.3211
218936_s_at	coiled-coil domain containing 59	<i>CCDC59</i>	0.3828
218937_at	zinc finger protein 434	<i>ZNF434</i>	0.4493
218949_s_at	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	<i>QRSL1</i>	0.4362
218954_s_at	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	<i>BRF2</i>	0.4137
218956_s_at	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2/pentatricopeptide repeat domain 1	<i>ATP5J2/PTCD1</i>	0.3065
218968_s_at	zinc finger protein 64 homolog (mouse)	<i>ZFP64</i>	0.3632
218975_at	collagen, type V, alpha 3	<i>COL5A3</i>	1.9309
218979_at	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	<i>RMI1</i>	0.4321
218989_x_at	solute carrier family 30 (zinc transporter), member 5	<i>SLC30A5</i>	0.4995
218993_at	RNA methyltransferase like 1	<i>RNMTL1</i>	0.3736
219002_at	FAST kinase domains 1	<i>FASTKD1</i>	0.4351

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
219006_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	<i>NDUF4F4</i>	0.3950
219035_s_at	ring finger protein 34	<i>RNF34</i>	0.4554
219037_at	ribosomal RNA processing 15 homolog (S. cerevisiae)	<i>RRP15</i>	0.4922
219053_s_at	vacuolar protein sorting 37 homolog C (S. cerevisiae)	<i>VPS37C</i>	0.4707
219068_x_at	ATPase family, AAA domain containing 3A	<i>ATAD3A</i>	1.5119
219074_at	transmembrane protein 184C	<i>TMEM184C</i>	0.3334
219083_at	SHQ1 homolog (S. cerevisiae)	<i>SHQ1</i>	0.3460
219089_s_at	zinc finger protein 576	<i>ZNF576</i>	0.4950
219094_at	armadillo repeat containing 8	<i>ARMC8</i>	1.5443
219099_at	chromosome 12 open reading frame 5	<i>C12orf5</i>	0.3527
219120_at	chromosome 2 open reading frame 44	<i>C2orf44</i>	0.3376
219124_at	chromosome 8 open reading frame 41	<i>C8orf41</i>	0.2379
219129_s_at	SAP30-like	<i>SAP30L</i>	0.4656
219131_at	UbiA prenyltransferase domain containing 1	<i>UBIAD1</i>	0.4726
219133_at	3-oxoacyl-ACP synthase, mitochondrial	<i>OXSM</i>	0.2486
219141_s_at	autophagy/beclin-1 regulator 1	<i>AMBRA1</i>	0.3719
219146_at	chromosome 17 open reading frame 42	<i>C17orf42</i>	0.3709
219149_x_at	debranching enzyme homolog 1 (S. cerevisiae)	<i>DBR1</i>	0.2660
219166_at	chromosome 14 open reading frame 104	<i>C14orf104</i>	0.2330
219169_s_at	transcription factor B1, mitochondrial	<i>TFB1M</i>	0.4230
219176_at	chromosome 2 open reading frame 47	<i>C2orf47</i>	0.4093
219177_at	brix domain containing 2	<i>BXDC2</i>	0.2745
219200_at	FAST kinase domains 3	<i>FASTKD3</i>	0.4598
219212_at	heat shock 70 kDa protein 14	<i>HSPA14</i>	0.4119
219226_at	Cdc2-related kinase, arginine/serine-rich	<i>CRKRS</i>	0.4183
219231_at	trimethylguanosine synthase homolog (S. cerevisiae)	<i>TGS1</i>	0.2814
219238_at	phosphatidylinositol glycan anchor biosynthesis, class V	<i>PIGV</i>	0.4570
219244_s_at	mitochondrial ribosomal protein L46	<i>MRPL46</i>	0.2915
219253_at	transmembrane protein 185B (pseudogene)	<i>TMEM185B</i>	0.4733
219258_at	TIMELESS interacting protein	<i>TIPIN</i>	0.3193
219261_at	chromosome 7 open reading frame 26	<i>C7orf26</i>	0.2648
219276_x_at	chromosome 9 open reading frame 82	<i>C9orf82</i>	0.4413
219286_s_at	RNA binding motif protein 15	<i>RBM15</i>	0.3621
219296_at	zinc finger, DHHC-type containing 13	<i>ZDHHC13</i>	0.4559

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
219321_at	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	<i>MPP5</i>	0.3634
219322_s_at	WD repeat domain 8	<i>WDR8</i>	0.2845
219328_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	<i>DDX31</i>	0.4878
219343_at	cell division cycle 37 homolog (S. cerevisiae)-like 1	<i>CDC37L1</i>	0.4838
219353_at	NHL repeat containing 2	<i>NHLRC2</i>	0.4431
219420_s_at	chromosome 1 open reading frame 163	<i>C1orf163</i>	0.4056
219433_at	BCL6 co-repressor	<i>BCOR</i>	0.4976
219439_at	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	<i>C1GALT1</i>	0.2997
219446_at	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	<i>RIC8B</i>	0.4257
219459_at	polymerase (RNA) III (DNA directed) polypeptide B	<i>POLR3B</i>	0.2239
219460_s_at	transmembrane protein 127	<i>TMEM127</i>	0.4847
219467_at	gypsy retrotransposon integrase 1	<i>GIN1</i>	0.4355
219486_at	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	<i>DUS2L</i>	0.3491
219492_at	cysteine-rich hydrophobic domain 2	<i>CHIC2</i>	0.1870
219494_at	RAD54 homolog B (S. cerevisiae)	<i>RAD54B</i>	0.3937
219502_at	nei endonuclease VIII-like 3 (E. coli)	<i>NEIL3</i>	0.3179
219512_at	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	<i>DSN1</i>	0.4496
219522_at	four jointed box 1 (Drosophila)	<i>FJX1</i>	0.4767
219530_at	partner and localizer of BRCA2	<i>PALB2</i>	0.3512
219541_at	Lck interacting transmembrane adaptor 1	<i>LIME1</i>	1.5240
219544_at	chromosome 13 open reading frame 34	<i>C13orf34</i>	0.4483
219551_at	ELL associated factor 2	<i>EAF2</i>	0.4522
219565_at	cytochrome P450, family 20, subfamily A, polypeptide 1	<i>CYP20A1</i>	0.4158
219575_s_at	component of oligomeric golgi complex 8///peptide deformylase (mitochondrial)	<i>COG8/PDF</i>	0.3377
219577_s_at	ATP-binding cassette, sub-family A (ABC1), member 7	<i>ABCA7</i>	1.6990
219581_at	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	<i>TSEN2</i>	0.4815
219595_at	similar to zinc finger protein 26 (KOX 20)///zinc finger protein 26	<i>LOC100287515/ ZNF26</i>	1.6049

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
219640_at	claudin 15	<i>CLDN15</i>	1.7002
219662_at	chromosome 2 open reading frame 49	<i>C2orf49</i>	0.3197
219679_s_at	WW domain containing adaptor with coiled-coil	<i>WAC</i>	0.4837
219707_at	copine VII	<i>CPNE7</i>	1.6723
219731_at	weakly similar to zinc finger protein 195	<i>FLJ34077</i>	0.4269
219733_s_at	solute carrier family 27 (fatty acid transporter), member 5	<i>SLC27A5</i>	1.5024
219753_at	stromal antigen 3	<i>STAG3</i>	1.5460
219787_s_at	epithelial cell transforming sequence 2 oncogene	<i>ECT2</i>	0.3472
219798_s_at	methylphosphate capping enzyme	<i>MEPCE</i>	0.2431
219816_s_at	RNA binding motif protein 23	<i>RBM23</i>	0.4890
219918_s_at	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	<i>ASPM</i>	0.2807
219920_s_at	GDP-mannose pyrophosphorylase B	<i>GMPPB</i>	1.5074
219966_x_at	BTG3 associated nuclear protein	<i>BANP</i>	0.2767
219971_at	interleukin 21 receptor	<i>IL21R</i>	0.3546
219981_x_at	zinc finger protein 587	<i>ZNF587</i>	0.4436
220035_at	nucleoporin 210 kDa	<i>NUP210</i>	1.8905
220046_s_at	cyclin L1	<i>CCNL1</i>	2.7922
220104_at	zinc finger CCCH-type, antiviral 1	<i>ZC3HAV1</i>	1.9500
220235_s_at	chromosome 1 open reading frame 103	<i>C1orf103</i>	0.2879
220253_s_at	low density lipoprotein-related protein 12	<i>LRP12</i>	0.4186
220295_x_at	DEP domain containing 1	<i>DEPDC1</i>	0.3436
220319_s_at	myosin regulatory light chain interacting protein	<i>MYLIP</i>	2.9232
220330_s_at	SAM domain, SH3 domain and nuclear localization signals 1	<i>SAMSN1</i>	0.4535
220367_s_at	Sin3A-associated protein, 130 kDa	<i>SAP130</i>	0.3837
220485_s_at	signal-regulatory protein gamma	<i>SIRPG</i>	1.5937
220651_s_at	minichromosome maintenance complex component 10	<i>MCM10</i>	0.2639
220742_s_at	N-glycanase 1	<i>NGLY1</i>	0.3378
220924_s_at	solute carrier family 38, member 2	<i>SLC38A2</i>	0.3783
220926_s_at	ER degradation enhancer, mannosidase alpha-like 3	<i>EDEM3</i>	0.4270
220934_s_at	transmembrane protein 223	<i>TMEM223</i>	0.3533
220937_s_at	ST6 alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	<i>ST6GALNAC4</i>	1.6597
220949_s_at	chromosome 7 open reading frame 49	<i>C7orf49</i>	0.3213

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
220964_s_at	RAB1B, member RAS oncogene family	<i>RAB1B</i>	1.5938
221007_s_at	FIP1 like 1 (S. cerevisiae)	<i>FIP1L1</i>	0.4228
221020_s_at	solute carrier family 25, member 32	<i>SLC25A32</i>	0.3938
221122_at	HRAS-like suppressor 2	<i>HRASLS2</i>	1.6261
221190_s_at	chromosome 18 open reading frame 8	<i>C18orf8</i>	0.4621
221193_s_at	zinc finger, CCHC domain containing 10	<i>ZCCHC10</i>	0.3544
221229_s_at	tRNA methyltransferase 61 homolog B (S. cerevisiae)	<i>TRMT61B</i>	0.3567
221257_x_at	F-box protein 38	<i>FBXO38</i>	0.4407
221258_s_at	kinesin family member 18A	<i>KIF18A</i>	0.2360
221277_s_at	pseudouridylate synthase 3	<i>PUS3</i>	0.4712
221286_s_at	hypothetical protein MGC29506	<i>MGC29506</i>	1.5510
221311_x_at	LYR motif containing 2	<i>LYRM2</i>	0.3475
221480_at	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37 kDa)	<i>HNRNPD</i>	1.5003
221497_x_at	egl nine homolog 1 (C. elegans)	<i>EGLN1</i>	0.3536
221518_s_at	ubiquitin specific peptidase 47	<i>USP47</i>	0.4135
221520_s_at	cell division cycle associated 8	<i>CDCA8</i>	0.4572
221528_s_at	engulfment and cell motility 2	<i>ELMO2</i>	0.4304
221536_s_at	large subunit GTPase 1 homolog (S. cerevisiae)	<i>LSG1</i>	0.4939
221547_at	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	<i>PRPF18</i>	0.4500
221549_at	glutamate-rich WD repeat containing 1	<i>GRWD1</i>	0.3243
221552_at	abhydrolase domain containing 6	<i>ABHD6</i>	0.2271
221563_at	dual specificity phosphatase 10	<i>DUSP10</i>	0.4966
221571_at	TNF receptor-associated factor 3	<i>TRAF3</i>	0.4973
221586_s_at	E2F transcription factor 5, p130-binding	<i>E2F5</i>	0.4568
221593_s_at	ribosomal protein L31	<i>RPL31</i>	3.1404
221649_s_at	peter pan homolog (Drosophila)	<i>PPAN</i>	0.1407
221657_s_at	ankyrin repeat and SOCS box-containing 6	<i>ASB6</i>	0.3319
221658_s_at	interleukin 21 receptor	<i>IL21R</i>	0.3316
221679_s_at	abhydrolase domain containing 6	<i>ABHD6</i>	0.3234
221688_s_at	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	<i>IMP3</i>	0.2570
221706_s_at	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	<i>USE1</i>	0.4624
221741_s_at	YTH domain family, member 1	<i>YTHDF1</i>	0.3452
221751_at	Solute carrier family 2 (facilitated glucose transporter), member 3 pseudogene 1	<i>SLC2A3P1</i>	0.4337

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
221758_at	armadillo repeat containing 6	<i>ARMC6</i>	1.7673
221768_at	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	<i>SFPQ</i>	3.4452
221772_s_at	protein phosphatase 2, regulatory subunit B, delta isoform	<i>PPP2R2D</i>	0.3882
221804_s_at	family with sequence similarity 45, member A/ pseudogene	<i>FAM45A/FAM45B</i>	0.4349
221808_at	RAB9A, member RAS oncogene family	<i>RAB9A</i>	0.3243
221813_at	F-box protein 42	<i>FBXO42</i>	0.3475
221817_at	dolichyl pyrophosphate phosphatase 1	<i>DOLPP1</i>	0.4425
221823_at	chromosome 5 open reading frame 30	<i>C5orf30</i>	0.3585
221825_at	angel homolog 2 (Drosophila)	<i>ANGEL2</i>	0.4710
221848_at	zinc finger, CCCH-type with G patch domain	<i>ZGPAT</i>	0.3737
221855_at	succinate dehydrogenase complex assembly factor 1	<i>SDHAF1</i>	0.4928
221860_at	heterogeneous nuclear ribonucleoprotein L	<i>HNRNPL</i>	4.4629
221890_at	zinc finger protein 335	<i>ZNF335</i>	0.4138
221918_at	PCTAIRE protein kinase 2	<i>PCTK2</i>	0.3562
221922_at	G-protein signaling modulator 2 (AGS3-like, C. elegans)	<i>GPSM2</i>	0.2972
221937_at	synergins, gamma	<i>SYNRG</i>	0.4075
221940_at	RNA pseudouridylation synthase domain containing 2	<i>RPUSD2</i>	0.3840
221942_s_at	guanylate cyclase 1, soluble, alpha 3	<i>GUCY1A3</i>	0.3812
221970_s_at	nucleolar protein 11	<i>NOL11</i>	0.3515
221989_at	ribosomal protein L10	<i>RPL10</i>	4.1064
222000_at	chromosome 1 open reading frame 174	<i>C1orf174</i>	0.3803
222018_at	nascent polypeptide-associated complex alpha subunit/nascent-polypeptide-associated complex alpha polypeptide pseudogene 1	<i>NACA/NACAP1</i>	14.4151
222028_at	zinc finger protein 45	<i>ZNF45</i>	0.3808
222030_at	SIVA1, apoptosis-inducing factor	<i>SIVA1</i>	3.5677
222034_at	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	<i>GNB2L1</i>	8.4318
222040_at	heterogeneous nuclear ribonucleoprotein A1	<i>HNRNPA1</i>	4.1086
222044_at	PDX1 C-terminal inhibiting factor 1	<i>PCIF1</i>	1.6084
222045_s_at	PDX1 C-terminal inhibiting factor 1	<i>PCIF1</i>	1.6823

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
222067_x_at	histone cluster 1, H2bd	<i>HIST1H2BD</i>	1.5425
222103_at	activating transcription factor 1	<i>ATF1</i>	0.4888
222118_at	centromere protein N	<i>CENPN</i>	0.4874
222119_s_at	F-box protein 11	<i>FBXO11</i>	0.4165
222130_s_at	FtsJ homolog 2 (E. coli)	<i>FTSJ2</i>	0.4062
222163_s_at	spermatogenesis associated 5-like 1	<i>SPATA5L1</i>	0.3379
222165_x_at	chromosome 9 open reading frame 16	<i>C9orf16</i>	1.7473
222182_s_at	CCR4-NOT transcription complex, subunit 2	<i>CNOT2</i>	0.3781
222199_s_at	bridging integrator 3	<i>BIN3</i>	0.3904
222201_s_at	caspase 8 associated protein 2	<i>CASP8AP2</i>	0.4551
222203_s_at	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	<i>RDH14</i>	0.3862
222239_s_at	integrator complex subunit 6	<i>INTS6</i>	0.2361
222243_s_at	transducer of ERBB2, 2	<i>TOB2</i>	0.3560
222250_s_at	integrator complex subunit 7	<i>INTS7</i>	0.3006
222251_s_at	glucocorticoid modulatory element binding protein 2	<i>GMEB2</i>	0.4407
222294_s_at	—	—	1.7564
222311_s_at	splicing factor, arginine/serine-rich 15	<i>SFRS15</i>	1.9966
31826_at	FK506 binding protein 15, 133 kDa	<i>FKBP15</i>	0.3552
31845_at	E74-like factor 4 (ets domain transcription factor)	<i>ELF4</i>	0.3654
32032_at	DiGeorge syndrome critical region gene 14	<i>DGCR14</i>	0.4587
32069_at	NEDD4 binding protein 1	<i>N4BPI</i>	0.2485
32541_at	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	<i>PPP3CC</i>	0.4408
32723_at	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50 kDa	<i>CSTF1</i>	0.3728
34031_i_at	KRIT1, ankyrin repeat containing	<i>KRIT1</i>	0.4720
34225_at	Wolf-Hirschhorn syndrome candidate 2	<i>WHSC2</i>	0.4894
34689_at	three prime repair exonuclease 1	<i>TREX1</i>	0.4046
35254_at	TRAF-type zinc finger domain containing 1	<i>TRAFD1</i>	0.4147
35974_at	lymphoid-restricted membrane protein	<i>LRMP</i>	1.6055
37028_at	protein phosphatase 1, regulatory (inhibitor) subunit 15A	<i>PPP1R15A</i>	1.7214
38157_at	dom-3 homolog Z (C. elegans)	<i>DOM3Z</i>	1.5789
38398_at	MAP-kinase activating death domain	<i>MADD</i>	0.4570
40562_at	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	<i>GNA11</i>	0.4928
44146_at	glucocorticoid modulatory element binding protein 2	<i>GMEB2</i>	0.4711

Table S1. *Cont.*

Probe Set ID	Gene Title	Gene Symbol	ADE_ave/Corresponding DMSO
44669_at	succinate dehydrogenase complex assembly factor 1	<i>SDHAF1</i>	0.4631
44783_s_at	hairy/enhancer-of-split related with YRPW motif 1	<i>HEY1</i>	0.3914
45288_at	abhydrolase domain containing 6	<i>ABHD6</i>	0.3247
46167_at	tetratricopeptide repeat domain 4	<i>TTC4</i>	0.2003
46665_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	<i>SEMA4C</i>	0.4710
47083_at	chromosome 7 open reading frame 26	<i>C7orf26</i>	0.3791
47105_at	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	<i>DUS2L</i>	0.4074
47773_at	F-box protein 42	<i>FBXO42</i>	0.4573
49485_at	PR domain containing 4	<i>PRDM4</i>	0.4940
51146_at	phosphatidylinositol glycan anchor biosynthesis, class V	<i>PIGV</i>	0.3683
51176_at	mediator complex subunit 27	<i>MED27</i>	0.3524
52731_at	autophagy/beclin-1 regulator 1	<i>AMBRA1</i>	0.4066
53968_at	integrator complex subunit 5	<i>INTS5</i>	0.1323
53987_at	RAN binding protein 10	<i>RANBP10</i>	0.4756
55065_at	MAP/microtubule affinity-regulating kinase 4	<i>MARK4</i>	0.4114
57532_at	dishevelled, dsh homolog 2 (Drosophila)	<i>DVL2</i>	0.4147
57539_at	zinc finger, CCCH-type with G patch domain	<i>ZGPAT</i>	0.4107
58696_at	exosome component 4	<i>EXOSC4</i>	0.2509
59999_at	hypoxia inducible factor 1, alpha subunit inhibitor	<i>HIF1AN</i>	0.4728
63009_at	SHQ1 homolog (S. cerevisiae)	<i>SHQ1</i>	0.3676
64371_at	splicing factor, arginine/serine-rich 14	<i>SFRS14</i>	2.0881
64474_g_at	DiGeorge syndrome critical region gene 8	<i>DGCR8</i>	0.4713
91684_g_at	exosome component 4	<i>EXOSC4</i>	0.2755
91952_at	DDB1 and CUL4 associated factor 15	<i>DCAF15</i>	0.4751