Table S2. Transcripts modified in BAHD1 knockdown HEK293 cells

Probe set	Gene Title	Gene Symbol	Fold change	Adjacent p-Value	Chromosomal Location	AccNum	Gene ID
Induced transcripts							
202409_at	insulin-like growth factor 2 (somatomedin A)	IGF2	2,27	4,51799E-06	chr11p15.5	X07868	3481
266_s_at	CD24 molecule	CD24	2,14	3,5543E-06	chr6q21	L33930	934
209763_at	chordin-like 1	CHRDL1	2,12	0,000101708	chrXq22.3	AL049176	91851
223500_at	complexin 1	CPLX1	2,04	2,26786E-06	chr4p16.3	BC002471	10815
229485_x_at	hypothetical protein BC012029	LOC152573	2,03	1,30654E-10	chr4p13	AI735586	152573
227705_at	transcription elongation factor A (SII)-like 7	TCEAL7	2,02	0,000341203	chrXq22.1	BF591534	56849
1559072_a_at	leucine rich repeat containing 62	LRRC62	2,00	0,000454616	chr22q13.1	BC032083	114794
232231_at	runt-related transcription factor 2	RUNX2	1,96	0,000187825	chr6p21	AL353944	860
236359_at	sodium channel, voltage-gated, type IV, beta	SCN4B	1,94	0,02642903	chr11q23.3	AW026241	6330
234016_at	hypothetical protein LOC90499	ANKRD20B	1,90	0,008971144	chr18p11.21 /// chr2q11.1	AL137712	90499
230316_at	SEC14-like 2 (S. cerevisiae)	SEC14L2	1,83	9,84188E-07	chr22q12.2	R49343	200312
1554549_a_at	WD repeat domain 20	WDR20	1,83	0,000832047	chr14q32.31	BC030654	91833
204120_s_at	adenosine kinase	ADK	1,82	2,18165E-09	chr10q22|10q11-q24	NM_001123	132
228463_at	forkhead box A3	FOXA3	1,82	0,02816691	chr19q13.2-q13.4	R99562	3171
226675_s_at	metastasis associated lung adenocarcinoma transcript 1	MALAT1	1,81	1,16475E-09	chr11q13.1	W80468	378938
203989_x_at	coagulation factor II (thrombin) receptor	F2R	1,78	6,40732E-09	chr5q13	NM_001992	2149
204446_s_at	arachidonate 5-lipoxygenase	ALOX5	1,76	0,005604599	chr10q11.2	NM_000698	240
208949_s_at	lectin, galactoside-binding, soluble, 3	LGALS3	1,76	0,04348753	chr14q21-q22	BC001120	3958
209981_at	cold shock domain containing C2, RNA binding	CSDC2	1,75	0,000946192	chr22q13.2-q13.31	AL023553	27351
211668_s_at	plasminogen activator, urokinase	PLAU	1,74	0,00076113	chr10q24	K03226	5328
212417_at	secretory carrier membrane protein 1	SCAMP1	1,74	2,52636E-11	chr5q13.3-q14.1	BF058944	9522
214414_x_at	hemoglobin, alpha 1	HBA1	1,73	0,009947431	chr16p13.3	T50399	3039
211421_s_at	ret proto-oncogene	RET	1,72	0,03524844	chr10q11.2	M31213	5979
218254_s_at	SAR1 gene homolog B (S. cerevisiae)	SAR1B	1,71	1,70874E-11	chr5q31.1	NM_016103	51128
242385_at	RAR-related orphan receptor B	RORB	1,71	0,02944577	chr9q22	R18374	6096
213479_at	neuronal pentraxin II	NPTX2	1,71	1,02019E-05	chr7q21.3-q22.1	U26662	4885
219347_at	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NUDT15	1,70	4,59076E-11	chr13q14.2	NM_018283	55270
214314_s_at	eukaryotic translation initiation factor 5B	EIF5B	1,70	2,03416E-08	chr2q11.2	BE138647	9669
228176_at	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	EDG3	1,69	0,00613117	chr9q22.1-q22.2	AA534817	286223
221276_s_at	syncoilin, intermediate filament 1	SYNC1	1,69	0,000263696	chr1p34.3-p33	NM_030786	81493
238622_at	RAP2B, member of RAS oncogene family	RAP2B	1,67	0,001645201	chr3q25.2	AW269686	5912
205619_s_at	mesenchyme homeobox 1	MEOX1	1,67	3,25444E-06	chr17q21	NM_004527	4222
223651_x_at	cell division cycle 23 homolog (S. cerevisiae)	CDC23	1,66	0,000326867	chr5q31	BC005258	8697
225497_at	arginyltransferase 1	ATE1	1,66	1,1343E-09	chr10q26.13	AL589591	11101
226690_at	Adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	ADCYAP1R1	1,65	0,003771459	chr7p14	AW451961	117
200821_at	lysosomal-associated membrane protein 2	LAMP2	1,65	3,82943E-12	chrXq24	NM_013995	3920
227899_at	vitrin	VIT	1,64	1,53166E-07	chr2p22-p21	AI817458	5212
214068_at	brain expressed, associated with Nedd4	BEAN	1,64	0,001883455	chr16q21	AF070610	146227
229254_at	major facilitator superfamily domain containing 4	MFSD4	1,63	0,02623782	chr1q32.1	BE550027	148808

227856_at	chromosome 4 open reading frame 32	C4orf32	1,63	1,37246E-08	chr4q25	AI110850	132720
204807_at	transmembrane protein 5	TMEM5	1,63	4,41098E-07	chr12q14.2	BF224146	10329
223843_at	scavenger receptor class A, member 3	SCARA3	1,63	0,004107223	chr8p21	AB007830	51435
225079_at	epithelial membrane protein 2	EMP2	1,63	0,000397831	chr16p13.2	AI089325	2013
1556015_a_at	mesoderm posterior 2 homolog (mouse)	MESP2	1,62	0,00850892	chr15q26.1	AL360139	145873
236533_at	development and differentiation enhancing factor 1	DDEF1	1,62	0,002914433	chr8q24.1-q24.2	AW236958	50807
228568_at	GRINL1A combined protein	Gcom1	1,62	0,01102865	chr15q21.3	AI926697	145781
216860_s_at	growth differentiation factor 11	GDF11	1,62	3,24479E-07	chr12q13.2	AF028333	10220
223821_s_at	sushi domain containing 4	SUSD4	1,62	0,000887802	chr1q41	BC004888	55061
204040_at	ring finger protein 144A	RNF144A	1,61	0,006895418	chr2p25.2-p25.1	NM_014746	9781
228715_at	zinc finger, CCHC domain containing 12	ZCCHC12	1,61	4,25922E-08	chrXq24	AV725825	170261
239913_at	solute carrier family 10, member 4	SLC10A4	1,61	0,00237624	chr4p12	AI421796	201780
206850_at	RAS-like, family 10, member A	RASL10A	1,60	0,03197565	chr22q12.2	NM_006477	10633
1554069_at	EPH receptor A8	EPHA8	1,60	0,00423041	chr1p36.12	BC038796	2046
201427_s_at	selenoprotein P, plasma, 1	SEPP1	1,60	1,61211E-10	chr5q31	NM_005410	6414
219520_s_at	WWC family member 3	WWC3	1,60	0,00552501	chrXp22.32	NM_018458	55841
209574_s_at	chromosome 18 open reading frame 1	C18orf1	1,60	0,004157257	chr18p11.2	AI349506	753
202007_at	nidogen 1	NID1	1,60	1,26352E-09	chr1q43	BF940043	4811
203455_s_at	spermidine/spermine N1-acetyltransferase 1	SAT1	1,60	2,07338E-08	chrXp22.1	NM_002970	6303
226548_at	SH3-binding domain kinase 1	SBK1	1,59	0,001169908	chr16p11.2	AI935915	112868
226913_s_at	SRY (sex determining region Y)-box 8	SOX8	1,58	0,01833992	chr16p13.3	BF527050	30812
202422_s_at	acyl-CoA synthetase long-chain family member 4	ACSL4	1,58	0,003567397	chrXq22.3-q23	NM_022977	2182
233329_s_at	lysine-rich coiled-coil 1	KRCC1	1,57	2,10235E-06	chr2p11.2	AK025986	51315
203485_at	reticulon 1	RTN1	1,57	0,0272523	chr14q23.1	NM_021136	6252
225516_at	solute carrier family 7, member 2	SLC7A2	1,57	5,77419E-07	chr8p22-p21.3	AA876372	6542
225802_at	topoisomerase (DNA) I, mitochondrial	TOP1MT	1,57	5,17971E-05	chr8q24.3	AW592604	116447
229849_at	WAS/WASL interacting protein family, member 3	WIPF3	1,57	0,000685469	chr7p15.1	AI807950	NA
235057_at	itchy homolog E3 ubiquitin protein ligase (mouse)	ITCH	1,57	0,003713306	chr20q11.22-q11.23	AW089307	83737
216497_at	heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	1,57	0,04783598	chr10q11.22 /// chr11p15.4 /// chr11q23.1 /// chr12q13.1 /// chr12q22 /// chr13q12.11 /// chr13q14.3 /// chr19p13.2 /// chr19q13.2 /// chr1p13.1 /// chr1q32.1 /// chr2q31.1 /// chr2q32.3 /// chr2q33.1 /// chr2q33.3 /// chr3p22.1 /// chr3q24 /// chr4q21.1	AL390738	219409
244264_at	killer cell lectin-like receptor subfamily G, member 2	KLRG2	1,57	0,02274599	chr7q34	AW197495	346689
227813_at	THAP domain containing 6	THAP6	1,56	0,006343741	chr4q21.1	AW058657	152815
229850_at	follicular lymphoma variant translocation 1	FVT1	1,56	4,51799E-06	chr18q21.3	N30152	NA
219858_s_at	FLJ20160 protein	FLJ20160	1,56	0,02872208	chr2q32.2	NM_017694	54842
210138_at	regulator of G-protein signaling 20	RGS20	1,56	0,02761309	chr8q12.1	AF074979	8601
235170_at	zinc finger protein 92	ZNF92	1,56	6,57701E-09	chr7q11.21	T52999	168374
211343_s_at	collagen, type XIII, alpha 1	COL13A1	1,55	0,00011693	chr10q22	M33653	1305
1552439_s_at	multiple EGF-like-domains 11	MEGF11	1,55	0,009395786	chr15q22.31	NM_032445	84465
207156_at	histone cluster 1, H2ag	HIST1H2AG	1,55	3,55575E-05	chr6p22.1	NM_021064	8969
1554542_at	similar to CG4995 gene product	LOC153328	1,55	0,03914669	chr5q31.1	BC025747	153328
209451_at	TRAF family member-associated NFKB activator	TANK	1,55	3,10698E-06	chr2q24-q31	U59863	10010

205191_at	retinitis pigmentosa 2 (X-linked recessive)	RP2	1,55	0,005480873	chrXp11.4-p11.21	NM_006915	6102
206315_at	cytokine receptor-like factor 1	CRLF1	1,54	0,01602843	chr19p12	NM_004750	9244
201839_s_at	tumor-associated calcium signal transducer 1	TACSTD1	1,54	0,01347745	chr2p21	NM_002354	4072
224712_x_at	chromosome 19 open reading frame 42	C19orf42	1,54	0,01817747	chr19p13.11	AI656658	79086
205286_at	transcription factor AP-2 gamma	TFAP2C	1,54	0,000129548	chr20q13.2	U85658	7022
210175_at	chromosome 2 open reading frame 3	C2orf3	1,54	5,20923E-06	chr2p11.2-p11.1	BC000853	6936
204755_x_at	hepatic leukemia factor	HLF	1,54	0,00423041	chr17q22	M95585	3131
228924_s_at	Ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1	1,54	0,01710196	chr6q15	AA491236	51465
202391_at	brain abundant, membrane attached signal protein 1	BASP1	1,53	2,48507E-07	chr5p15.1-p14	NM_006317	10409
228454_at	ligand dependent nuclear receptor corepressor	LCOR	1,53	7,86371E-08	chr10q24	AW663968	84458
210380_s_at	calcium channel, voltage-dependent, T type, alpha 1G subunit	CACNA1G	1,53	0,0302633	chr17q22	AF126966	8913
223288_at	ubiquitin specific peptidase 38	USP38	1,53	4,25922E-08	---	AW977401	84640
215073_s_at	nuclear receptor subfamily 2, group F, member 2	NR2F2	1,53	1,85315E-07	chr15q26	AL554245	7026
222751_at	HERPUD family member 2	HERPUD2	1,53	1,06328E-06	chr7p14.2	AA536012	64224
205113_at	neurofilament, medium polypeptide 150kDa	NEFM	1,52	1,70335E-05	chr8p21	NM_005382	4741
228754_at	solute carrier family 6, member 6	SLC6A6	1,51	0,03543398	chr3p25-p24	BG150485	80852
202158_s_at	CUG triplet repeat, RNA binding protein 2	CUGBP2	1,51	0,000920671	chr10p13	NM_006561	10659
218900_at	cyclin M4	CNNM4	1,51	0,01531443	chr2p12-p11.2	NM_020184	26504
218871_x_at	chondroitin sulfate GalNAcT-2	GALNACT-2	1,51	8,54455E-07	chr10q11.21	NM_018590	55454
203845_at	p300/CBP-associated factor	PCAF	1,51	0,000476079	chr3p24	AV727449	8850
209786_at	high mobility group nucleosomal binding domain 4	HMGN4	1,51	4,50036E-07	chr6p21.3	BC001282	10473
230001_at	membrane-associated ring finger (C3HC4) 9	9-Mar	1,50	0,04701235	chr12q14.1	AI807693	92979
1554314_at	chromosome 6 open reading frame 141	C6orf141	1,50	0,03838336	chr6p12.3	BC036917	135398
214240_at	galanin	GAL	1,50	0,000128676	chr11q13.2	AL556409	51083
204447_at	ProSAPiP1 protein	ProSAPiP1	1,50	3,59401E-06	chr20p13	NM_014731	9762
222103_at	activating transcription factor 1	ATF1	1,50	4,9498E-09	chr12q13	AI434345	466
224772_at	neuron navigator 1	NAV1	1,50	0,01536971	---	AB032977	89796
231567_s_at	coiled-coil domain containing 62	CCDC62	1,49	0,04739882	chr12q24.31	AI027946	84660
242517_at	KISS1 receptor	KISS1R	1,49	0,00337594	chr19p13.3	AI819198	84634
218424_s_at	STEAP family member 3	STEAP3	1,48	0,01501934	chr2q14.2	NM_018234	55240
203066_at	B cell RAG associated protein	GALNAC4S-6ST	1,48	0,000365149	chr10q26	NM_014863	51363
201163_s_at	insulin-like growth factor binding protein 7	IGFBP7	1,48	2,01261E-05	chr4q12	NM_001553	3490
209544_at	receptor-interacting serine-threonine kinase 2	RIPK2	1,48	0,01738217	chr8q21	AF027706	8767
201304_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NDUFA5	1,48	2,82476E-07	chr7q32	NM_005000	4698
243463_s_at	Ras-like without CAAX 1	RIT1	1,48	0,000237432	chr1q22	AA417878	NA
228802_at	RNA binding protein with multiple splicing 2	RBPMS2	1,48	0,01574586	chr15q22.31	BE348466	348093
225022_at	golgi associated PDZ and coiled-coil motif containing	GOPC	1,48	0,001774715	chr6q21	AW271409	57120
201915_at	SEC63 homolog (S. cerevisiae)	SEC63	1,48	0,01079859	chr6q21	AI806665	11231
200606_at	desmoplakin	DSP	1,48	1,58258E-07	chr6p24	NM_004415	1832
226430_at	RELT-like 1	RELL1	1,47	5,65572E-08	---	AI394438	253981
209575_at	interleukin 10 receptor, beta	IL10RB	1,47	0,00062672	chr21q22.1-q22.2|21q22.11	BC001903	3588
209803_s_at	pleckstrin homology-like domain, family A, member 2	PHLDA2	1,47	4,74729E-06	chr11p15.5	AF001294	7262
205296_at	retinoblastoma-like 1 (p107)	RBL1	1,47	0,002664397	chr20q11.2	AL365505	5933
210681_s_at	ubiquitin specific peptidase 15	USP15	1,47	9,57446E-05	chr12q14	AF153604	9958

227015_at	aspartate beta-hydroxylase domain containing 2	ASPHD2	1,47	0,03140279	chr22q12.1	Z99714	24144
201963_at	acyl-CoA synthetase long-chain family member 1	ACSL1	1,47	0,00176519	chr4q34-q35	NM_021122	2180
215071_s_at	histone cluster 1, H2ac	HIST1H2AC	1,47	8,57423E-05	chr6p21.3	AL353759	3008
1553479_at	transmembrane protein 145	TMEM145	1,47	0,03063325	chr19q13.2	NM_173633	284339
222765_x_at	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	ESF1	1,46	0,0367495	chr20p12.1	AL161659	79133
1564207_at	hypothetical protein FLJ35390	FLJ35390	1,46	0,002384459	chr7p13	BC014556	255031
201020_at	tyrosine 3-monooxygenase	YWHAH	1,46	1,19248E-06	chr22q12.3	NM_003405	7533
217144_at	ubiquitin B /// similar to ubiquitin B precursor	UBB	1,46	0,0026089	chr17p12-p11.2	X04801	7315
222459_at	chromosome 1 open reading frame 108	C1orf108	1,46	9,34549E-06	chr1p34.3	BG109865	79647
226333_at	interleukin 6 receptor	IL6R	1,46	0,005022682	chr1q21	AV700030	3570
1558014_s_at	male sterility domain containing 2	MLSTD2	1,46	1,1146E-06	chr11p15.2	BG261090	84188
238199_x_at	OK/SW-cl.16	LOC440552	1,46	0,000732094	chr1p36.33	AI708524	440552
1553096_s_at	BCL2-like 11 (apoptosis facilitator)	BCL2L11	1,46	0,004705645	chr2q13	NM_138627	10018
212449_s_at	lysophospholipase I	LYPLA1	1,46	2,83778E-08	chr8q11.23	BG288007	10434
205194_at	phosphoserine phosphatase	PSPH	1,46	1,76188E-06	chr7p15.2-p15.1	NM_004577	5723
231579_s_at	TIMP metallopeptidase inhibitor 2	TIMP2	1,46	0,00011254	chr17q25	BE968786	7077
211709_s_at	C-type lectin domain family 11, member A	CLEC11A	1,46	0,00497526	chr19q13.3	BC005810	6320
200603_at	protein kinase, cAMP-dependent	PRKAR1A	1,46	2,10194E-06	chr17q23-q24	AL050038	5573
201951_at	activated leukocyte cell adhesion molecule	ALCAM	1,46	0,005738057	chr3q13.1	BF242905	214
212262_at	quaking homolog, KH domain RNA binding (mouse)	QKI	1,45	6,20387E-05	chr6q26-q27	AA149639	9444
244467_at	transmembrane protein 46-like	C22:CTA-250D10.9	1,45	0,01771496	chr22q13.2	AW136354	440829
210029_at	indoleamine-pyrrole 2,3 dioxygenase	INDO	1,45	0,002339924	chr8p12-p11	M34455	3620
208762_at	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	SUMO1	1,45	1,23834E-05	chr2q33	U83117	7341
205583_s_at	chromosome X open reading frame 45	CXorf45	1,45	7,53772E-08	chrXq23	NM_024810	79868
242136_x_at	Hypothetical LOC403340	MGC70870	1,45	0,04866097	---	T66145	403340
206214_at	phospholipase A2, group VII	PLA2G7	1,45	0,01789758	chr6p21.2-p12	NM_005084	7941
222637_at	COMM domain containing 10	COMMD10	1,45	7,30089E-05	chr5q23.1	BC005179	51397
224786_at	short coiled-coil protein	SCOC	1,45	5,93781E-11	chr4q31.1	AL133580	60592
219669_at	CD177 molecule	CD177	1,45	4,12384E-05	chr19q13.2	NM_020406	57126
234971_x_at	phospholipase C, delta 3	PLCD3	1,45	0,009070529	chr17q21.31	AI521584	113026
220958_at	unc-51-like kinase 4 (C. elegans)	ULK4	1,45	0,000925599	chr3p22.1	NM_017886	54986
217127_at	cystathionase (cystathionine gamma-lyase)	CTH	1,44	6,98108E-08	chr1p31.1	AL354872	1491
202289_s_at	transforming, acidic coiled-coil containing protein 2	TACC2	1,44	0,04644117	chr10q26	NM_006997	10579
225448_at	N-ethylmaleimide-sensitive factor attachment protein, gamma	NAPG	1,44	0,02702152	chr18p11.22	AL519376	8774
229804_x_at	COBW domain containing 1	CBWD1	1,44	0,02111859	chr2q14.1 /// chr9p24.3 /// chr9q12 /// chr9q13	AW169333	55871
205774_at	coagulation factor XII (Hageman factor)	F12	1,44	0,000204244	chr5q33-qter	NM_000505	2161
213245_at	adenylate cyclase 1 (brain)	ADCY1	1,44	0,03115297	chr7p13-p12	AL120173	107
219301_s_at	contactin associated protein-like 2	CNTNAP2	1,43	1,05752E-05	chr7q35-q36	AU144598	26047
209569_x_at	DNA segment on chromosome 4 (unique) 234 expressed sequence	D4S234E	1,43	0,01848932	chr4p16.3	NM_014392	27065
201505_at	laminin, beta 1	LAMB1	1,43	2,15974E-05	chr7q22	NM_002291	3912
241734_at	serum response factor binding protein 1	SRFBP1	1,43	0,007025972	chr5q23.1	AI391443	153443
219157_at	kelch-like 2, Mayven (Drosophila)	KLHL2	1,43	0,002082349	chr4q21.2	NM_007246	11275
226628_at	THO complex 2	THOC2	1,43	0,007613273	chrXq25-q26.3	BG259856	57187
203840_at	basic leucine zipper nuclear factor 1 (JEM-1)	BLZF1	1,43	0,01371854	chr1q24	NM_003666	8548

213348_at	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C	1,43	0,003104109	chr11p15.5	N33167	1028
205531_s_at	glutaminase 2 (liver, mitochondrial)	GLS2	1,43	0,04185452	chr12q13	NM_013267	27165
212440_at	putative nucleic acid binding protein RY-1	RY1	1,43	1,48015E-06	chr2p14	X76302	11017
206552_s_at	tachykinin, precursor 1	TAC1	1,43	0,03058159	chr7q21-q22	NM_003182	6863
230056_at	bromodomain PHD finger transcription factor	BPTF	1,43	0,002872774	chr17q24.3	AI735696	2186
225431_x_at	aminoacylase 1-like 2	ACY1L2	1,42	1,39484E-09	chr6q15	BE779764	135293
223551_at	protein kinase (cAMP-dependent, catalytic) inhibitor beta	PKIB	1,42	0,003632432	chr6q22.31	AF225513	5570
1555824_a_at	phosphofurin acidic cluster sorting protein 2	PACS2	1,42	0,00720534	chr14q32.33	AK098354	NA
222490_at	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	POLR3E	1,42	2,26539E-06	chr16p12.1	AK023160	55718
204619_s_at	versican	VCAN	1,42	0,00028905	chr5q14.3	BF590263	1462
216806_at	similar to laminin receptor 1 (ribosomal protein SA)	LOC652411	1,42	0,000121504	---	AL136306	NA
212637_s_at	WW domain containing E3 ubiquitin protein ligase 1	WWP1	1,42	0,0228142	chr8q21	AU155187	11059
224649_x_at	cyclin Y	CCNY	1,42	7,11554E-06	chr10p11.21	AI765014	219771
1557132_at	WD repeat domain 17	WDR17	1,42	0,01711633	chr4q34	BI713506	116966
228915_at	dachshund homolog 1 (Drosophila)	DACH1	1,42	0,005604599	chr13q22	AI650353	1602
226686_at	CDGSH iron sulfur domain 2	CISD2	1,41	0,000243655	chr4q24	AI188518	493856
233970_s_at	tRNA methyltransferase 6 homolog (S. cerevisiae)	TRMT6	1,41	7,42846E-05	chr20p12.3	AB032979	51605
217996_at	pleckstrin homology-like domain, family A, member 1	PHLDA1	1,41	0,009062491	chr12q15	AA576961	22822
219895_at	family with sequence similarity 70, member A	FAM70A	1,41	0,01950408	chrXq24	NM_017938	55026
232224_at	mannan-binding lectin serine peptidase 1	MASP1	1,41	0,00038423	chr3q27-q28	AI274095	5648
227180_at	ELOVL family member 7, elongation of long chain fatty acids (yeast)	ELOVL7	1,41	0,000795458	chr5q12.1	AW138767	79993
212353_at	sulfatase 1	SULF1	1,41	0,0186831	chr8q13.2-q13.3	AI479175	23213
231001_at	fin bud initiation factor	FIBIN	1,41	0,0244448	chr11p14.2	AI755024	387758
1558212_at	hypothetical LOC401491	FLJ35024	1,41	0,03966825	chr9p24.2	BC004474	401491
201701_s_at	progesterone receptor membrane component 2	PGRMC2	1,41	0,000842835	chr4q26	NM_006320	10424
Repressed transcripts							
207746_at	polymerase (DNA directed), theta	POLQ	-1,41	0,02882389	chr3q13.33	NM_014125	10721
215711_s_at	WEE1 homolog (S. pombe)	WEE1	-1,41	0,01792984	chr11p15.3-p15.1	AJ277546	7465
236966_at	armadillo repeat containing 8	ARMC8	-1,41	0,03713555	chr3q22.3	BF942281	347736
203343_at	UDP-glucose dehydrogenase	UGDH	-1,41	7,30089E-05	chr4p15.1	NM_003359	7358
231297_at	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	DOT1L	-1,41	0,002009508	chr19p13.3	AI479899	84444
228998_at	trinucleotide repeat containing 6B	TNRC6B	-1,41	0,02725063	chr22q13.1	AV693653	NA
214877_at	CDK5 regulatory subunit associated protein 1-like 1	CDKAL1	-1,41	0,002946474	chr6p22.3	BE794663	54901
222665_at	family with sequence similarity 82, member B	FAM82B	-1,41	0,000970234	chr8q21.3	AK000672	51115
219158_s_at	NMDA receptor regulated 1	NARG1	-1,42	9,95583E-05	chr4q31.1	NM_025085	80155
233827_s_at	suppressor of Ty 16 homolog (S. cerevisiae)	SUPT16H	-1,42	9,19268E-05	chr14q11.2	AK024072	11198
202647_s_at	neuroblastoma RAS viral (v-ras) oncogene homolog	NRAS	-1,42	4,41098E-07	chr1p13.2	NM_002524	4893
209680_s_at	kinesin family member C1	KIFC1	-1,42	0,001883455	chr6p21.3	BC000712	3833
221104_s_at	nipsnap homolog 3B (C. elegans)	NIPSNAP3B	-1,42	0,000181148	chr9q31.1	NM_018376	55335
214946_x_at	family with sequence similarity 21, member B /// family with sequence similarity 21, member A	FAM21A	-1,42	0,00174287	chr10q11.1 /// chr10q11.22 /// chr10q11.23	AV728658	387680
217811_at	selenoprotein T	SELT	-1,42	4,38967E-05	chr3q25.1	NM_016275	51714
1558561_at	histocompatibility (minor) 13	HM13	-1,42	0,04683448	chr20q11.21	AK074686	81502
202038_at	ubiquitination factor E4A (UFD2 homolog, yeast)	UBE4A	-1,42	3,10698E-06	chr11q23.3	NM_004788	9354
238443_at	transcription factor A, mitochondrial	TFAM	-1,42	0,000700031	chr10q21	BE546873	7019
201337_s_at	vesicle-associated membrane protein 3 (cellubrevin)	VAMP3	-1,42	4,74729E-06	chr1p36.23	NM_004781	9341
211228_s_at	RAD17 homolog (S. pombe)	RAD17	-1,42	0,000522092	chr5q13	AF085736	5884

200770_s_at	laminin, gamma 1 (formerly LAMB2)	LAMC1	-1,42	1,03906E-05	chr1q31	J03202	3915
224676_at	transmembrane emp24 protein transport domain containing 4	TMED4	-1,42	4,19116E-06	chr7p13	AI472339	222068
239950_at	homeo box A11, antisense	HOXA11S	-1,42	0,01358209	chr7p15.2	AW137133	NA
224064_s_at	dehydrodolichyl diphosphate synthase	DHDDS	-1,42	0,001325151	chr1p36.11	BC004117	79947
226506_at	thrombospondin, type I, domain containing 4	THSD4	-1,42	0,0272523	chr15q23	AI742570	79875
206852_at	EPH receptor A7	EPHA7	-1,42	0,001772201	chr6q16.1	NM_004440	2045
203885_at	RAB21, member RAS oncogene family	RAB21	-1,42	0,000107135	chr12q21.1	NM_014999	23011
225665_at	sterile alpha motif and leucine zipper containing kinase AZK	ZAK	-1,42	9,34549E-06	chr2q24.2	AI129320	51776
207464_at	S-adenosylhomocysteine hydrolase-like 1	AHCYL1	-1,42	0,002868094	chr1p13.2	NM_014121	10768
204369_at	phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	-1,43	0,001543983	chr3q26.3	NM_006218	5290
223274_at	transcription factor 19 (SC1)	TCF19	-1,43	0,000327912	chr6p21.3	BC002493	6941
203870_at	ubiquitin specific peptidase 46	USP46	-1,43	0,004005294	chr4q12	BE856374	64854
225440_at	1-acylglycerol-3-phosphate O-acyltransferase 3	AGPAT3	-1,43	0,000318038	chr21q22.3	BE737251	56894
212300_at	taxilin alpha	TXLNA	-1,43	0,000561495	chr1p35.1	AL049795	8668
213238_at	ATPase, Class V, type 10D	ATP10D	-1,43	0,01075097	chr4p12	AI478147	57205
200813_s_at	platelet-activating factor acetylhydrolase, isoform Ib	PAFAH1B1	-1,43	2,01466E-06	chr17p13.3	BE256969	5048
204233_s_at	choline kinase alpha	CHKA	-1,43	0,01358209	chr11q13.2	AI991328	1119
244698_at	CMT1A duplicated region transcript 4	CDRT4	-1,43	0,019582	chr17p12	AW297656	284040
203967_at	cell division cycle 6 homolog (S. cerevisiae)	CDC6	-1,43	4,02507E-06	chr17q21.3	U77949	990
221771_s_at	M-phase phosphoprotein, mpp8	HSMPP8	-1,43	0,01055064	chr13q12.11	BC003542	54737
228455_at	RNA binding motif protein 15	RBM15	-1,43	0,03856401	chr1p13	AI092824	9122
210756_s_at	Notch homolog 2 (Drosophila)	NOTCH2	-1,43	0,0004794	chr1p13-p11	AF308601	4853
221041_s_at	solute carrier family 17 (anion/sugar transporter), member 5	SLC17A5	-1,43	0,02680892	chr6q14-q15	NM_012434	26503
206500_s_at	chromosome 14 open reading frame 106	C14orf106	-1,43	0,01281857	chr14q21.3	NM_018353	55320
202526_at	SMAD family member 4	SMAD4	-1,43	0,007756548	chr18q21.1	U44378	4089
204341_at	tripartite motif-containing 16 /// tripartite motif-containing 16-like	TRIM16	-1,43	0,001045701	chr17p11.2	NM_006470	10626
211665_s_at	son of sevenless homolog 2 (Drosophila)	SOS2	-1,43	0,03830453	chr14q21	L20686	6655
209234_at	kinesin family member 1B	KIF1B	-1,43	0,000227303	chr1p36.2	BF939474	23095
232591_s_at	transmembrane protein 30A	TMEM30A	-1,43	0,000149105	chr6q14.1	AK022883	55754
211814_s_at	cyclin E2	CCNE2	-1,43	0,00813838	chr8q22.1	AF112857	9134
201779_s_at	ring finger protein 13	RNF13	-1,43	5,53854E-07	chr3q25.1	AF070558	11342
202470_s_at	cleavage and polyadenylation specific factor 6, 68kDa	CPSF6	-1,43	0,003259391	chr12q15	NM_007007	11052
1555112_a_at	chromosome 1 open reading frame 114	C1orf114	-1,43	0,001005364	chr1q24	BC026073	57821
212393_at	SET binding factor 1	SBF1	-1,43	0,001045701	chr22q13.33	AL096767	6305
218072_at	COMM domain containing 9	COMMD9	-1,43	0,000139015	chr11p13	NM_014186	29099
213679_at	tetratricopeptide repeat domain 30A	TTC30A	-1,43	0,002896609	chr2q31.2	AL049329	92104
224455_s_at	ADP-dependent glucokinase	ADPGK	-1,43	0,01025905	chr15q24.1	BC006112	83440
201668_x_at	myristoylated alanine-rich protein kinase C substrate	MARCKS	-1,44	0,00410563	chr6q22.2	AW163148	4082
1553117_a_at	serine/threonine kinase 38	STK38	-1,44	0,02196018	chr6p21	NM_007271	11329
225401_at	chromosome 1 open reading frame 85	C1orf85	-1,44	0,001050922	chr1q22	BF977145	112770
238416_x_at	conserved nuclear protein NHN1	NHN1	-1,44	0,03993592	chr16q24.2-q24.3	BF968618	124245
225162_at	SH3 domain protein D19	SH3D19	-1,44	0,001025303	chr4q31.3	BG285417	152503
222476_at	CCR4-NOT transcription complex, subunit 6	CNOT6	-1,44	3,34504E-05	chr5q35.3	AA633196	57472
1554794_a_at	ubiquitin protein ligase E3C	UBE3C	-1,44	8,74732E-05	chr7q36.3	BC014029	9690
219493_at	SHC SH2-domain binding protein 1	SHCBP1	-1,44	8,22828E-09	chr16q11.2	NM_024745	79801

211984_at	calmodulin 1 (phosphorylase kinase, delta)	CALM1	-1,44	4,74729E-06	chr14q24-q31	AI653730	801
217620_s_at	phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	-1,44	0,02108757	chr3q22.3	AA805318	5291
218192_at	inositol hexaphosphate kinase 2	IHPK2	-1,44	0,002747842	chr3p21.31	NM_016291	51447
218362_s_at	DIS3 mitotic control homolog (S. cerevisiae)	DIS3	-1,44	0,000109138	chr13q22.1	NM_014953	22894
214446_at	elongation factor, RNA polymerase II, 2	ELL2	-1,44	0,02784748	chr5q15	NM_012081	22936
202247_s_at	metastasis associated 1	MTA1	-1,44	0,003368513	chr14q32.3	BE561596	9112
206184_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	CRKL	-1,44	0,01493411	chr22q11|22q11.21	NM_005207	1399
202719_s_at	testis derived transcript (3 LIM domains)	TES	-1,44	4,19116E-06	chr7q31.2	BC001451	26136
200800_s_at	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	HSPA1A	-1,44	0,001716531	chr6p21.3	NM_005345	3303
1566324_a_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF	-1,44	0,01736716	chr16q22-q23	AA442149	4094
203051_at	bromo adjacent homology domain containing 1	BAHD1	-1,45	0,004474236	chr15q15.1	NM_014952	22893
34858_at	potassium channel tetramerisation domain containing 2	KCTD2	-1,45	0,01618524	chr17q25.1	D79998	23510
226647_at	transmembrane protein 25	TMEM25	-1,45	0,0339796	chr11q23.3	AL562445	84866
208493_at	homeobox A11	HOXA11	-1,45	0,008444999	chr7p15-p14	NM_005523	3207
212602_at	WD repeat and FYVE domain containing 3	WDFY3	-1,45	0,02761309	chr4q21.23	AI806395	23001
240551_at	zinc finger and BTB domain containing 45	ZBTB45	-1,45	0,000795458	chr19q13.43	BE550601	84878
212150_at	KIAA0143 protein	KIAA0143	-1,45	0,001611241	chr8q24.22	AA805651	23167
201775_s_at	KIAA0494	KIAA0494	-1,45	0,03035844	chr1pter-p22.1	AA676790	9813
219978_s_at	nucleolar and spindle associated protein 1	NUSAP1	-1,45	6,62059E-06	chr15q15.1	NM_018454	51203
1555408_at	B melanoma antigen family, member 4	BAGE2	-1,45	4,43152E-26	chr21p /// chr21p11.1	AF218570	85317
200672_x_at	spectrin, beta, non-erythrocytic 1	SPTBN1	-1,45	0,008343976	chr2p21	NM_003128	6711
1564282_a_at	hypothetical protein LOC285708	LOC285708	-1,45	0,01001464	chr5q21.2	AK092078	285708
224149_x_at	sarcolemma associated protein	SLMAP	-1,46	4,28366E-05	chr3p21.2-p14.3	AF304450	7871
234929_s_at	spermatogenesis associated 7	SPATA7	-1,46	0,00048746	chr14q31.3	AF144488	55812
1554397_s_at	UEV and lactate/malate dehyrogenase domains	UEVLD	-1,46	0,000796013	chr11p15.1	BC011011	55293
224097_s_at	F11 receptor	F11R	-1,46	0,03032018	chr1q21.2-q21.3	AF191495	50848
204426_at	transmembrane emp24 domain trafficking protein 2	TMED2	-1,46	2,59265E-06	chr12q24.31	NM_006815	10959
1552627_a_at	Rho GTPase activating protein 5	ARHGAP5	-1,46	0,04733453	chr14q12	NM_001173	394
209897_s_at	slit homolog 2 (Drosophila)	SLIT2	-1,46	5,09069E-06	chr4p15.2	AF055585	9353
227713_at	katanin p60 subunit A-like 1	KATNAL1	-1,46	0,001057542	chr13q12.3	AI807482	84056
225046_at	Hypothetical gene supported by AL713796	LOC389831	-1,46	0,000959188	---	AL521247	389831
204833_at	ATG12 autophagy related 12 homolog (S. cerevisiae)	ATG12	-1,46	1,31114E-05	chr5q21-q22	NM_004707	9140
215215_s_at	exonuclease NEF-sp	LOC81691	-1,46	0,003746964	chr16p12.2	AC004381	6296
228282_at	Major facilitator superfamily domain containing 8	MFSD8	-1,46	0,002087986	chr4q28.1-q28.2	AW611550	256471
1557950_at	serologically defined colon cancer antigen 1	SDCCAG1	-1,46	0,000604683	chr14q22	BF984340	9147
38241_at	butyrophilin, subfamily 3, member A3	BTN3A3	-1,46	0,02147843	chr6p21.3	U90548	10384
1554251_at	heterochromatin protein 1, binding protein 3	HP1BP3	-1,46	0,01810978	chr1p36.12	BC022342	50809
226095_s_at	ataxin 1-like	ATXN1L	-1,46	4,92926E-05	chr16q22.3	AW138861	146517
220299_at	spermatogenesis associated 6	SPATA6	-1,46	0,02125522	chr1p33	NM_019073	54558
217539_at	chromosome 18 open reading frame 25	C18orf25	-1,46	0,0198719	chr18q21.1	W28849	147339
242984_at	muskelin 1, intracellular mediator containing kelch motifs	MKLN1	-1,46	0,02945376	chr7q32	BF723626	4289
214672_at	tubulin tyrosine ligase-like family, member 5	TTLL5	-1,46	0,001633772	chr14q24.3	AB023215	23093
228191_at	feline leukemia virus subgroup C cellular receptor 1	FLVCR1	-1,46	9,12501E-06	chr1q32.3	AA206016	NA
226648_at	hypoxia-inducible factor 1, alpha subunit inhibitor	HIF1AN	-1,47	5,53563E-05	chr10q24	AI769745	NA
206686_at	pyruvate dehydrogenase kinase, isozyme 1	PDK1	-1,47	0,00095555	chr2q31.1	NM_002610	5163
233141_s_at	suppression of tumorigenicity 7 like	ST7L	-1,47	0,03968098	chr1p13.2	AK021719	54879
236313_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	-1,47	0,01079108	chr9p21	AW444761	1030

222661_at	angiogenic factor with G patch and FHA domains 1	AGGF1	-1,47	4,3263E-06	chr5q13.3	AA528017	55109
208926_at	sialidase 1 (lysosomal sialidase)	NEU1	-1,47	0,000706064	chr6p21.3	U84246	4758
242963_at	sphingomyelin synthase 2	SGMS2	-1,47	0,006199709	chr4q25	AI160370	166929
223582_at	G protein-coupled receptor 98	GPR98	-1,47	0,007613273	chr5q13	AF055084	84059
202626_s_at	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	-1,47	0,02527125	chr8q13	NM_002350	4067
229664_at	mitogen-activated protein kinase 8	MAPK8	-1,47	0,008736427	chr10q11.22	AI379407	5599
225366_at	phosphoglucomutase 2	PGM2	-1,47	0,000112995	chr4p14	AI652855	55276
1553338_at	chromosome 1 open reading frame 55	C1orf55	-1,47	0,000190745	chr1q42.12	NM_152608	163859
232708_at	galactose-1-phosphate uridylyltransferase	GALT	-1,47	0,03090305	chr9p13	AA453223	2592
215991_s_at	KIAA0090	KIAA0090	-1,47	0,01435044	chr1p36.13	AU121504	23065
232553_at	phosphate cytidylyltransferase 1, choline, beta	PCYT1B	-1,48	0,004769376	chrXp22.11	AI857508	9468
200988_s_at	proteasome (prosome, macropain) activator subunit 3	PSME3	-1,48	0,02473125	chr17q21	NM_005789	10197
203630_s_at	component of oligomeric golgi complex 5	COG5	-1,48	6,94748E-06	chr7q22-q31	NM_006348	10466
225414_at	ring finger protein 149	RNF149	-1,48	7,79839E-06	chr2q11.2	AL558987	284996
207219_at	zinc finger protein 643	ZNF643	-1,48	0,01862546	chr1p34.2	NM_023070	65243
210224_at	major histocompatibility complex, class I-related	MR1	-1,48	0,02091254	chr1q25.3	AF031469	3140
226150_at	phosphatidic acid phosphatase type 2 domain containing 1B	PPAPDC1B	-1,48	0,000387686	chr8p12	BF111651	84513
216266_s_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1	ARFGEF1	-1,48	5,87162E-05	chr8q13	AK025637	10565
207590_s_at	centromere protein I	CENPI	-1,48	0,0389701	chrXq22.1	NM_006733	2491
228725_x_at	protein arginine methyltransferase 2	PRMT2	-1,48	1,05836E-07	chr21q22.3	BF003112	3275
214918_at	heterogeneous nuclear ribonucleoprotein M	HNRPM	-1,48	0,03422539	chr19p13.3-p13.2	AK024911	4670
201335_s_at	Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	-1,48	0,01347745	chr11q23.3	NM_015313	23365
238421_at	Ring finger and CCCH-type zinc finger domains 2	RC3H2	-1,49	0,02173186	chr9q34	N86386	54542
210484_s_at	tumor necrosis factor receptor superfamily, member 10c	TNFRSF10C	-1,49	0,04039031	chr8p21.2 /// chr8p22-p21	BC005043	8794
202129_s_at	RIO kinase 3 (yeast)	RIOK3	-1,49	4,74729E-06	chr18q11.2	AW006290	8780
213039_at	rho/rac guanine nucleotide exchange factor (GEF) 18	ARHGEF18	-1,49	9,83585E-06	chr19p13.3	AB011093	23370
219774_at	coiled-coil domain containing 93	CCDC93	-1,49	0,003993352	chr2q14.1	NM_019044	54520
1555326_a_at	ADAM metallopeptidase domain 9 (meltrin gamma)	ADAM9	-1,49	4,68314E-06	chr8p11.23	AF495383	8754
235024_at	PHD finger protein 17	PHF17	-1,49	0,000245434	chr4q26-q27	AI868315	79960
209878_s_at	v-rel reticuloendotheliosis viral oncogene homolog A	RELA	-1,49	0,02293315	chr11q13	M62399	5970
236227_at	transmembrane protein 161B	TMEM161B	-1,49	0,01464503	chr5q14.3	BF106392	153396
231886_at	similar to hypothetical protein LOC284701	DKFZP434B2016	-1,49	0,0191567	chr16q24.3	AL137655	388572
223594_at	transmembrane protein 117	TMEM117	-1,49	0,01912392	chr12q12	AL136855	84216
220658_s_at	aryl hydrocarbon receptor nuclear translocator-like 2	ARNTL2	-1,49	0,03071038	chr12p12.2-p11.2	NM_020183	56938
1555225_at	chromosome 1 open reading frame 43	C1orf43	-1,49	0,001939665	chr1q21.2	BC008306	25912
204357_s_at	LIM domain kinase 1	LIMK1	-1,50	0,03838182	chr7q11.23	NM_002314	3984
206113_s_at	RAB5A, member RAS oncogene family	RAB5A	-1,50	8,32178E-06	chr3p24-p22	NM_004162	5868
205409_at	FOS-like antigen 2	FOSL2	-1,50	0,01693318	chr2p23.3	NM_005253	2355
238427_at	GrpE-like 2, mitochondrial (E. coli)	GRPEL2	-1,50	0,03499667	chr5q33.1	C15005	134266
202064_s_at	sel-1 suppressor of lin-12-like (C. elegans)	SEL1L	-1,50	0,008033444	chr14q24.3-q31	AF052059	6400
226038_at	LON peptidase N-terminal domain and ring finger 1	LONRF1	-1,50	5,6818E-05	chr8p23.1	BF680438	91694
223251_s_at	ankyrin repeat domain 10	ANKRD10	-1,50	0,000632732	chr13q34	BC001727	55608
203736_s_at	PTPRF interacting protein, binding protein 1 (liprin beta 1)	PPFIBP1	-1,50	0,005172444	chr12p11.23-p11.22	NM_003622	8496
206383_s_at	GTPase activating protein (SH3 domain) binding protein 2	G3BP2	-1,50	4,29523E-05	chr4q21.1	NM_012297	9908
1555564_a_at	complement factor I	CFI	-1,50	0,01388627	chr4q25	BC020718	3426

213805_at	abhydrolase domain containing 5	ABHD5	-1,51	0,007336186	chr3p21	AI692428	51099
208710_s_at	adaptor-related protein complex 3, delta 1 subunit	AP3D1	-1,51	0,000795458	chr19p13.3	AI424923	8943
208902_s_at	ribosomal protein S28	RPS28	-1,51	0,003151686	chr19p13.2	BF431363	256949
229559_at	hypothetical protein FLJ40125	FLJ40125	-1,51	0,01013932	chr19q13.32	BE732320	147699
235588_at	establishment of cohesion 1 homolog 2 (S. cerevisiae)	ESCO2	-1,51	0,02198536	chr8p21.1	AA740849	157570
202316_x_at	ubiquitination factor E4B (UFD2 homolog, yeast)	UBE4B	-1,51	0,006460136	chr1p36.3	AW241715	10277
238759_at	coiled-coil domain containing 88A	CCDC88A	-1,51	0,004778953	chr2p16.1	AI681810	55704
1570523_s_at	ATG10 autophagy related 10 homolog (S. cerevisiae)	ATG10	-1,51	0,000886153	chr5q14.2	AF318326	83734
1554417_s_at	anterior pharynx defective 1 homolog A (C. elegans)	APH1A	-1,51	5,35116E-05	chr1p36.13-q31.3	AY113699	51107
208997_s_at	uncoupling protein 2 (mitochondrial, proton carrier)	UCP2	-1,51	0,000439407	chr11q13	U82819	7351
217790_s_at	signal sequence receptor, gamma	SSR3	-1,51	0,000974794	chr3q25.31	NM_007107	6747
212851_at	DCN1, defective in cullin neddylation 1, domain containing 4	DCUN1D4	-1,51	2,23297E-05	chr4q12	AA194584	23142
214056_at	Myeloid cell leukemia sequence 1 (BCL2-related)	MCL1	-1,52	0,02556069	chr1q21	BF981280	4170
203628_at	insulin-like growth factor 1 receptor	IGF1R	-1,52	0,008283178	chr15q26.3	H05812	3480
216855_s_at	heterogeneous nuclear ribonucleoprotein U	HNRNPU	-1,52	0,02399395	chr1q44	D13413	3192
204568_at	KIAA0831	KIAA0831	-1,52	0,003746964	chr14q22.3	NM_014924	22863
208853_s_at	calnexin	CANX	-1,52	1,74647E-11	chr5q35	L18887	821
230534_at	hypothetical protein MGC15634	MGC15634	-1,52	0,000157385	chr1q42.13	AW025362	84841
203096_s_at	Rap guanine nucleotide exchange factor (GEF) 2	RAPGEF2	-1,52	0,04667966	chr4q32.1	BF439282	9693
209456_s_at	F-box and WD repeat domain containing 11	FBXW11	-1,52	0,000875339	chr5q35.1	AB033281	23291
215891_s_at	GM2 ganglioside activator	GM2A	-1,52	0,005428052	chr5q31.3-q33.1	X61094	2760
205321_at	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	EIF2S3	-1,52	4,67781E-06	chrXp22.2-p22.1	NM_001415	1968
217173_s_at	low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	-1,52	0,03445698	chr19p13.3	S70123	3949
206139_at	phosphatidylinositol 4-kinase, catalytic, beta	PI4KB	-1,52	0,004769376	chr1q21	NM_002651	5298
76897_s_at	FK506 binding protein 15, 133kDa	FKBP15	-1,52	0,02907499	chr9q32	AA628140	23307
212690_at	DDHD domain containing 2	DDHD2	-1,52	1,58801E-07	chr8p12	AB018268	23259
210653_s_at	branched chain keto acid dehydrogenase E1, beta polypeptide	BCKDHB	-1,52	0,000107549	chr6q13-q15	M55575	594
207403_at	insulin receptor substrate 4	IRS4	-1,52	1,90851E-05	chrXq22.3	NM_003604	8471
230163_at	Hypothetical protein LOC143381	LOC143381	-1,53	0,0109085	chr10q26.11	AW263087	2674
202249_s_at	WD repeat domain 42A	WDR42A	-1,53	0,000063039	chr1q22-q23	AU146233	50717
212253_x_at	dystonin	DST	-1,53	0,000112626	chr6p12.1	BG253119	667
1553962_s_at	ras homolog gene family, member B	RHOB	-1,53	0,007336186	chr2p24	BI668074	388
217859_s_at	solute carrier family 39 (zinc transporter), member 9	SLC39A9	-1,53	0,001331983	chr14q24.1	NM_018375	55334
226557_at	tetratricopeptide repeat domain 5	TTC5	-1,53	0,008120254	chr14q11.2	AW044606	91875
212899_at	cell division cycle 2-like 6 (CDK8-like)	CDC2L6	-1,53	0,000543984	chr6q21	AB028951	23097
221765_at	UDP-glucose ceramide glucosyltransferase	UGCG	-1,53	0,005910053	chr9q31	AI378044	7357
202667_s_at	solute carrier family 39 (zinc transporter), member 7	SLC39A7	-1,53	5,63976E-05	chr6p21.3	NM_006979	7922
212619_at	KIAA0286 protein	KIAA0286	-1,53	1,01893E-05	chr12q13.3	AW205215	23306
224078_at	hippocampus abundant gene transcript-like 2	HIATL2	-1,53	0,000390116	chr9q22.33	BC005058	84278
211068_x_at	family with sequence similarity 21, member C	FAM21C	-1,53	0,000756646	chr10q11.1 /// chr10q11.23	BC006456	253725
217310_s_at	forkhead box J3	FOXJ3	-1,53	0,04061638	chr1pter-q31.3	AK027075	22887
235333_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6	-1,53	4,19116E-06	chr18q11	BG503479	9331
225375_at	chromosome 17 open reading frame 32	C17orf32	-1,53	0,001032529	chr17q11.2	AW975808	147007
201638_s_at	cleavage and polyadenylation specific factor 1, 160kDa	CPSF1	-1,54	0,01247134	chr8q24.23	BE676642	29894

218643_s_at	cysteine-rich PDZ-binding protein	CRIPT	-1,54	6,02079E-05	chr2p21	NM_014171	9419
1555469_a_at	cytoplasmic linker associated protein 2	CLASP2	-1,54	0,003046698	chr3p22.3	BC029035	23122
232235_at	dermatan sulfate epimerase-like	DSEL	-1,54	0,04690383	chr18q22.1	AK021539	92126
222507_s_at	TMEM9 domain family, member B	TMEM9B	-1,54	3,6766E-06	chr11p15.3	AI188389	56674
230697_at	Bardet-Biedl syndrome 5	BBS5	-1,54	0,04123778	chr2q31.1	AW418788	129880
202262_x_at	dimethylarginine dimethylaminohydrolase 2	DDAH2	-1,54	0,01780729	chr6p21.3	NM_013974	23564
232981_s_at	AP1 gamma subunit binding protein 1	AP1GBP1	-1,55	0,000103659	chr17q12	AF090924	11276
231793_s_at	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	CAMK2D	-1,55	0,001887304	chr4q26	AA448956	817
204317_at	G-2 and S-phase expressed 1	GTSE1	-1,55	0,000107135	chr22q13.2-q13.3	BF305380	51512
221220_s_at	SCY1-like 2 (S. cerevisiae)	SCYL2	-1,55	0,000484192	chr12q23.1	NM_017988	55681
226155_at	KIAA1600	KIAA1600	-1,56	0,000282217	chr10q25.3	AB046820	57700
219760_at	lin-7 homolog B (C. elegans)	LIN7B	-1,56	0,008634456	chr19q13.3	NM_022165	64130
201159_s_at	N-myristoyltransferase 1	NMT1	-1,56	0,005628019	chr17q21.31	NM_021079	4836
217770_at	phosphatidylinositol glycan anchor biosynthesis, class T	PIGT	-1,56	3,16816E-08	chr20q12-q13.12	NM_015937	51604
225631_at	KIAA1706 protein	KIAA1706	-1,56	0,02903477	chr7p14	BE501865	80820
214157_at	GNAS complex locus	GNAS	-1,56	0,002132488	chr20q13.3	AA401492	2778
231997_at	tubulin folding cofactor E-like	TBCEL	-1,56	0,04749948	chr11q23.3	R69910	219899
237856_at	RAP1, GTP-GDP dissociation stimulator 1	RAP1GDS1	-1,56	0,00166422	chr4q23-q25	AI052055	5910
200742_s_at	tripeptidyl peptidase I	TPP1	-1,56	0,000238583	chr11p15	BG231932	1200
225930_at	NFKB inhibitor interacting Ras-like 1	NKIRAS1	-1,56	8,34663E-05	chr3p24.2	AI970120	28512
225613_at	microtubule associated serine/threonine kinase family member 4	MAST4	-1,56	0,001325686	chr5q12.3	AI096389	23227
228569_at	poly(A) polymerase alpha	PAPOLA	-1,56	3,03777E-08	chr14q32.31	AV683473	10914
1552612_at	CDC42 small effector 2	CDC42SE2	-1,56	0,01757326	chr5q31.1	NM_020240	NA
243225_at	hypothetical protein LOC283481	LOC283481	-1,57	0,01797719	chr13q33.1	AI042341	2259
226583_at	FLJ40142 protein	FLJ40142	-1,57	0,000118618	chr12q24.11	AL560962	400073
204659_s_at	growth factor, augmenter of liver regeneration	GFER	-1,57	0,02435136	chr16p13.3-p13.12	AF124604	2671
229946_at	p20	LOC130074	-1,57	0,003726664	chr2q21.1	BF056651	389039
210664_s_at	tissue factor pathway inhibitor	TFPI	-1,57	0,00050553	chr2q32	AF021834	7035
221673_s_at	casein kinase 1, gamma 1	CSNK1G1	-1,57	0,001795443	chr15q22.1-q22.31	AB042563	53944
224304_x_at	ninein (GSK3B interacting protein)	NIN	-1,57	0,002339924	chr14q22.1	AF223939	51199
236328_at	zinc finger protein 285A	ZNF285A	-1,57	0,000352184	---	AW513227	26974
1553148_a_at	sorting nexin 13	SNX13	-1,57	0,003909016	chr7p21.1	R75838	23161
233882_s_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	SEMA6D	-1,57	0,02000088	chr15q21.1	AK022831	80031
206777_s_at	crystallin, beta B2	CRYBB2	-1,57	2,07116E-06	chr22q11.2-q12.1|22q11.23	NM_000496	1415
214895_s_at	ADAM metallopeptidase domain 10	ADAM10	-1,58	0,002980303	chr15q2|15q22	AU135154	102
1552660_a_at	chromosome 5 open reading frame 22	C5orf22	-1,58	2,76897E-09	chr5p13.3	BC021215	55322
211085_s_at	serine/threonine kinase 4	STK4	-1,58	0,03968098	chr20q11.2-q13.2	Z25430	6789
212157_at	syndecan 2	SDC2	-1,58	5,21997E-05	chr8q22-q23	BE048514	6383
209629_s_at	nuclear transport factor 2-like export factor 2	NXT2	-1,58	0,00062672	chrXq22.3	AF201942	55916
1554481_a_at	erythrocyte membrane protein band 4.1	EPB41	-1,58	0,006885592	chr1p33-p32	BC039079	2035
1556551_s_at	solute carrier family 39 (zinc transporter), member 6	SLC39A6	-1,59	3,41195E-08	chr18q12.2	BQ027619	25800
1564066_at	spermatogenesis associated, serine-rich 1	C6orf137	-1,59	0,01017889	chr6p21.1	AL833884	441151
220458_at	FLJ10246	FLJ10246	-1,59	5,53854E-07	chr5p12	NM_018038	55104
215501_s_at	dual specificity phosphatase 10	DUSP10	-1,59	0,002728423	chr1q41	AK022513	11221
1553691_at	beta-1,3-N-acetylgalactosaminyltransferase 2	B3GALNT2	-1,60	0,00023597	chr1q42.3	NM_152490	148789

216125_s_at	RAN binding protein 9	RANBP9	-1,60	0,000145474	chr6p23	AF064606	10048
231921_at	chromosome 2 open reading frame 37	C2orf37	-1,60	2,73216E-05	chr2q31.1	AK021599	80067
235683_at	sestrin 3	SESN3	-1,60	0,000591803	chr11q21	BF685808	143686
226709_at	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ROBO2	-1,60	0,01077193	chr3p12.3	BE858548	6092
243937_x_at	centaurin, gamma-like family, member 2	CTGLF2	-1,60	0,02356204	chr10q22.2	BF436377	439983
228816_at	hypothetical protein LOC92270	LOC92270	-1,60	0,005537472	chr5q14.2	AK022625	92270
212478_at	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	RMND5A	-1,60	0,000964254	chr2p11.2	H65865	64795
222074_at	uroporphyrinogen decarboxylase	UROD	-1,61	0,00850892	chr1p34	AW614435	7389
208899_x_at	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	ATP6V1D	-1,61	2,93595E-11	chr14q23-q24.2	AF100741	51382
207826_s_at	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	-1,61	3,1236E-11	chr1p36.13-p36.12	NM_002167	3399
220260_at	TBC1 domain family, member 19	TBC1D19	-1,61	0,02599533	chr4p15.2	NM_018317	55296
211602_s_at	transient receptor potential cation channel, subfamily C, member 1	TRPC1	-1,61	4,83761E-06	chr3q22-q24	U31110	7220
225337_at	abhydrolase domain containing 2	ABHD2	-1,61	0,003751667	chr15q26.1	AI346910	11057
223078_s_at	tropomodulin 3 (ubiquitous)	TMOD3	-1,62	0,000880301	chr15q21.1-q21.2	AF177171	29766
1558807_at	ATPase family, AAA domain containing 2B	ATAD2B	-1,62	0,04231011	chr2p24.1-p23.3	AK094821	54454
202128_at	KIAA0317	KIAA0317	-1,62	5,35507E-06	chr14q24.3	NM_014821	9870
219222_at	ribokinase	RBKS	-1,63	0,001169908	chr2p23.3	NM_022128	64080
210734_x_at	MYC associated factor X	MAX	-1,63	0,000168058	chr14q23	M64240	4149
1563687_a_at	FRY-like	FRYL	-1,63	0,01227528	chr4p12	U80082	23045
209862_s_at	centrosomal protein 57kDa	CEP57	-1,63	2,38533E-08	chr11q21	BC001233	9702
212337_at	taurine upregulated gene 1	TUG1	-1,63	1,48699E-12	chr22q12.2	AI687738	55000
204209_at	phosphate cytidylyltransferase 1, choline, alpha	PCYT1A	-1,63	0,007418134	chr3q29	AI638771	5130
225333_at	zinc finger protein 496	ZNF496	-1,64	0,02006291	chr1q44	AI218383	84838
224868_at	zinc finger, DHHC-type containing 5	ZDHHC5	-1,64	3,08543E-05	chr11q12.1	BE961925	25921
235314_at	ribosomal protein L32 pseudogene 3	RPL32P3	-1,64	0,04383745	chr3q21.3	W73195	132241
226545_at	CD109 molecule	CD109	-1,64	1,17177E-05	chr6q13	AL110152	135228
222153_at	myelin expression factor 2	MYEF2	-1,64	0,02593568	chr15q21.1	AK023133	50804
201942_s_at	carboxypeptidase D	CPD	-1,64	1,87554E-06	chr17q11.2	D85390	1362
200952_s_at	cyclin D2	CCND2	-1,65	0,002716492	chr12p13	AI635187	894
205535_s_at	protocadherin 7	PCDH7	-1,65	1,29253E-06	chr4p15	NM_002589	5099
223200_s_at	large subunit GTPase 1 homolog (S. cerevisiae)	LSG1	-1,65	2,61964E-06	chr3q29	AI219740	55341
218282_at	ER degradation enhancer, mannosidase alpha-like 2	EDEM2	-1,66	0,000123805	chr20q11.22	NM_018217	55741
229178_at	hypothetical protein LOC145786	LOC145786	-1,66	0,003860442	chr15q21.1	AV699825	145786
203639_s_at	fibroblast growth factor receptor 2	FGFR2	-1,66	6,3508E-05	chr10q26	M80634	2263
203641_s_at	COBL-like 1	COBLL1	-1,66	0,01435044	chr2q24.3	BF002844	22837
223241_at	sorting nexin 8	SNX8	-1,66	0,04803939	chr7p22.2	AF121858	29886
216549_s_at	TBC1 domain family, member 22B	TBC1D22B	-1,66	0,01039667	chr6p21.2	AL096712	9025
213073_at	zinc finger, FYVE domain containing 26	ZFYVE26	-1,66	6,4179E-05	chr14q24.1	AB002319	23503
203811_s_at	DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	-1,66	9,83585E-06	chr1p31.1	NM_007034	11080
229611_at	leishmanolysin-like (metallopeptidase M8 family)	LMLN	-1,66	0,002009508	chr3q29	BF056991	89782
208530_s_at	retinoic acid receptor, beta	RARB	-1,67	9,13731E-05	chr3p24	NM_016152	5915
202453_s_at	general transcription factor IIH, polypeptide 1, 62kDa	GTF2H1	-1,67	1,1146E-06	chr11p15.1-p14	NM_005316	2965
231926_at	epidermal growth factor receptor pathway substrate 15-like 1	EPS15L1	-1,67	0,00120471	chr19p13.11	AK023744	58513
1565651_at	ADP-ribosylation factor 1	ARF1	-1,68	0,009277492	chr1q42	BI868311	NA

240793_at	Titin	TTN	-1,68	0,005818769	chr2q31	BF224054	7273
1553978_at	myocyte enhancer factor 2B	MEF2B	-1,68	4,04127E-07	chr19p12	BC010931	4207
213982_s_at	RAB GTPase activating protein 1-like	RABGAP1L	-1,69	0,02332989	chr1q24	BG107203	9910
214474_at	protein kinase, AMP-activated, beta 2 non-catalytic subunit	PRKAB2	-1,69	1,70335E-05	chr1q21.1	NM_005399	5565
214098_at	KIAA1107	KIAA1107	-1,69	0,002900858	chr1p22.1	AB029030	23285
207073_at	cyclin-dependent kinase-like 2 (CDC2-related kinase)	CDKL2	-1,69	0,01043808	chr4q21.1	NM_003948	8999
203248_at	zinc finger protein 24	ZNF24	-1,71	7,53772E-08	chr18q12	NM_006965	7572
1569057_s_at	melanoma inhibitory activity family, member 3	MIA3	-1,71	1,40669E-07	chr1q41	BC031805	375056
201988_s_at	cAMP responsive element binding protein-like 2	CREBL2	-1,71	2,49633E-07	chr12p13	BF438056	1389
235955_at	MARVEL domain containing 2	MARVELD2	-1,72	0,000482828	chr5q13.2	N57927	153562
1555144_at	ADP-ribosylation factor-like 17	ARL17	-1,72	5,07006E-05	chr17q21.31	BC020869	51326
224835_at	hypothetical protein KIAA1434	RP5-1022P6.2	-1,72	6,24189E-07	chr20p12.3	AL109935	1980
202124_s_at	trafficking protein, kinesin binding 2	TRAK2	-1,73	0,000361362	chr2q33	AV705253	66008
200935_at	calreticulin	CALR	-1,73	4,1697E-12	chr19p13.3-p13.2	NM_004343	811
213472_at	heterogeneous nuclear ribonucleoprotein H1 (H)	HNRPH1	-1,73	0,000736931	chr5q35.3	AI022387	3187
210790_s_at	SAR1 gene homolog A (S. cerevisiae)	SAR1A	-1,74	1,69374E-07	chr10q22.1	BC003658	56681
222716_s_at	sorting nexin 24	SNX24	-1,74	7,33181E-07	chr5q23.2	AU144093	28966
200615_s_at	adaptor-related protein complex 2, beta 1 subunit	AP2B1	-1,74	1,80525E-13	chr17q11.2-q12	AL567295	163
235016_at	receptor accessory protein 3	REEP3	-1,75	0,000123748	chr10q21.3	AL118571	221035
220019_s_at	zinc finger protein 224	ZNF224	-1,75	0,004748773	chr19q13.2	NM_005774	7767
203758_at	cathepsin O	CTSO	-1,75	0,001592126	chr4q31-q32	AV729484	1519
1556344_at	hypothetical LOC150051	LOC150051	-1,75	7,10884E-05	chr21q22.11	BU621258	150051
1568873_at	zinc finger protein 519	ZNF519	-1,75	0,01062275	chr18p11.21	BC010705	162655
226570_at	ATPase, Na+/K+ transporting, beta 3 polypeptide	ATP1B3	-1,76	0,003370107	chr3q23	BF059073	483
221185_s_at	IQ motif containing G	IQCG	-1,77	0,000123748	chr3q29	NM_025111	84223
218817_at	signal peptidase complex subunit 3 homolog (S. cerevisiae)	SPCS3	-1,79	6,126E-06	chr4q34.2	NM_021928	60559
1552481_s_at	mannosidase, alpha, class 1A, member 2	MAN1A2	-1,79	4,92926E-05	chr1p13	NM_006699	10905
208430_s_at	dystrobrevin, alpha	DTNA	-1,79	0,000834052	chr18q12	NM_001390	1837
230285_at	hypothetical protein DKFZp313A2432	DKFZp313A2432	-1,80	5,7047E-07	chr11p14.2	BF447829	258010
222853_at	fibronectin leucine rich transmembrane protein 3	FLRT3	-1,80	3,10084E-09	chr20p11	N71923	23767
219632_s_at	transient receptor potential cation channel, subfamily V, member 1	TRPV1	-1,81	0,01022748	chr17p13.3	AF196175	7442
205868_s_at	protein tyrosine phosphatase, non-receptor type 11	PTPN11	-1,81	5,92176E-07	chr12q24	L07527	5781
202136_at	zinc finger, MYND domain containing 11	ZMYND11	-1,82	1,03655E-13	chr10p14	BE250417	10771
1559469_s_at	signal-induced proliferation-associated 1 like 2	SIPA1L2	-1,85	0,001581097	chr1q42.2	BC006013	57568
244481_at	Solute carrier family 25, member 24	SLC25A24	-1,86	0,003230707	chr1p13.3	BF196523	29957
1566403_at	small nucleolar RNA, H/ACA box 68	SNORA68	-1,87	2,07116E-06	chr19p13	Y11162	26780
203834_s_at	trans-golgi network protein 2	TGOLN2	-1,88	0,000653768	chr2p11.2	NM_006464	10618
204047_s_at	phosphatase and actin regulator 2	PHACTR2	-1,89	0,01414782	chr6q24.2	AW295193	9749
1552737_s_at	WW domain containing E3 ubiquitin protein ligase 2	WWP2	-1,89	1,64076E-05	chr16q22.1	NM_007014	11060
1569652_at	myeloid/lymphoid or mixed-lineage leukemia	MLLT3	-1,89	0,04939732	chr9p22	BC030550	4300
242812_at	Tripartite motif-containing 26	TRIM26	-1,90	0,03402253	chr6p21.3	AW294604	414777
1560017_at	transmembrane and tetratricopeptide repeat containing 3	TMTC3	-1,91	0,02603392	chr12q21.32	AK074973	160418
216250_s_at	leupaxin	LPXN	-1,91	0,009725719	chr11q12.1	X77598	9404
215358_x_at	zinc finger protein 37B	ZNF37B	-1,91	4,51946E-05	chr10q11.21	AK026980	256112
206241_at	karyopherin alpha 5 (importin alpha 6)	KPNA5	-1,92	5,9009E-08	chr6q22.2	NM_002269	3841
226761_at	IKAROS family zinc finger 4 (Eos)	IKZF4	-1,93	0,000836736	chr12q13	BF940979	64375

1560006_a_at	hypothetical protein LOC646762	LOC646762	-1,93	1,97749E-05	chr7p15.1	BG501482	442522
210930_s_at	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2	ERBB2	-1,95	6,1709E-05	chr17q11.2-q12|17q21.1	AF177761	2064
228635_at	protocadherin 10	PCDH10	-1,95	1,80525E-13	chr4q28.3	AI640307	57575
203788_s_at	sema domain, immunoglobulin domain (Ig)	SEMA3C	-1,97	0,02518691	chr7q21-q31	AI962897	10512
1555829_at	family with sequence similarity 62 (C2 domain containing) member B	FAM62B	-1,97	0,00015404	chr7q36.3	BC001224	NA
220220_at	leucine rich repeat containing 37, member A4 (pseudogene)	LRRC37A4	-2,01	4,86569E-05	chr17q21.31	NM_018001	55073
219543_at	phenazine biosynthesis-like protein domain containing	PBLD	-2,04	6,05642E-21	chr10pter-q25.3	NM_022129	64081
205822_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	-2,05	2,09429E-13	chr5p14-p13	NM_002130	3157
201876_at	paraoxonase 2	PON2	-2,09	9,721E-20	chr7q21.3	NM_000305	5445
223853_at	blood vessel epicardial substance	BVES	-2,12	4,02507E-06	chr6q21	AF204172	11149
222562_s_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	TNKS2	-2,13	1,119E-13	chr10q23.3	BF060683	80351
244321_at	GPI deacylase	PGAP1	-2,19	9,10762E-05	chr2q33.1	BF063546	80055
201852_x_at	collagen, type III, alpha 1	COL3A1	-2,33	4,12246E-06	chr2q31	AI813758	1281
201012_at	annexin A1	ANXA1	-2,82	4,77434E-12	chr9q12-q21.2|9q12-q21.2	NM_000700	301