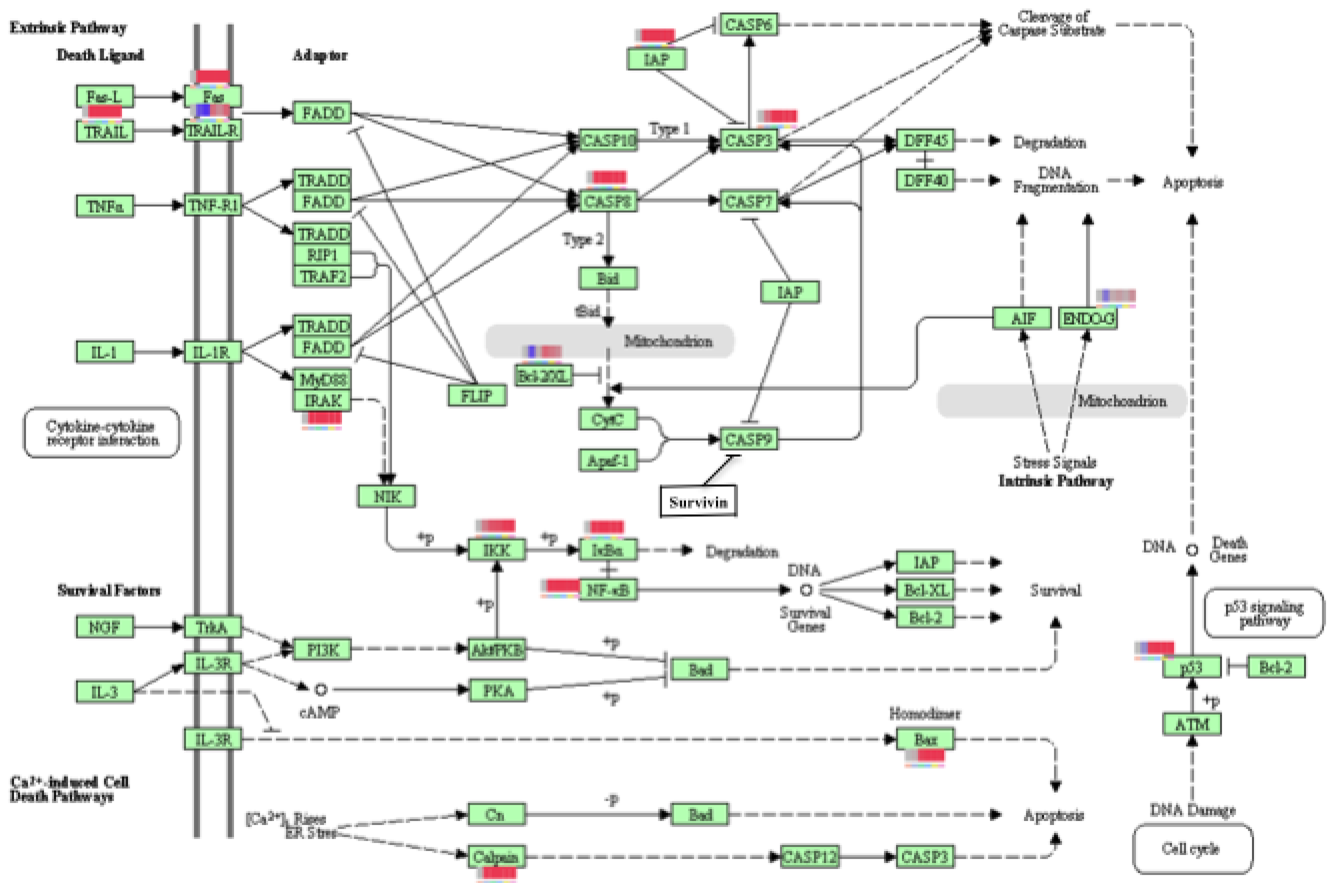
Apoptosis pathway

A)



B)

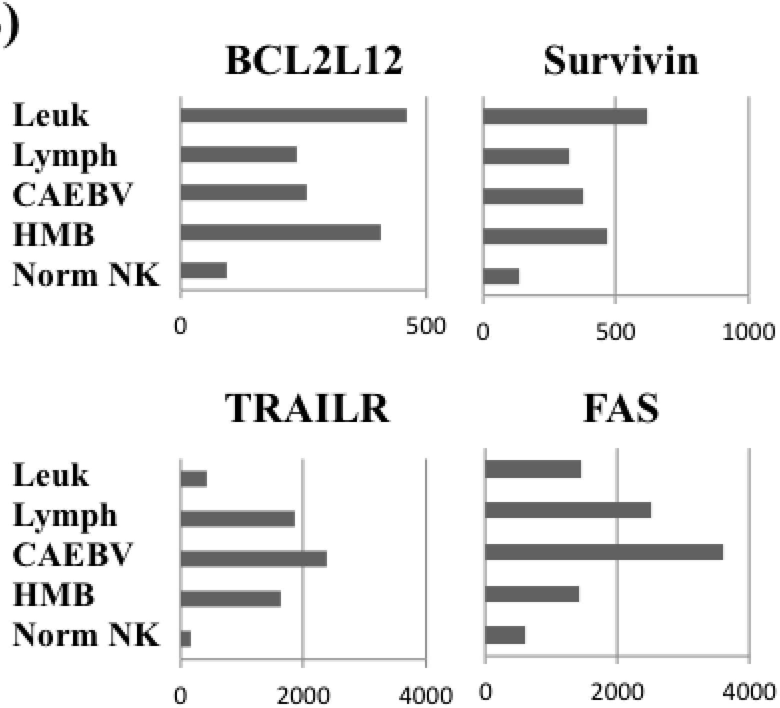


Figure S1

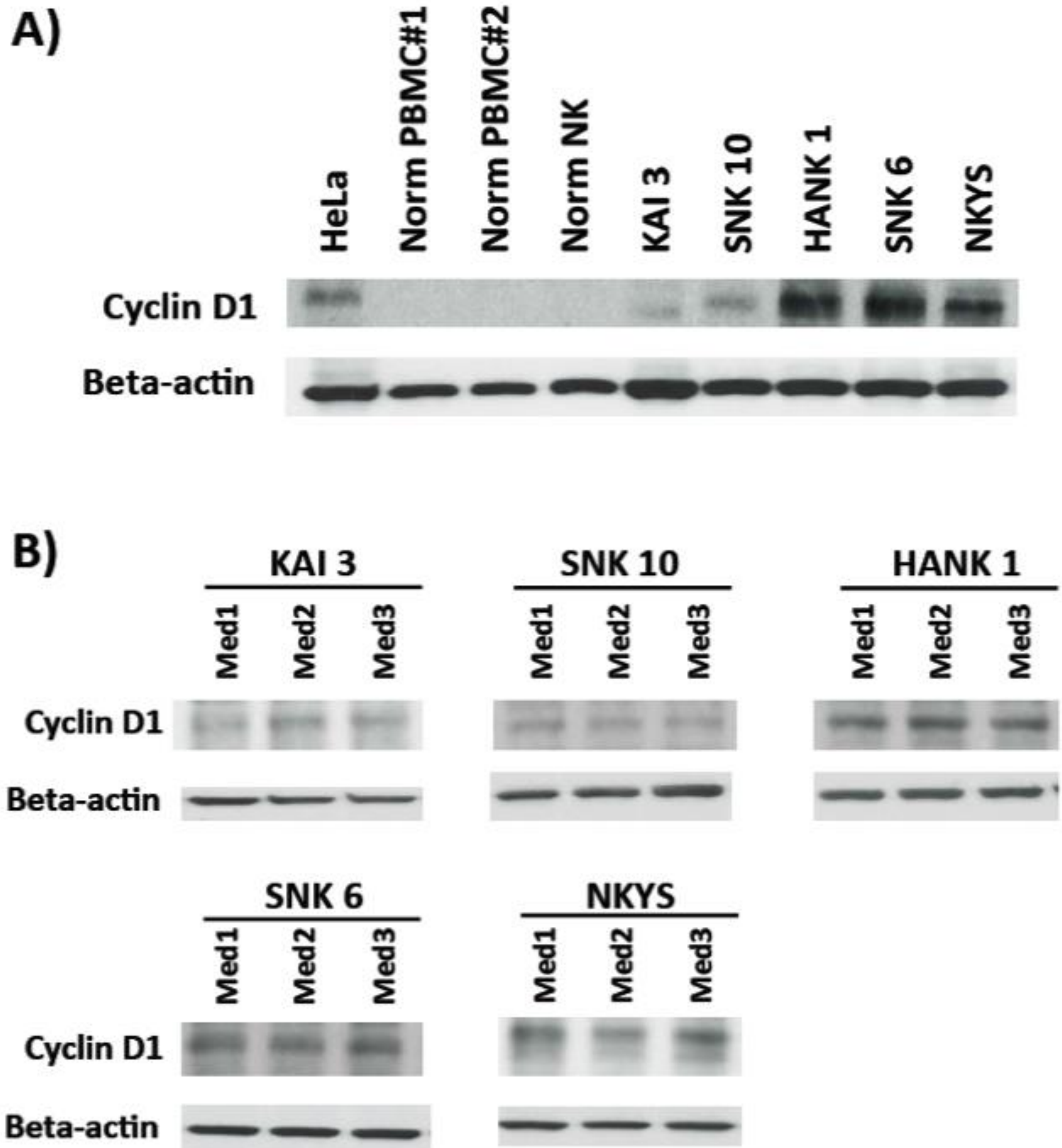

A)
HeLa
Norm PBMC#1
Norm PBMC#2
Norm NK
KAI 3
SNK 10
HANK 1
SNK 6
NKYS
Cyclin D1
Beta-actin
B)
KAI 3
SNK 10
HANK 1
Med1
Med2
Med3
Cyclin D1
Beta-actin
SNK 6
NKYS
Med1
Med2
Med3
Cyclin D1
Beta-actin

Figure S2

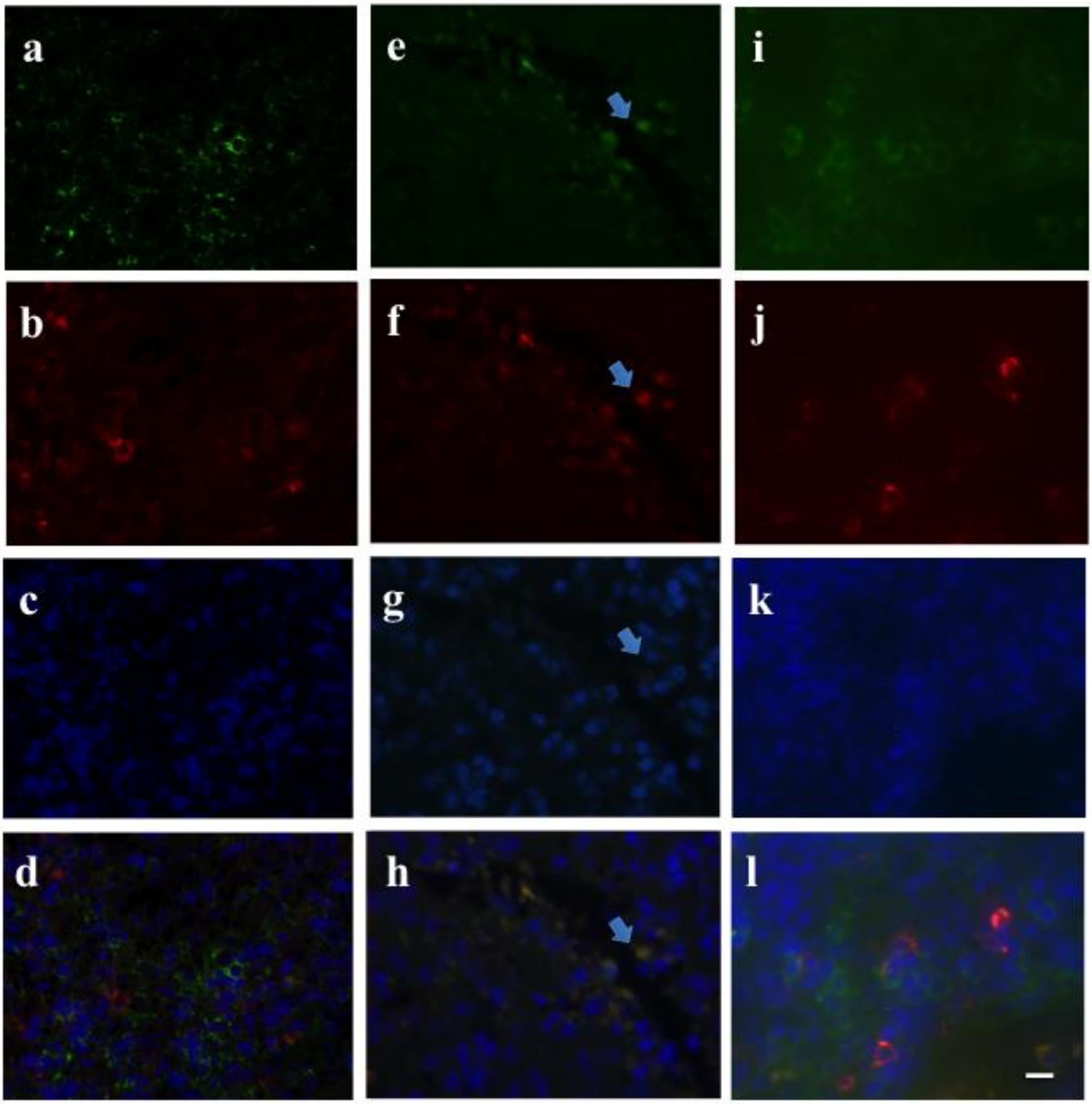


Figure S4

Table S1. Origin and characters of cell lines and normal CD16(-) NK cells

Cells	Origin	EBV infection	LMP1	EBNA1	EBV clonality	CD56	CD16
PBMC	healthy, peripheral blood	-	-	-	-	n.d.	n.d.
CD16(-) normal NK	healthy, tonsil	-	-	-	-	+	-
KAI3	HMB patient	+	+	+	+	+	-
SNK10	CAEBV patient	+	+	+	+	+	-
HANK1	NK/T lymphoma, primary lesion	+	+	+	+	+	-
SNK6	NK/T lymphoma, primary lesion	+	+	+	+	+	-
NK-YS	leukemic-state nasal angiocentric NK cell lymphoma, peripheral blood	+	+	+	+	+	-

n.d. : not done

Table S2. Gene cluster (A-1) which shows down regulation in HMB, CAEBV, NK lymphoma and NK leukemia compared to Norm NK

ID	PBMC1,PBMC2	CD16(-)NK1/2	KAI3-1,KAI3-2	SNK10	HANK,SNK6	NK-YS	Gene Title	Gene Symbol
status	PBMC	Normal NK CD16(-)	HMB	CAEBV	NK lymphoma	NK leukemia		
measurement ID	1	2	3	4	5	6		
1552924_a_at	155.4	41.65	4.55	3.1	1.8	2.1	phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2
1553316_at	19.05	204.4	16.8	14.9	13.450001	4.1	G protein-coupled receptor 82	GPR82
1553317_s_at	2.6999998	192.6	7.5	1.6	3.1999998	0.3	G protein-coupled receptor 82	GPR82
1554335_at	79	91.600006	36.449997	8.7	35.25	21.8	cytohesin 4	CYTH4
1554579_a_at	7.95	505.65002	52.6	1.1	3.6999998	0.9	myosin XVIIIB	MYO18B
1554733_at	0.95	122.6	90.95	1.6	1.75	0.8	hypothetical protein MGC24125	MGC24125
1554876_a_at	43.9	100.25	8.45	4	9.7	10.4	S100 calcium binding protein Z	S100Z
1555181_a_at	88.2	48.25	105.75	24.7	35.95	10.7	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	ST3GAL3
1556601_a_at	824.1	168.1	104.549995	87	96.450005	79.4	Spermatogenesis associated 13	SPATA13
1557098_s_at	32	131.1	27.150002	1.9	10.849999	2.7	highly accelerated region 1A (non-protein coding)	HAR1A
1557621_at	16.05	161.35	11.349999	3.3	3.4499998	1.7	kielin/chordin-like protein	KCP
1557835_at	199.40001	36.95	42.75	8.3	15.2	0.8	---	---
1558345_a_at	214.4	61.100002	34.85	32.3	30	35.8	hypothetical gene supported by NM_194304	LOC439911
1558496_at	2.95	108	3.45	1.7	70.75	2.5	---	---
1558497_a_at	1.2	148.4	4.3999996	0.8	96.15	0.5	---	---
1559025_at	129.5	90.75	71.75	21.6	18.35	7.3	septin 9	9-Sep
1560014_s_at	277.7	54.15	42.25	34	47.350002	16	pyridoxal-dependent decarboxylase domain containing 1	PDXDC1
1560128_x_at	494.15002	84.55	35.1	54.7	65.9	24.6	Hypothetical gene supported by AK128882	LOC441108
1560562_a_at	110.2	25.55	0.70000005	0.6	0.55	0.4	zinc finger protein 677	ZNF677
1560814_a_at	110.75	111.55	63.15	17.8	29.2	26.8	chromosome 15 open reading frame 57	C15orf57
1562255_at	1179.8	129.65	55.649998	34.6	20.2	19.4	synaptotagmin-like 3	SYTL3
1562587_at	10.7	98.8	42.05	11.2	7.6	1.6	cytokine-dependent hematopoietic cell linker	CLNK
1564031_a_at	131.55	116.9	37.35	52	65.25	31.5	RELT-like 2	RELL2
1565701_at	127	99.15	119.649994	26.4	57.25	20.1	---	---
1565863_at	16	188.55	55.1	19.5	5.8500004	4	---	---
1566448_at	647.05005	46.2	3.8	3	2.8	5.8	CD6 molecule	CD6
1569091_at	208.85	77.85	135.25	49.5	57.05	21.8	---	---
1569180_at	551.1	183.04999	130.3	51.7	70.75	11.1	---	---
1569181_x_at	574.9	227.95	145.5	62.9	72.6	14.9	---	---
1569496_s_at	234.85	109.55	40.65	33.4	35.65	47.2	hypothetical LOC100130872	LOC100130872
1569542_at	3.2	120.15	69.95	4.1	3.6000001	11	---	---
1569741_at	4.8	87.5	13.6	13.5	14.900001	12.8	---	---
201218_at	504.80002	151.9	7.1000004	7.2	80.35	2.2	C-terminal binding protein 2	CTBP2
201219_at	218	73.05	14.5	5.3	26.45	5.7	C-terminal binding protein 2	CTBP2
201340_s_at	712.89996	28.05	57.5	0.5	1.8000001	0.4	ectodermal-neural cortex (with BTB-like domain)	ENC1
201540_at	447.09998	150.1	12.35	10.6	11.950001	3	four and a half LIM domains 1	FHL1
201691_s_at	55.05	94.8	40.8	27.4	78.25	19.4	tumor protein D52	TPD52
201841_s_at	203.20001	79.2	49.95	16.6	97.55	0.9	heat shock 27kDa protein 1	HSPB1
202018_s_at	11.450001	96.95	1.55	1	1.3499999	1.2	lactotransferrin	LTF
202191_s_at	724.05005	167.6	8.35	9.8	59.100002	3.9	growth arrest-specific 7	GAS7
202192_s_at	642.9	163.05	44.800003	27.8	69.6	33.5	growth arrest-specific 7	GAS7
202435_s_at	597.25	266.85	6.45	7.7	5.3	1.1	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1
202436_s_at	1070.3	490.75	8.799999	6.1	5.3	9	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1
202437_s_at	754.85	415.59998	0.55	0.1	0.35000002	0.2	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1
202587_s_at	225.75	178.55	114.85	68.8	47.649998	7.7	adenylate kinase 1	AK1
202917_s_at	14751.949	348.85	32.1	1.9	6.3500004	13	S100 calcium binding protein A8	S100A8
203413_at	1157.7	69.850006	22.3	16.7	13.35	9.9	NEL-like 2 (chicken)	NELL2
203636_at	8.2	210.35	4.7999997	3.4	11.4	2.1	midline 1 (Opitz/BBB syndrome)	MID1
203637_s_at	30.8	302.40002	18.05	0.7	1.05	0.7	midline 1 (Opitz/BBB syndrome)	MID1
204018_x_at	6809.5996	138.25	6.65	4.8	5	8	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
204081_at	2079.2002	43.75	66.25	1.9	4.9	3.7	neurogranin (protein kinase C substrate, RC3)	NRGN
204561_x_at	7.25	86.75	3.4499998	2.4	2.3	2.2	apolipoprotein C-II	APOC2
204621_s_at	10606.5	395.65002	29.4	24.4	23	23.8	nuclear receptor subfamily 4, group A, member 2	NR4A2
204622_x_at	7547.8	415.90002	31.85	39.9	24.900002	34	nuclear receptor subfamily 4, group A, member 2	NR4A2
204749_at	122.2	59.300003	0.65	0.4	1.75	0.2	nucleosome assembly protein 1-like 3	NAP1L3
205051_s_at	28.45	173.5	19.8	3.6	2.3	3	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	KIT
205123_s_at	12.5	264.8	50.3	14.2	9.65	5.3	transmembrane protein with EGF-like and two follistatin-like domains 1	TMEFF1

205182_s_at	205.35	63.399998	65.75	21.5	24.3	6.6	zinc finger protein 324	ZNF324
205239_at	2023.3999	779.3	6.85	9.1	44.65	6	amphiregulin	AREG
205277_at	258.3	87.8	30.95	34.3	69.7	21.5	PR domain containing 2, with ZNF domain	PRDM2
205425_at	147.2	62.3	101.7	25.9	19.5	6.8	huntingtin interacting protein 1	HIP1
205758_at	3716.6	68.7	2.4	3.4	2.1	1.8	CD8a molecule	CD8A
205856_at	49.699997	263.4	65.95	28.8	52.75	3.9	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	SLC14A1
205883_at	493.55	83.6	12.45	19.5	10.1	13.4	zinc finger and BTB domain containing 16	ZBTB16
206307_s_at	17.65	128.45	12.65	9.1	70.1	17.1	forkhead box D1	FOXD1
206335_at	309	66.25	67.350006	24.1	26.45	24.2	galactosamine (N-acetyl)-6-sulfate sulfatase	GALNS
206390_x_at	4353.2	126.45	19.650002	11.1	17.7	3.9	platelet factor 4	PF4
206635_at	137.20001	54.5	36.9	11.5	48.7	8.9	cholinergic receptor, nicotinic, beta 2 (neuronal)	CHRNB2
207571_x_at	1948.15	156.75	61.65	16.8	8.1	2.2	chromosome 1 open reading frame 38	C1orf38
207857_at	957.05	146.7	20.9	7.6	6.5	25.5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
208078_s_at	4088.9	139.65	41.35	14.6	73.5	59.6	salt-inducible kinase 1	SIK1
208189_s_at	4.4	149.65	4.2	4.1	2.5	1.2	myosin VIIA	MYO7A
208594_x_at	347.4	115.4	42	8.6	23.25	24.6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	LILRA6
208602_x_at	482.05	67.05	6.8500004	1.8	1.3	1.5	CD6 molecule	CD6
208981_at	1815.85	53.05	55.85	6.8	8.15	1.2	platelet/endothelial cell adhesion molecule	PECAM1
209116_x_at	9533.65	108.85	7.9	3.6	31.75	3.3	hemoglobin, beta	HBB
209318_x_at	455.95	74.6	28.05	22.4	123.299995	9.8	pleiomorphic adenoma gene-like 1	PLAGL1
209458_x_at	7566.65	141.35	5.3500004	7.8	9.75	3.6	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
209460_at	133.4	157.6	61.05	14.7	40.35	0.8	4-aminobutyrate aminotransferase	ABAT
209468_at	4.3	101.7	9.75	8	4.9	6.3	low density lipoprotein receptor-related protein 5	LRP5
209538_at	268.2	55.25	6.1	0.9	21.8	1.2	zinc finger protein 32	ZNF32
209726_at	109.2	115.9	100.850006	36.3	40.6	24.5	carbonic anhydrase XI	CA11
209818_s_at	120.25	62.85	58.8	22.5	34.65	41.5	hyaluronan binding protein 4	HABP4
210370_s_at	333.09998	131.15	61.55	5.7	6.0499997	1	lymphocyte antigen 9	LY9
210461_s_at	159.1	100.2	43.95	9.1	20.099998	39.1	actin binding LIM protein 1	ABLIM1
210690_at	104.75	180.70001	14.15	15.1	52.5	5.9	killer cell lectin-like receptor subfamily C, member 4	KLRC4
210835_s_at	1162.7	371.3	31.699999	14.9	70.049995	5.9	C-terminal binding protein 2	CTBP2
210872_x_at	104.25	40.25	7.45	3.2	19	2	growth arrest-specific 7	GAS7
210879_s_at	219.9	117.05	53.55	31.6	24.849998	24.2	RAB11 family interacting protein 5 (class I)	RAB11FIP5
211026_s_at	163.79999	195.4	37.35	23.6	74.15	23.6	monoglyceride lipase	MGLL
211100_x_at	435.3	162.95	29.5	30.1	18.45	41.8	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
211101_x_at	436.95	169.55	29.5	17.6	16.75	40.6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
211102_s_at	102.35	60.600002	6.4500003	1.1	1	1.7	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2
211135_x_at	810.2	54.6	12.45	4.2	19.85	3.8	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	LILRB3
211336_x_at	463.8	245.95001	102.75	12.9	69.8	45	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	LILRB1
211696_x_at	10538.25	219.95	27.849998	21.5	34.6	29.5	hemoglobin, beta	HBB
211699_x_at	5830	128.85	17.7	2.1	2.3	4.2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
211745_x_at	9002	152.65	32.9	26.8	17.55	21.9	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
211748_x_at	1640.1	83.75	54.45	21.8	49.3	41.3	prostaglandin D2 synthase 21kDa (brain)	PTGDS
211794_at	516.75	76.6	2.0500002	1.7	1.55	1	FYN binding protein (FYB-120/130)	FYB
211893_x_at	525.14996	91.95	31	7	8.55	8.7	CD6 molecule	CD6
211900_x_at	675.85	117.850006	34.4	7.6	15.5	9.4	CD6 molecule	CD6
212445_s_at	70.5	249.54999	122.15	15.5	45.199997	7.6	neural precursor cell expressed, developmentally down-regulated 4-like	NEDD4L
212823_s_at	204.5	37.5	2.35	1.7	1.2	1.1	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	PLEKHG3
212912_at	94.05	24.55	33.4	1.1	1.85	0.9	ribosomal protein S6 kinase, 90kDa, polypeptide 2	RPS6KA2
212957_s_at	108.4	34.1	1.25	1.4	1.25	0.7	hypothetical LOC92249	LOC92249
213158_at	651.6	80.100006	47.6	32	36.5	20.3	---	---
213236_at	89.7	130.1	34.4	29.8	36.45	14.4	SAM and SH3 domain containing 1	SASH1
213280_at	1366.5	53	1.3499999	0.4	0.55	0.5	GTPase activating Rap/RanGAP domain-like 4	GARNL4
213395_at	87.850006	268.7	1.8	0.4	3.85	0.6	megalencephalic leukoencephalopathy with subcortical cysts 1	MLC1
213471_at	34.7	348.7	29.6	34.1	36.6	6.8	nephronophthisis 4	NPHP4
213659_at	139.2	68.8	47.1	24.8	50.1	25.9	zinc finger protein 75D	ZNF75D
213778_x_at	220.25	45.9	30.099998	14.7	36.65	7.7	zinc finger protein 276	ZNF276
213908_at	244.85	85.1	13.25	0.8	6.85	5.2	WAS protein homolog associated with actin, golgi membranes and microtubules-like 1 /// WAS protein homolog associated with actin, golgi membranes and microtubules-like 2 (pseudogene)	WHAMML1 ///WHAMML2
213958_at	2508.5498	500.45	110.899994	31.5	45.25	6.8	CD6 molecule	CD6
213975_s_at	15438.75	166.8	0.5	0.7	0.25	0.1	lysozyme (renal amyloidosis)	LYZ
214146_s_at	8126.1	308	1.8000001	0.5	0.5	0.6	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	PPBP
214241_at	331.65	67.75	59.050003	47.1	66.100006	37.9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFB8

214255_at	243.79999	53.4	11.95	2.6	15.95	2.3	ATPase, class V, type 10A	ATP10A
214414_x_at	10142.25	180.4	10	4.8	6.5	3	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
214579_at	83.05	90.850006	43.35	43.4	61.449997	18.2	NIPA-like domain containing 3	NIPAL3
214656_x_at	315.1	79.9	115.350006	55.5	112.549995	53.6	myosin IC	MYO1C
214677_x_at	4379.05	46.35	5.45	5	2.35	3	immunoglobulin lambda locus	IGL@
214719_at	264.7	84.399994	121.350006	19.8	18.95	1.1	solute carrier family 46, member 3	SLC46A3
214850_at	414.85	68.45	86.45	48.2	47.85	16.6	glucuronidase, beta pseudogene	LOC100170939
215152_at	20.5	101.55	14.25	22.8	31.2	13.8	v-myb myeloblastosis viral oncogene homolog (avian)	MYB
215191_at	347.85	64.65	107.899994	31	51.25	13	---	---
215221_at	648.5	71.8	42.75	36.6	23.2	19	---	---
215359_x_at	1408.95	265.4	191.25	69.6	120.6	25.5	zinc finger protein 44	ZNF44
215894_at	91.4	142.95001	1.8499999	3.2	4.1	0.2	prostaglandin D2 receptor (DP)	PTGDR
215967_s_at	495.75	240.55	66.55	3	11.85	3.2	lymphocyte antigen 9	LY9
216248_s_at	9220.8	380.25	22.85	40	30.3	26.6	nuclear receptor subfamily 4, group A, member 2	NR4A2
217022_s_at	4749.05	115.8	70.75	0.7	1.75	0.9	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// hypothetical LOC100126583	IGH@ /// IGHA1 /// IGHA2 /// LOC100126583
217414_x_at	5458.15	89.05	2.5	1.8	1.65	1.5	hemoglobin, alpha 1 /// hemoglobin, alpha 2	HBA1 /// HBA2
217655_at	909.85	67.7	44.8	32.1	50.949997	18.4	hypothetical LOC100127972	LOC100127972
217865_at	1429.95	47.7	1.95	1.4	117.549995	1	ring finger protein 130	RNF130
217963_s_at	1157.5	94.899994	10.299999	1.6	4.15	6	nerve growth factor receptor (TNFRSF16) associated protein 1	NGFRAP1
218066_at	993.6	210.3	35.65	10.7	27.599998	58.4	solute carrier family 12 (potassium/chloride transporters), member 7	SLC12A7
218312_s_at	357.85	108.65	2.9499998	1	9	3.2	zinc finger and SCAN domain containing 18	ZSCAN18
218523_at	151.4	40.550003	48.9	19.4	20.15	2.2	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP
218806_s_at	244.1	39.5	1.65	1.4	6.85	0.4	vav 3 guanine nucleotide exchange factor	VAV3
219229_at	313.7	44.1	57	7.3	9.2	0.5	solute carrier organic anion transporter family, member 3A1	SLCO3A1
219288_at	152.25	298.85	2.45	0.3	0.7	3	chromosome 3 open reading frame 14	C3orf14
219359_at	493	202.25	30.95	24.2	41.1	37.4	ATH1, acid trehalase-like 1 (yeast)	ATHL1
219396_s_at	108	42.6	17.45	12.4	8.55	6	nei endonuclease VIII-like 1 (E. coli)	NEIL1
219452_at	607.30005	52.550003	1.4	1.9	1.6	1	dipeptidase 2	DPEP2
219529_at	439.35	194.54999	6.1499996	5.2	3.15	3.3	chloride intracellular channel 3	CLIC3
219541_at	462.5	337.55	29.8	45.2	24.85	9	Lck interacting transmembrane adaptor 1	LIME1
219765_at	224.25	34.85	4	0.6	24.300001	0.4	zinc finger protein 329	ZNF329
219846_at	211.9	55.300003	56.15	40.7	54.25	22.1	gon-4-like (C. elegans)	GON4L
220016_at	151.25	98.850006	9.6	9.7	25.9	15.9	AHNAK nucleoprotein	AHNAK
220123_at	150.70001	66	108.25	37.2	39.5	22.6	solute carrier family 35, member F5	SLC35F5
220196_at	7.1499996	133.95001	1.3	1.9	1.15	4.8	mucin 16, cell surface associated	MUC16
220404_at	107.1	69.05	17.400002	10.9	14.95	19.2	G protein-coupled receptor 97	GPR97
220558_x_at	217.75	97.100006	85.2	44.3	25.95	25.3	tetraspanin 32	TSPAN32
220646_s_at	2202.9	1627.8501	12.3	5.8	83.350006	1.8	killer cell lectin-like receptor subfamily F, member 1	KLRF1
221185_s_at	57.25	1258.6	34.5	21.6	68.8	9.5	IQ motif containing G	IQCG
221195_at	132.6	83.2	96.55	24.4	20.849998	18.6	ring finger protein, transmembrane 1	RNFT1
221601_s_at	4794.15	173.35	12.049999	13.3	6.05	8.8	Fas apoptotic inhibitory molecule 3	FAIM3
221602_s_at	1794.3999	89.8	3.15	2.6	2.35	1.8	Fas apoptotic inhibitory molecule 3	FAIM3
221756_at	5170.35	189.5	30.35	30.8	8.75	19.2	phosphoinositide-3-kinase interacting protein 1	PIK3IP1
221841_s_at	6503.95	132.4	6.45	4.9	2.4	2.1	Kruppel-like factor 4 (gut)	KLF4
221958_s_at	67.5	178.5	0.79999995	2.4	1.1	1.7	G protein-coupled receptor 177	GPR177
222557_at	412.7	121.6	31.650002	15.6	30.1	11.2	stathmin-like 3	STMN3
222788_s_at	145.70001	78.95	101.649994	41	47.15	20.2	round spermatid basic protein 1	RSBN1
222996_s_at	591.4	302.95	79.9	35.1	41.65	2.5	CXXC finger 5	CXXC5
223594_at	26.849998	87.9	64.149994	10.7	18.6	12.7	transmembrane protein 117	TMEM117
223836_at	4852.3	1028.65	10.8	31.9	10.05	47.4	fibroblast growth factor binding protein 2	FGFBP2
224065_at	59.2	59.949997	38.2	25.7	66	25.1	homeodomain interacting protein kinase 2	HIPK2
224215_s_at	96.7	57.65	0.9	1.2	1.05	0.3	delta-like 1 (Drosophila)	DLL1
224794_s_at	62.3	87.8	121.35	15	10.6	17.5	cerebral endothelial cell adhesion molecule	CERCAM
224970_at	98.55	105	61.9	20.5	33.2	28.6	nuclear factor I/A	NFIA
224975_at	69.05	106.1	68.85	19.2	24.05	26	nuclear factor I/A	NFIA
224976_at	96.75	76.1	51.5	16.6	30.35	30.3	nuclear factor I/A	NFIA
225102_at	182.8	166.04999	27.1	15.5	49.9	18.7	monoglyceride lipase	MGLL
225166_at	126.8	89.55	35.6	15.2	17.35	23.4	Rho GTPase activating protein 18	ARHGAP18
225214_at	224.20001	56.6	114.6	4.5	8.45	7.7	hypothetical protein LOC100129034	LOC100129034
225224_at	635.25	119.45	102.2	47.1	47.7	14.4	chromosome 20 open reading frame 112	C20orf112
225562_at	1836.2	82.95	1.9000001	2.1	1.5	0.9	RAS p21 protein activator 3	RASA3

225591_at	460.35	58.75	4.1	13.1	58.25	2.2	F-box protein 25	FBXO25
226125_at	32.25	158.9	92.3	27.4	53.65	33.9	---	---
226247_at	706.65	83.1	1.6999999	3.3	14.6	1.1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	PLEKHA1
226252_at	424.6	79	28.650002	19.6	28.5	24.8	---	---
226279_at	570.55	56.449997	3.4	2.3	4.05	3.8	protease, serine, 23	PRSS23
226388_at	132.55	117.9	13.25	3.8	4.2	12.4	transcription elongation factor A (SII), 3	TCEA3
226431_at	986.4	216.7	284.2	25.4	67.4	24.9	family with sequence similarity 117, member B	FAM117B
226548_at	343.45	124.6	23.25	10.5	16.449999	29.1	SH3-binding domain kinase 1	SBK1
226564_at	111.5	62.350002	60.75	24.3	49.899998	30.7	zinc finger and AT hook domain containing	ZFAT
226791_at	248	128.4	139.85	43	56.1	26.2	kinesin family member C2	KIFC2
226792_s_at	183.55	89.100006	79.4	21.8	42.2	2.8	kinesin family member C2	KIFC2
226806_s_at	98	112.65	32.4	6.7	18.55	16.2	nuclear factor I/A	NFIA
226869_at	128.9	184.5	0.90000004	1.5	0.8	0.8	multiple EGF-like-domains 6	MEGF6
226879_at	700.4	133.95	14.1	29.5	42.5	8.7	hydrogen voltage-gated channel 1	HVCN1
227053_at	59.35	119.25	3.5	4.7	7.65	0.7	protein kinase C and casein kinase substrate in neurons 1	PACSIN1
227121_at	393.3	62.95	28.45	22.3	32.75	29.4	---	---
227232_at	621.94995	147.55	154.4	65.1	32.65	11.7	Enah/Vasp-like	EVL
227233_at	65.45	142.79999	91.5	11.1	7	5.6	tetraspanin 2	TSPAN2
227279_at	219.35	63.6	7.15	6.7	10.05	2.7	transcription elongation factor A (SII)-like 3	TCEAL3
227367_at	623.15	63.75	80.05	21.8	12.4	1	solute carrier organic anion transporter family, member 3A1	SLCO3A1
227432_s_at	466.5	45.550003	13.6	1.4	7.1499996	11.9	---	---
227474_at	83	240.79999	10.85	13	149.05	5.4	hypothetical LOC654433	LOC654433
227646_at	255.1	619.8	326.6	20.9	24.199999	6.5	early B-cell factor 1	EBF1
227762_at	515.1	125.55	10.85	19.5	8.25	20.6	---	---
227769_at	267.8	605.9	426.5	18.6	7.4	11	---	---
227804_at	3.7	114.8	101.7	57.6	56.25	13	TLC domain containing 1	TLCD1
227949_at	12.900001	108.25	8.55	10.1	8.85	7.4	phosphatase and actin regulator 3	PHACTR3
228010_at	25	143.8	7.65	4.2	10.200001	14.2	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	PPP2R2C
228071_at	1787.1	87.649994	2.65	0.9	3.2	2.9	GTPase, IMAP family member 7	GIMAP7
228083_at	367.75	236.65	57.800003	17.8	3.75	1.2	calcium channel, voltage-dependent, alpha 2/delta subunit 4	CACNA2D4
228094_at	1245.7	1363.5	5.7	3.2	7	19.5	adhesion molecule, interacts with CXADR antigen 1	AMICA1
228333_at	673.55	83.8	99.7	27.1	38.35	29.8	---	---
228411_at	7.9500003	289.25	11.650001	11.3	13.15	0.9	par-3 partitioning defective 3 homolog B (C. elegans)	PARD3B
228532_at	1908.6499	171.79999	95.05	2.1	21.95	3	chromosome 1 open reading frame 162	C1orf162
228731_at	3.95	234.95001	36.1	4	2.4	4.2	---	---
228742_at	121.3	58.3	71.25	35.2	33.550003	15.3	---	---
228771_at	265.45	104.05	24.6	6.7	143.4	27.4	adrenergic, beta, receptor kinase 2	ADRBK2
228854_at	1034.65	204.5	5.2	4.4	1.55	3.8	---	---
228857_at	232.4	92.3	38.2	31.5	41.9	30.3	guanine nucleotide binding protein-like 1 /// hypothetical protein LOC285831	GNL1 /// LOC285831
228885_at	3.85	217.65	1.7	1	1.35	8.8	MAM domain containing 2	MAMDC2
229151_at	28.6	108.350006	38.1	17	17.7	7.3	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	SLC14A1
229177_at	25	906.75	12.55	2.5	2.5	2.1	chromosome 16 open reading frame 89	C16orf89
229221_at	346.05	86.8	59.2	24.2	81.15	43.5	CD44 molecule (Indian blood group)	CD44
229390_at	2022.95	25.35	0.75	0.4	1.2	1.7	family with sequence similarity 26, member F	FAM26F
229487_at	42.65	82.649994	76.3	12.5	13.35	8.2	early B-cell factor 1	EBF1
229550_at	9.25	126.35	5.25	3.7	8.45	3.5	KIAA1409	KIAA1409
229596_at	61	48.4	103.5	31.1	28.5	4.5	amidohydrolase domain containing 1	AMDHD1
229844_at	606.9	48	46.15	4.2	5	9.3	---	---
230203_at	126.55	59.65	34.9	31.4	51.25	20.3	hypothetical LOC440918	FLJ46875
230206_at	307.84998	144.75	8.65	1.4	29.099998	1.2	Dedicator of cytokinesis 5	DOCK5
230207_s_at	370.15002	189	10.35	5	32.8	5.2	Dedicator of cytokinesis 5	DOCK5
230233_at	6502.45	119.600006	65.149994	18.8	53.2	8.2	---	---
230263_s_at	402.2	153.15	7.7999997	3.9	24.7	4.4	Dedicator of cytokinesis 5	DOCK5
230277_at	25.65	80.399994	50.95	12.4	59.85	19.4	hypothetical protein LOC100294023	LOC100294023
230529_at	611.3	92.95	36.25	23.7	37.05	22.3	headcase homolog (Drosophila)	HECA
230563_at	181.55	369.15	7.05	1.4	1.3000001	3.6	RasGEF domain family, member 1A	RASGEF1A
230590_at	344.25	53.05	41.4	23.5	15.4	15	---	---
230756_at	184.35	149	40.5	3.9	17.25	9.7	zinc finger protein 683	ZNF683
230925_at	2426.65	175.5	12.1	1.1	73.799995	4.8	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	APBB1IP
230934_at	59.85	161.5	105.4	61.6	36.550003	18	serine/threonine kinase 32C	STK32C
230958_s_at	71.8	125.75	56.95	12.8	20.05	16.9	---	---

231093_at	884.35	166.85	8.5	12.9	127.4	6.8	Fc receptor-like 3	FCRL3
231124_x_at	2295.6	334.55	278.6	36.6	84.9	24.6	lymphocyte antigen 9	LY9
231166_at	190.75	147.5	147.1	9.8	32.65	13.5	G protein-coupled receptor 155	GPR155
231291_at	59.55	77.7	59.9	6.4	11.200001	7.9	---	---
231770_x_at	203.25	102.600006	70.5	23.4	50.35	29.6	chromosome 2 open reading frame 86	C2orf86
231835_at	189.2	79.55	57.25	21.9	31	1.6	chromosome 1 open reading frame 93	C1orf93
231873_at	118.85	289.55	278.7	45.4	50.65	16	bone morphogenetic protein receptor, type II (serine/threonine kinase)	BMPR2
232180_at	108.9	60.85	37.85	37.1	60.9	15.1	UDP-glucose pyrophosphorylase 2	UGP2
232204_at	165.5	341.45	174.7	23	13.6	0.8	early B-cell factor 1	EBF1
232234_at	963.45	160.05	17.699999	1.9	73.350006	91.6	Src-like-adaptor 2	SLA2
232436_at	381.84998	94.600006	39.65	34.2	35.5	16.3	zinc finger protein 274	ZNF274
232463_at	64.55	103.45	77.35	23.5	40.35	11.1	non-protein coding RNA 107	NCRNA00107
232978_at	139.70001	31.2	67.7	11.9	13.4	0.8	---	---
232991_at	297.85	144.6	145.79999	56	76.05	22.6	ADP-ribosylation factor-like 17	ARL17
233330_s_at	22.95	254.25	252.20001	35.8	16.65	4.6	---	---
233425_at	137.45	108.9	31.05	39.3	46.550003	11.4	---	---
233440_at	22.449999	43.6	86.9	18.7	34.25	7.4	---	---
233528_s_at	93.85	58.55	93.75	38.6	50.1	19.4	GATS protein-like 3 /// TBC1 domain family, member 10A	GATSL3 /// TBC1D10A
233955_x_at	713.7	465.75	62	22.8	36.75	2.6	CXXC finger 5	CXXC5
234151_at	222.25	90.7	83.5	27.4	42.800003	45.2	---	---
235000_at	66.8	60.399998	85.95	38	35.1	8.4	---	---
235308_at	1070.65	201.55	59.550003	25.5	56.75	31.4	zinc finger and BTB domain containing 20	ZBTB20
235369_at	206.95	180.15	223.6	86.1	80	16.8	chromosome 14 open reading frame 28	C14orf28
235652_at	793.4	36.1	0.65000004	0.6	0.35000002	0.4	---	---
235739_at	4016.5498	319.45	28.449999	29.5	11.5	26.4	---	---
235756_at	42.2	110.5	77.05	15.6	28.9	36.3	---	---
235847_at	888.45	54.550003	89.4	21.9	33.75	14.8	---	---
236335_at	8.65	164.45	34.4	6.8	3.6499999	2.8	---	---
236485_at	83	47.15	48.300003	6	21.650002	0.7	Similar to ZNF124 protein	LOC100129837
236655_at	38.6	121.65	47.15	18.4	90.55	12.4	tumor protein D52	TPD52
236668_at	99.75	72.15	31.9	29.7	36.85	19.7	---	---
236699_at	334.8	53.65	126.4	24.5	23.900002	6.1	---	---
236719_at	52.600002	81.7	29.75	9.6	17.400002	29	---	---
237201_at	94.899994	82.25	114.3	33	27.2	19.7	---	---
237875_at	179.25	71.95	33.5	28	22.150002	13.8	---	---
238044_at	81.3	38.05	51.25	18.7	20.55	1.1	---	---
238218_at	15.75	142.15	16.8	7.6	11.55	20.9	oocyte expressed protein homolog (dog)	OOEP
238649_at	82.75	83.100006	90	25.1	73.9	38.5	phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1
238678_at	221.55	56	123.35	41.2	51.85	17.4	hypothetical LOC402483	tcag7.907
238684_at	101.55	73.5	87.85	52	42.75	11.2	SET domain, bifurcated 2	SETDB2
238774_at	411.95	102.149994	64.6	26.1	39.9	17.4	---	---
238850_at	13.75	112	15.6	2.9	9.25	8.4	hypothetical LOC645323	LOC645323
238893_at	1478.6	124.85	88.8	26.1	96	38.4	hypothetical LOC338758	LOC338758
238900_at	10.95	271	1.9	4	211.09999	0.4	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to HLA class II histocompatibility antigen, DRB1-7 beta chain	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100294036
239179_at	169.25	59.95	64.9	25.2	50.8	48.5	---	---
239624_at	8.3	243.04999	7.2	6.3	7.4	0.8	---	---
239862_at	77.2	147.5	25.6	11.7	32.25	11.3	---	---
239892_at	153.85	57.949997	52.75	36.2	48.75	18.9	---	---
240061_at	226.65	52.9	11.95	0.6	2.8	5.8	Pigeon homolog (Drosophila)	PION
240094_at	255.35	115.15	100.4	49.4	60.550003	19.2	---	---
240189_at	28.75	54.75	59.35	12.6	59.75	1.9	acyl-Coenzyme A oxidase-like	ACOXL
240434_at	24.65	120.9	60.149998	30	19.1	52.4	---	---
240458_at	333.4	59.800003	84.65	38.1	54.3	16.9	---	---
241065_x_at	52.35	81.3	89.2	54.7	64.45	19.6	Cytidine monophosphate N-acetylneuraminic acid synthetase	CMAS
241402_at	931.7	100.75	29.6	26.8	32.05	26.4	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	TSEN54
241460_at	268.7	89.75	154.15	19.7	65	17.3	---	---
241905_at	675.30005	106.7	49.85	47.1	72.5	18.7	Phosphoinositide-3-kinase, class 2, alpha polypeptide	PIK3C2A
242052_at	66.25	54.9	101.950005	44.2	66.45	21.7	---	---

242080_at	195.6	124.65	168.45	58	66.65	16.7	---	---
242108_at	95.05	93	45.25	54.4	51.85	19.2	---	---
243030_at	489.3	53.15	51.15	36.4	44.550003	19.1	---	---
243178_at	746.95	67.25	13.25	20.6	50.95	8.1	---	---
243216_x_at	123.20001	79.600006	99.95	25.5	26	19.1	---	---
244075_at	163.25	144.2	173.6	45.8	44.05	12.1	---	---
244413_at	288.25	1061.4	436.35	4.7	9	6.4	C-type lectin-like 1	CLECL1
244434_at	1.55	226.8	3.75	1.5	1.95	1.1	---	---
244677_at	1215.85	97.45	25.8	25.5	28.85	15.6	---	---
244716_x_at	132.15	93.25	30.25	33.9	77.799995	17.7	transmembrane and immunoglobulin domain containing 2	TMIGD2
33197_at	72.3	240.05	27.5	17.2	9.1	7.2	myosin VIIA	MYO7A
37254_at	66.05	69.9	90.45	53.1	60.45	20.2	zinc finger protein 133	ZNF133

Table S3. Gene cluster (A-2) which shows up regulation in HMB, CAEBV, NK lymphoma and NK leukemia compared to Norm NK

ID status measurement ID	PBMC1,PBMC2 PBMC 1	CD16(-)NK1/2 Normal NK CD16(-) 2	KAI3-1, KAI3-2 HMB 3	SNK10 CAEBV 4	HANK, SNK6 NK lymphoma 5	NK-YS NK leukemia 6	Gene Title	Gene Symbol
1053_at	170.45	130.75	670.35	471	607.19995	880.6	replication factor C (activator 1) 2, 40kDa	RFC2
1552625_a_at	97.8	50.75	442.09998	222.2	328.8	314.7	tRNA nucleotidyl transferase, CCA-adding, 1	TRNT1
1552660_a_at	105.05	90.55	293.1	289.7	294.35	322.5	chromosome 5 open reading frame 22	C5orf22
1552921_a_at	29.2	83.5	414.45	370.1	393	360.9	fidgetin-like 1	FIGNL1
1553510_s_at	147.1	107.600006	410.45	310.1	378.1	655.6	RCD1 required for cell differentiation1 homolog (S. pombe)	RQCD1
1553587_a_at	180.04999	126.05	315.55	321.3	328.4	829.5	polymerase (DNA-directed), epsilon 4 (p12 subunit)	POLE4
1554080_at	170.65	96.7	345.4	260.3	324.05	494.9	RCD1 required for cell differentiation1 homolog (S. pombe)	RQCD1
1554082_a_at	298.2	72.149994	227.05	217.4	175.4	404.5	nucleolar protein 9	NOL9
1554089_s_at	1959.2	205.85	416.65002	436.6	498.05	513.4	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	SBDS /// SBDSP
1554351_a_at	352.05	252.70001	880.35	824.7	1057.45	1519.2	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	TIPRL
1554390_s_at	1238.6	167.85	847.05	736.2	560.5	774.4	ARP2 actin-related protein 2 homolog (yeast)	ACTR2
1554433_a_at	368.84998	88.95	560.05	320.7	366.5	336	zinc finger protein 146	ZNF146
1554482_a_at	267.1	142.75	426.1	423.5	349.40002	625.1	SAR1 homolog B (S. cerevisiae)	SAR1B
1554600_s_at	390.2	96.15	2797.5	1061.3	685.85	973.3	lamin A/C	LMNA
1554747_a_at	338.65002	293.15	1501.85	770.5	961.7	851.7	septin 2	2-Sep
1554868_s_at	1148.95	463.15002	1606.95	1584.1	1518.05	1202.5	PEST proteolytic signal containing nuclear protein	PCNP
1555167_s_at	1264.85	109.3	299	389	279.9	386.5	nicotinamide phosphoribosyltransferase	NAMPT
1555594_a_at	223.05	60.3	538.55	307.8	322.1	471.7	muscleblind-like (Drosophila)	MBNL1
1555760_a_at	313.95	193.15	392.59998	363.2	465.1	479.7	RNA binding motif protein 15	RBM15
1555971_s_at	556.2	125.05	757.55	701.9	536.85	636.7	F-box protein 28	FBXO28
1555996_s_at	540.05	72.05	317.84998	487.1	271.65	454.5	eukaryotic translation initiation factor 4A, isoform 2	EIF4A2
1556988_s_at	284.84998	100.55	353.6	283	353.2	408.7	chromodomain helicase DNA binding protein 1-like	CHD1L
1557915_s_at	1659.8	406.2	1419.8501	1407.6	1897.15	1712.6	glutathione S-transferase omega 1	GSTO1
1558015_s_at	598.85	149.55	678.85	571.4	438.7	663.7	ARP2 actin-related protein 2 homolog (yeast)	ACTR2
1558080_s_at	559	187.3	1105.5	981.6	436.7	733.3	DnaJ (Hsp40) homolog, subfamily C, member 3	DNAJC3
1558233_s_at	348.3	157.1	555.4	334.1	338.15002	291.5	activating transcription factor 1	ATF1
1560116_a_at	768.65	202	443.5	383.5	486.95	414.7	neural precursor cell expressed, developmentally down-regulated 1	NEDD1
1560339_s_at	504.80002	302.75	820.19995	1403.3	796.95	1166.9	nucleosome assembly protein 1-like 4	NAP1L4
1564164_at	371.55	113.75	369.84998	235	353.95	141.7	DENN/MADD domain containing 1B	DENND1B
1564637_a_at	214.9	152	521.25	411.5	496.95	531.9	family with sequence similarity 98, member B	FAM98B
1565717_s_at	729.5	155.25	896.75	832.6	836.60004	1844	fusion (involved in t(12;16) in malignant liposarcoma) /// nuclear receptor subfamily 1, group H, member 3	FUS /// NR1H3
1568618_a_at	1011	103	520.8	431.5	263.7	829.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1
200593_s_at	1372.7	273.84998	1533.25	1350.2	997.45	2162.3	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	HNRNPU
200607_s_at	881.35	750.15	1996.1499	1609	1669.55	1373.9	RAD21 homolog (S. pombe)	RAD21
200615_s_at	184.95	202.79999	673.6	942.3	659.9	579.1	adaptor-related protein complex 2, beta 1 subunit	AP2B1
200686_s_at	6105.55	1757.95	4042.75	4483.5	4787.55	3425.4	splicing factor, arginine/serine-rich 11	SFRS11
200690_at	408.85	89.649994	413.3	293.3	383.55	447.4	heat shock 70kDa protein 9 (mortalin)	HSPA9
200727_s_at	1646	170.85	834.25	804.1	569.3	898.7	ARP2 actin-related protein 2 homolog (yeast)	ACTR2
200730_s_at	546.45	80.9	460.55	934	494.35	648.8	protein tyrosine phosphatase type IVA, member 1	PTP4A1
200731_s_at	1466.55	144.6	532.35	646.8	497.84998	457.4	protein tyrosine phosphatase type IVA, member 1	PTP4A1
200733_s_at	2726.9	644.15	2080.9	3008.8	1806.95	1740.5	protein tyrosine phosphatase type IVA, member 1	PTP4A1
200768_s_at	1153.75	338.6	1293.25	1171.1	1492.3	1778	methionine adenosyltransferase II, alpha	MAT2A
200769_s_at	55.9	41.4	175.79999	272.8	275.85	540.6	methionine adenosyltransferase II, alpha	MAT2A
200782_at	3023	471	1447.3	2226.4	1122.1	1710.1	annexin A5	ANXA5
200787_s_at	387.2	78.05	390.3	189.6	205.45001	399	phosphoprotein enriched in astrocytes 15	PEA15
200815_s_at	846.55005	176.95001	455.05	542.2	444.05	614.2	platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45kDa)	PAFAH1B1
200825_s_at	495	223.5	490.5	702.5	547.8	851.4	hypoxia up-regulated 1	HYOU1
200839_s_at	2730.15	43.85	693.19995	547	324.09998	287.6	cathepsin B	CTSB
200841_s_at	128.6	75.3	714.6	608.5	574.3	452.2	glutamyl-prolyl-tRNA synthetase	EPRS
200842_s_at	496.2	641.44995	2374.8	1681.5	1801.05	1271.1	glutamyl-prolyl-tRNA synthetase	EPRS
200843_s_at	547.25	404.7	1493	1765.2	1456.25	1201.3	glutamyl-prolyl-tRNA synthetase	EPRS
200844_s_at	1606.55	1451.2	4360.6	2577.2	4797.85	2697.5	peroxiredoxin 6	PRDX6
200864_s_at	477.1	153.15	409.45	452.4	277.6	365	RAB11A, member RAS oncogene family	RAB11A
200917_s_at	204.20001	114.35	310.05	250.2	235.05	440.5	signal recognition particle receptor (docking protein)	SRPR
200935_at	189.55	55.75	263	140.3	148.05	497.4	calreticulin	CALR
200950_at	304.09998	228.09999	785.8	902.3	688.95	809	actin related protein 2/3 complex, subunit 1A, 41kDa	ARPC1A
200951_s_at	219.1	53.75	318.85	1053.9	1168.75	1146.8	cyclin D2	CCND2

200953_s_at	2110.0498	475.95	1787.05	4099	3845.9502	4559.4	cyclin D2	CCND2
200956_s_at	408.59998	229.4	657.15	592.2	557.6	1050.3	structure specific recognition protein 1	SSRP1
200957_s_at	576.05	234.35	776.9	639.8	659.25	1184.7	structure specific recognition protein 1	SSRP1
201020_at	327.40002	142.6	753.15	621	718.75	1058.7	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	YWHAH
201027_s_at	363.35	178.5	460.25	377.5	508.2	453.3	eukaryotic translation initiation factor 5B	EIF5B
201043_s_at	243.3	251.6	728.44995	1428.1	651.4	1640.4	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	ANP32A
201046_s_at	918.3	437.45	1053.8	945.9	1109.6001	760	RAD23 homolog A (S. cerevisiae)	RAD23A
201076_at	478.5	150.45001	370.35	287.6	324.3	604.1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	NHP2L1
201079_at	910.94995	190.2	1270.45	829	718.30005	656.8	synaptogyrin 2	SYNGR2
201083_s_at	831.85	106.3	366.40002	215.1	255.05	445.1	BCL2-associated transcription factor 1	BCLAF1
201097_s_at	3180.2998	906	2685	1962	1872.65	1865.2	ADP-ribosylation factor 4	ARF4
201101_s_at	944.45	174.4	622.8	326.1	370.55	842.9	BCL2-associated transcription factor 1	BCLAF1
201118_at	915.3	463.35	931.6	1383.6	1580.1499	1681.6	phosphogluconate dehydrogenase	PGD
201120_s_at	370.40002	145.1	621.1	911	577.45	831.2	progesterone receptor membrane component 1	PGRMC1
201121_s_at	1309.35	415.95	1393.85	1742.9	1245.5	1708.1	progesterone receptor membrane component 1	PGRMC1
201122_x_at	374.1	69.95	573.55	260	336.9	629.6	eukaryotic translation initiation factor 5A	EIF5A
201123_s_at	516.45	59.949997	1310.1	951.5	1004.80005	3573.7	eukaryotic translation initiation factor 5A	EIF5A
201132_at	1180.75	173.95001	1662.2	883.7	495.05	920	heterogeneous nuclear ribonucleoprotein H2 (H'')	HNRNPH2
201161_s_at	830.15	250.40001	1150.9	1204.8	1083.15	1323.4	cold shock domain protein A	CSDA
201164_s_at	1633.35	388.2	683.65	657.7	660.80005	538.4	pumilio homolog 1 (Drosophila)	PUM1
201169_s_at	793.44995	172.35	402.85	595.7	727.6	507.5	basic helix-loop-helix family, member e40	BHLHE40
201170_s_at	5232.5996	1360.45	1937.3	2947.2	3131.85	2368.3	basic helix-loop-helix family, member e40	BHLHE40
201200_at	1817.25	575.85	1712.45	2824.8	1501.1	1692.2	cellular repressor of E1A-stimulated genes 1	CREG1
201211_s_at	155.5	43.3	391.3	256.9	234.2	542.5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X
201233_at	253	136.2	306.75	310.8	342.7	585.6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	PSMD13
201237_at	869.9	174.2	813.75	631.3	602.35	801.2	capping protein (actin filament) muscle Z-line, alpha 2	CAPZA2
201259_s_at	650.85	335.8	976.80005	1090.7	935.7	1218.1	synaptophysin-like 1	SYPL1
201260_s_at	757.4	292.84998	771.55005	969.1	720.35004	980.9	synaptophysin-like 1	SYPL1
201263_at	708.3	536.35	1830.95	1933	2183	1781.9	threonyl-tRNA synthetase	TARS
201266_at	611.80005	507.44998	1065.55	1878.9	2325.1	2015.7	thioredoxin reductase 1	TXNRD1
201362_at	1366.75	180.5	1117.85	846.3	612.15	387.5	influenza virus NS1A binding protein	IVNS1ABP
201363_s_at	1425.3	157.85	1139.3	789.6	521.4	390.5	influenza virus NS1A binding protein	IVNS1ABP
201366_at	1634.9	682.95	1501.9	1700.5	1776.75	1312.7	annexin A7	ANXA7
201378_s_at	663.35	147.25	679.5	280.8	413.4	977.7	ubiquitin associated protein 2-like	UBAP2L
201404_x_at	171.5	89.600006	383.85	314.9	328.3	533.4	proteasome (prosome, macropain) subunit, beta type, 2	PSMB2
201409_s_at	1755	271.15	974.25	563.1	790.55	609.5	protein phosphatase 1, catalytic subunit, beta isoform	PPP1CB
201414_s_at	613.45	298.55	707.1	774.1	549.9	520.8	nucleosome assembly protein 1-like 4	NAP1L4
201415_at	398.84998	232.85	773.05005	548.8	634.9	554.1	glutathione synthetase	GSS
201420_s_at	129.6	63.550003	535.9	216.4	283.45	496.5	WD repeat domain 77	WDR77
201450_s_at	549.7	243.35	738.55	660.3	637.05	634.2	TIA1 cytotoxic granule-associated RNA binding protein	TIA1
201456_s_at	932.30005	293.5	635.2	1115.5	884.7	1017.7	budding uninhibited by benzimidazoles 3 homolog (yeast)	BUB3
201475_x_at	568.5	321.55	1134.95	1961.3	1450.3	1105.9	methionyl-tRNA synthetase	MARS
201487_at	1945.7	928.5	2311.6	3550.6	1769.85	2685.4	cathepsin C	CTSC
201490_s_at	1149.8501	331.05	1125.1	1215.1	1360.55	3842.8	peptidylprolyl isomerase F	PPIF
201514_s_at	279	82.25	406.25	381.2	414.59998	717.4	GTPase activating protein (SH3 domain) binding protein 1	G3BP1
201528_at	792.35	386.7	1540.75	1745.4	1458.6001	2236.7	replication protein A1, 70kDa	RPA1
201529_s_at	399.25	170.2	880.05005	1057.2	855.85	1543.4	replication protein A1, 70kDa	RPA1
201533_at	915.05	245.5	1193.35	1048.4	824.75	1125.5	catenin (cadherin-associated protein), beta 1, 88kDa	CTNNB1
201555_at	303.6	263.55	2369.4	1508.1	2054.85	1944.6	minichromosome maintenance complex component 3	MCM3
201571_s_at	203.4	230.29999	689.75	790.3	688.15	674.2	dCMP deaminase	DCTD
201572_x_at	484.5	194.85	866.75	791.8	620.9	858.3	dCMP deaminase	DCTD
201585_s_at	362.15	174.65	578.5	598.4	497.55	1094.3	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	SFPQ
201587_s_at	1441.2	397.85	728.85	978.4	807.2	755.1	interleukin-1 receptor-associated kinase 1	IRAK1
201595_s_at	1860.1	760.5	1490.45	1368.4	1610.95	1421.7	zinc finger CCCH-type containing 15	ZC3H15
201609_x_at	233.95	247.85	760.4	809.8	497.59998	1015.1	isoprenylcysteine carboxyl methyltransferase	ICMT
201660_at	190.6	22.8	397.75	221.6	531.95	353	Acyl-CoA synthetase long-chain family member 3	ACSL3
201661_s_at	394.4	15.65	615.85	288.1	807.75	470.6	acyl-CoA synthetase long-chain family member 3	ACSL3
201662_s_at	632.15	39.1	763.45	473.6	847.19995	1139.6	acyl-CoA synthetase long-chain family member 3	ACSL3
201722_s_at	802.5	104.600006	579.95	872.1	392	1621.7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1

201723_s_at	658.35	72.15	464.35	479.9	290.9	961.1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1
201724_s_at	638.15	74.25	387.05	467.7	286.6	791	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1
201739_at	5726.75	40.05	215.5	511.5	193.85	825.5	serum/glucocorticoid regulated kinase 1	SGK1
201746_at	306.84998	47.300003	530.1	1005.6	419.7	720.6	tumor protein p53	TP53
201748_s_at	346.4	83.95	264.15	288.2	260.85	388.7	scaffold attachment factor B	SAFB
201755_at	164.79999	117.950005	737.1	430.7	551.55	705.8	minichromosome maintenance complex component 5	MCM5
201772_at	1414.95	361.15	2002.9	1553	1987.7999	1732.7	antizyme inhibitor 1	AZIN1
201807_at	1608.75	728.80005	1676.95	1675.7	1216.65	1083.5	vacuolar protein sorting 26 homolog A (S. pombe)	VPS26A
201817_at	347.6	145.6	505.15002	445.6	350.85	495.6	ubiquitin protein ligase E3C	UBE3C
201830_s_at	180.45001	131.55	397.9	460.8	361.05002	612.8	neuroepithelial cell transforming 1	NET1
201937_s_at	292.2	120.9	301.3	211.4	393.75	265.7	aspartyl aminopeptidase	DNPEP
201948_at	647.85	241.4	644.75	550.9	757.55	717.9	guanine nucleotide binding protein-like 2 (nucleolar)	GNL2
201956_s_at	534.75	470.35	1135.35	1084.9	966.85	829.1	glyceronephosphate O-acyltransferase	GNPAT
201963_at	3737	65.65	681.2	515.6	1090.1499	742	acyl-CoA synthetase long-chain family member 1	ACSL1
201971_s_at	255.9	147.45	741.6	336.4	548.8	292.9	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A
202047_s_at	842.75	313.55	1000.95	855.7	1230.6	665	chromobox homolog 6	CBX6
202069_s_at	214.4	127.6	677.5	602	616.15	1549.4	isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A
202070_s_at	150.1	41.2	253.09999	218.4	221.70001	591.1	isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A
202097_at	1277.3	364.34998	1106.7	1150.9	1540.7	1239.5	nucleoporin 153kDa	NUP153
202113_s_at	1692.35	255.09999	999.64996	1444.1	1208.1499	803.7	sorting nexin 2	SNX2
202114_at	987.15	109.8	328	709.4	389.7	367.7	sorting nexin 2	SNX2
202148_s_at	65.899994	89.95	457.35	287.4	415.2	186	pyrroline-5-carboxylate reductase 1	PYCR1
202170_s_at	616.35	256.2	876.55005	746	498.5	679.3	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT
202200_s_at	491.9	301.7	1558.45	794.5	1241.6	1040.2	SFRS protein kinase 1	SRPK1
202212_at	233.79999	104	398.90002	248.5	250.95	481.1	pescadillo homolog 1, containing BRCT domain (zebrafish)	PES1
202223_at	91.75	74.85	347.5	454.2	224.70001	720.9	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	STT3A
202236_s_at	152.35	122.25	1212	983.4	654.25	1672.2	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	SLC16A1
202240_at	10	156.2	346.95	458.3	227.7	566.1	polo-like kinase 1 (Drosophila)	PLK1
202243_s_at	1271.8	1165.3999	2419.15	2442.1	3163.1501	2354	proteasome (prosome, macropain) subunit, beta type, 4	PSMB4
202272_s_at	601.9	216.65	902	898.2	673.05	885.8	F-box protein 28	FBXO28
202284_s_at	1495.65	87.2	1950.7999	1241.6	577.1	1120.4	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A
202293_at	485.2	116.3	398.15002	330.3	392	382.4	stromal antigen 1	STAG1
202303_x_at	493.3	215.4	714.5	819	676.65	916.7	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SMARCA5
202314_at	548.95	32.3	651.35	417.1	691.8	462.4	cytochrome P450, family 51, subfamily A, polypeptide 1	CYP51A1
202330_s_at	172.29999	94.3	268.4	291	678.2	441.3	uracil-DNA glycosylase	UNG
202337_at	582.05	161.04999	461.8	362.9	336.09998	901.3	polyamine-modulated factor 1	PMF1
202346_at	422.9	249.65	658.35	669	516.05	612.1	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	UBE2K
202347_s_at	893.69995	309.6	580.05	931.5	747.75	968.3	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	UBE2K
202362_at	4143.7	1299.3999	3326.6	3837.8	4718.1	2306.1	RAP1A, member of RAS oncogene family	RAP1A
202381_at	432.7	258.05	702.75	1246.2	890.44995	878.1	ADAM metallopeptidase domain 9 (meltrin gamma)	ADAM9
202397_at	301.6	123.9	858.15	827.8	731.15	1200.1	nuclear transport factor 2	NUTF2
202416_at	517.55005	222.85	681.1	581.1	404.3	596.3	DnaJ (Hsp40) homolog, subfamily C, member 7	DNAJC7
202417_at	258.35	197.45001	517.75	493.5	567.95	439.1	kelch-like ECH-associated protein 1	KEAP1
202420_s_at	529.4	165.5	917.95	458.6	489.8	1198.6	DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9
202431_s_at	773.85	259.3	1769.3999	572.8	1532.75	766	v-myc myelocytomatosis viral oncogene homolog (avian)	MYC
202446_s_at	1484.8	193.65	466.15	994.3	450.35	2157.9	phospholipid scramblase 1	PLSCR1
202451_at	209.6	210.15	545.1	508.4	367.3	630.7	general transcription factor IIH, polypeptide 1, 62kDa	GTF2H1
202468_s_at	124.1	216	1906.25	1125.3	1333	553.7	catenin (cadherin-associated protein), alpha-like 1	CTNNAL1
202498_s_at	1852.1499	104.95	421.35	285.3	403.35	546	solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A3
202520_s_at	962.65	668	1859.15	1485.3	1402.75	1382.7	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	MLH1
202533_s_at	36.7	89.9	567.1	635.6	541.95	943.9	dihydrofolate reductase	DHFR
202536_at	1188.25	349.40002	930.5	974.5	522.5	661.4	chromatin modifying protein 2B	CHMP2B
202543_s_at	473.25	159.35	552.4	472.7	332.6	610.5	glia maturation factor, beta	GMFB
202557_at	937.85	442.45	966.85	1126.2	797.85	650.8	heat shock protein 70kDa family, member 13	HSPA13
202564_x_at	207.4	221.2	720	453.5	642.85	487.5	ADP-ribosylation factor-like 2	ARL2
202580_x_at	23.75	175.95	407.35	556	433.9	479.5	forkhead box M1	FOXM1
202602_s_at	1014.2	643.9	1332.6	1293	1261.1	1172.7	HIV-1 Tat specific factor 1	HTATSF1
202613_at	206.9	107	947.30005	532.2	655.05	1116.7	CTP synthase	CTPS
202634_at	687.8	299	635.05	551.9	666.94995	511.8	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	POLR2K
202637_s_at	593.4	63.6	316.2	460.5	434.5	600.6	intercellular adhesion molecule 1	ICAM1

202638_s_at	344.55	34.35	289.05	433.1	297.15	473	intercellular adhesion molecule 1	ICAM1
202647_s_at	392.4	179.15	657.5	551.4	577	827.9	neuroblastoma RAS viral (v-ras) oncogene homolog	NRAS
202653_s_at	2148.4	542.35	1453.6001	1306.5	1401.55	1129.3	membrane-associated ring finger (C3HC4) 7	7-Mar
202654_x_at	1001.2	268.5	1342.2	814.9	892.2	822.5	membrane-associated ring finger (C3HC4) 7	7-Mar
202687_s_at	297.45	289.09998	942.3	2156.2	1200.75	1150.4	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10
202702_at	574.35	164	436.15002	381.7	487.5	288.4	tripartite motif-containing 26	TRIM26
202706_s_at	223	70.6	437.5	254.5	278.6	558.8	uridine monophosphate synthetase	UMPS
202726_at	167.5	110.15	467.3	348.7	374.9	385	ligase I, DNA, ATP-dependent	LIG1
202763_at	832.25	159.75	642.35	1288.3	841.2	870.6	caspase 3, apoptosis-related cysteine peptidase	CASP3
202817_s_at	277.45	107.8	434.44998	551.6	175.65	569.2	synovial sarcoma translocation, chromosome 18	SS18
202829_s_at	1333.65	607	1418.8	1413.5	1623.15	1071.2	vesicle-associated membrane protein 7	VAMP7
202862_at	93.2	288.4	806	1093.1	728	929.8	fumarylacetoacetate hydrolase (fumarylacetoacetase)	FAH
202883_s_at	283.55	91.1	371	242.5	212.79999	676.9	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	PPP2R1B
202886_s_at	87.05	46.6	245.55	176.6	148.95	527.2	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	PPP2R1B
202892_at	239.90001	163.75	622.75	523.5	666.6	708	cell division cycle 23 homolog (S. cerevisiae)	CDC23
202907_s_at	722	275.3	619.4	810.6	789.2	813	nibrin	NBN
202911_at	448.05	317.45	2567.8	976.4	2288.9502	1260.9	mutS homolog 6 (E. coli)	MSH6
202934_at	425.35	33.2	602	214.7	214.7	281.8	hexokinase 2	HK2
202949_s_at	29.699999	32.3	531.5	458.7	423.75	104.3	four and a half LIM domains 2	FHL2
203007_x_at	1091.75	453.59998	1441.65	1867.6	1364.25	1536.6	lysophospholipase I	LYPLA1
203032_s_at	53.1	72.1	733.8	560.7	765.4	671.4	fumarate hydratase	FH
203033_x_at	385.7	440.9	2107.4	1569.9	2060.2998	1747.9	fumarate hydratase	FH
203079_s_at	543.05	123.100006	395.85	293.6	253.6	429.2	cullin 2	CUL2
203082_at	484.65	153.2	561.4	441.7	383.40002	604.1	BMS1 homolog, ribosome assembly protein (yeast)	BMS1
203086_at	334.5	86.6	289.7	421.8	411.25	300.2	kinesin heavy chain member 2A	KIF2A
203087_s_at	1011.5	369.05	1037.75	1795	1933	1797.3	kinesin heavy chain member 2A	KIF2A
203089_s_at	280.55	126.45	746.65	982.5	786.19995	573.7	HtrA serine peptidase 2	HTRA2
203091_at	230.20001	110.05	301.7	274.3	254.7	578.6	far upstream element (FUSE) binding protein 1	FUBP1
203094_at	293.45	155.3	528.7	376.3	310.40002	401.1	MAD2L1 binding protein	MAD2L1BP
203098_at	239.3	164.3	595.75	388.9	423	290.6	chromodomain protein, Y-like	CDYL
203103_s_at	415.8	237.2	759.3	636.7	567.4	1312.7	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	PRPF19
203105_s_at	234.70001	158.35	643.45	464.8	477.5	416.2	dynamin 1-like	DNM1L
203109_at	254.65	136.4	531.4	471.7	567.2	829.9	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	UBE2M
203119_at	168.95001	76.5	413.09998	173.2	256.3	451.8	coiled-coil domain containing 86	CCDC86
203120_at	619.19995	183.1	535.75	596	501.1	740.3	tumor protein p53 binding protein, 2	TP53BP2
203176_s_at	357.84998	90.8	718.64996	374.5	350	899.1	transcription factor A, mitochondrial	TFAM
203210_s_at	72.9	69.25	427.45	325.6	420.7	469.3	replication factor C (activator 1) 5, 36.5kDa	RFC5
203218_at	686.45	328.7	677.65	611.1	669	465.8	mitogen-activated protein kinase 9	MAPK9
203233_at	975.55	209	680.6	279.9	516.95	311.4	interleukin 4 receptor	IL4R
203270_at	40.65	124.75	435.44998	302.8	306.3	642.9	deoxythymidylate kinase (thymidylate kinase)	DTYMK
203275_at	424.05	101.6	353.6	394.6	446.95	404.9	interferon regulatory factor 2	IRF2
203276_at	224.55	181.70001	831.05	925	971	1991.7	lamin B1	LMNB1
203311_s_at	439.69998	97.55	373.5	718	333.6	758	ADP-ribosylation factor 6	ARF6
203328_x_at	184.95001	119.850006	450.15002	279.1	211	468.3	insulin-degrading enzyme	IDE
203333_at	201.20001	208.85	588.95	994.6	908.89996	806.8	kinesin-associated protein 3	KIFAP3
203336_s_at	481.45	255.15	1727.8	461.9	949.65	552.7	integrin beta 1 binding protein 1	ITGB1BP1
203358_s_at	237.90001	212.9	1321.4	1466.8	2068.2	1165.3	enhancer of zeste homolog 2 (Drosophila)	EZH2
203392_s_at	1350.95	208.85	909.9	759.1	547.75	706.5	C-terminal binding protein 1	CTBP1
203405_at	383.25	344.85	1674.75	1410.9	1443.55	1307	proteasome (prosome, macropain) assembly chaperone 1	PSMG1
203410_at	602.75	78.15	490.2	400.3	272.85	277.2	adaptor-related protein complex 3, mu 2 subunit	AP3M2
203411_s_at	578.75	124.8	3768.75	1299.5	823.94995	1304.5	lamin A/C	LMNA
203418_at	4.1000004	235.45001	691.55	594.9	572.1	1275.4	cyclin A2	CCNA2
203427_at	1060.55	104.6	450.8	500.5	343.35	459.6	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A
203428_s_at	647.30005	97.15	450.5	458.8	494.75	649.5	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	ASF1A
203465_at	269.2	148.04999	711.55	588.6	596.4	777.5	mitochondrial ribosomal protein L19	MRPL19
203537_at	499.80002	154.45	998.15	656.9	531.6	703.8	phosphoribosyl pyrophosphate synthetase-associated protein 2	PRPSAP2
203611_at	338.55	207.54999	388.55002	366.2	363.6	294.5	telomeric repeat binding factor 2	TERF2
203612_at	47.9	69.75	566.05	232.9	328.95	535.4	bystin-like	BYSL
203629_s_at	320.8	97.55	304.1	258	305.9	194.4	component of oligomeric golgi complex 5	COG5
203630_s_at	507.55	197	587.85	431.2	600.55	354.3	component of oligomeric golgi complex 5	COG5
203694_s_at	401.35	174.6	451.84998	415.6	317.45	473.8	DEAH (Asp-Glu-Ala-His) box polypeptide 16	DHX16

203696_s_at	155.05	97.15	1035.25	762.3	850.14996	1445.7	replication factor C (activator 1) 2, 40kDa	RFC2
203714_s_at	323.8	220.9	607.44995	550.9	806.35	722.7	tubulin folding cofactor E	TBCE
203744_at	51.6	111.75	507.9	446.3	201.20001	712.5	high-mobility group box 3	HMGB3
203814_s_at	345.90002	72.8	499.95	257.1	387.3	182.5	NAD(P)H dehydrogenase, quinone 2	NQO2
203830_at	140.05	101.600006	433.80002	371.1	287.85	470.6	chromosome 17 open reading frame 75	C17orf75
203837_at	1103.35	93.7	225.20001	442.1	294.55	261.6	mitogen-activated protein kinase kinase kinase 5	MAP3K5
203840_at	177.05	75.35	388.65	286.4	301.15	515.7	basic leucine zipper nuclear factor 1	BLZF1
203880_at	567.1	413.5	2019.5	1309.1	2035.45	1383.5	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	COX17
203881_s_at	20.8	288.45	2610.4	2050.5	1905.4	1018	dystrophin	DMD
203893_at	486.8	343.90002	868.35	847.9	1181.25	1212.7	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	TAF9
203956_at	384.8	229.35	478.75	401.6	420.8	322.9	MORC family CW-type zinc finger 2	MORC2
203966_s_at	1272.8	259.2	704.30005	493.8	545.35	429.2	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	PPM1A
203967_at	7.55	29.05	316.5	207.4	184.9	450.5	cell division cycle 6 homolog (S. cerevisiae)	CDC6
203968_s_at	10.15	36.949997	346.75	209.9	243.95001	479.2	cell division cycle 6 homolog (S. cerevisiae)	CDC6
203974_at	180.95	58.4	816.35	381.1	359.25	745.7	haloacid dehalogenase-like hydrolase domain containing 1A	HDHD1A
204126_s_at	2.55	84.55	489.55	266.4	467.8	528.3	CDC45 cell division cycle 45-like (S. cerevisiae)	CDC45L
204128_s_at	49.4	115.5	731.35	597.6	548.5	915.9	replication factor C (activator 1) 3, 38kDa	RFC3
204171_at	791.1	114.65	514.7	433.2	491	556.9	ribosomal protein S6 kinase, 70kDa, polypeptide 1	RPS6KB1
204172_at	384.59998	530.5	4863.8	1210.4	2779.7002	1366.4	coproporphyrinogen oxidase	CPOX
204208_at	300.6	145.65	481	370.7	463.3	298.9	RNA guanylyltransferase and 5''-phosphatase	RNGTT
204211_x_at	368.9	45.35	350.7	617.3	554.05	776.2	eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2
204238_s_at	105.55	167.1	667.55	302.8	478.8	383.2	chromosome 6 open reading frame 108	C6orf108
204269_at	334.8	85.8	493.55002	699.4	578.30005	404.3	pim-2 oncogene	PIM2
204391_x_at	286.2	111.399994	426.3	275.2	425.95	283.7	tripartite motif-containing 24	TRIM24
204407_at	118.2	128.05	660.5	446.5	670.35	361.5	transcription termination factor, RNA polymerase II	TTF2
204426_at	222	155.45	584.55	823.1	513.55	973.2	transmembrane emp24 domain trafficking protein 2	TMED2
204427_s_at	277.59998	195.15	582.35	832.5	527.3	1104.9	transmembrane emp24 domain trafficking protein 2	TMED2
204435_at	716.85	82.399994	332.7	242.9	388.35	194.5	nucleoporin like 1	NUPL1
204441_s_at	119.85001	99.15	446.19998	287.1	362.34998	528.4	polymerase (DNA directed), alpha 2 (70kD subunit)	POLA2
204478_s_at	419.35	117.6	315.95	265.4	288.7	394.9	RAB interacting factor	RABIF
204496_at	429.94998	151.75	439.95	323.5	400.15002	283.9	striatin, calmodulin binding protein 3	STRN3
204513_s_at	416.35	184.54999	935	667.8	543.15	442.9	engulfment and cell motility 1	ELMO1
204528_s_at	3596	1718.8	3593.5	3525.3	4188.9	2554.7	nucleosome assembly protein 1-like 1	NAP1L1
204533_at	79.6	7.1	2399.75	867.8	1444.85	70.6	chemokine (C-X-C motif) ligand 10	CXCL10
204566_at	722.55	184.25	1070.95	810.3	704.25	352.6	protein phosphatase 1D magnesium-dependent, delta isoform	PPM1D
204603_at	18.9	67.95	490.59998	339	503.09998	574.1	exonuclease 1	EXO1
204634_at	317.75	135.6	457.5	600.6	323.7	440.4	NIMA (never in mitosis gene a)-related kinase 4	NEK4
204641_at	18.95	278.65	907.2	1149.7	869	924.4	NIMA (never in mitosis gene a)-related kinase 2	NEK2
204699_s_at	272.95	78.25	422.84998	203.5	226.05	487.4	chromosome 1 open reading frame 107	C1orf107
204700_x_at	307.45	69.05	512.3	279.8	244.8	433.3	chromosome 1 open reading frame 107	C1orf107
204702_s_at	104.60001	16.75	708.4	582.9	435.95	136.1	nuclear factor (erythroid-derived 2)-like 3	NFE2L3
204716_at	122.6	39.85	324.65	643.8	278.55	145.5	coiled-coil domain containing 6	CCDC6
204831_at	224.75	158.9	536.05	407.4	397.40002	387.3	cyclin-dependent kinase 8	CDK8
204896_s_at	488.95	62.449997	381.65	235.2	289.05	203.6	prostaglandin E receptor 4 (subtype EP4)	PTGER4
204897_at	8565.1	1408.3	3415.1	3176.2	2720.6	2388.9	prostaglandin E receptor 4 (subtype EP4)	PTGER4
204900_x_at	458.65002	243.75	936.35004	855.3	1068.75	1067	Sin3A-associated protein, 30kDa	SAP30
204905_s_at	383.09998	302.75	671.5	776.2	886.80005	1423.7	eukaryotic translation elongation factor 1 epsilon 1	EEF1E1
204976_s_at	500.90002	146.1	570.35	374.6	366.3	289.5	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	AMMECR1
205034_at	79.2	86.35	295.4	453.8	378.2	622.4	cyclin E2	CCNE2
205053_at	123.25	454.3	1274.15	968.3	1331.25	938.9	primase, DNA, polypeptide 1 (49kDa)	PRIM1
205063_at	231.8	109.45	392.09998	265.2	306.7	448.7	survival of motor neuron protein interacting protein 1	SIP1
205085_at	15.5	60	198.65	176.4	286.65	401.5	origin recognition complex, subunit 1-like (yeast)	ORC1L
205065_s_at	28.25	11.55	58.35	90.2	61.6	94.9	protein tyrosine phosphatase, non-receptor type 11	PTPN11
205126_at	405.1	173.45	585.5	507.8	544	513.6	vaccinia related kinase 2	VRK2
205173_x_at	1167.15	234.95001	2346.25	2236	2183.4	617	CD58 molecule	CD58
205321_at	229.5	99.8	1337.6	1511.3	862.5	2036.9	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	EIF2S3
205339_at	77.100006	173.85	508.30002	530.5	714.44995	839.4	SCL/TAL1 interrupting locus	STIL
205393_s_at	22.45	96.85	608.05	613.4	485.25	935.8	CHK1 checkpoint homolog (S. pombe)	CHEK1
205394_at	38.8	104.4	616.1	717.4	527.45	902	CHK1 checkpoint homolog (S. pombe)	CHEK1

205401_at	173.85	104.65	472.55	593.9	523.4	844	alkylglycerone phosphate synthase	AGPS
205527_s_at	175.5	23.85	291.75	131.1	187.15	376.9	gem (nuclear organelle) associated protein 4	GEMIN4
205548_s_at	673.30005	233.29999	1332.85	1170.8	1335.25	440.4	BTG family, member 3	BTG3
205788_s_at	2195.05	1016.6	2433.45	2385.4	2395.2	1737.7	zinc finger CCCH-type containing 11A	ZC3H11A
205804_s_at	803.95	340.84998	1169.6	1179	921.5	1072.4	TRAF3 interacting protein 3	TRAF3IP3
205961_s_at	924.25	870.65	2219.7	1828.4	1797.7	1462.8	PC4 and SFRS1 interacting protein 1	PSIP1
205963_s_at	240	154.6	534.85	415.1	505.2	535	DnaJ (Hsp40) homolog, subfamily A, member 3	DNAJA3
205995_x_at	321.05	101.55	302.95	367.3	351.35	250.5	IQ motif containing B1	IQCB1
206042_x_at	760.35	131.95	617.6	517.8	487.6	443.4	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	SNRPN /// SNURF
206061_s_at	697.9	167.35	605.75	275.1	430.5	253.4	dicer 1, ribonuclease type III	DICER1
206066_s_at	233.5	74.3	458.95	323.1	456.5	539.6	RAD51 homolog C (S. cerevisiae)	RAD51C
206102_at	31.8	311.2	1080.6001	707.9	1273.8501	1423.2	GINS complex subunit 1 (Psf1 homolog)	GINS1
206113_s_at	363.2	140.8	408.9	487.3	289.9	337.5	RAB5A, member RAS oncogene family	RAB5A
206173_x_at	225.15	64.65	180.35	158.2	206.65	588.7	GA binding protein transcription factor, beta subunit 1	GABPB1
206245_s_at	4270.8	339.2	2217.45	1777.8	1328.15	1533	influenza virus NS1A binding protein	IVNS1ABP
206302_s_at	256.90002	124	409.75	553.2	965.65	499.2	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	NUDT4 /// NUDT4P1
206316_s_at	93.95	104.25	375.09998	391.1	548.6	350.9	kinetochore associated 1	KNTC1
206461_x_at	1913.3999	185.7	301.55	411.8	1891.75	1978.7	metallothionein 1H	MT1H
206499_s_at	195.54999	73.25	505.80002	336	431.40002	628.7	regulator of chromosome condensation 1 /// SNHG3-RCC1 readthrough transcript	RCC1 /// SNHG3-RCC1
206550_s_at	204.25	66.45	248	183.4	365.75	302.8	nucleoporin 155kDa	NUP155
206562_s_at	834.55005	248.5	991.65	1127.3	681.35	743.8	casein kinase 1, alpha 1	CSNK1A1
206571_s_at	517.45	60.15	255.25	284.6	387.95	232.1	mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4
206729_at	120.55	167.55	526.15	746.9	674.9	1475.2	tumor necrosis factor receptor superfamily, member 8	TNFRSF8
206788_s_at	171.15	122.45	375.95	693.2	556.25	1258.7	core-binding factor, beta subunit	CBFB
207088_s_at	167.4	103.55	387.7	433.2	380.45	796.1	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	SLC25A11
207275_s_at	1820.05	27.099998	322.9	187.7	502.55002	368.4	acyl-CoA synthetase long-chain family member 1	ACSL1
207391_s_at	206.65	76.95	447.3	338.8	411.90002	485.7	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	PIP5K1A
207396_s_at	175.9	119.149994	351.5	246.6	270.25	458.5	asparagine-linked glycosylation 3, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	ALG3
207431_s_at	998.1	406.15	1536.35	1348.9	1150.05	1854.6	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	DEGS1
207543_s_at	221.55	113.65	1054.4	628.5	477.05	418.6	prolyl 4-hydroxylase, alpha polypeptide I	P4HA1
207549_x_at	493.05	191.5	648.3	486.3	480.8	344.3	CD46 molecule, complement regulatory protein	CD46
207614_s_at	505.75	248.45	1082.85	648.5	690.80005	577.4	cullin 1	CUL1
207719_x_at	729.7	188.75	1483	673.2	818.80005	639.1	centrosomal protein 170kDa	CEP170
207760_s_at	1343.5	184.1	487.59998	441.6	344.7	569.6	nuclear receptor co-repressor 2	NCOR2
207813_s_at	19.1	60.75	1232.9	843.7	397.40002	247.4	ferredoxin reductase	FDXR
208091_s_at	1872.3501	194.45	2988.25	1721.7	1341.85	1085	vesicular, overexpressed in cancer, prosurvival protein 1	VOPP1
208093_s_at	1471.7	167.04999	343.15	411.4	458.6	429.3	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	NDEL1
208478_s_at	131.4	83.75	514.6	1117.7	670.65	902.4	BCL2-associated X protein	BAX
208541_x_at	145.2	24.9	206.1	133.1	142.4	358.8	transcription factor A, mitochondrial	TFAM
208624_s_at	267.85	68.7	493	161.5	231.70001	476.8	eukaryotic translation initiation factor 4 gamma, 1	EIF4G1
208648_at	789.44995	115.2	405	301.3	250.95001	504.1	valosin-containing protein	VCP
208653_s_at	649	298.75	673.65	665.7	553.75	1341.7	CD164 molecule, sialomucin	CD164
208680_at	1111.4	758.9	6015.0996	2324.5	5141.5996	2523.1	peroxiredoxin 1	PRDX1
208683_at	5150.1504	1614.3	4435.05	4862.5	3626.15	3022.6	calpain 2, (m/II) large subunit	CAPN2
208694_at	684.15	306.6	1584.2	893.5	1205.95	1058.8	protein kinase, DNA-activated, catalytic polypeptide	PRKDC
208775_at	3008.2	1756.8	5399.75	4204.1	4623.5996	4116.2	exportin 1 (CRM1 homolog, yeast)	XPO1
208803_s_at	433.75	169.75	369.34998	424.9	404.59998	459.1	signal recognition particle 72kDa	SRP72
208811_s_at	1186.35	198.5	569.6	563.4	783.5	767.9	DnaJ (Hsp40) homolog, subfamily B, member 6 /// transmembrane protein 135	DNAJB6 /// TMEM135
208838_at	313.4	178.75	1232.1	522.4	878.5	690.6	cullin-associated and neddylation-dissociated 1	CAND1
208839_s_at	285.6	181.54999	1230.35	486.6	734.4	547.8	cullin-associated and neddylation-dissociated 1	CAND1
208840_s_at	863.05	180.75	605.5	912	463.2	848.5	GTPase activating protein (SH3 domain) binding protein 2	G3BP2
208864_s_at	1161.45	2140.4	4653.1504	5934.3	6730.7	4660.2	thioredoxin	TXN
208921_s_at	1203.5	1550.25	2668.6	3027.9	3501.4	3198.1	sorcin	SRI
208930_s_at	302.55	63.800003	445.8	179.4	218.79999	368.5	interleukin enhancer binding factor 3, 90kDa	ILF3
208931_s_at	339.1	72.399994	369.65	261.1	266.8	647.1	interleukin enhancer binding factor 3, 90kDa	ILF3
208938_at	229.75	66.149994	458.09998	185.1	272.9	383.5	papillary renal cell carcinoma (translocation-associated)	PRCC
208967_s_at	246.45	270.8	1262.8999	963.9	1373.9	1473	adenylate kinase 2	AK2
208990_s_at	2154.95	916.19995	1685	1826.9	1985.8	1605.1	heterogeneous nuclear ribonucleoprotein H3 (2H9)	HNRNPH3
209003_at	167.1	84.399994	274.15	352.7	272.25	658.2	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	SLC25A11
209015_s_at	227.05	73.3	621.6	416.2	382.45	244	DnaJ (Hsp40) homolog, subfamily B, member 6	DNAJB6
209017_s_at	365.40002	194.4	615.05005	654	437.75	446	lon peptidase 1, mitochondrial	LONP1

209027_s_at	1261.45	317.35	1202.7	1308.2	709.45	1327	abl-interactor 1	ABI1
209046_s_at	1325.65	919.85	1777.65	2001.7	1787.35	1472.3	GABA(A) receptor-associated protein-like 2	GABARAPL2
209052_s_at	27	61.1	156	315.2	174.25	285	Wolf-Hirschhorn syndrome candidate 1	WHSC1
209085_x_at	361.45	205.5	580.55	601.5	453.9	477.3	replication factor C (activator 1) 1, 145kDa	RFC1
209092_s_at	628.3	172.9	816.9	689.3	477.15	932.2	glyoxalase domain containing 4	GLOD4
209142_s_at	658.9	317.40002	1010.10004	1278.8	1120	1538.2	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	UBE2G1
209157_at	797.25	271.7	890.5	1099.9	633	843.7	DnaJ (Hsp40) homolog, subfamily A, member 2	DNAJA2
209162_s_at	565.95	188.7	472.55002	355.8	405	301.1	PRP4 pre-mRNA processing factor 4 homolog (yeast)	PRPF4
209175_at	189.85	96.05	473	273	315.65002	450	SEC23 interacting protein	SEC23IP
209193_at	629.80005	217.5	407.65002	701.6	699.75	804.7	pim-1 oncogene	PIM1
209208_at	299.34998	84.35	426.75	385.7	310.75	730	mannose-P-dolichol utilization defect 1	MPDU1
209231_s_at	217.65	74.15	295.8	274.3	202.45001	367.2	dynactin 5 (p25)	DCTN5
209233_at	541.5	209.1	734.55	372.7	446.9	1177.7	EMG1 nucleolar protein homolog (S. cerevisiae)	EMG1
209259_s_at	748.1	389.65	882.15	1314	1212.55	1441.6	structural maintenance of chromosomes 3	SMC3
209295_at	1437.25	150.45001	1634.8	2373.8	1868.25	414.3	tumor necrosis factor receptor superfamily, member 10b	TNFRSF10B
209331_s_at	577.05	122.25	512.25	394	304.45	391.9	MYC associated factor X	MAX
209433_s_at	132.6	59.050003	620.95	322.7	270.15	660.6	phosphoribosyl pyrophosphate amidotransferase	PPAT
209463_s_at	145.2	130.45001	272.75	235.9	245.95001	431.6	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	TAF12
209509_s_at	181.65	121.55	373	295.7	229.2	482.7	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	DPAGT1
209523_at	858.45	384.25	738.85	665	773.15	568.6	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	TAF2
209527_at	320.55	62.300003	319.35	175.8	144.35	609.1	exosome component 2	EXOSC2
209533_s_at	434.75	114.7	332.85	407.7	260.75	424.4	phospholipase A2-activating protein	PLAA
209567_at	359.85	144.1	713.25	340.4	405.55	344.3	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	RRS1
209572_s_at	853.8	359.9	1955.95	1674.2	1262.1	1321.6	embryonic ectoderm development	EED
209630_s_at	650.2	327.59998	623.9	593.4	537.95	461.7	F-box and WD repeat domain containing 2	FBXW2
209642_at	37.35	418.35	1056.6499	1045.9	1431	1236.5	budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1
209666_s_at	396.3	137.45	466.35	359.2	404.84998	392.3	conserved helix-loop-helix ubiquitous kinase	CHUK
209680_s_at	4.1499996	138.54999	385.45	384	268.8	453.5	kinesin family member C1	KIFC1
209715_at	128.34999	112.399994	314.85	269.6	294.40002	549.8	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5
209748_at	326.09998	133.3	514.5	286.4	390.09998	212.5	spastin	SPAST
209751_s_at	370.8	58.25	455.5	222	214.4	394	trafficking protein particle complex 2 /// trafficking protein particle complex 2 pseudogene 1	TRAPPC2 /// TRAPPC2P1
209753_s_at	139.05	92.15	452.45	521.9	461.05	747.9	thymopoietin	TMPO
209754_s_at	169.8	55.05	615.65	639.8	577.4	894.6	thymopoietin	TMPO
209788_s_at	1553.3501	358.3	1073.7	1231.7	820.25	1354.2	endoplasmic reticulum aminopeptidase 1	ERAP1
209814_at	1132.6499	212.15	544.1	960.3	877.4	1101.8	zinc finger protein 330	ZNF330
209824_s_at	1019.5	180.6	435.40002	378	530.3	374.9	aryl hydrocarbon receptor nuclear translocator-like	ARNTL
209849_s_at	106.9	146.55	969.4	716.8	1132.3	1065.6	RAD51 homolog C (S. cerevisiae)	RAD51C
209860_s_at	1297.55	806.15	1561.4	1606.7	1979	1693.5	annexin A7	ANXA7
209884_s_at	337.05	119.9	917.25	361.2	609.9	266	solute carrier family 4, sodium bicarbonate cotransporter, member 7	SLC4A7
209896_s_at	485.35	220.20001	495.84998	637.4	542.4	764.1	protein tyrosine phosphatase, non-receptor type 11	PTPN11
210028_s_at	242.95001	134.7	578.7	486.8	534.5	443	origin recognition complex, subunit 3-like (yeast)	ORC3L
210076_x_at	398.15	167.15	944.45	941.8	629	687.6	SERPINE1 mRNA binding protein 1	SERBP1
210092_at	842.1	320.85	608.3	683.7	933.1	938.5	mago-nashi homolog, proliferation-associated (Drosophila)	MAGOH
210093_s_at	1102.05	316.90002	698.05005	908.3	878.69995	1208.6	mago-nashi homolog, proliferation-associated (Drosophila)	MAGOH
210115_at	64.9	101.7	622.9	406.8	385.5	666.9	ribosomal protein L39-like	RPL39L
210137_s_at	496.9	234.4	848.15	861.8	683.6	802.5	dCMP deaminase	DCTD
210154_at	231.6	210.7	583.4	609.1	556.1	600.3	malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2
210180_s_at	319	96.850006	379.25	275.8	224.2	496.2	transformer 2 beta homolog (Drosophila)	TRA2B
210317_s_at	129.5	46.199997	465.7	767.8	465.15002	1050.7	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	YWHAE
210334_x_at	35.9	133.55	466.6	375.8	324.6	615.5	baculoviral IAP repeat-containing 5	BIRC5
210371_s_at	594.75	302.59998	1024.45	1269.2	1119.25	1653.3	retinoblastoma binding protein 4	RBBP4
210385_s_at	221.5	148.85	383.85	509.6	280.25	516.9	endoplasmic reticulum aminopeptidase 1	ERAP1
210416_s_at	34.2	85.15	232.4	153.6	294.6	190.9	CHK2 checkpoint homolog (S. pombe)	CHEK2
210458_s_at	288.5	98.2	779.2	755.7	725.75	285.2	TRAF family member-associated NFKB activator	TANK
210512_s_at	1522.7	44.949997	790.8	924	238.95	180.1	vascular endothelial growth factor A	VEGFA
210527_x_at	365.84998	109.55	574.19995	765.6	1551.7001	186.4	tubulin, alpha 3c	TUBA3C
210538_s_at	2363.4	146.35	1416.3	910.9	2249.65	1503.2	baculoviral IAP repeat-containing 3	BIRC3
210541_s_at	217	147.45	486.8	354	386.6	309.3	tripartite motif-containing 27	TRIM27
210543_s_at	237.20001	111.85	656.05	428.3	555.2	572.5	protein kinase, DNA-activated, catalytic polypeptide	PRKDC

210567_s_at	93.55	55.55	184.5	188.5	343.05002	465.3	S-phase kinase-associated protein 2 (p45)	SKP2
210616_s_at	798.55005	190.85	464.6	355.9	415.8	326.1	SEC31 homolog A (S. cerevisiae)	SEC31A
210681_s_at	1844.1499	218.75	659.44995	719	369.8	652.8	ubiquitin specific peptidase 15	USP15
210768_x_at	281.09998	161.45	765.4	511	567.9	1219.9	transmembrane and coiled-coil domains 1	TMCO1
210840_s_at	1632.7	401.34998	1182.05	1276.6	683.75	862.1	IQ motif containing GTPase activating protein 1	IQGAP1
210966_x_at	337.55	124.600006	575.6	274	361.3	250.7	La ribonucleoprotein domain family, member 1	LARP1
210970_s_at	840.95	375.45	698.15	654	679	482.9	inhibitor of Bruton agammaglobulinemia tyrosine kinase	IBTK
210996_s_at	1271.95	445.15	1911.25	1930.9	1468.95	1741	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	YWHAE
211074_at	1836.55	628.95	1533.05	1874.8	1581.55	1633.3	folate receptor 1 (adult)	FOLR1
211080_s_at	22.9	121.7	525.75	624.6	458.4	411.1	NIMA (never in mitosis gene a)-related kinase 2	NEK2
211098_x_at	307.59998	177.54999	740.2	522.8	493.09998	1196.7	transmembrane and coiled-coil domains 1	TMCO1
211108_s_at	10.7	2.15	20.7	49.8	33.25	82.6	Janus kinase 3	JAK3
211136_s_at	225.45	142.15	497.85	233.6	266.85	439.9	cleft lip and palate associated transmembrane protein 1	CLPTM1
211152_s_at	224.45	100.100006	468.65002	689.6	551.15	408.3	HtrA serine peptidase 2	HTRA2
211505_s_at	583.65	263.95	525.3	593.8	489	419.9	staufen, RNA binding protein, homolog 1 (Drosophila)	STAU1
211630_s_at	386.15002	222.3	758.85	610.6	690.8	572.4	glutathione synthetase	GSS
211707_s_at	352.8	77.95	308.05	402.9	348.3	230.6	IQ motif containing B1	IQCB1
211744_s_at	592.30005	136.8	1340.55	1169	1299.8501	313.2	CD58 molecule	CD58
211754_s_at	114.85001	62.300003	465.69998	229.9	331.25	442.1	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	SLC25A17
211764_s_at	1094.4	172.45001	850.45	609.8	464.19998	704.3	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	UBE2D1
211804_s_at	39.25	53.65	388.75	171.5	323.45	558.5	cyclin-dependent kinase 2	CDK2
211833_s_at	159.75	96.850006	579.95	1090.7	692.94995	859.9	BCL2-associated X protein	BAX
211930_at	1040.5	266.6	732.8	683.1	894.05005	572	heterogeneous nuclear ribonucleoprotein A3	HNRNPA3
211949_s_at	158.9	47.4	174.4	124.2	159.65	378.9	nucleolar and coiled-body phosphoprotein 1	NOLC1
212003_at	187.45001	120.7	318.85	360.1	302.25	588.6	chromosome 1 open reading frame 144	C1orf144
212004_at	244.75	153.35	428.5	450.5	443.34998	508.4	chromosome 1 open reading frame 144	C1orf144
212006_at	1172.95	385.85	1123.2	1053	1039.2	783.8	UBX domain protein 4	UBXN4
212008_at	441.90002	205.9	797.4	716.8	753.69995	530.6	UBX domain protein 4	UBXN4
212024_x_at	840.05	149.35	711.5	339.5	405.40002	303.1	flightless I homolog (Drosophila)	FLII
212031_at	1145.55	162.1	565.65	453.3	416	787.8	RNA binding motif protein 25	RBM25
212105_s_at	153.65	61.2	621.8	181.4	261.25	565.2	DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9
212115_at	140.6	135.35	596.05	577.8	548.25	695.7	hematological and neurological expressed 1-like	HN1L
212116_at	298.65	187.9	618.9	547.2	466.75	512.5	tripartite motif-containing 27	TRIM27
212136_at	1309.65	233.9	819.55	1037.1	939.65	1161.2	ATPase, Ca++ transporting, plasma membrane 4	ATP2B4
212137_at	1945.9	1158.6	2693.4	2864.8	2958.75	2284.7	La ribonucleoprotein domain family, member 1	LARP1
212139_at	442.7	163.5	368.8	342.3	482.5	418.2	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	GCN1L1
212142_at	44.75	30.949999	626.6	253.5	321.95	603.4	minichromosome maintenance complex component 4	MCM4
212175_s_at	474.15002	386.5	1423.25	1266.5	1937.25	1881.4	adenylate kinase 2	AK2
212193_s_at	249.75	119.05	595.5	319.8	389.95	324.6	La ribonucleoprotein domain family, member 1	LARP1
212211_at	219.7	96.2	455.65	361.5	335.84998	384.2	ankyrin repeat domain 17	ANKRD17
212217_at	89.5	113.3	593.8	262.7	321.25	243.8	prolyl endopeptidase-like	PREPL
212264_s_at	625.69995	202.65	507.09998	543.5	547.94995	710.8	wings apart-like homolog (Drosophila)	WAPAL
212277_at	477.1	160	923.85	361.3	663.44995	309	myotubularin related protein 4	MTMR4
212301_at	915.8	300.8	738.3	534.2	573.9	456.8	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	RTF1
212311_at	418.55	47.7	168.15	677.5	278.45	486	KIAA0746 protein	KIAA0746
212371_at	605.9	327.59998	1010.15	1207.4	961.85	921.1	PPPDE peptidase domain containing 1	PPPDE1
212379_at	71.4	102.55	873.95	396	686.6	748	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	GART
212432_at	496.09998	166	426.5	368.1	328.75	937.8	GrpE-like 1, mitochondrial (E. coli)	GRPEL1
212442_s_at	773.2	66.85	1971.95	757.6	519.25	651.8	LAG1 homolog, ceramide synthase 6	LASS6
212446_s_at	462.4	31.15	1203.7	551.3	347.95	497.4	LAG1 homolog, ceramide synthase 6	LASS6
212461_at	2281.55	497	2553.5498	1266.6	2193.55	1523.2	antizyme inhibitor 1	AZIN1
212467_at	428.95	179.20001	478.95	438.6	329.25	368.9	DnaJ (Hsp40) homolog, subfamily C, member 13	DNAJC13
212470_at	621.55	235.25	664.9	539	548.15	399.8	sperm associated antigen 9	SPAG9
212474_at	356.25	207.79999	524.3	461	538.95	399.4	AVL9 homolog (S. cerevisiase)	AVL9
212515_s_at	1257.2	223.8	1447.05	1157.1	934	2119.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X

212527_at	104.85001	82.149994	310.4	469.1	413.75	415.1	PPPDE peptidase domain containing 2	PPPDE2
212532_s_at	523.2	164.8	920.85	811.2	503.7	507.8	LSM12 homolog (S. cerevisiae)	LSM12
212556_at	242.04999	149.5	536.3	377.8	435.8	327.1	scribbled homolog (Drosophila)	SCRIB
212561_at	703.44995	86.2	955.2	366.6	511	193.7	DENN/MADD domain containing 5A	DENND5A
212589_at	343.75	225.45	703.5	1742.8	1282.35	926.8	related RAS viral (r-ras) oncogene homolog 2	RRAS2
212623_at	438.40002	197.85	486	501.2	299.15	658.1	transmembrane protein 41B	TMEM41B
212709_at	396.59998	94.8	365.6	335.8	353	550.4	nucleoporin 160kDa	NUP160
212714_at	127.45001	149.4	732.9	360.1	674.05005	307.9	La ribonucleoprotein domain family, member 4	LARP4
212725_s_at	1368.9	445.7	868.65	1041.8	866.75	614	taurine upregulated 1 (non-protein coding)	TUG1
212773_s_at	2659.2	1135.6	2206.75	2112.6	2249.25	1928.9	translocase of outer mitochondrial membrane 20 homolog (yeast)	TOMM20
212795_at	1473.35	341.95	816.85	1050.2	631.94995	637.3	KIAA1033	KIAA1033
212815_at	263.55	72.75	1091.3	415.2	514.85	602.6	activating signal cointegrator 1 complex subunit 3	ASCC3
212836_at	206.15	107.149994	408.19998	438	437.15002	546.3	polymerase (DNA-directed), delta 3, accessory subunit	POLD3
212840_at	552.7	120.45	333.65	223.1	330.75	155.6	UBX domain protein 7	UBXN7
212854_x_at	1785.7	781.65	1765.7001	2134.9	1953.85	1412	neuroblastoma breakpoint family, member 10	NBPF10
212888_at	1102	222.45	1006.95	408.5	681.9	388	dicer 1, ribonuclease type III	DICER1
212943_at	874.9	349.45	884.4	620.1	759.8	580.8	KIAA0528	KIAA0528
213007_at	101.25	305.7	653.45	896.1	901.05	1172.8	Fanconi anemia, complementation group I	FANCI
213008_at	85.8	255.79999	595.45	590.7	806.69995	733.7	Fanconi anemia, complementation group I	FANCI
213019_at	879.5	138.4	469.25	351.9	305.4	822	RAN binding protein 6	RANBP6
213026_at	2461.4	380.05	934.8	958.6	754.69995	593.8	ATG12 autophagy related 12 homolog (S. cerevisiae)	ATG12
213027_at	629.05005	340.84998	800.55	635.7	759.55	492.9	TROVE domain family, member 2	TROVE2
213038_at	442.05	45.4	262.5	703	551.95	155.6	ring finger protein 19B	RNF19B
213092_x_at	213.05	129.15	601.6	499.6	519.55005	942.3	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9
213128_s_at	670.15	183.54999	610.3	550.6	451.6	496.9	ubiquitin protein ligase E3A	UBE3A
213149_at	246.7	105.05	378.3	278.6	248.15001	415.8	dihydrolipoamide S-acetyltransferase	DLAT
213188_s_at	371.4	157.35	1816.95	2684.7	2063.6	1097.1	MYC induced nuclear antigen	MINA
213189_at	269.7	72.4	1456.8501	1739.7	1334.5	757.8	MYC induced nuclear antigen	MINA
213212_x_at	405.25	85.149994	468.05	468	339	269.7	golgi autoantigen, golgin subfamily a-like pseudogene /// golgi autoantigen, golgin subfamily a, 6D-like	FLJ40113 /// LOC440295
213233_s_at	512.7	135.55	574.85	357.7	366.95	298	kelch-like 9 (Drosophila)	KLHL9
213282_at	224.79999	17.400002	545	305.2	188.05	132.6	Apolipoprotein O-like	APOOL
213294_at	467.84998	43.1	349.9	682.5	612.45	577.9	---	---
213302_at	141.2	91.850006	521	322.9	437.9	684.3	phosphoribosylformylglycinamidine synthase	PFAS
213320_at	255.05	115.100006	697.75	417.5	483.34998	646	protein arginine methyltransferase 3	PRMT3
213322_at	365.65002	285.3	612.5	641	536.4	446.7	chromosome 6 open reading frame 130	C6orf130
213330_s_at	257.75	280.75	1557.55	1380.9	1200.75	1750.5	stress-induced-phosphoprotein 1	STIP1
213390_at	787.9	398.95	948.1	1168	802.8	1220.4	zinc finger CCCH-type containing 4	ZC3H4
213446_s_at	1266.35	87	475.34998	408	212.54999	293.8	IQ motif containing GTPase activating protein 1	IQGAP1
213461_at	175.65	129.5	481.35	464	277.84998	628.5	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NUDT21
213528_at	326.7	155.70001	492.15	328.8	276.35	511.5	chromosome 1 open reading frame 156	C1orf156
213532_at	858.55	139.4	519.85	301.8	318.95	239.8	ADAM metallopeptidase domain 17	ADAM17
213534_s_at	1081.8501	50.800003	663.95	284.9	359.8	142.4	PAS domain containing serine/threonine kinase	PASK
213548_s_at	357.35	90.05	380.84998	321	350.8	435.7	CDV3 homolog (mouse)	CDV3
213599_at	17.85	153.2	465.6	482.5	508.45	800	Opa interacting protein 5	OIP5
213608_s_at	190.6	79.149994	411	182.7	207.75	462.9	SRR1 domain containing	SRRD
213647_at	48.85	68.4	502.25	210.4	377.35	456.3	DNA replication helicase 2 homolog (yeast)	DNA2
213754_s_at	386.85	179.2	372.75	479.7	415.8	460.6	similar to poly(A) binding protein interacting protein 1 /// poly(A) binding protein interacting protein 1	LOC645139 /// PAIP1
213761_at	361.8	143.85	538.9	357.8	429.2	284.4	Mdm1 nuclear protein homolog (mouse)	MDM1
213812_s_at	778.55	340.85	665.75	623.8	650.85	540.5	calcium/calmodulin-dependent protein kinase kinase 2, beta	CAMKK2
213918_s_at	1981.65	284.9	783.55005	544.1	540.75	460.6	Nipped-B homolog (Drosophila)	NIPBL
214079_at	27.25	13.6	178.3	2715.1	3111.7998	968.4	dehydrogenase/reductase (SDR family) member 2	DHRS2
214096_s_at	839.65	1410.6499	3029.95	3024.8	2509.65	2226.2	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2
214170_x_at	375.5	373.7	1820.3501	1476.3	1832.65	1655.9	fumarate hydratase	FH
214179_s_at	160.3	73.850006	295.85	462.3	305.5	146.9	nuclear factor (erythroid-derived 2)-like 1	NFE2L1
214205_x_at	139.1	88.95	369.65002	259.4	293.35	489.9	glutaredoxin 3	GLRX3
214268_s_at	388.75	128.95001	638.5	333.5	542.15	282.5	myotubularin related protein 4	MTMR4
214329_x_at	240	231.70001	1362.8	2257	1392.3999	1344.1	tumor necrosis factor (ligand) superfamily, member 10	TNFSF10
214437_s_at	212.45	481.5	1231.65	1616.3	1219	1172.8	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2
214446_at	87.15	41.1	444.4	497.8	561.15	545.3	elongation factor, RNA polymerase II, 2	ELL2
214499_s_at	866.69995	109.9	399	229.9	245.54999	549.2	BCL2-associated transcription factor 1	BCLAF1
214507_s_at	70.350006	54.7	343.35	230.3	227.7	796.5	exosome component 2	EXOSC2

214544_s_at	215.5	151.85	379.45	474.2	307.45	537.7	synaptosomal-associated protein, 23kDa	SNAP23
214553_s_at	384.65002	192.05	531.45	415.1	461.8	512.1	cAMP-regulated phosphoprotein, 19kDa	ARPP19
214662_at	326.5	42	689.25	230.4	278.59998	197.7	WD repeat domain 43	WDR43
214697_s_at	285.4	132.6	402.34998	528.6	361.34998	157.8	ROD1 regulator of differentiation 1 (S. pombe)	ROD1
214766_s_at	373.05	66.1	423.9	261.3	362.6	391.7	AT hook containing transcription factor 1	AHCTF1
214787_at	354.8	78.1	342.3	360.2	450.7	147	DENN/MADD domain containing 4A	DENND4A
214845_s_at	89.4	125.45	285.65	284.7	345.95	500.4	calumenin	CALU
214937_x_at	756.3	444.4	969.44995	832.5	881.35	762.1	pericentriolar material 1	PCM1
214943_s_at	373.1	131.7	468.2	510.2	497.3	482.7	RNA binding motif protein 34	RBM34
215009_s_at	1263.85	200.15	462.65002	482.9	533.55	441.6	SEC31 homolog A (S. cerevisiae)	SEC31A
215088_s_at	714	229.75	956.5	773.6	678.5	718.3	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	SDHC
215450_at	221.25	260.1	528.55005	518.1	717	723.9	---	---
215501_s_at	598.15	72.55	373.5	502.6	530.05	301.4	dual specificity phosphatase 10	DUSP10
215509_s_at	7.1	185.70001	590.2	486.7	744.8	671.6	budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1
215708_s_at	91	56.4	368.95	274.8	383	768.5	primase, DNA, polypeptide 2 (58kDa)	PRIM2
215719_x_at	413.15	309.75	1163.9	3222.5	1811.75	1277.8	Fas (TNF receptor superfamily, member 6)	FAS
215728_s_at	50.6	76.4	351.3	226.2	344.1	367.5	acyl-CoA thioesterase 7	ACOT7
215780_s_at	362.05	270.6	862.15	1292.9	1173.05	1651.2	SET translocation (myeloid leukemia-associated) pseudogene /// SET nuclear oncogene	hCG_1644608 /// SET
215794_x_at	235.79999	117.299995	227.29999	261	247.1	392.6	glutamate dehydrogenase 2	GLUD2
215905_s_at	139.25	59.9	275.6	438.3	426.65002	813.6	small nuclear ribonucleoprotein 40kDa (U5)	SNRNP40
216064_s_at	252.2	150	445.15	488.4	232.25	525.4	aspartylglucosaminidase	AGA
216100_s_at	241.15	87.85	362.1	300.4	279.7	607.3	torsin A interacting protein 1	TOR1AIP1
216212_s_at	184.2	70.95	531.1	275	413.9	665	dyskeratosis congenita 1, dyskerin	DKC1
216236_s_at	1749.2	97.4	332.65002	287.2	403.85	656.5	solute carrier family 2 (facilitated glucose transporter), member 14 /// solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A14 /// SLC2A3
216252_x_at	269.25	225.45	845.60004	2185.6	1347.8	830.7	Fas (TNF receptor superfamily, member 6)	FAS
216323_x_at	297.3	135.45	719.35	641.8	1102.55	249.7	tubulin, alpha 3d	TUBA3D
216336_x_at	1632.1001	98.95	252.7	204.5	357.05	416.9	metallothionein 1E /// metallothionein 1H /// metallothionein 1M	MT1E /// MT1H /// MT1M
216532_x_at	117	74.4	730.85004	225.7	400.15002	546	glutaredoxin 3	GLRX3
216591_s_at	233.2	154.7	648.69995	523.4	515.45	562.1	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	SDHC
216593_s_at	333.90002	150.5	428.1	370.1	291.55	491.3	similar to phosphatidylinositol glycan, class C /// phosphatidylinositol glycan anchor biosynthesis, class C	LOC100289848 /// PIGC
216607_s_at	197.05	26.65	453.8	258.9	467.8	355.8	cytochrome P450, family 51, subfamily A, polypeptide 1	CYP51A1
216883_x_at	152.1	135.1	580.15	373.4	321.65	305.6	phosphodiesterase 6D, cGMP-specific, rod, delta	PDE6D
216942_s_at	626.4	130.05	1666.4501	1317.3	1447.3999	351.2	CD58 molecule	CD58
217099_s_at	141.6	26.35	404	199.6	242.6	408.8	gem (nuclear organelle) associated protein 4	GEMIN4
217165_x_at	1493.2	83.35	327.4	273.9	565	815.2	metallothionein 1F	MT1F
217168_s_at	6095.65	772.05	1749.95	1669.2	1749.6	1255.3	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	HERPUD1
217370_x_at	402.05	118.149994	433.8	437.6	352.7	816	nuclear receptor subfamily 1, group H, member 3	NR1H3
217388_s_at	1279.45	37.2	211.85	279	400.65	139	kynureninase (L-kynurenine hydrolase)	KYNU
217427_s_at	673.9	177.75	444.25	474.3	354.90002	347	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	HIRA
217445_s_at	23.599998	53.8	411.5	269.5	411.3	431.3	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	GART
217496_s_at	165.35	135.1	543.2	358.2	280.9	600.1	insulin-degrading enzyme	IDE
217741_s_at	3538	710.95	2392.1	2472.1	2721.1	1423.2	zinc finger, AN1-type domain 5	ZFAND5
217748_at	972.44995	217.9	797.85	692.1	686.25	570.9	adiponectin receptor 1	ADIPOR1
217750_s_at	678.4	266.2	1384.3	910.5	967.6	722.2	ubiquitin-conjugating enzyme E2Z	UBE2Z
217777_s_at	82.85	101.3	694.2	370.6	517.94995	691.4	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
217778_at	109.64999	55.75	269.95	134.2	238.05	388.1	solute carrier family 39 (zinc transporter), member 1	SLC39A1
217814_at	350.8	64.2	582.45	313.3	296.5	581.3	coiled-coil domain containing 47	CCDC47
217816_s_at	3020.2998	1155.8	2613.85	2560.5	2269.8	2009.5	PEST proteolytic signal containing nuclear protein	PCNP
217826_s_at	757.7	210.45001	622.85	645.4	398.8	457.5	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1
217831_s_at	212.65	65.600006	367.30002	186	502.45	490.2	NSFL1 (p97) cofactor (p47)	NSFL1C
217839_at	845.55	514.25	1354	1497.6	1214.3999	1032.1	TRK-fused gene	TFG
217885_at	721.55	255.5	1057.95	763.1	1006.55	794.4	importin 9	IPO9
217960_s_at	116.7	58.1	234.45	294.2	330.40002	448.9	translocase of outer mitochondrial membrane 22 homolog (yeast)	TOMM22
218007_s_at	2388.25	2653.0498	5842.2	6380	6569.55	5870.6	ribosomal protein S27-like	RPS27L
218036_x_at	355.5	143.15	666	620.8	437.34998	619	NMD3 homolog (S. cerevisiae)	NMD3
218046_s_at	176.70001	242.35	621	676.7	680.65	1071.1	mitochondrial ribosomal protein S16	MRPS16
218073_s_at	146.85	90.9	477.65	343.2	321.3	553.4	transmembrane protein 48	TMEM48
218078_s_at	301.8	157.45001	367.85	306.4	224.20001	405.8	zinc finger, DHHC-type containing 3	ZDHHC3
218090_s_at	820	45.75	612.55	741.3	445.65	202.8	bromodomain and WD repeat domain containing 2	BRWD2
218129_s_at	90.1	125.65	279.5	339.8	237.25	482.9	nuclear transcription factor Y, beta	NFYB

218156_s_at	228.9	49.4	355.84998	430.2	340.25	838.5	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	TSR1
218170_at	417.8	348.3	1439.2	1533.7	1383.25	1561.3	isochorismatase domain containing 1	ISOC1
218185_s_at	661.15	349.6	1498.1001	788.4	1101.8	933.1	armadillo repeat containing 1	ARMC1
218210_at	444.85	151.20001	385.5	323.9	314.95	524.3	fructosamine 3 kinase related protein	FN3KRP
218254_s_at	462.69998	272.7	870.9	884	697.85	1121.3	SAR1 homolog B (S. cerevisiae)	SAR1B
218260_at	383.45	183.45001	580.25	551.6	405	643.9	DET1 and DDB1 associated 1	DDA1
218264_at	101.35	26.95	331.40002	211.4	357.09998	390.7	BRCA2 and CDKN1A interacting protein	BCCIP
218294_s_at	329.2	66.75	615.8	372.1	313.90002	439.8	nucleoporin 50kDa	NUP50
218295_s_at	208.85	84.35	351.45	305.7	266.5	403.5	nucleoporin 50kDa	NUP50
218313_s_at	462.15	229.95	1024.05	747	592.4	592.7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	GALNT7
218331_s_at	598.65	168.15	499	366.2	424.4	423.6	chromosome 10 open reading frame 18	C10orf18
218333_at	1162.05	201.55	469.5	574.9	395.2	874.5	Der1-like domain family, member 2	DERL2
218335_x_at	293.9	140.65	355.65	479.1	284.7	361	TNFAIP3 interacting protein 2	TNIP2
218361_at	87.65	138.8	578	256.3	386.35	221.6	golgi phosphoprotein 3-like	GOLPH3L
218392_x_at	249.75	136.4	489.8	420.9	474	587.4	sideroflexin 1	SFXN1
218397_at	136.85	190.4	923.8	592.2	759.5	530.6	Fanconi anemia, complementation group L	FANCL
218403_at	718.85	318.7	1515.35	1714	1300.55	1435.9	TP53 regulated inhibitor of apoptosis 1	TRIAP1
218404_at	963.55	242.95	1032.85	1671.6	993.45	828.9	sorting nexin 10	SNX10
218423_x_at	439.75	206.7	670.7	469.5	656.65	432.2	vacuolar protein sorting 54 homolog (S. cerevisiae)	VPS54
218446_s_at	818.94995	116.9	529.1	659.4	404.05	422.2	family with sequence similarity 18, member B	FAM18B
218459_at	351.1	110.399994	656.3	353.9	266.15	630.1	torsin family 3, member A	TOR3A
218461_at	276.7	226.15	840	664.3	906.35	892.6	GPN-loop GTPase 3	GPN3
218465_at	256.55	130.79999	363.65	296	189.09999	489.1	transmembrane protein 33	TMEM33
218481_at	164.2	111.4	452.45	272.6	350.95	597.2	exosome component 5	EXOSC5
218527_at	199.29999	150.7	452.25	371.1	241.1	467.1	aprataxin	APTX
218529_at	112.8	110.8	479.5	291.9	330.5	785.8	CD320 molecule	CD320
218535_s_at	403.65002	132.9	324.65	307.8	314.45	522.6	RIO kinase 2 (yeast)	RIOK2
218583_s_at	354.55	257	682.45	627.7	447.75	516.3	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	DCUN1D1
218585_s_at	38.65	297.15002	2032.7001	1524.4	2092.2	1664.5	denticleless homolog (Drosophila)	DTL
218607_s_at	329.7	113.9	370.25	411.4	223.8	584.2	SDA1 domain containing 1	SDAD1
218627_at	145.5	67.05	329.90002	530.1	510.8	213.9	DNA-damage regulated autophagy modulator 1	DRAM1
218640_s_at	657.75	143.05	383.7	514.6	299	361.8	pleckstrin homology domain containing, family F (with FYVE domain) member 2	PLEKHF2
218647_s_at	1021.25	193.8	548.1	501.3	709.35	646.9	yrdC domain containing (E. coli)	YRDC
218649_x_at	1099.85	335.65002	695.7	599.9	626.5	537.7	serologically defined colon cancer antigen 1	SDCCAG1
218662_s_at	49.95	283.25	631.65	762.1	832	1089.7	non-SMC condensin I complex, subunit G	NCAPG
218713_at	297.45	112	389.1	495.6	336.2	469.5	NMDA receptor regulated 2	NARG2
218728_s_at	600.55005	218.9	567.15	857	699.75	780.4	cornichon homolog 4 (Drosophila)	CNIH4
218739_at	274	43.949997	236.25	434.8	417.7	256.8	abhydrolase domain containing 5	ABHD5
218748_s_at	105.25	91	601.65	413.8	318.2	373.2	exocyst complex component 5	EXOC5
218754_at	433.4	112.350006	323.5	255.3	250.05	394.1	nucleolar protein 9	NOL9
218777_at	355.3	165.29999	397.25	343.4	406.25	309.3	receptor accessory protein 4	REEP4
218782_s_at	170.6	304.85	1038.8	688.6	1358.2	1446	ATPase family, AAA domain containing 2	ATAD2
218817_at	161.9	73.399994	250.65	314.6	186.05	476.4	signal peptidase complex subunit 3 homolog (S. cerevisiae)	SPCS3
218842_at	428.3	240.40001	747.85	651.1	791.5	813.5	RNA polymerase II associated protein 3	RPAP3
218853_s_at	167.65	120.4	395.35	369.3	223.5	501.9	motile sperm domain containing 1	MOSPD1
218878_s_at	1254.1001	167.45	383.25	436.1	346.5	476.9	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	SIRT1
218883_s_at	199.2	160.2	979.05005	1579.2	1614.7	1561.1	MLF1 interacting protein	MLF1IP
218886_at	286.34998	71.35	202.15	217.6	256	460.5	PAK1 interacting protein 1	PAK1IP1
218929_at	1082.7	76.95	339.75	436	259.95	436.2	CDKN2A interacting protein	CDKN2AIP
218930_s_at	383.55	217.55	554.3	466.6	641.3	454.3	transmembrane protein 106B	TMEM106B
218962_s_at	300.65	142.04999	613.65	481.6	519.25	300.1	transmembrane protein 168	TMEM168
218989_x_at	405.85	204.4	479.1	480.6	580.35	624.7	solute carrier family 30 (zinc transporter), member 5	SLC30A5
218993_at	497.75	91.95	314.05	272.9	249.15	396	RNA methyltransferase like 1	RNMTL1
219000_s_at	13.6	83.899994	535.05005	390.7	597.55	571.9	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	DSCC1
219031_s_at	422.7	151.8	682.35	376.3	382.2	907.2	nuclear import 7 homolog (S. cerevisiae)	NIP7
219037_at	378.65	68.7	436.84998	434.5	341.90002	781.3	ribosomal RNA processing 15 homolog (S. cerevisiae)	RRP15
219076_s_at	58.600002	174.85	461.25	477.2	348.65	484.9	peroxisomal membrane protein 2, 22kDa	PXMP2
219099_at	675.45	182.9	1190.15	1454.9	776.95	848.3	chromosome 12 open reading frame 5	C12orf5
219125_s_at	84.3	123.25	386.1	255.7	337.65	536.3	recombination activating gene 1 activating protein 1	RAG1AP1
219148_at	26.3	572.65	1100.2	1530.8	1882.05	2185.1	PDZ binding kinase	PBK

219176_at	601.9	249.05	737.7	762.9	913.5	891.5	chromosome 2 open reading frame 47	C2orf47
219244_s_at	281.4	154.6	396.6	347.6	508.45	368.5	mitochondrial ribosomal protein L46	MRPL46
219248_at	418.1	84.8	513	657.4	439.94998	392.6	THUMP domain containing 2	THUMPD2
219258_at	117	96.25	380.65002	457	446.1	1030.8	TIMELESS interacting protein	TIPIN
219260_s_at	146.6	77.25	385.3	237.4	350.1	499	chromosome 17 open reading frame 81	C17orf81
219275_at	115.89999	104.25	573.1	373	538.05	782.8	programmed cell death 5	PDCD5
219276_x_at	574.15	278.95	773.05	764.2	486.95	669.6	chromosome 9 open reading frame 82	C9orf82
219347_at	436.84998	112.6	545.4	608.5	575.35	459.2	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NUDT15
219356_s_at	756.15	824.80005	1366.6	1942.7	1454.8501	1197.4	chromatin modifying protein 5	CHMP5
219399_at	294.65	53.55	410	434.7	310.7	489	lin-7 homolog C (C. elegans)	LIN7C
219494_at	15.2	15	238.7	181.2	201.79999	333.4	RAD54 homolog B (S. cerevisiae)	RAD54B
219520_s_at	301.35	52.45	574.05	382.8	254.35	124.3	WWC family member 3	WWC3
219549_s_at	693.65	197.4	414.25	579.4	613.9	632.8	reticulon 3	RTN3
219575_s_at	222.35	93.55	343.09998	326.4	294.09998	452.6	component of oligomeric golgi complex 8 /// peptide deformylase (mitochondrial)	COG8 /// PDF
219753_at	62.05	83.5	203.95	345.2	921.85	1089.1	stromal antigen 3	STAG3
219787_s_at	28.8	256.4	857.95	722.4	680.05	1422.5	epithelial cell transforming sequence 2 oncogene	ECT2
219979_s_at	184.95	250.45	696.35	626.8	416.5	537.3	chromosome 11 open reading frame 73	C11orf73
220044_x_at	1223.75	784.85	1819.55	1782.5	1749.5	1516.2	LUC7-like 3 (S. cerevisiae)	LUC7L3
220083_x_at	118.3	71.6	439.3	241.2	312.05	554.1	ubiquitin carboxyl-terminal hydrolase L5	UCHL5
220085_at	27.5	81.5	257.4	356.2	533.6	260.2	helicase, lymphoid-specific	HELLS
220368_s_at	841.6	124.15	660.3	608.8	380.8	475.1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	SMEK1
220651_s_at	9.45	58.35	544.5	289.3	465.09998	728.3	minichromosome maintenance complex component 10	MCM10
220688_s_at	253.25	126.25	637.95	334.5	361.59998	1011.3	mRNA turnover 4 homolog (S. cerevisiae)	MRTO4
220865_s_at	143.15	34.95	419.05	145.2	238.85	394	prenyl (decaprenyl) diphosphate synthase, subunit 1	PDSS1
221007_s_at	373.45	164.6	342.45	401.5	351.35	372.3	FIP1 like 1 (S. cerevisiae)	FIP1L1
221090_s_at	302.6	142.35	402.75	281	198.65	393.5	2-oxoglutarate and iron-dependent oxygenase domain containing 1	OGFOD1
221094_s_at	267.55	142.7	445.25	387.2	353.40002	384.3	elongation protein 3 homolog (S. cerevisiae)	ELP3
221158_at	399.69998	103.5	314.65002	241.5	278.84998	202.9	chromosome 21 open reading frame 66	C21orf66
221196_x_at	317.45	167.55	665.69995	524.8	516.3	608.8	BRCA1/BRCA2-containing complex, subunit 3	BRCC3
221223_x_at	274.4	83.649994	1102.85	741.3	1245.95	391.1	cytokine inducible SH2-containing protein	CISH
221229_s_at	287.75	129	566.9	304.2	405.85	301.2	tRNA methyltransferase 61 homolog B (S. cerevisiae)	TRMT61B
221428_s_at	280.65002	171.7	484.15	495.3	415.05	523.9	transducin (beta)-like 1 X-linked receptor 1	TBL1XR1
221480_at	201.85	75.850006	423.6	174	225.1	515.5	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	HNRNPD
221497_x_at	192.15	51.05	335.1	561.7	285.75	310.1	egl nine homolog 1 (C. elegans)	EGLN1
221517_s_at	793.45	214.55	476.6	483.1	341.25	654.5	mediator complex subunit 17	MED17
221521_s_at	41.4	69.8	899	460.4	811.5	1313.3	GINS complex subunit 2 (Psf2 homolog)	GINS2
221559_s_at	1052.2	132.85	756.85	569.9	547.5	692.6	MIS12, MIND kinetochore complex component, homolog (S. pombe)	MIS12
221561_at	625.9	195.35	771.65	694.2	403.6	1046.1	sterol O-acyltransferase 1	SOAT1
221563_at	1284.35	147.75	628.3	459.4	761.8	356.1	dual specificity phosphatase 10	DUSP10
221568_s_at	1203.3	333	1107.35	1077.2	659.35	712.5	lin-7 homolog C (C. elegans)	LIN7C
221618_s_at	93.35	82.55	593.65	421.2	349.34998	422.3	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	TAF9B
221620_s_at	120.35001	149.8	703.05005	330.5	465.2	317.2	apolipoprotein O	APOO
221658_s_at	632.15	154.8	335.5	452.9	479.85	485.6	interleukin 21 receptor	IL21R
221677_s_at	127.55	215.45001	636.30005	532.5	840	873.8	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit /// downstream neighbor of SON	ATP5O /// DONSON
221693_s_at	361.1	86	342.3	348.4	235.05	366.1	mitochondrial ribosomal protein S18A	MRPS18A
221767_x_at	549.4	286.2	568.7	483.3	691.25	436.5	high density lipoprotein binding protein	HDLBP
221782_at	342.7	128.3	420.3	476.6	408.55	431	DnaJ (Hsp40) homolog, subfamily C, member 10	DNAJC10
221873_at	337.25	140.45	362.8	284.2	270	384.2	zinc finger protein 143	ZNF143
222036_s_at	149.65	119.200005	1408.55	840.3	1104.6	1702.3	minichromosome maintenance complex component 4	MCM4
222037_at	7.65	20.55	395.7	230.4	224.6	520.6	minichromosome maintenance complex component 4	MCM4
222040_at	862.7	94.15	254.6	495.7	383.09998	425.7	heterogeneous nuclear ribonucleoprotein A1	HNRNPA1
222077_s_at	204.6	794.9	2519.35	2005.1	2221.6	1797.1	Rac GTPase activating protein 1	RACGAP1
222103_at	960.15	344.75	985.75	686.8	620.15	529.5	activating transcription factor 1	ATF1
222158_s_at	472.8	172.7	711	648	460.80002	433.7	PPPDE peptidase domain containing 1	PPPDE1
222204_s_at	707.8	130.75	481.30002	394.8	382.2	484.2	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	RRN3
222250_s_at	120.8	123	295.45	333.1	478.35	464.6	integrator complex subunit 7	INTS7
222385_x_at	242.2	148.95	559.5	428.1	307.84998	705.7	Sec61 alpha 1 subunit (S. cerevisiae)	SEC61A1
222387_s_at	245.8	169.45	552.35	388.3	251.4	524	vacuolar protein sorting 35 homolog (S. cerevisiae)	VPS35
222393_s_at	572.9	161.15	853.65	418.5	374.7	980.7	N-acetyltransferase 13 (GCN5-related)	NAT13

222395_s_at	608.65	179.2	909.4	611.7	615.9	442.9	ubiquitin-conjugating enzyme E2Z	UBE2Z
222399_s_at	1228.6	453.4	1738	1874.2	1113.6	2916.8	transmembrane 9 superfamily member 3	TM9SF3
222402_at	166.3	62.25	307.35	245	210.75	459.7	proteasome maturation protein	POMP
222406_s_at	545.45	127.25	646.8	518.3	354.15002	513.3	proline-rich nuclear receptor coactivator 2	PNRC2
222411_s_at	910.89996	765.3	1535.45	1434.6	1412.25	1193.1	signal sequence receptor, gamma (translocon-associated protein gamma)	SSR3
222424_s_at	235.79999	186.25	840.6	956.6	666.9	517.9	nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1
222432_s_at	252.35	83.75	329.5	340.8	285.25	715.4	coiled-coil domain containing 47	CCDC47
222442_s_at	550.85	166.54999	603.4	574.1	453.25	822	ADP-ribosylation factor-like 8B	ARL8B
222452_s_at	631.45	170.70001	326.4	442.7	389.55	341.5	GC-rich promoter binding protein 1-like 1	GPBP1L1
222458_s_at	340.8	102.55	337.8	322.5	254.75	418.1	akirin 1	AKIRIN1
222464_s_at	731.65	193.3	894.85	847.1	1061.85	1601.9	chromosome 10 open reading frame 119	C10orf119
222474_s_at	368.90002	140.55	461.85	436.1	539.5	589.4	translocase of outer mitochondrial membrane 22 homolog (yeast)	TOMM22
222477_s_at	333.25	331.59998	1994.6001	1238.5	1159.3	1296.6	transmembrane 7 superfamily member 3	TM7SF3
222497_x_at	1087.35	330.84998	1329.6	1329.8	904.69995	1164.7	NMD3 homolog (S. cerevisiae)	NMD3
222532_at	65.45	49.050003	248.20001	276	213.79999	398.2	signal recognition particle receptor, B subunit	SRPRB
222555_s_at	289.1	147.3	478.75	374.7	339.09998	464.3	mitochondrial ribosomal protein L44	MRPL44
222581_at	192.45001	100.7	476.55	360.3	256.84998	416.1	xenotropic and polytropic retrovirus receptor	XPR1
222608_s_at	22.75	196.95001	952.2	475.8	604.15	538.2	anillin, actin binding protein	ANLN
222624_s_at	304.45	74.25	271.90002	298.2	254.5	535.8	zinc finger protein 639	ZNF639
222680_s_at	60.6	184.35	1351.45	1011.3	1469.6	1475.8	denticleless homolog (Drosophila)	DTL
222700_at	643.95	261.15	1719.2	833.5	1100.3	916.1	atlastin GTPase 2	ATL2
222703_s_at	212.95	109.149994	514.15	340.4	507.5	814.3	yrdC domain containing (E. coli)	YRDC
222726_s_at	217.15	99.45	567.65	532.1	358.40002	514.5	exocyst complex component 5	EXOC5
222745_s_at	314.7	149	389.85	381.5	358.4	376	chromosome 15 open reading frame 29	C15orf29
222752_s_at	268.65	123	482.05	388.3	371.85	433.8	transmembrane protein 206	TMEM206
222753_s_at	753.69995	129.85	336.9	384.2	286.55	610	signal peptidase complex subunit 3 homolog (S. cerevisiae)	SPCS3
222754_at	410.59998	108.5	1035.4	649.8	931.85004	757.7	tRNA nucleotidyl transferase, CCA-adding, 1	TRNT1
222762_x_at	388.65	189.85	809.65	501.2	517.85	436.3	LIM domains containing 1	LIMD1
222791_at	1021.5	257.4	577	471.2	447.9	357.5	round spermatid basic protein 1	RSBN1
222825_at	391.9	148.65	604.8	482.7	458.4	366.4	OTU domain containing 6B	OTUD6B
222843_at	131.15	264.40002	1130.95	972.1	1134.8	1005.4	fidgetin-like 1	FIGNL1
222846_at	520.9	88.85	609.85	329.2	291.75	351.4	RAB8B, member RAS oncogene family	RAB8B
222848_at	313.5	296.05	608.4	1332.6	951.8	1199.8	centromere protein K	CENPK
222875_at	305.34998	91.75	509.65	478.2	588.5	694.8	DEAH (Asp-Glu-Ala-His) box polypeptide 33	DHX33
222980_at	1575.8	917.1	3102.55	2665.8	2372.85	1835.3	RAB10, member RAS oncogene family	RAB10
222981_s_at	486.3	334.8	1882.1499	1637	1435.8	1289.6	RAB10, member RAS oncogene family	RAB10
222989_s_at	294.3	65.850006	237.29999	293.2	217.59999	560.8	ubiquilin 1	UBQLN1
222991_s_at	566.5	106.25	330.8	338.4	281.7	645.5	ubiquilin 1	UBQLN1
223046_at	508	178.54999	1055.1	1737.5	798.30005	831.7	egl nine homolog 1 (C. elegans)	EGLN1
223076_s_at	442.05002	113.7	673.5	398.2	565.30005	838.4	NOL1/NOP2/Sun domain family, member 2	NSUN2
223090_x_at	798.45	109.95	795.85	645.7	590.85	774.1	vezatin, adherens junctions transmembrane protein	VEZT
223144_s_at	882.65	120.899994	398.55	771.4	386.45	560.4	akirin 2	AKIRIN2
223151_at	501.5	295.65	1174.45	1132.8	838.80005	1100.9	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	DCUN1D5
223160_s_at	1146.35	139.79999	728.85	765.9	556.35	620.9	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	SMEK1
223180_s_at	269.7	218.2	858.80005	712	952.65	1227.9	chromosome 18 open reading frame 55	C18orf55
223184_s_at	170.75	123.649994	532.55	290.3	348.55	202.5	1-acylglycerol-3-phosphate O-acyltransferase 3	AGPAT3
223211_at	467.09998	214	441.9	389.6	401	290.2	2-hydroxyacyl-CoA lyase 1	HACL1
223221_at	202.1	72.75	482.2	272.5	289.59998	387	SCO cytochrome oxidase deficient homolog 1 (yeast)	SCO1
223225_s_at	101.5	58.4	420.09998	127.7	236.7	452	SEH1-like (S. cerevisiae)	SEH1L
223229_at	24.25	318.55	1134.25	973.7	2272.65	1601.4	ubiquitin-conjugating enzyme E2T (putative)	UBE2T
223263_s_at	693.9	154.70001	553.7	496.7	365.3	370.2	FGFR1 oncogene partner 2	FGFR1OP2
223271_s_at	384.40002	151.75	466.25	415.8	341.3	639.1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	CTDSPL2
223274_at	52.4	96.7	330.6	338.5	423.4	420.2	transcription factor 19	TCF19
223286_at	169	129.35	505	363.9	305.8	500	chromosome 17 open reading frame 81	C17orf81
223288_at	633.65	369.25	672.94995	796.2	623.25	610.4	ubiquitin specific peptidase 38	USP38
223290_at	144.45001	128.55	402.25	330.5	357.65002	407.9	pyridoxal (pyridoxine, vitamin B6) phosphatase	PDXP
223320_s_at	423.7	251.95001	960.45	989.3	985.69995	906.3	ATP-binding cassette, sub-family B (MDR/TAP), member 10	ABCB10
223335_at	498.40002	170.9	836.05	732.4	684.55	479.1	transmembrane protein 69	TMEM69
223336_s_at	1062.35	344.6	786.94995	803.9	857	524.3	RAB18, member RAS oncogene family	RAB18
223338_s_at	730.35	387.90002	899.94995	1000.2	735.25	758.3	ATPase inhibitory factor 1	ATPIF1

223354_x_at	162.4	180.4	571.25	322.9	475.6	403.3	mitochondrial fission factor	MFF
223377_x_at	279.84998	110.2	1189.2	784.1	1311.6	473.4	cytokine inducible SH2-containing protein	CISH
223413_s_at	441.6	77.7	518.65	157.9	252.05	524.6	Ly1 antibody reactive homolog (mouse)	LYAR
223490_s_at	87.05	88.45	451.3	360.2	322.65002	748.2	exosome component 3	EXOSC3
223542_at	338.65	139.1	451.55	467.8	354.7	519.1	ankyrin repeat domain 32	ANKRD32
223556_at	55.1	68.8	688.4	566.5	658.55	638.6	helicase, lymphoid-specific	HELLS
223592_s_at	1013.9	51.95	607.6	306.3	282.55	157.1	ring finger protein 135	RNF135
223619_x_at	496.4	110.2	419.55	469.1	428.7	273.9	peroxisomal trans-2-enoyl-CoA reductase	PECR
223675_s_at	381.05	56.4	451.55	441.6	383.25	515.6	vezatin, adherens junctions transmembrane protein	VEZT
223804_s_at	351.35	201.85	571.1	547	469.4	540.7	THUMP domain containing 3	THUMPD3
223808_s_at	247.04999	149.6	337.9	328.7	293.8	523.5	protein tyrosine phosphatase, mitochondrial 1	PTPMT1
223961_s_at	112.3	30.900002	650.85	421.4	754.05	252.6	cytokine inducible SH2-containing protein	CISH
224130_s_at	383.25	218.6	435.85	695.8	570.85	592.7	steroid receptor RNA activator 1	SRA1
224177_s_at	213.45001	111.1	456.1	260.6	244.45001	468.6	chromosome X open reading frame 26	CXorf26
224247_s_at	223.6	195.29999	535.6	512.8	382.2	689.6	mitochondrial ribosomal protein S10	MRPS10
224281_s_at	397.15	129.45	351.05	294.2	267.9	370.1	neugrin, neurite outgrowth associated	NGRN
224311_s_at	185.25	120.299995	411.2	411.4	302.05	648.9	calcium binding protein 39	CAB39
224468_s_at	154.85	162.7	558.9	717.1	767.05005	621.3	chromosome 19 open reading frame 48	C19orf48
224564_s_at	876.65	278.4	805.80005	1043.6	937.35004	1150.8	reticulon 3	RTN3
224581_s_at	1250.25	455.55	2017	1556.1	1816	1577.8	nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1
224582_s_at	334.1	185.25	961.44995	1036.7	863.19995	1016.2	nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1
224626_at	456.9	186.85	459.65002	478.5	521.25	637.8	solute carrier family 35, member A4	SLC35A4
224629_at	1153.55	985.65	1797.3	2516	1898.9	1768.9	lectin, mannose-binding, 1	LMAN1
224634_at	348.4	80.2	592.85	265.6	417.05	1055.6	G patch domain containing 4	GPATCH4
224661_at	213	136.65	384.15	360.9	209.54999	463.8	phosphatidylinositol glycan anchor biosynthesis, class Y	PIGY
224695_at	412.25	181.3	766.4	587.1	598.05	571.8	chromosome 2 open reading frame 29	C2orf29
224764_at	471.7	34.95	516.55005	314.8	203.79999	164.8	Rho GTPase activating protein 21	ARHGAP21
224787_s_at	1471.8	431.5	1055.85	1034.7	1029.6	767.8	RAB18, member RAS oncogene family	RAB18
224830_at	969.4	593.1	1639.3999	1985.4	1168.7	2268.8	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NUDT21
224855_at	127.35001	117.149994	533	393.8	305.55	366.9	left-right determination factor 1 /// pyrroline-5-carboxylate reductase family, member 2	LEFTY1 /// PYCR2
224856_at	1446.6	78.95	692.25	365.4	299.1	870.7	FK506 binding protein 5	FKBP5
224866_at	796.94995	151.35	642.25	473.4	365.7	670.5	fatty acyl CoA reductase 1	FAR1
224878_at	118.8	84.850006	327.75	287.7	171.2	383	ubiquitin family domain containing 1	UBFD1
224879_at	332.59998	332.8	827.35	860.2	597.15	999.6	chromosome 9 open reading frame 123	C9orf123
224893_at	745.45	70.2	365.45	803.2	531.35	828.2	atlastin GTPase 3	ATL3
224966_s_at	259.15002	23.65	220.05	99.3	110.45	235.2	dihydrouridine synthase 3-like (S. cerevisiae)	DUS3L
225039_at	67.7	158.2	593.35	302.7	409	345.1	ribulose-5-phosphate-3-epimerase	RPE
225040_s_at	121.55	273.85	1182.45	489.6	889.35	643.1	ribulose-5-phosphate-3-epimerase	RPE
225046_at	44.949997	27.8	752.45	513.9	143.8	204.7	hypothetical gene supported by AL713796	LOC389831
225049_at	1570.8	726.85	1534.05	2084.2	1804.6001	1471.6	biogenesis of lysosomal organelles complex-1, subunit 2	BLOC1S2
225064_at	570.65	73.350006	480.34998	299.6	394.84998	575.2	rabaptin, RAB GTPase binding effector protein 1	RABEP1
225070_at	416.75	55.6	258.75	147.8	164.9	372.3	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	NUS1
225092_at	777.35	102.149994	631.69995	444.8	546.9	706.4	rabaptin, RAB GTPase binding effector protein 1	RABEP1
225106_s_at	219.95001	103.9	491.25	427.1	331.5	677.2	2-oxoglutarate and iron-dependent oxygenase domain containing 1	OGFOD1
225114_at	403.5	146.75	869.2	737.3	584.85	724.5	alkylglycerone phosphate synthase	AGPS
225152_at	669.8	157.85	434.90002	328.8	378.55	389.7	zinc finger protein 622	ZNF622
225158_at	333.09998	107.2	741.7	494.3	359.7	724.1	G elongation factor, mitochondrial 1	GFM1
225160_x_at	403.40002	118.75	1268.35	1088.8	1389.45	940.2	Mdm2 p53 binding protein homolog (mouse)	MDM2
225194_at	797.85	268.2	995.39996	977.3	696.8	956.1	pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)	PLRG1
225200_at	292.25	133.25	704.45	592.2	335.55	467	DPH3, KTI11 homolog (S. cerevisiae)	DPH3
225243_s_at	619.9	198.35	579.55005	597.5	428.95	432.7	sarcolemma associated protein	SLMAP
225252_at	373.90002	155.2	502.8	172.2	883.65	392.4	sulfiredoxin 1 homolog (S. cerevisiae)	SRXN1
225264_at	652	219	596.4	533.5	410.7	474.1	arginyl-tRNA synthetase 2, mitochondrial	RARS2
225265_at	739.6	122.5	1411.85	975.9	947.15	798	RNA binding motif, single stranded interacting protein 1	RBMS1
225273_at	803.05005	84.7	899.9	699.5	463.85	296.8	WWC family member 3	WWC3
225289_at	512.65	77.75	255.2	244.9	193.35	288.8	Signal Tranducer and Activator of Transcription 3 (acute-phase response factor)	STAT3
225400_at	92.7	169.95001	606.05	600.4	416.45	673.2	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	TSEN15
225404_at	676.7	239	519.5	514.6	549.7	624.3	chromosome 1 open reading frame 212	C1orf212
225439_at	117.55	150.65	914.95	781.2	943.8	917.5	NudC domain containing 1	NUDCD1
225468_at	361	129.1	336.2	339.7	344.5	388.3	protein associated with topoisomerase II homolog 1 (yeast)	PATL1
225520_at	69.25	165.4	547.35	772	861.65	627.1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	MTHFD1L
225525_at	240.70001	51.449997	850.80005	765.7	343	122.9	KIAA1671	KIAA1671
225572_at	853.5	288.2	754.6	607.7	615.69995	462.8	cAMP responsive element binding protein 1	CREB1
225581_s_at	501.65	166.45	608.5	409.6	358.45	342.8	mitochondrial ribosomal protein L50	MRPL50
225638_at	297.3	214.75	939.3	755.6	1042.15	789.1	chromosome 1 open reading frame 31	C1orf31
225644_at	177.4	86.65	398.4	379.3	489.90002	570.3	coiled-coil domain containing 117	CCDC117
225647_s_at	725.15	650.75	2231.1	4211.2	1648.45	2548.2	cathepsin C	CTSC
225655_at	19.5	84.7	1275.8	564.4	869.05005	1219	ubiquitin-like with PHD and ring finger domains 1	UHRF1
225674_at	401.1	436.45	889.1	1231.6	1494	1346.8	B-cell receptor-associated protein 29	BCAP29
225692_at	982.6	561.45	1512.4	1130.2	1076.45	864.2	calmodulin binding transcription activator 1	CAMTA1

225734_at	74.25	103.95	563.75	935	657.35	618.9	F-box protein 22	FBXO22
225736_at	89.5	99.5	356.15	559.1	420	353.2	F-box protein 22	FBXO22
225748_at	447.45	100.35	279	225.5	298.55	495.7	LTV1 homolog (S. cerevisiae)	LTV1
225751_at	250.5	183.6	566.55	443	307.55	692.7	RNA binding motif protein 17	RBM17
225761_at	750.35	216.7	481.8	650.5	376.75	525.8	PAP associated domain containing 4	PAPD4
225775_at	338.45	34.65	1169.85	597.9	862.39996	241.8	tetraspanin 33	TSPAN33
225836_s_at	150.8	83.65	530.8	370.3	292.45	457.7	chromosome 12 open reading frame 32	C12orf32
225847_at	81.15	53.45	319.3	332.9	222.8	394.8	neutral cholesterol ester hydrolase 1	NCEH1
225885_at	316.40002	99.2	527.4	283.7	497	183.1	early endosome antigen 1	EEA1
225889_at	625.05	234	1397.6499	1249.8	1115	1203.2	AE binding protein 2	AEBP2
225890_at	299.8	371.09998	1128.65	764	960.9	634.9	chromosome 20 open reading frame 72	C20orf72
225932_s_at	3140.7	1123.4	2080.55	2109.3	2427.5	1631.4	heterogeneous nuclear ribonucleoprotein A2/B1	HNRNPA2B1
225953_at	167.6	146.3	327.85	304.5	343.34998	288.8	regulation of nuclear pre-mRNA domain containing 1A	RPRD1A
225984_at	351.44998	105.95	419.95	302.8	397.5	230	protein kinase, AMP-activated, alpha 1 catalytic subunit	PRKAA1
225994_at	275.3	219.95001	765.75	650.9	489.09998	563.7	cleavage and polyadenylation specific factor 2, 100kDa	CPSF2
226003_at	345.55	222	885.6	350.4	660.3	420.8	kinesin family member 21A	KIF21A
226005_at	647.85	186.7	465.7	579	540.80005	598.2	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	UBE2G1
226050_at	84.850006	93.399994	784.75	462.3	313.59998	357.3	transmembrane and coiled-coil domains 3	TMCO3
226077_at	787.5	507.69998	1218.4	2068.9	987.25	2172.5	ring finger protein 145	RNF145
226099_at	862.85	307.8	2925.8	2700.8	3124.7	2889.1	elongation factor, RNA polymerase II, 2	ELL2
226117_at	473.7	736.65	1740.85	1651.5	1680.45	1186.3	TRAF-interacting protein with forkhead-associated domain	TIFA
226159_at	341.8	126	399.3	426.4	399.2	195.4	chromosome 5 open reading frame 51	C5orf51
226254_s_at	1364.95	323.5	1245.75	1258.3	1182.8999	1010.1	KIAA1430	KIAA1430
226294_x_at	685.4	222.5	862.35	707.7	763.35	588.9	family with sequence similarity 91, member A1	FAM91A1
226320_at	365.1	99.149994	775.60004	453.8	405.90002	1252.2	THO complex 4	THOC4
226329_s_at	628.2	468.25	1320.8	1160.2	1211.3999	888.1	MIT, microtubule interacting and transport, domain containing 1	MITD1
226350_at	323.09998	99.45	947	462.2	905.8	791.9	choroideremia-like (Rab escort protein 2)	CHML
226354_at	793.7	127	1442	812.4	714	450	lactamase, beta	LACTB
226400_at	4777.4	1101.7	3300	2374.7	2699.7	2109.6	Cell division cycle 42 (GTP binding protein, 25kDa)	CDC42
226456_at	48.55	121.100006	438.3	429.5	515.6	255.8	chromosome 16 open reading frame 75	C16orf75
226468_at	341.75	123.7	316.25	309.8	275.85	383.8	---	---
226503_at	308.95	145.8	559.75	375.4	522	346.8	RAP1 interacting factor homolog (yeast)	RIF1
226567_at	747.05	243.8	602.2	435.9	502.1	384	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	USP14
226574_at	389.05	203.7	476.95	551.2	395.59998	770.9	paraspeckle component 1	PSPC1
226686_at	175.6	147.85	382.75	320.1	234.65	451.9	CDGSH iron sulfur domain 2	CISD2
226801_s_at	1798.3999	895	1941.2999	1997.7	1887.8999	1738.7	axin interactor, dorsalization associated	AIDA
226813_at	145.95001	101.549995	308.2	422.2	447.09998	325.5	chromosome 1 open reading frame 57	C1orf57
226831_at	248.75	229.3	1053.45	374.9	640.1	438.3	Solute carrier family 25, member 46	SLC25A46
226958_s_at	188.7	89.9	449.75	320.8	334.15	437.4	mediator complex subunit 11	MED11
226982_at	331.59998	206.75	1148.8999	453.2	1520.95	458.9	elongation factor, RNA polymerase II, 2	ELL2
227075_at	318.55	178.6	443	372.4	378.6	287.6	elongation protein 3 homolog (S. cerevisiae)	ELP3
227117_at	169.15	147.5	533.6	584.6	633	213.1	---	---
227158_at	240.65	103.5	370.6	204.3	209.35	415.1	chromosome 14 open reading frame 126	C14orf126
227295_at	247.25	202.45	794.2	900.5	633.3	877.4	IKK interacting protein	IKIP
227309_at	280.75	65.5	343.25	201.2	226.7	434.9	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	YOD1
227350_at	49.2	155.5	554	917.9	1085.05	646	helicase, lymphoid-specific	HELLS
227545_at	86.35	142.85	653.35	471.5	617.45	369.4	---	---
227606_s_at	262.9	141.6	190.05	231.8	746.75	688.8	STAM binding protein-like 1	STAMBPL1
227653_at	137.70001	122.6	401.09998	221.7	247.35	400.7	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	TRMT5
227680_at	512.55	101	388.95	404.4	376.35	587	zinc finger protein 326	ZNF326
227696_at	410.85	109.25	249.6	522.2	319.05	371.3	Exosome component 6	EXOSC6
227697_at	2482	79.25	216.4	168.4	239.65	378.1	suppressor of cytokine signaling 3	SOCS3
227740_at	1151	322.8	755.9	642.6	673.65	550.2	U2AF homology motif (UHM) kinase 1	UHMK1
227786_at	626.15	171	628.6	540.2	511.2	492	mediator complex subunit 30	MED30
227818_at	137.8	81.8	224.9	258.2	392.7	278.4	coiled-coil domain containing 21	CCDC21
227861_at	484.65	269.6	597.05	593.7	544.05	445.6	transmembrane protein 161B	TMEM161B
227916_x_at	225.75	194.6	633.55005	560.8	538.7	925.8	exosome component 3	EXOSC3
227973_at	827	254.75	584.65	461.1	585.35	428.8	chromosome 2 open reading frame 69	C2orf69
227993_at	419.6	85.8	348.05	223.1	203.95	465.9	methionyl aminopeptidase 2	METAP2
228095_at	263.15	197.85	547.4	467.3	513.05	563.6	PHD finger protein 14	PHF14
228183_s_at	659.9	251.65	562.45	751.8	744.19995	772.1	RPA interacting protein	RPAIN
228189_at	541.05	178.75	802.55005	410.6	654.5	392.5	BCL2-associated athanogene 4	BAG4
228217_s_at	385.35	193.20001	1103.05	529.1	626.4	404.1	proteasome (prosome, macropain) assembly chaperone 4	PSMG4
228378_at	236	110.8	464.25	327.2	356.55	524.3	chromosome 12 open reading frame 29	C12orf29
228385_at	405.45	104	255.45	452.4	499	305.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	DDX59
228597_at	182.70001	132.29999	747.4	499.3	664.85	878	chromosome 21 open reading frame 45	C21orf45
228606_at	126.85	183.7	449.35	519.4	351.90002	441.5	Tctex1 domain containing 2	TCTEX1D2
228650_at	177.15	93	537.95	513.2	364.4	313.4	---	---
228729_at	1.8	188.9	446.2	435.8	376.75	752.4	cyclin B1	CCNB1
228785_at	733.2	229.25	1038.95	670.1	801.85	455.8	Zinc finger protein 281	ZNF281
229075_at	114.6	45.3	246.7	288.9	372.95	179.6	spermatogenesis associated 5	SPATA5

229097_at	39.15	246.25	825.89996	752.9	451.9	585.1	diaphanous homolog 3 (Drosophila)	DIAPH3
229120_s_at	1320.1	310.65002	671.95	576.1	565.7	475.7	CDC42 small effector 1	CDC42SE1
229353_s_at	2845.25	1744.25	6159.15	4506.1	5093.9	3938.4	nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1
229437_at	261.34998	19.45	902.1	2965.4	4893.6997	563.3	MIR155 host gene (non-protein coding)	MIR155HG
229551_x_at	222.8	90.8	582.4	534	951.35	467.6	zinc finger protein 367	ZNF367
229610_at	19.6	127.9	330.5	382.5	396.90002	321.8	cytoskeleton associated protein 2-like	CKAP2L
229711_s_at	533.05005	167.1	1651.7999	1319.4	1914.8999	1194.9	Mdm2 p53 binding protein homolog (mouse)	MDM2
229733_s_at	427.8	358.05	1710.7	1242.5	1728	1016	---	---
229861_at	302.90002	141.7	593.2	295	392.5	236.1	---	---
230026_at	204.25	38.05	304.75	469.5	345.15	529.4	mitochondrial ribosomal protein L43	MRPL43
230027_s_at	247.5	122.6	438.05	319.5	312.95	605.6	mitochondrial ribosomal protein L43	MRPL43
230075_at	131.7	90	352.15	472	509.35	133.7	RAB39B, member RAS oncogene family	RAB39B
230329_s_at	42.550003	156.1	356.95	373.8	394.7	412.8	nudix (nucleoside diphosphate linked moiety X)-type motif 6	NUDT6
231269_at	212.25	27.2	291.9	141.1	203.35	204.9	activating signal cointegrator 1 complex subunit 3	ASCC3
231713_s_at	424.7	127.100006	361.3	430	358.45	426.4	elongation protein 2 homolog (S. cerevisiae)	ELP2
231715_s_at	299.6	258.34998	1319.7	957.9	798.25	840.3	left-right determination factor 1 /// pyrroline-5-carboxylate reductase family, member 2	LEFTY1 /// PYCR2
231772_x_at	81.35	156.7	588.75	996.4	1048.4	818	centromere protein H	CENPH
231784_s_at	112.35001	96.55	530.45	298.7	290.25	484.6	DDB1 and CUL4 associated factor 13	DCAF13
231852_at	62.899998	32.1	323.15	742.8	332.25	221.9	exoribonuclease 1	ERI1
231862_at	121.39999	68.75	455.9	403.7	374.5	535.8	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5
232065_x_at	177.2	224.6	637.15	535	442.59998	514.3	centromere protein L	CENPL
232432_s_at	324.8	197.75	477.65002	485.7	573.94995	718	solute carrier family 30 (zinc transporter), member 5	SLC30A5
233013_x_at	414.2	150.7	437.95	393.6	310.40002	456	hypothetical protein LOC220906	LOC220906
233110_s_at	97.9	92.8	407.55	255.6	235.35	459	BCL2-like 12 (proline rich)	BCL2L12
233124_s_at	434.5	169.25	506.05	312.5	369.25	1013.8	enoyl Coenzyme A hydratase domain containing 1	ECHDC1
233655_s_at	144.9	92.8	234.65	188.2	240.85	391	HAUS augmin-like complex, subunit 6	HAUS6
233757_x_at	195.05	101.8	442.15	374.4	221.1	535.1	---	---
234405_s_at	490.35	116.2	368.84998	404.4	319.40002	600.3	phosphorylated adaptor for RNA export	PHAX
234915_s_at	185.29999	134.54999	384.15002	372.1	375.25	653.9	density-regulated protein	DENR
234982_at	621.85	104.45	730.30005	418.3	392.8	327	ubiquitin protein ligase E3 component n-recognin 3 (putative)	UBR3
234984_at	730.8	145	461.65	407.2	417.1	478.2	neural precursor cell expressed, developmentally down-regulated 1	NEDD1
234992_x_at	18.4	69.5	255.5	251.1	173.65	367.7	epithelial cell transforming sequence 2 oncogene	ECT2
235067_at	312.2	89	322.9	267.9	288.85	164.4	muskelin 1, intracellular mediator containing kelch motifs	MKLN1
235088_at	89.55	199.6	588.65	1262.4	725.65	786	chromosome 4 open reading frame 46	C4orf46
235158_at	393.7	234.4	627.05	598.2	663.75	557.2	transmembrane protein 209	TMEM209
235189_at	116.4	35	223.65001	189.9	165.7	218.2	NMDA receptor regulated 2	NARG2
235252_at	376	84.399994	1606.05	709	807.44995	612.5	kinase suppressor of ras 1	KSR1
235940_at	69.65	71.15	354.6	769.6	327.45	201.2	chromosome 9 open reading frame 64	C9orf64
237215_s_at	53.85	132.85	264.25	303.4	866.45	510.1	transferrin receptor (p90, CD71)	TFRC
237737_at	20.15	18.55	688.55	946.4	2373.4	326.6	similar to hCG1744891	LOC100289026
237753_at	711.1	104.7	564.80005	399	711.6	437.5	---	---
238015_at	73.85	147.95	464.45	972.8	607.8	571.6	chromosome 4 open reading frame 46	C4orf46
238057_at	124.89999	22.05	231.5	78.5	142.54999	244.4	ubiquitin specific peptidase 45	USP45
238075_at	62.65	95.2	448.45	459.4	379.75	435.5	CHK1 checkpoint homolog (S. pombe)	CHEK1
238600_at	215.9	201.54999	571.3	591.9	338.05	419.4	janus kinase and microtubule interacting protein 1	JAKMIP1
238619_at	1441.95	122.85	347.6	461.2	401.5	145	---	---
238695_s_at	107.25	68.350006	276.05	335.1	324.05	108.3	RAB39B, member RAS oncogene family	RAB39B
239331_at	1234.05	126.649994	430.3	437.3	457.05	150.4	---	---
239346_at	283.9	164.6	521.05	639.3	420.25	628.7	---	---
244026_at	1034	56.05	569.05	358.4	702.6	240.7	---	---
244103_at	2265.8	413.2	1258.05	1450	1103	1103	chromosome 1 open reading frame 55	C1orf55
244187_at	163.85	13.6	588	264.4	189	110.8	---	---
244669_at	588.6	91.649994	329.7	531.9	293.90002	408.9	small nucleolar RNA host gene 5 (non-protein coding) /// small nucleolar RNA, C/D box 50A /// small nucleolar RNA, C/D box 50B	SNHG5 /// SNORD50A /// SNORD50B
244811_at	547.4	72.45	439.84998	340.3	366.3	373.8	pleckstrin homology domain interacting protein	PHIP
244828_x_at	307.25	54.1	212.65	296.4	217.95	432.3	nuclear assembly factor 1 homolog (S. cerevisiae)	NAF1
34689_at	548.75	239.95001	539.05	445.7	515.95	370.5	three prime repair exonuclease 1	TREX1
35201_at	527.3	107.1	482.75	253.9	237.05	514.9	heterogeneous nuclear ribonucleoprotein L	HNRNPL
36564_at	457	32.8	242.95001	673.5	518.55	147.4	ring finger protein 19B	RNF19B
37577_at	150.75	162.55	292.95	365.7	409.1	378	Rho GTPase activating protein 19	ARHGAP19
44563_at	203.2	97.350006	346.75	222.1	291.7	401.7	WD repeat containing, antisense to TP53	WRAP53
45633_at	35.55	36.25	205.79999	205.8	166.45	514.6	GINS complex subunit 3 (Psf3 homolog)	GINS3
52285_f_at	116.8	105.6	317.35	270.1	273.3	427.8	centrosomal protein 76kDa	CEP76

Table S4. Gene cluster (B-1) which shows down regulation in CAEBV, NK lymphoma and NK leukemia compared to Norm NK/HMB

measurement ID	PBMC1, PBMC2	CD16(-)NK1/2	KAI3-1, KAI3-2	SNK10	HANK, SNK6	NK-YS	Gene Title	Gene Symbol
status	PBMC	Normal NK CD16(-)	HMB	CAEBV	NK lymphoma	NK leukemia		
MeasurementID	1	2	3	4	5	6		
200897_s_at	311.15	335.9	774.25	217.9	9.95	6.5	palladin, cytoskeletal associated protein	PALLD
201059_at	160.5	93.2	165.5	98.9	53.55	44.8	cortactin	CTTN
201828_x_at	406.8	306.45	693.45	313	21.3	31.7	family with sequence similarity 127, member A	FAM127A
202096_s_at	1664.6499	102.7	654.15	139.9	12.25	13.8	translocator protein (18kDa)	TSPO
202367_at	308.15002	111.95	159.4	85.3	59.6	41.6	cut-like homeobox 1	CUX1
202545_at	364.7	84.75	254.05	37.6	55.95	29.6	protein kinase C, delta	PRKCD
203029_s_at	196.2	229.85	1308.05	85.8	510	39.3	protein tyrosine phosphatase, receptor type, N polypeptide 2	PTPRN2
203030_s_at	36.85	179	554.15	22	246.95	24.1	protein tyrosine phosphatase, receptor type, N polypeptide 2	PTPRN2
205308_at	232.05	168.95001	699.95	320.9	5.25	16.3	family with sequence similarity 164, member A	FAM164A
205479_s_at	58.35	99.55	123.1	36	6.1499996	11.7	plasminogen activator, urokinase	PLAU
205729_at	6.05	91.5	42.15	8.9	3	5	oncostatin M receptor	OSMR
206272_at	164.7	81.15	298.3	90.6	55.55	57.7	RAB4A, member RAS oncogene family /// S-phase response (cyclin related)	RAB4A /// SPHAR
206914_at	551.6	82.85	1899.4	3.6	1.3	0.6	cytotoxic and regulatory T cell molecule	CRTAM
208657_s_at	644.95	208.05	336.3	88	15.35	46.7	septin 9	9-Sep
209030_s_at	121.10001	100.350006	1888.15	102.2	48.05	26	cell adhesion molecule 1	CADM1
209031_at	92.3	177.20001	1799.95	84	109.55	21.2	cell adhesion molecule 1	CADM1
209032_s_at	64.3	42.1	693.8	44.1	20.150002	10.5	cell adhesion molecule 1	CADM1
209574_s_at	267.85	134.55	978.9	67	92.200005	18.5	chromosome 18 open reading frame 1	C18orf1
210785_s_at	2317.55	218.4	83.45	37.8	7.3	8.5	chromosome 1 open reading frame 38	C1orf38
211534_x_at	48.449997	76.9	354.95	43	149.4	26.1	protein tyrosine phosphatase, receptor type, N polypeptide 2	PTPRN2
211864_s_at	173.70001	174.54999	471.65002	124.3	363.94998	51.4	myoferlin	MYOF
212070_at	1733.2	139.55	251.9	15.9	11.75	20	G protein-coupled receptor 56	GPR56
212509_s_at	2496.2	361.55	1383.8	50.2	52.1	12	matrix-remodelling associated 7	MXRA7
212609_s_at	184.1	100.45	267.9	99.4	67.25	18.6	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3
215175_at	402.3	149.55	240.54999	82.2	28.25	22.8	pecanex homolog (Drosophila)	PCNX
216997_x_at	442.90002	88.2	256.9	159.9	63.55	50.8	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4
217983_s_at	6664.5	409.40002	1352.25	81.9	26.95	21.4	ribonuclease T2	RNASET2
217984_at	4574.7	208.35	597.15	29.7	14.200001	22.3	ribonuclease T2	RNASET2
218326_s_at	34.800003	436.7	355.9	67.2	3.75	1.9	leucine-rich repeat-containing G protein-coupled receptor 4	LGR4
219228_at	5573.3	143.25	179.3	81	27.65	41.5	zinc finger protein 331	ZNF331
221766_s_at	913.2	479.15002	656.2	146.8	63.45	18.5	family with sequence similarity 46, member A	FAM46A
224412_s_at	30.4	269.85	821.45	50.2	27.6	25.4	transient receptor potential cation channel, subfamily M, member 6	TRPM6
226621_at	20.1	229.25	236.1	32.8	10.35	9.8	---	---
227985_at	23.3	79.45	487.40002	53.5	37.949997	55.5	---	---
228384_s_at	52.9	501.45	599.5	64.6	5	2.3	pyridine nucleotide-disulphide oxidoreductase domain 2	PYROXD2
229764_at	29.25	242.2	3666.1501	31.5	14.6	1.3	tumor protein p63 regulated 1	TPRG1
230538_at	18.8	139.35	357.5	58.7	70.200005	38.4	SHC (Src homology 2 domain containing) family, member 4	SHC4
230864_at	5.3500004	117.9	359.15002	169.6	17.75	14.6	serine/threonine-protein kinase NIM1	MGC42105
232629_at	178.15	441.8	602.35	102	0.8	0.4	prokineticin 2	PROK2
235238_at	3.8999999	100.55	278.90002	38.6	44.7	39.7	SHC (Src homology 2 domain containing) family, member 4	SHC4
235333_at	48.65	43	659.2	69	62.649998	21.7	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6
240389_at	5.6499996	156.20001	317.85	42.6	24.800001	25.7	Transient receptor potential cation channel, subfamily M, member 6	TRPM6

Table S5. Gene cluster (B-2) which shows up regulation in CAEBV, NK lymphoma and NK leukemia compared to Norm NK and HMB

ID	PBMC1,PBMC2	CD16(-)NK1/2	KAI3-1,KAI3-2	SNK10	HANK,SNK6	NK-YS	Gene Title	Gene Symbol
status	PBMC	Normal NK CD16(-)	HMB	CAEBV	NK lymphoma	NK leukemia		
MeasurementID	1	2	3	4	5	6		
1552648_a_at	80.2	15.2	26	139.2	86.6	147.7	tumor necrosis factor receptor superfamily, member 10a	TNFRSF10A
1553542_at	60.5	9.6	22.599998	44.1	70.25	156	coiled-coil domain containing 125	CCDC125
1554292_a_at	74.45	16.7	48.1	67.7	83.60001	124.1	UHRF1 binding protein 1-like	UHRF1BP1L
1555464_at	126.75	18.5	54.95	89.6	174.45	92.3	interferon induced with helicase C domain 1	IFIH1
1556172_at	4.25	14.549999	6.6	32.1	76.2	150.7	---	---
1556173_a_at	31.3	28.650002	11.8	59.4	84.35	161.6	---	---
1564746_at	23.9	15.65	45.2	66.2	60.45	100.1	Na+/H+ exchanger domain containing 2	NHEDC2
200952_s_at	71.5	17.3	106.05	227.1	174.45	403.8	cyclin D2	CCND2
202218_s_at	35.55	18.1	16.85	44.2	57.15	172.2	fatty acid desaturase 2	FADS2
203131_at	4.05	1	12.200001	136.1	89.39999	1029.8	platelet-derived growth factor receptor, alpha polypeptide	PDGFRA
203498_at	29.300001	9.799999	25.95	140.9	407.95	2520.3	regulator of calcineurin 2	RCAN2
204113_at	53.25	20.650002	62.65	82.7	72.15	115.1	CUG triplet repeat, RNA binding protein 1	CUGBP1
204795_at	98.45	36.7	97.05	90.3	190.65	389.8	proline rich 3	PRR3
207528_s_at	19.25	17.3	23.9	108.3	93.45	97.9	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	SLC7A11
207824_s_at	77.7	30.7	74.95	69.9	84.5	124.2	MYC-associated zinc finger protein (purine-binding transcription factor)	MAZ
208844_at	26.349998	48.949997	43.65	90	97.95001	119.4	voltage-dependent anion channel 3	VDAC3
208962_s_at	168	16.85	1.75	145.8	158.5	482.9	fatty acid desaturase 1	FADS1
208963_x_at	156.85	15.95	14.450001	104	115.7	290.4	fatty acid desaturase 1	FADS1
208964_s_at	214.04999	25.25	21.7	217.9	209.4	490	fatty acid desaturase 1	FADS1
209961_s_at	39.75	11.900001	32	82.9	303.15	109.1	hepatocyte growth factor (hepapoietin A; scatter factor)	HGF
210098_s_at	67.5	29.300001	22.5	89.2	81.2	126	---	---
210755_at	16.1	0.75	4.6	108.6	324	72.2	hepatocyte growth factor (hepapoietin A; scatter factor)	HGF
210997_at	30.4	2.9	1.45	43.5	450.65	69.1	hepatocyte growth factor (hepapoietin A; scatter factor)	HGF
211162_x_at	4.2	36.85	41.300003	47.4	70.2	225.6	stearoyl-CoA desaturase (delta-9-desaturase)	SCD
212383_at	255.2	19.900002	45.2	156.1	184.95	127.8	ATPase, H+ transporting, lysosomal V0 subunit a1	ATP6V0A1
212641_at	222.5	10.75	25.3	51.4	53.65	79.7	human immunodeficiency virus type I enhancer binding protein 2	HIVEP2
213415_at	81.5	4.95	9.5	287.6	872.55	387.2	chloride intracellular channel 2	CLIC2
213758_at	425.45	29.25	30.25	58.5	61.55	72.1	cytochrome c oxidase subunit IV isoform 1	COX4I1
214190_x_at	111.4	23.5	12.700001	73.4	104.15	195.6	golgi associated, gamma adaptin ear containing, ARF binding protein 2	GGA2
216962_at	2.1999998	8.3	22.650002	61	63.15	120.5	RPA interacting protein	RPAIN
218148_at	107.3	25.95	35.95	60.4	69.45	71.6	centromere protein T	CENPT
218536_at	172.9	17.9	60.050003	109.1	100.7	107.5	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	MRS2
218634_at	53.05	9.450001	38.15	87.9	70.15	125.5	pleckstrin homology-like domain, family A, member 3	PHLDA3
219714_s_at	139.3	1.9	1.95	57.6	218.55	2226	calcium channel, voltage-dependent, alpha 2/delta subunit 3	CACNA2D3
219938_s_at	288.7	11.75	5.6499996	36.3	79.75	63.2	proline-serine-threonine phosphatase interacting protein 2	PSTPIP2
220800_s_at	80	26.1	116.25	174.2	121.95	251.7	tropomodulin 3 (ubiquitous)	TMOD3
221011_s_at	1104.35	46.25	23.5	82.7	104.15	254.5	limb bud and heart development homolog (mouse)	LBH
221210_s_at	250.85	8.95	49.5	120.5	79.35	243.9	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NPL
222038_s_at	18.7	11.25	36.95	46.4	52.35	154.6	UTP18, small subunit (SSU) processome component, homolog (yeast)	UTP18
222565_s_at	173.35	5.75	8.25	32.1	126.05	137	protein kinase D3	PRKD3
223405_at	458.35	9.95	80.8	196.9	146.75	211.6	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NPL
223452_s_at	169.25	4.3	43.1	177.2	129.3	351.6	atlastin GTPase 3	ATL3
224496_s_at	73.649994	22.95	84.899994	135.4	184.05	189.5	transmembrane protein 107	TMEM107
226064_s_at	81.8	5.5	2.95	30.3	75.6	144.1	diacylglycerol O-acyltransferase homolog 2 (mouse)	DGAT2
226448_at	66.45	14.299999	17.8	53.4	68.95	401.1	family with sequence similarity 89, member A	FAM89A
226537_at	64.350006	22.9	39.55	66.7	57.85	127.5	histidine triad nucleotide binding protein 3	HINT3
227171_at	72.55	45.4	54.35	86.5	115.65	132.7	---	---
227438_at	52.35	13.85	38.75	130.9	168.55	211.1	alpha-kinase 1	ALPK1
227461_at	119.60001	10.6	5.3	33	28.1	147.4	stonin 2	STON2
229082_at	22.6	18.2	41.15	63.9	86.20001	266.2	coiled-coil domain containing 125	CCDC125
230170_at	1793.5	34.4	45.2	141.8	447.45	176.8	oncostatin M	OSM
232291_at	149.75	8.150001	70.45	76.8	158.4	296.1	MIR17 host gene (non-protein coding)	MIR17HG
233016_at	17.55	2.1	2.5500002	92.8	186.1	227.3	---	---
234347_s_at	39.95	17.65	31.85	58.5	61.5	108.5	density-regulated protein	DENR

235102_x_at	697.7	15.849999	117.6	108.8	253.4	574.6	---	---
235286_at	33.9	21.15	39.35	65.1	70.35	120.1	---	---
235846_at	83.15	11.950001	54.1	62	100.95	112.7	---	---
237203_at	17.05	13.099999	10.35	87	119.15	178.7	---	---
241371_at	153.7	8.650001	13.3	129	98.39999	131.5	---	---
242705_x_at	134.25	20.8	62.85	57.3	61.95	91	similar to hCG1981348	LOC100289219
242918_at	153.9	12.200001	36.45	33.6	49.4	94	Nuclear autoantigenic sperm protein (histone-binding)	NASP
243840_at	13.45	12	42.95	77.9	84.25	135.6	arsenic transactivated protein 1	LOC100289612
244030_at	51.5	22.7	48.7	74.4	77.15	76.3	serine/threonine/tyrosine interacting protein	STYX
244219_at	224.2	23.35	56.25	53.6	63.7	101.1	---	---

Table S6. Gene cluster (C) which shows down regulation in NK lymphoma and NK leukemia compared to Norm NK, HMB and CAEBV

ID	PBMC1,PBMC2	CD16(-)NK1/2	KAI3-1,KAI3-2	SNK10	HANK,SNK6	NK-YS	Gene Title	Gene Symbol
status	PBMC	Normal NK CD16(-)	HMB	CAEBV	NK lymphoma	NK leukemia		
measurement ID	1	2	3	4	5	6		
1552400_a_at	16.9	75.55	253.20001	200	42.25	18.1	chromosome 15 open reading frame 27	C15orf27
1552627_a_at	88	43.8	194.6	168.3	57.75	0.6	Rho GTPase activating protein 5	ARHGAP5
1553132_a_at	695.1	241.75	727.15	201.7	9.1	2.4	tandem C2 domains, nuclear	TC2N
1563641_a_at	179.45001	52.7	83.25	67.2	23.75	3.4	sorting nexin 20	SNX20
1569077_x_at	128.75	80.8	82.95	77.1	22.3	22.3	zinc finger protein 836	ZNF836
1569366_a_at	137.54999	14.049999	95.85	61	16.2	0.5	zinc finger protein 569	ZNF569
1569387_at	110.65	73.05	84.45	39.4	8.1	1	---	---
1570360_s_at	86.15	48.15	131.65	70.8	25.550001	2.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	DDX3Y
200906_s_at	60.65	37.6	104.05	39.9	6.9	2.9	palladin, cytoskeletal associated protein	PALLD
200907_s_at	246.55	228.5	596.75	146.2	3.8999999	0.5	palladin, cytoskeletal associated protein	PALLD
201416_at	74.55	65.8	143	56.7	2.5	1	SRY (sex determining region Y)-box 4	SOX4
201417_at	299	114.05	362.95	339.9	8.65	0.9	SRY (sex determining region Y)-box 4	SOX4
202085_at	229.35	1723.6001	1138.9	405.9	41.65	8.2	tight junction protein 2 (zona occludens 2)	TJP2
202481_at	257.3	61.699997	58.15	37.1	2	1.7	dehydrogenase/reductase (SDR family) member 3	DHRS3
203081_at	135.8	78	175.54999	33	19.65	6	catenin, beta interacting protein 1	CTNNBIP1
203215_s_at	22.599998	105.600006	436.80002	99.9	71.9	1.9	myosin VI	MYO6
203633_at	475.90002	264.65	277.8	504	9.95	1.5	carnitine palmitoyltransferase 1A (liver)	CPT1A
203763_at	60.15	43.85	142.05	97.3	85.1	1.1	dynein, cytoplasmic 2, light intermediate chain 1	DYNC2LI1
203787_at	461.09998	161.25	521.4	210.7	4.8	1.5	single-stranded DNA binding protein 2	SSBP2
203928_x_at	47.199997	33.65	121.95	100.6	20.25	2.8	microtubule-associated protein tau	MAPT
204048_s_at	667.4	167.15	393.35	85.2	10.95	0.9	phosphatase and actin regulator 2	PHACTR2
204049_s_at	1054.05	179.1	453.85	116	9.9	0.4	phosphatase and actin regulator 2	PHACTR2
204403_x_at	235.4	86.100006	145	101.1	58	36.8	family with sequence similarity 115, member A	FAM115A
204409_s_at	1078.4	499.5	1082.45	1353.9	334	4.5	eukaryotic translation initiation factor 1A, Y-linked	EIF1AY
204497_at	142.05	30.25	66.3	36.4	19.1	0.7	adenylate cyclase 9	ADCY9
205000_at	3508.9	1611.5	1189.1	1100.3	466.05	5.5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	DDX3Y
205001_s_at	620.4	268.85	292.45	212.3	96.15	6.8	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	DDX3Y
205125_at	380.40002	55.1	105.2	52.7	28.849998	7.8	phospholipase C, delta 1	PLCD1
206059_at	2243.0498	527.69995	455.8	311.9	103.65	1	zinc finger protein 91	ZNF91
207761_s_at	1422	213.04999	1611.2	205.2	110.7	0.8	methyltransferase like 7A	METTL7A
207996_s_at	189.55	83.85	218.15	19.5	19.050001	1	chromosome 18 open reading frame 1	C18orf1
209014_at	439.9	352.5	650.3	177.1	91.299995	18.1	melanoma antigen family D, 1	MAGED1
209122_at	2602.05	502.15002	543.9	534.2	117.100006	1.8	perilipin 2	PLIN2
209576_at	20.6	60.949997	147.79999	131.5	3.8	4	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1
209674_at	1345.3501	374.3	413.7	379.6	303.94998	2.8	cryptochrome 1 (photolyase-like)	CRY1
209703_x_at	309.65	46	278.65002	32.9	26.05	1.8	methyltransferase like 7A	METTL7A
210045_at	159.9	71.350006	106.75	81	26	7.5	isocitrate dehydrogenase 2 (NADP+), mitochondrial	IDH2
210778_s_at	436.85	112.850006	123.299995	81.1	27.800001	25.3	MAX dimerization protein 4	MXD4
210829_s_at	235.29999	84.05	377.30002	135.6	9.6	2.6	single-stranded DNA binding protein 2	SSBP2
210948_s_at	370.34998	39.9	47.45	61.6	0.84999996	0.8	lymphoid enhancer-binding factor 1	LEF1
211704_s_at	109.7	59.2	98.850006	82.8	27.25	1.3	spindlin family, member 2A /// spindlin family, member 2B	SPIN2A /// SPIN2B
212945_s_at	227.35	32.7	59.6	57.3	46.9	0.5	MAX gene associated	MGA
213353_at	243.85	161.55	57.5	46.1	11.6	3.9	ATP-binding cassette, sub-family A (ABC1), member 5	ABCA5
213385_at	395.55	70.850006	953.95	59.1	52.75	1.1	chimerin (chimaerin) 2	CHN2
213435_at	26.15	137.54999	253.45	154.7	6.8	0.7	SATB homeobox 2	SATB2
213657_s_at	150.45	108.25	130.85	72.1	22.05	1.1	---	---
213658_at	79.2	48.15	87.7	43.4	10.7	6.8	---	---
214228_x_at	91.7	118.799995	468.35	204.5	150.65	3	tumor necrosis factor receptor superfamily, member 4	TNFRSF4
214470_at	3957.8499	2039.4	2159.45	1859.6	2.5	1.7	killer cell lectin-like receptor subfamily B, member 1	KLRB1
214749_s_at	1244.65	597.85	464.9	441.5	183.9	8.9	armadillo repeat containing, X-linked 6 /// similar to armadillo repeat containing, X-linked 6	ARMCX6 /// LOC653354
215749_s_at	201.1	59.55	190.6	77.6	70.299995	30.6	golgi reassembly stacking protein 1, 65kDa	GORASP1
218589_at	1015.4	613.7	795.9	1634.7	6.8	2.4	lysophosphatidic acid receptor 6	LPAR6
218676_s_at	181.20001	277.25	1216.55	620.4	105.4	0.8	phosphatidylcholine transfer protein	PCTP
219049_at	725.44995	1229.6499	792	462.8	165.55	7.6	chondroitin sulfate N-acetylgalactosaminyltransferase 1	CSGALNACT1

219259_at	274.3	57.2	70.9	26.6	2.75	2	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	SEMA4A
219355_at	193.1	499.55	548.35	141.5	133.2	1.2	chromosome X open reading frame 57	CXorf57
219559_at	63.2	92.55	167.35	81.5	61.3	15.4	solute carrier family 17, member 9	SLC17A9
219826_at	125.35	26.25	130.8	70.8	23.6	1.1	zinc finger protein 419	ZNF419
219878_s_at	186.90001	58.05	155.1	86.2	21.6	3.9	Kruppel-like factor 13	KLF13
220198_s_at	63.7	37.4	106.45	54.8	19.1	1.1	eukaryotic translation initiation factor 5A2	EIF5A2
221558_s_at	2665.0498	392.65002	442	701.4	2.55	0.3	lymphoid enhancer-binding factor 1	LEF1
221666_s_at	932.3	72.45	478.6	396.2	59.15	2	PYD and CARD domain containing	PYCARD
222987_s_at	162.35	73.7	91.4	88.1	3.3	7.4	transmembrane protein 9	TMEM9
222988_s_at	267.5	76.3	127.3	95.7	11	9	transmembrane protein 9	TMEM9
223380_s_at	881.5	147.25	498.4	188.1	64.4	8.6	LATS, large tumor suppressor, homolog 2 (Drosophila)	LATS2
224492_s_at	504.65	184.4	318.45	180.2	115.6	12.9	zinc finger protein 627	ZNF627
225272_at	820.55005	206.4	379.34998	262.5	58.25	2.1	spermidine/spermine N1-acetyltransferase family member 2	SAT2
225447_at	286.65002	188.8	496.35	118.5	12.2	5	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	GPD2
225579_at	838.75	262.3	900.65	170.9	44.15	4.9	PQ loop repeat containing 3	PQLC3
225912_at	1132.2	136.85	257.45	273.5	116.549995	20.7	tumor protein p53 inducible nuclear protein 1	TP53INP1
225949_at	112.6	103.399994	62.3	71.5	14.35	7.7	nuclear receptor binding protein 2	NRBP2
226039_at	1408.6	47	112.25	51.5	16.05	2.6	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	MGAT4A
226127_at	339.84998	94.4	267.45	239.1	89.799995	2.4	alkB, alkylation repair homolog 3 (E. coli)	ALKBH3
226137_at	326.05	80.2	112.75	194.2	13.25	10.4	zinc finger homeobox 3	ZFHX3
226264_at	466.15002	48.6	64.95	80.4	4.85	3.2	sushi domain containing 1	SUSD1
227009_at	116.95	45.3	61.199997	48.8	11.35	9.2	---	---
227013_at	617.65	69.899994	331.45	153.3	52.050003	3.6	LATS, large tumor suppressor, homolog 2 (Drosophila)	LATS2
227134_at	1524	341.25	335.75	319.1	46.75	3.5	synaptotagmin-like 1	SYTL1
227195_at	136.65	31.25	122.1	31.8	32.3	1.3	zinc finger protein 503	ZNF503
227379_at	225.4	124.7	121.850006	218.7	150.95	0.9	membrane bound O-acyltransferase domain containing 1	MBOAT1
227534_at	577.6	54.55	207.35	133	86.1	0.9	chromosome 9 open reading frame 21	C9orf21
227670_at	564.75	88.6	91.5	110.5	30	25.4	zinc finger protein 75a	ZNF75A
227947_at	965.3	154.75	356	84.3	5.5499997	0.1	phosphatase and actin regulator 2	PHACTR2
228115_at	5.5	22.05	89.8	134.1	11.099999	0.4	---	---
228492_at	536.1	103.15	170.15	163.6	2.7	6.1	ubiquitin specific peptidase 9, Y-linked	USP9Y
228678_at	58.85	117.7	370.59998	169.1	16.35	1.3	family with sequence similarity 116, member B	FAM116B
228869_at	1232	473.1	511.8	350.7	146.45	17.9	---	---
229040_at	225.35	23.3	28.099998	24.8	2.3000002	1.3	---	---
229327_s_at	419.65	142.95001	188.55	540.2	5.2	6.9	---	---
229739_s_at	59.9	98.3	262.1	152.1	25.45	4.3	family with sequence similarity 116, member B	FAM116B
230012_at	366.1	41.6	47.7	39.6	19.1	8.8	chromosome 17 open reading frame 44	C17orf44
230454_at	72.25	82.7	97.95	83.5	18.45	14.8	islet cell autoantigen 1,69kDa-like	ICA1L
231817_at	152.95	26.85	79.55	45	22.9	2.5	ubiquitin specific peptidase 53	USP53
233198_at	170.70001	116.4	198.35	155.3	20.05	26.4	golgi autoantigen, golgin subfamily a, 2-like 1	GOLGA2L1
233241_at	32.550003	82.25	150.8	41.2	18.95	3.2	chromosome 20 open reading frame 19	C20orf19
233849_s_at	475.19998	168.9	647.85	563.9	169.4	1.4	Rho GTPase activating protein 5	ARHGAP5
234970_at	595.5	106.9	311.2	114	14.7	0.6	tandem C2 domains, nuclear	TC2N
235289_at	123.9	60.7	83.25	50.2	18.8	4	eukaryotic translation initiation factor 5A2	EIF5A2
235296_at	129.15	128.05	159.9	113.7	47.85	7.2	eukaryotic translation initiation factor 5A2	EIF5A2
235410_at	361.95	53	65	66.8	23.65	12.7	nephronophthisis 3 (adolescent)	NPHP3
235432_at	670.65	64.45	108.450005	69.9	37.85	10.6	nephronophthisis 3 (adolescent)	NPHP3
235635_at	59.4	25.2	86.85	43.9	48.3	1.4	Rho GTPase activating protein 5	ARHGAP5
239142_at	56	47.35	97.35	42.4	45.649998	0.4	Rieske (Fe-S) domain containing	RFESD
239300_at	212.2	76.95	135.75	68	36.1	13.8	---	---
242277_at	263.85	90	171.05	40.1	4.3500004	2.1	---	---
242738_s_at	159	45.5	76.05	92.1	21.2	3.6	zinc finger homeobox 3	ZFHX3
244050_at	1152.1	87.5	114.5	254.8	3.25	6.6	protein tyrosine phosphatase-like A domain containing 2	PTPLAD2
244482_at	554.95	40.25	75.8	116	19.15	0.2	---	---
244881_at	113.95	76.65	144.55	66.4	68.6	19.3	leishmanolysin-like (metallopeptidase M8 family)	LMLN
37590_g_at	111.950005	82.2	130.15	69.3	17.4	10.5	---	---

Table S7. Gene cluster (D-1) which shows down regulation in NK leukemia compared to Norm NK. HMB, CAEBV and NK lymphoma

ID	PBMC1,PBMC2	CD16(-)NK1/2	KAI3-1,KAI3-2	SNK10	HANK,SNK6	NK-YS	Gene Title	Gene Symbol
status	PBMC	Normal NK CD16(-)	HMB	CAEBV	NK lymphoma	NK leukemia		
MeasurementID	1	2	3	4	5	6		
1553145_at	63.3	59.8	142.95	69.5	62.05	14.5	hypothetical FLJ39653	FLJ39653
1553185_at	631.80005	163.2	390.95	114.8	197.79999	20.7	RAS and EF-hand domain containing	RASEF
1553645_at	100.75	30.3	281.9	202.5	186.85	0.5	coiled-coil domain containing 141	CCDC141
1553856_s_at	1152.15	193.9	738.75	508.3	823.44995	26.3	purinergic receptor P2Y, G-protein coupled, 10	P2RY10
1554397_s_at	92.8	172.65	359.65	436.3	279.15	8.7	UEV and lactate/malate dehyrogenase domains	UEVLD
1555465_at	42.4	265.35	398.6	560	328.8	46.2	mucolipin 2	MCOLN2
1555888_at	128.85	93.6	121	96	106.05	18.3	Ubiquitin protein ligase E3 component n-recognin 5	UBR5
1555945_s_at	1049.6	223.6	493.6	463	339.35	110.4	family with sequence similarity 120A	FAM120A
1556658_a_at	1250.25	237.8	665	258.6	414.05	55	---	---
1557051_s_at	84.149994	130.2	62.6	206.5	146.6	1.7	---	---
1557270_at	371.85	100.65	168.45	79.8	76.65	16	---	---
1557632_at	769.95	125.05	160.95001	68	107.45	13.8	---	---
1558827_a_at	437.90002	133.75	64.95	55.2	28.099998	1	zinc finger protein 831	ZNF831
1558922_at	252	84.55	115.15	80.2	86.95	15.5	---	---
1559957_a_at	27.1	53.8	131.05	74.1	90.15	11.8	hypothetical LOC642852	LOC642852
1561346_at	459	90.55	131.35	143.2	80.75	11.3	---	---
1562529_s_at	672.3	96	205.45001	111.8	101.5	13.5	---	---
1564424_at	965.15	104.850006	96.100006	58.4	61.149998	10.5	---	---
1565804_at	156.05	60.3	18	38.8	23.5	0.8	---	---
1567628_at	891.3	420.3	343.55	1166.8	677.25	17.5	CD74 molecule, major histocompatibility complex, class II invariant chain	CD74
1568623_a_at	45.649998	37.25	139.75	46.2	74.3	1.1	solute carrier family 35, member E4	SLC35E4
200600_at	6962.45	1780.05	3886.9502	3524.1	3443.5	8.6	moesin	MSN
201003_x_at	721.19995	305.85	799.25	699.2	331.75	8.5	arginyl aminopeptidase (aminopeptidase B) /// transmembrane protein 189 /// TMEM189-UBE2V1 readthrough transcript /// ubiquitin-conjugating enzyme E2 variant 1	RNPEP /// TMEM189 /// TMEM189-UBE2V1 /// UBE2V1
201137_s_at	11439.6	5796.45	2319.3	4667.9	6227.55	95.3	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
201328_at	725.7	285.6	326.3	277.1	153.95	85.4	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2
201413_at	608.85	229.4	904.5	683.4	635.3	93.3	hydroxysteroid (17-beta) dehydrogenase 4	HSD17B4
201494_at	1016.69995	387.34998	490.75	408.8	217.4	97.7	prolylcarboxypeptidase (angiotensinase C)	PRCP
201631_s_at	6867.6	246.8	679.7	937	406.05002	24.9	immediate early response 3	IER3
201720_s_at	5988.85	435.09998	2580.2998	1495.8	703.1	13.7	lysosomal protein transmembrane 5	LAPTM5
201721_s_at	13966.9	938.6	3982	2185	1080.15	23.3	lysosomal protein transmembrane 5	LAPTM5
201986_at	953.85	358.1	888.65	755.8	675.44995	187.3	mediator complex subunit 13	MED13
201987_at	1102.8	772	2068.35	841.1	1046.8	165.1	mediator complex subunit 13	MED13
202073_at	699.25	251.95	603.1	502.1	334.3	83.6	optineurin	OPTN
202108_at	350.8	86.600006	291.85	57.3	109.6	0.7	peptidase D	PEPD
202615_at	1453.55	313	574.95	273.8	250	6.3	Guanine nucleotide binding protein (G protein), q polypeptide	GNAQ
202822_at	871.9	624.9	378.3	168.3	187.35	18.7	LIM domain containing preferred translocation partner in lipoma	LPP
202838_at	384.75	585.8	2463	803.2	140.8	3.1	fucosidase, alpha-L- 1, tissue	FUCA1
202853_s_at	532.2	93.05	338.95	177.1	197.4	3	RYK receptor-like tyrosine kinase	RYK
202855_s_at	171.75	84	102.15	160.7	123.25	5.9	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	SLC16A3
202856_s_at	765.05005	195.95	255.95	243.7	193.90001	1	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	SLC16A3
202880_s_at	2281.9	357.7	431.1	836.1	173.35	141.9	cytohesin 1	CYTH1
202910_s_at	2695.75	470.75	319.45	726.3	536.6	90.4	CD97 molecule	CD97
202931_x_at	678.55	546.35	43.449997	229.9	180.2	1.5	bridging integrator 1	BIN1
203045_at	586.7	142.85	473.6	225.2	303.2	2.1	ninjurin 1	NINJ1
203140_at	2999.25	517.5	485.15	488.6	820.80005	34.1	B-cell CLL/lymphoma 6	BCL6
203216_s_at	112.85	318.55	690.35	697.1	249.15001	0.1	myosin VI	MYO6
203232_s_at	1249.1	718.55	334.3	577.1	374.1	71.5	ataxin 1	ATXN1
203271_s_at	257.55	55.05	131.7	91.9	93.450005	21.4	unc-119 homolog (C. elegans)	UNC119
203303_at	1080.2	612.6	1252.25	967.6	704	8	dynein, light chain, Tctex-type 3	DYNLT3
203384_s_at	169.8	59.6	67.95	79.7	70.5	19.7	golgi autoantigen, golgin subfamily a, 1	GOLGA1
203401_at	485.55	469.05	1408.65	487.7	693.55	0.4	phosphoribosyl pyrophosphate synthetase 2	PRPS2
203414_at	1109.25	321.09998	547.2	1225.8	696.1	143.8	monocyte to macrophage differentiation-associated	MMD
203518_at	659.65	182.85	380.65	528.2	515.15	35.3	lysosomal trafficking regulator	LYST
203528_at	1664.35	356.05	361.45	370.8	373.65002	87.9	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	SEMA4D
203556_at	783.65	67.2	156.45	117.9	25.400002	0.3	zinc fingers and homeoboxes 2	ZHX2
203557_s_at	47.75	205.45001	274.35	104.4	232.5	5.7	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	PCBD1
203739_at	1603.3	495.25	1069.5	493.2	546.44995	127.8	zinc finger protein 217	ZNF217

203831_at	861	301.85	440.25	283.4	252.75	101.5	R3H domain containing 2	R3HDM2
203932_at	3639.2998	508.1	613.95	1493.7	1334.75	27.5	major histocompatibility complex, class II, DM beta	HLA-DMB
204067_at	70.8	60.949997	103.15	84	30.35	1.1	sulfite oxidase	SUOX
204094_s_at	1851.9501	257.45	507.25	287.9	373.45	127.3	TSC22 domain family, member 2	TSC22D2
204158_s_at	1282.95	427.15002	243.79999	233.4	196.79999	1.5	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	TCIRG1
204254_s_at	336.35	427.3	223.70001	552.5	393.05	5.2	vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR
204255_s_at	219.45	445.55	279.5	546.9	437.55	1.9	vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR
204290_s_at	192.3	352.09998	482.35	323.3	312.7	67.9	aldehyde dehydrogenase 6 family, member A1	ALDH6A1
204374_s_at	8.75	43.5	139.9	48.6	75	2.1	galactokinase 1	GALK1
204523_at	428.35	44.15	113.05	172.3	85.75	0.2	zinc finger protein 140	ZNF140
204552_at	642.4	425.8	415.35	471.3	299.6	124.2	inositol polyphosphate-4-phosphatase, type I, 107kDa	INPP4A
204629_at	159.25	63.75	499.90002	257.1	172.70001	41.4	parvin, beta	PARVB
204670_x_at	9214.65	5388.2	4773.3	6443.1	6998.75	13.2	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 4	HLA-DRB1 /// HLA-DRB4
204674_at	1021.6	438.6	1557.65	601.3	514.1	78.9	lymphoid-restricted membrane protein	LRMP
204867_at	149.75	321.9	223.45001	180.7	272.69998	15.3	GTP cyclohydrolase I feedback regulator	GCHFR
204985_s_at	415	504	638.7	339.2	378.95	100	trafficking protein particle complex 6A	TRAPPC6A
205022_s_at	1702.3501	504.19998	461.35	374.3	264.25	127.3	forkhead box N3	FOXN3
205047_s_at	457.65	315.45	466.8	1599.5	1466.05	0.6	asparagine synthetase	ASNS
205052_at	234.15	628.65	540.7	660.6	624.6	107.8	AU RNA binding protein/enoyl-Coenzyme A hydratase	AUH
205081_at	2030.9	1071.75	1239.75	631.6	378.15	0.9	cysteine-rich protein 1 (intestinal)	CRIP1
205397_x_at	129.70001	61.1	53.199997	87.8	64.55	3	SMAD family member 3	SMAD3
205398_s_at	228.55	136.35	164.75	351.7	168.85	16.2	SMAD family member 3	SMAD3
205453_at	227.85	419.3	300.75	649.7	354.5	8.1	homeobox B2	HOXB2
205603_s_at	524.85	120.399994	371.45	158.5	167.2	0.4	diaphanous homolog 2 (Drosophila)	DIAPH2
205652_s_at	43.1	56.15	106.55	102	62.15	2.8	tubulin tyrosine ligase-like family, member 1	TTLL1
205681_at	3320.2	96.8	137.25	172.2	126.7	16.5	BCL2-related protein A1	BCL2A1
205718_at	877.85	1559	978.7	1396.9	449.65002	152.7	integrin, beta 7	ITGB7
205726_at	278.1	70.05	166	70.3	66.15	7.4	diaphanous homolog 2 (Drosophila)	DIAPH2
205756_s_at	156.55	244.75	421.8	717.9	497.85	89.2	coagulation factor VIII, procoagulant component	F8
205798_at	9475.85	457.4	1194.1	854.9	364.95	19.6	interleukin 7 receptor	IL7R
205831_at	3035.75	1526.35	2721.15	3199.5	1590.8501	22.6	CD2 molecule	CD2
205871_at	74.05	21.35	175.9	62.8	42.6	2.1	plasminogen-like A /// plasminogen-like B1 /// plasminogen-like B2	PLGLA /// PLGLB1 /// PLGLB2
206081_at	57.699997	82.25	179.45	70.9	57.4	6.9	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	SLC24A1
206240_s_at	827.15	116.95	207.75	142.5	122.399994	10.6	zinc finger protein 136	ZNF136
206313_at	98.15	101.05	220.1	242.6	145.55	4.9	major histocompatibility complex, class II, DO alpha	HLA-DOA
206385_s_at	318.05	252.15001	508.7	1178.3	424.65002	92.4	ankyrin 3, node of Ranvier (ankyrin G)	ANK3
206632_s_at	292.75	1195.4	2624.85	1591.6	1988.3501	4.6	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	APOBEC3B
206756_at	168.05	68.25	137.8	119.7	300.65	3.3	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	CHST7
207001_x_at	3003.0498	222.15	69.6	80	109.55	4.4	TSC22 domain family, member 3	TSC22D3
207426_s_at	152.54999	1041.1499	4687.35	2497.1	444.1	9.3	tumor necrosis factor (ligand) superfamily, member 4	TNFSF4
207578_s_at	139.95	74.6	84.35	86.4	76.7	11.7	5-hydroxytryptamine (serotonin) receptor 4	HTR4
207651_at	757.15	992.35	4122.6	4052.2	2298.3	89	G protein-coupled receptor 171	GPR171
207836_s_at	4.5	182.45001	340.35	170.3	158.70001	2.2	RNA binding protein with multiple splicing	RBPMS
207843_x_at	186.85	162.35	249.45	453.9	362.65	1.2	cytochrome b5 type A (microsomal)	CYB5A
208270_s_at	728.25	440.8	1213.6	830.2	412.8	2	arginyl aminopeptidase (aminopeptidase B)	RNPEP
208306_x_at	13477.051	7906.6504	7183.2	8358.9	8755.5	21.2	---	---
208763_s_at	10905.85	1333.2	404.5	491.7	531.7	18.7	TSC22 domain family, member 3	TSC22D3
208894_at	12474.4	8360.85	9666.3	9108	11185.35	35	major histocompatibility complex, class II, DR alpha	HLA-DRA
209034_at	7481.8496	1455.45	2250.25	980.1	847.05	139.1	proline-rich nuclear receptor coactivator 1	PNRC1
209262_s_at	7	25.650002	196.95	61	83.100006	0.7	nuclear receptor subfamily 2, group F, member 6	NR2F6
209312_x_at	12586.5	8500.75	6968	9801.5	9943.2	25.6	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5	HLA-DRB1 /// HLA-DRB4 /// HLA-DRB5
209366_x_at	205.85	215.79999	328.65	522.4	396.35	0.8	cytochrome b5 type A (microsomal)	CYB5A
209459_s_at	286	234.65	195.54999	21	64.45	0.2	4-aminobutyrate aminotransferase	ABAT
209487_at	22.8	295.05	1054.9	418.1	235.2	1.5	RNA binding protein with multiple splicing	RBPMS

209488_s_at	1.9	177.65	895.05	251.2	310.9	0.9	RNA binding protein with multiple splicing	RBPMS
209568_s_at	133.95	131.55	724.05	191.8	195.1	25.3	ral guanine nucleotide dissociation stimulator-like 1	RGL1
209585_s_at	210.6	156.45	632.85	351.4	468.4	6.1	multiple inositol polyphosphate histidine phosphatase, 1	MINPP1
209670_at	3847.05	313.2	1077.5	537.7	1177.55	55.9	T cell receptor alpha constant	TRAC
209671_x_at	3613.4502	275.95	1065.75	535.3	1433.95	19.1	T cell receptor alpha locus /// T cell receptor alpha constant	TRA@ /// TRAC
209728_at	6185.95	255	2419.7	3249.2	94.6	0.6	major histocompatibility complex, class II, DR beta 4	HLA-DRB4
209823_x_at	1639.75	333.40002	716.9	2539.2	956.35	4.2	major histocompatibility complex, class II, DQ beta 1	HLA-DQB1
209829_at	1537.25	116.25	106.450005	95.3	56.8	12.5	family with sequence similarity 65, member B	FAM65B
209863_s_at	15.9	269.35	1578.85	110	307.15	0.5	tumor protein p63	TP63
209916_at	164.75	97.350006	207.7	105.1	188.7	21.5	dehydrogenase E1 and transketolase domain containing 1	DHTKD1
210001_s_at	526.45	188.45	316.25	516.2	650.94995	132.2	suppressor of cytokine signaling 1	SOCS1
210058_at	177.7	103.8	120.100006	318.5	152.7	12.7	mitogen-activated protein kinase 13	MAPK13
210201_x_at	934.9	748.15	75.35	316.5	241.05	4.1	bridging integrator 1	BIN1
210205_at	255.4	128.75	57.85	133.7	54.6	1.6	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	B3GALT4
210425_x_at	1603.35	292.15	333.6	1289	273.9	104.2	golgi autoantigen, golgin subfamily a, 8B	GOLGA8B
210426_x_at	1091.3	122.65	140	139.9	97.399994	19.8	RAR-related orphan receptor A	RORA
210439_at	805.25	189.2	672.19995	1516.5	898.69995	0.8	inducible T-cell co-stimulator	ICOS
210479_s_at	1066.55	90.05	136.55	148.7	76.4	12.7	RAR-related orphan receptor A	RORA
210972_x_at	4082.7998	307.5	1319.1001	598.3	1437.65	45.6	T cell receptor alpha locus /// T cell receptor alpha constant /// T cell receptor alpha joining 17 /// T cell receptor alpha variable 20	TRA@ /// TRAC /// TRAJ17 /// TRAV20
210982_s_at	10026.35	6381.6	6102.95	6450.1	7538.15	11.9	major histocompatibility complex, class II, DR alpha	HLA-DRA
211068_x_at	2054.35	522.9	748.4	463	327.7	95	family with sequence similarity 21, member C /// family with sequence similarity 21, member D	FAM21C /// FAM21D
211370_s_at	200.55	95.2	104.3	91.8	55.1	4.5	mitogen-activated protein kinase kinase 5	MAP2K5
211426_x_at	122.05	59.350002	213.5	109.2	106.8	17.5	guanine nucleotide binding protein (G protein), q polypeptide	GNAQ
211654_x_at	619.65	3572.9	1350.1	1959.2	2675	25.7	major histocompatibility complex, class II, DQ beta 1	HLA-DQB1
211656_x_at	2214.0498	607.85	953.4	2862.7	1006.25	20	major histocompatibility complex, class II, DQ beta 1 /// similar to major histocompatibility complex, class II, DQ beta 1	HLA-DQB1 /// LOC100294318
211729_x_at	936.55005	67	2788.85	495.7	675.6	25.5	biliverdin reductase A	BLVRA
211902_x_at	2267.9502	299.84998	1410.55	601.6	1269.55	34	T cell receptor alpha locus	TRA@
211991_s_at	5152.9	5248.4004	3695.25	4530.7	5053.6	158.3	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1
212099_at	2577.8	104.55	562.1	125.1	353	2.2	ras homolog gene family, member B	RHOB
212326_at	154.6	56.45	69	57.6	32.75	2.9	vacuolar protein sorting 13 homolog D (S. cerevisiae)	VPS13D
212335_at	683.65	181.9	495.69998	463.2	406.65	133	glucosamine (N-acetyl)-6-sulfatase	GNS
212370_x_at	2174.35	594.30005	819.19995	515.8	357.59998	115	family with sequence similarity 21, member A /// family with sequence similarity 21, member B /// family with sequence similarity 21, member C	FAM21A /// FAM21B /// FAM21C
212372_at	28.15	151	4436.0996	406.6	538.7	16.6	myosin, heavy chain 10, non-muscle	MYH10
212492_s_at	1186.5	340.7	497.1	270.7	278.2	118	lysine (K)-specific demethylase 4B	KDM4B
212510_at	412	155.45	560.75	152.3	145.35	0.9	glycerol-3-phosphate dehydrogenase 1-like	GPD1L
212522_at	433.75	89.55	216.04999	103.7	102.75	14	phosphodiesterase 8A	PDE8A
212566_at	626.05	394.5	409.2	351.6	456.59998	112.7	microtubule-associated protein 4	MAP4
212572_at	675.65	159.79999	776.80005	440.6	324.6	5	serine/threonine kinase 38 like	STK38L
212607_at	444.3	224.65	971.35	333.8	191.9	11.4	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3
212671_s_at	7027.65	2589.25	6483.4004	7480.3	8235.35	24.1	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2 /// similar to MHC class II antigen /// similar to MHC HLA-DQ alpha	HLA-DQA1 /// HLA-DQA2 /// LOC100294224 /// LOC100294317
212774_at	1945.2	276.85	778.5	180	211.65	2.6	zinc finger protein 238	ZNF238
212777_at	129.95	337.45	356.05	443.3	256.55	88.7	son of sevenless homolog 1 (Drosophila)	SOS1
212779_at	1297.3501	295.55	404.69998	497.2	424.45	157	KIAA1109	KIAA1109
212798_s_at	401.9	479.75	332.25	459.3	324.4	92.8	ankyrin repeat and MYND domain containing 2	ANKMY2
212914_at	504.95	82.350006	41.35	55	60.5	3.4	chromobox homolog 7	CBX7
212928_at	766.25	223.9	422.05	337.3	432.35	64.3	TSPY-like 4	TSPYL4

212929_s_at	1133.1001	307.5	264.05	233.9	158.55	44.9	family with sequence similarity 21, member A /// family with sequence similarity 21, member B /// family with sequence similarity 21, member C /// family with sequence similarity 21, member D	FAM21A /// FAM21B /// FAM21C /// FAM21D
212998_x_at	2186.2998	3641.75	1729.7999	3103.7	3243.85	1.1	major histocompatibility complex, class II, DQ beta 1 /// similar to major histocompatibility complex, class II, DQ beta 1	HLA-DQB1 /// LOC100294318
213093_at	618.4	155.65	1177.05	564.5	201.84999	32.3	protein kinase C, alpha	PRKCA
213215_at	161.85	72.3	159.9	74.7	91.75	20.1	adaptor-related protein complex 3, sigma 2 subunit	AP3S2
213241_at	805	242.45001	772.75	537.2	489	37.9	plexin C1	PLXNC1
213295_at	1101.25	294.34998	512.4	346.5	449.1	118	cylindromatosis (turban tumor syndrome)	CYLD
213361_at	229.8	228.75	216.95001	384	321.44998	10.4	tudor domain containing 7	TDRD7
213537_at	824.3	750.25	563.35	875.5	445	93.1	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1
213906_at	1233.25	196	420.85	616.3	707.75	116.7	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	MYBL1
214415_at	107.25	28.699999	149.1	60.4	44.6	5.3	plasminogen-like B1 /// plasminogen-like B2	PLGLB1 /// PLGLB2
214439_x_at	654.05	382.6	47.85	268.4	187.8	2.2	bridging integrator 1	BIN1
214639_s_at	25.45	167.95001	171.70001	151.1	154.15	1.4	homeobox A1	HOXA1
214753_at	2183.85	431.6	395.1	385.4	305.4	91.9	NEDD4 binding protein 2-like 2	N4BP2L2
214946_x_at	1743.45	501.3	646.15	436.9	341	69.8	family with sequence similarity 21, member A /// family with sequence similarity 21, member B /// family with sequence similarity 21, member C /// family with sequence similarity 21, member D	FAM21A /// FAM21B /// FAM21C /// FAM21D
215111_s_at	1623.9	230.25	296.3	853.1	200.65	102.1	TSC22 domain family, member 1	TSC22D1
215193_x_at	8192.301	7987.05	6371.65	7523	8868.9	19.6	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4
215241_at	11.25	908.5	1081.95	557.8	264.95	38.9	anoctamin 3	ANO3
215659_at	45.25	148.05	61.2	48.9	79.85	6.6	Gasdermin B	GSDMB
215726_s_at	201.4	148.65	262.05	440	335.34998	5.7	cytochrome b5 type A (microsomal)	CYB5A
215990_s_at	314.59998	93.15	152.35	112.1	192.20001	5.6	B-cell CLL/lymphoma 6	BCL6
216682_s_at	273.4	47.55	75.9	47.4	45.45	2	Family with sequence similarity 48, member A	FAM48A
216983_s_at	154.4	72.85	87	96.2	68.4	15.2	zinc finger protein 224	ZNF224
217164_at	285.34998	84.399994	114.149994	82	94.75	22.2	---	---
217362_x_at	1244.2	230.05	678.55005	1198.9	106.75	15.9	major histocompatibility complex, class II, DR beta 6 (pseudogene)	HLA-DRB6
217478_s_at	2510.6	1738.2	1469.05	1925.4	1962.45	20.3	major histocompatibility complex, class II, DM alpha /// major histocompatibility complex, class II, DM beta	HLA-DMA /// HLA-DMB
217783_s_at	8571.35	886	1558.15	638.7	801.4	84.7	yippee-like 5 (Drosophila)	YPEL5
217869_at	632.3	190.35	697.1	1131.1	330	4	hydroxysteroid (17-beta) dehydrogenase 12	HSD17B12
217929_s_at	162.4	109.45	142.4	134	86.55	14.7	KIAA0319-like	KIAA0319L
217940_s_at	475.7	280	818.05	164	121.8	3.4	carbohydrate kinase domain containing	CARKD
217989_at	2369.95	548.65	146.9	553.5	331.45	4.4	hydroxysteroid (17-beta) dehydrogenase 11	HSD17B11
218031_s_at	1443.75	500.25	478.69998	371.3	288.45	100.3	forkhead box N3	FOXN3
218109_s_at	3172	298.15	35.35	405.6	229.65	1.4	major facilitator superfamily domain containing 1	MFSD1
218197_s_at	288.35	240.40001	661.6	353.8	291.05	88.2	oxidation resistance 1	OXR1
218284_at	400.25	179.55	195.29999	462	239.5	3.4	SMAD family member 3	SMAD3
218297_at	240.4	152.6	282	437.3	283.15	86.2	family with sequence similarity 188, member A	FAM188A
218504_at	114.350006	302.90002	572.45	671.8	492.9	168.8	fumarylacetoacetate hydrolase domain containing 2A	FAHD2A
218987_at	1134.45	264.85	366.05	534.7	371.15002	154.6	activating transcription factor 7 interacting protein	ATF7IP
219077_s_at	204.85	133.05	237.95	90.5	226.8	20.2	WW domain containing oxidoreductase	WWOX
219109_at	87.15	14.6	247.9	174.5	102.399994	0.2	sperm associated antigen 16	SPAG16
219376_at	92.2	63.4	117.299995	119.9	134.65	1.1	zinc finger protein 322B	ZNF322B
219433_at	209.54999	242.85	415.15	220.1	168.65	5.3	BCL6 co-repressor	BCOR
219443_at	252.7	78.55	122.299995	117	98.65	5	taspase, threonine aspartase, 1	TASP1

219595_at	246.70001	71.5	148.15	92.6	58.15	8.7	similar to zinc finger protein 26 (KOX 20) /// zinc finger protein 26	LOC100287515 /// ZNF26
219641_at	109.9	53.3	96	54.5	40.75	6.2	de-etiolated homolog 1 (Arabidopsis)	DET1
219665_at	115.25	103.15	122.299995	102.9	76.850006	20.5	nudix (nucleoside diphosphate linked moiety X)-type motif 18	NUDT18
219834_at	55.95	96.65	95.55	116.5	83.05	18.5	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	ALS2CR8
219836_at	13.65	154.9	377.3	280.8	829.65	43.8	zinc finger, BED-type containing 2	ZBED2
219957_at	884.85	111.2	129.65	120.6	183.6	14.7	RUN and FYVE domain containing 2	RUFY2
220775_s_at	107.55	116.25	229.1	365.9	191.65	2.4	UEV and lactate/malate dehyrogenase domains	UEVLD
221012_s_at	1179.75	367.65	482.25	397	332.45	144.9	tripartite motif-containing 8	TRIM8
221249_s_at	1392.75	589.45	571.55	813.6	248.5	72.4	family with sequence similarity 117, member A	FAM117A
221588_x_at	254.55	360.84998	663.35	369.9	335.35	78.4	aldehyde dehydrogenase 6 family, member A1	ALDH6A1
221589_s_at	199.55	234.29999	616.15	426.4	307.8	63.6	aldehyde dehydrogenase 6 family, member A1	ALDH6A1
221752_at	298.75	283.84998	290.5	632.3	198.6	133.6	slingshot homolog 1 (Drosophila)	SSH1
221824_s_at	942.25	180	302.8	172.6	199.1	8.2	membrane-associated ring finger (C3HC4) 8	8-Mar
221899_at	2725.95	475	389.65002	310.2	417.4	47.1	NEDD4 binding protein 2-like 2	N4BP2L2
221905_at	968.1	254.40001	468.55002	308.5	391.9	93.4	cylindromatosis (turban tumor syndrome)	CYLD
222408_s_at	6703	576.65	1038.5	651.7	685.25	124.3	yippee-like 5 (Drosophila)	YPEL5
222415_at	1652.95	317.25	597.8	410.8	533.1	135.7	myeloid/lymphoid or mixed-lineage leukemia 3	MLL3
222451_s_at	65.85	39.2	126.95	61.6	53.7	1	zinc finger, DHHC-type containing 9	ZDHHC9
222494_at	2376.2998	900	723.85	506.6	465.55	156.4	forkhead box N3	FOXN3
222553_x_at	369.95	347.6	841.89996	740.8	578.9	161.3	oxidation resistance 1	OXR1
222730_s_at	288.25	88.75	412.7	178	185.7	11.6	zinc finger, DHHC-type containing 2	ZDHHC2
222731_at	1102	388.25	1148.35	527.5	539.9	1.1	zinc finger, DHHC-type containing 2	ZDHHC2
223085_at	2154.75	319.45	326.45	587.7	679.85	136.1	ring finger protein 19A	RNF19A
223120_at	261.55	177	512.44995	36.9	61.6	1.4	fucosidase, alpha-L- 2, plasma	FUCA2
223257_at	157.3	55.3	222.25	149	89.1	10.5	G2/M-phase specific E3 ubiquitin ligase	G2E3
223260_s_at	144.65	73.4	188.4	65.6	85.8	5.4	polymerase (DNA directed) kappa	POLK
223261_at	577.15	211.5	514.94995	176.6	252.75	9.8	polymerase (DNA directed) kappa	POLK
223266_at	139.75	117.5	937.1	233.5	85.05	24.7	STE20-related kinase adaptor beta	STRADB
223305_at	257.55	154.25	294.85	251.8	144.75	10.5	transmembrane protein 216	TMEM216
223311_s_at	90.9	38.55	308.25	94.1	42.5	1.8	metastasis associated 1 family, member 3	MTA3
223360_at	108.7	131.55	375.05	88.8	166.6	13.1	chromosome 21 open reading frame 56	C21orf56
223398_at	403.3	219.1	324.75	274.3	276	117.6	chromosome 9 open reading frame 89	C9orf89
223434_at	560.3	258	211.15	929.9	394.75	48.7	guanylate binding protein 3	GBP3
223566_s_at	235.05	292.8	593.25	318.8	227.04999	1.2	BCL6 co-repressor	BCOR
223799_at	76.05	59.4	190.9	107	104	14.4	KIAA1826	KIAA1826
223915_at	567.4	170.35	178.1	109.6	74.2	0.5	BCL6 co-repressor	BCOR
223916_s_at	218.04999	49.95	113.25	55.6	45.35	3.9	BCL6 co-repressor	BCOR
224301_x_at	702.65	154.75	396.05	716.4	109.85	38.2	H2A histone family, member J	H2AFJ
224516_s_at	705.1	278.1	73.149994	48.3	42.35	1.8	CXXC finger 5	CXXC5
224571_at	700.95	459	1270.3	478	567.85	124	interferon regulatory factor 2 binding protein 2	IRF2BP2
224698_at	1901.6	690.65	485.05	545	289.5	115.4	extended synaptotagmin-like protein 2	ESYT2
224722_at	99.55	221	372.45	499.1	104.2	39.4	mindbomb homolog 1 (Drosophila)	MIB1
224759_s_at	707.6	391.35	931.55	367.8	655	0.5	chromosome 12 open reading frame 23	C12orf23
224767_at	147	142.55	222.54999	283.2	283.15	72.2	Ribosomal protein L37	RPL37
224811_at	629.4	278.05	316.05	114.5	150.70001	0.9	---	---
224861_at	679.45	106.7	246.3	150.7	119.850006	1.6	Guanine nucleotide binding protein (G protein), q polypeptide	GNAQ
224862_at	781.95	115.65	299.55	198.2	139.15	0.1	Guanine nucleotide binding protein (G protein), q polypeptide	GNAQ
224882_at	207.95001	87.55	56.2	77.2	71.6	5.4	acyl-CoA synthetase short-chain family member 1	ACSS1
224920_x_at	818	60.75	37.35	55.6	45.449997	1.9	myeloid-associated differentiation marker	MYADM
224952_at	142.05	111.3	73.75	55.1	155.9	0.8	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	TANC2
224973_at	207.29999	97.8	192.3	37.4	15.3	0.1	family with sequence similarity 46, member A	FAM46A
224989_at	209	98.45	129.15	184.2	111.05	13.7	---	---
224990_at	365.75	166.15	248.40001	509.2	227.05	41.8	chromosome 4 open reading frame 34	C4orf34
225060_at	25.7	114.850006	790.45	236.3	100.549995	15.9	low density lipoprotein receptor-related protein 11	LRP11
225081_s_at	382.2	389.25	251.35	494.3	587.35	7.1	cell division cycle associated 7-like	CDCA7L
225164_s_at	325.05	101.8	422.8	585.1	233.9	14.7	eukaryotic translation initiation factor 2 alpha kinase 4	EIF2AK4

225245_x_at	868.65	169.85	464.35	806.8	106.8	46.6	H2A histone family, member J	H2AFJ
225334_at	954.14996	249.15001	238	324.3	207.35	9.8	chromosome 10 open reading frame 32	C10orf32
225339_at	276.55	146.15	321.95	290.2	401.8	91.6	sperm associated antigen 9	SPAG9
225673_at	5892.8	265.75	205.7	305.4	260.55	2.4	myeloid-associated differentiation marker	MYADM
225922_at	599.15	348.2	361.4	733.8	766.80005	26.5	folliculin interacting protein 2	FNIP2
225924_at	493.15	374.8	353.3	455.9	750.55	26.5	folliculin interacting protein 2	FNIP2
225956_at	2014.45	410.5	323	262.9	261.8	56.6	chromosome 5 open reading frame 41	C5orf41
225970_at	375.15002	230.25	360.05	573.4	564.4	131.2	DDHD domain containing 1	DDHD1
225971_at	556.35	239.75	433.90002	590.2	711.35	170.1	DDHD domain containing 1	DDHD1
226063_at	220.4	23.45	102.600006	37.8	29.949999	3.5	vav 2 guanine nucleotide exchange factor	VAV2
226119_at	884.65	355.6	321.65	375.7	371	78.9	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	PCMTD1
226157_at	411.3	122.649994	287.2	176.4	108.899994	16.4	Transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2
226158_at	793.85	206.05	126.799995	125.2	89.100006	12.4	kelch-like 24 (Drosophila)	KLHL24
226218_at	9840.15	235.79999	976.65	708.8	237.6	8.6	interleukin 7 receptor	IL7R
226278_at	864.05	228.25	406.65	406.6	253.45	4.1	small VCP/p97-interacting protein	SVIP
226358_at	162.85	103.649994	68.399994	70.8	41.65	1.7	anterior pharynx defective 1 homolog B (C. elegans)	APH1B
226460_at	825.1	409	392.05	774.4	912.25	28.4	folliculin interacting protein 2	FNIP2
226649_at	17.8	59.4	211.95001	98.4	95.6	1.1	pantothenate kinase 1	PANK1
226682_at	3743.4	509.69998	959.55005	880.4	545.9	27.3	RAR-related orphan receptor A	RORA
226696_at	90.3	123.55	148.6	171.3	324.8	9.5	retinoblastoma binding protein 9	RBBP9
226752_at	529.55	174.5	124.2	255.7	221.5	5.7	family with sequence similarity 174, member A	FAM174A
226808_at	205.35	150.70001	158.3	104.4	149.65	10.1	zinc finger protein 862	ZNF862
226878_at	441.3	503.55	670.4	663.5	533	14	major histocompatibility complex, class II, DO alpha	HLA-DOA
226977_at	59.45	120.4	107.1	132.4	150.4	13.6	chromosome 5 open reading frame 53	C5orf53
226978_at	95.65	93	88.75	46.3	75.45	2	peroxisome proliferator-activated receptor alpha	PPARA
226981_at	620.5	258.8	564.4	600	524.6	161.4	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	MLL
226991_at	799.05005	563.30005	950.6	582.3	381.5	85.1	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	NFATC2
227020_at	1000.25	207.35	495.8	454.3	197.40001	15.9	yippee-like 2 (Drosophila)	YPEL2
227040_at	218.25	167.45	252.79999	340.7	320.05	101.9	NHL repeat containing 3	NHLRC3
227074_at	932.8	456.35	360.85	453.9	373.9	103.5	hypothetical protein LOC100131564	LOC100131564
227418_at	411.8	250.95001	707.3	513.9	500.7	59.4	KIAA1826	KIAA1826
227426_at	139.4	1255.95	1510.8	826.7	725.95	99.2	son of sevenless homolog 1 (Drosophila)	SOS1
227482_at	92	47.65	162.65	61.7	49.65	5.4	aarF domain containing kinase 1	ADCK1
227645_at	1339.4	124.399994	127.05	138.8	96.149994	1.6	phosphoinositide-3-kinase, regulatory subunit 5	PIK3R5
227767_at	613.9	206.54999	358.65	541.7	397.75	126	casein kinase 1, gamma 3	CSNK1G3
227915_at	45.1	328.65002	166.70001	206.7	182.15	0.6	ankyrin repeat and SOCS box-containing 2	ASB2
227921_at	18.099998	114.75	410.8	219.9	305.4	36.3	---	---
227930_at	774.44995	87.4	81.899994	215.3	129.05	2.8	Eukaryotic translation initiation factor 2C, 4	EIF2C4
227980_at	171.65	97.5	193.6	160.3	171.25	10.1	zinc finger protein 322A	ZNF322A
228062_at	522.95	165.6	88.4	108.4	83.75	0.1	nucleosome assembly protein 1-like 5	NAP1L5
228063_s_at	787.5	278.2	147.7	161.8	141.65	5.2	nucleosome assembly protein 1-like 5	NAP1L5
228108_at	196.75	28.55	350.8	107	80.05	0.3	---	---
228149_at	249.25	78.65	289.55	180.8	98.25	0.5	chromosome 7 open reading frame 60	C7orf60
228157_at	199.5	285.59998	382.15002	386.1	444.75	115.5	zinc finger protein 207	ZNF207
228290_at	88.95	184.1	149.15	107.5	63.4	3.4	Non-protein coding RNA 153	NCRNA00153
228318_s_at	527.6	156.9	91.649994	162.4	139.05	11.2	cysteine-rich PAK1 inhibitor	CRIPAK
228442_at	771.65	769	1072.2	686.7	529.8	149.5	---	---
228642_at	381.59998	232.95	121.6	324.4	222	12.8	---	---
228816_at	3.9499998	109.2	37.1	74.5	70.350006	1.6	ATPase, H+ transporting, lysosomal accessory protein 1-like	ATP6AP1L
228891_at	207.5	53.6	32.449997	53.2	38.3	3	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	SEMA4D
228932_at	101.149994	81.4	80.95	77.8	76.3	22.6	---	---
229000_at	82.05	51.3	93.25	38.6	39.4	0.6	zinc finger protein 77	ZNF77
229123_at	194.75	41.5	107.100006	78.6	56.65	8.5	---	---
229261_at	43.1	442.4	500.75	222.1	288.34998	24.4	---	---
229312_s_at	209.04999	83.75	130.4	87.3	111.15	15.9	G kinase anchoring protein 1	GKAP1
230005_at	321.2	38.75	178	258	206.65	0.2	small VCP/p97-interacting protein	SVIP

230006_s_at	484.85	108	309.45	299.7	242.29999	3.7	small VCP/p97-interacting protein	SVIP
230110_at	498.19998	750.65	610.85	1222.5	945.44995	62.9	mucolipin 2	MCOLN2
230120_s_at	131.7	63.7	146.8	86	82.350006	9.1	plasminogen-like B2	PLGLB2
230176_at	189.8	152.4	195.45001	358.7	180.20001	11.5	---	---
230180_at	881.45	96.25	221.1	539	105.7	60.7	---	---
230285_at	337.3	59.2	229.25	193.7	133.9	6.1	small VCP/p97-interacting protein	SVIP
230296_at	639.65	292.35	358.55	367.9	444.34998	106	Chromosome 16 open reading frame 52	C16orf52
230337_at	69.85	1127.85	712.2	342.5	562.05	24.6	son of sevenless homolog 1 (Drosophila)	SOS1
230352_at	157.2	564.9	1400.1499	451.6	692.30005	0.6	Phosphoribosyl pyrophosphate synthetase 2	PRPS2
230387_at	642.3	272.7	915.85	261.5	450.90002	51.6	---	---
231165_at	303.7	68.5	155.54999	111.2	105.75	21.3	---	---
231252_at	146.4	132.5	232.40001	197.2	328.75	86.8	chromosome 2 open reading frame 67	C2orf67
231929_at	306.15	117.2	965.35	180.1	78.049995	2.8	IKAROS family zinc finger 2 (Helios)	IKZF2
231940_at	621.9	31.5	109.950005	137.3	50.4	0.2	zinc finger protein 529	ZNF529
232077_s_at	286.3	115.3	26.85	35.2	35	1.1	yippee-like 3 (Drosophila)	YPEL3
232138_at	547.65	89.45	227.95001	98	68.1	14.1	Muscleblind-like 2 (Drosophila)	MBNL2
232344_at	137.5	41.45	147.55	60	58.25	8.8	---	---
232369_at	341.85	83.5	141.4	63.6	40.9	8.8	---	---
232431_at	2442.4502	480.15002	469.15	323.4	245.85	120.8	---	---
232527_at	607	158.4	218.75	260.9	295.45	87.5	---	---
232744_x_at	408.35	91.5	79.25	92.5	60.649998	9	---	---
232883_at	20.55	122.3	137.29999	70.3	72.2	10.9	---	---
233595_at	764.85	223.7	450.05	244.3	355.90002	65	ubiquitin specific peptidase 34	USP34
233651_s_at	142.95	156.8	374.95	128.7	99.3	13.1	MPN domain containing	MPND
233675_s_at	9.3	156.5	112.5	102.2	178.2	0.2	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	LOC374491
233857_s_at	20.150002	246.45	103.75	255.5	172.7	6.9	ankyrin repeat and SOCS box-containing 2	ASB2
234260_at	847.95	88.65	80.7	89.9	107.5	7.8	---	---
234994_at	39.3	222.35	757.25	616.4	585.30005	125.5	transmembrane protein 200A	TMEM200A
235028_at	713.25	128.35	277.45	72.7	147.75	14	---	---
235346_at	181.95	251.85	842.35	315.3	344.3	0.2	FUN14 domain containing 1	FUNDC1
235352_at	666.19995	190.05	443.90002	484	209.3	79.5	---	---
235409_at	207.3	35.25	54.1	45.2	31.6	1.6	MAX gene associated	MGA
235556_at	453.84998	111.85	103.4	66.7	82.25	19.2	---	---
235567_at	1197.7	42.75	162.1	187.1	87.5	3.5	RAR-related orphan receptor A	RORA
235601_at	154.9	83.850006	68.9	43.4	48	2	---	---
235912_at	827.25	105	107.5	64.5	69.85	13	---	---
235927_at	506.65002	233.95	265.5	324.3	390.85	98.5	exportin 1 (CRM1 homolog, yeast)	XPO1
236266_at	749.75	49.15	157.85	75.7	61.7	7.8	RAR-related orphan receptor A	RORA
236280_at	1993.6499	365.5	859.14996	622.3	1091.85	8.3	---	---
236398_s_at	20.7	75.2	155.35	43.6	29.95	1.7	---	---
237189_at	111.25	190.2	84.05	133.4	133.5	2.4	---	---
237460_x_at	49.65	284.75	527.05	338.1	369.1	107	chromosome 14 open reading frame 182	C14orf182
238476_at	574.55	75.75	77.4	75.3	68.4	18.9	chromosome 5 open reading frame 41	C5orf41
238494_at	89.75	35.05	153.95001	107.2	71.6	0.6	TNF receptor-associated factor 3 interacting protein 1	TRAF3IP1
238840_at	722.55	49.949997	37.2	63.4	57.300003	3.5	leucine rich repeat (in FLII) interacting protein 1	LRRFIP1
239302_s_at	54.25	74.15	135.75	79.9	72.75	17.1	---	---
239409_at	612.2	102.95	142.55	86.7	173.90001	20.3	---	---
239435_x_at	85.5	48.15	124.200005	106	199.4	2	shroom family member 1	SHROOM1
239448_at	599.35	187.95	103.700005	132.7	94.7	0.9	---	---
239453_at	392.6	123.9	190.45	80.8	174.70001	8.6	---	---
239557_at	195	80.45	164.05	75.1	62.449997	21.3	---	---
240070_at	436.25	138.5	2427.55	1481.6	84.25	4.8	T cell immunoreceptor with Ig and ITIM domains	TIGIT
240446_at	42	56.5	82.8	48.1	23.75	2.3	---	---
240499_at	825	84.65	187.4	107.4	129.8	22.5	---	---
240539_at	46.2	43.15	122.35	28.9	24.9	0.3	---	---
240572_s_at	1183.1001	836.15	827.8	775.7	206.45	75.7	CLR pseudogene	LOC374443
241681_at	1328.5	342.35	830.75	363	854.75	100.2	---	---
241879_at	390	209.85	152.54999	63.6	74.85	1.3	---	---
242343_x_at	439.65	238	404.90002	306.3	345.2	23.7	---	---

242515_x_at	135.55	139.20001	470.05	758.1	269.5	63.1	chromosome 11 open reading frame 17	C11orf17
242628_at	71.850006	72.15	109.6	56.8	65.65	5.7	---	---
243280_at	303.55	126.35	89.45	88.1	84.5	18.6	---	---
243528_at	124.4	40.5	106.45	63.1	47.800003	0.5	---	---
243601_at	264	255.8	280.85	423.2	388.65002	122	hypothetical protein LOC285957	LOC285957
243869_at	413.45	79.399994	81.149994	43.5	43.1	3.2	---	---
243981_at	615.69995	101.649994	84.4	74.9	97.7	19.1	serine/threonine kinase 4	STK4
244132_x_at	481.44998	223.75	528.75	339	327.15002	50.6	Zinc finger protein 518A	ZNF518A
244383_at	152.85	142.85	103.25	73.8	113.399994	6.3	---	---
244433_at	848.25	100.5	99.55	113.1	105.8	16.3	---	---
244457_at	335.5	47.35	161.1	107.6	97.2	17.2	---	---
244779_at	112.350006	37.25	100.649994	42.2	44.3	1.2	---	---
35974_at	754.85	274.75	1082.6001	446.2	362.45	53.1	lymphoid-restricted membrane protein	LRMP
37965_at	166.85	86.55	480.2	281	191.8	58.7	parvin, beta	PARVB

Table S8. Gene cluster (D-2) which shows up regulation in NK leukemia compared to Norm NK, HMB, CAEBV and NK lymphoma

ID	PBMC1,PBMC2	CD16(-)NK1/2	KAI3-1,KAI3-2	SNK10	HANK,SNK6	NK-YS	Gene Title	Gene Symbol
status	PBMC	Normal NK CD16(-)	CAEBV1	CAEBV2	lymphoma	leukemia		
measurement ID	1	2	3	4	5	6		
1552641_s_at	14.5	6.9	17.05	11.5	68.95	136	ATPase family, AAA domain containing 3A /// ATPase family, AAA domain containing 3B /// similar to AAA-ATPase TOB3	ATAD3A /// ATAD3B /// LOC732419
1552908_at	132.45	0.5	1.0999999	1.5	2.5	311.9	chromosome 1 open reading frame 150	C1orf150
1553023_a_at	14.950001	7.2	15.95	12.8	12.299999	153.2	NADPH oxidase, EF-hand calcium binding domain 5	NOX5
1554442_at	98.9	9.049999	24.6	17.6	30.849998	92.9	bestrophin 1	BEST1
1554508_at	193.15	28.8	38.7	4.5	98.899994	284.9	phosphoinositide-3-kinase adaptor protein 1	PIK3AP1
1556602_at	80.25	21.3	33.6	17.4	43.05	64.9	---	---
1559205_s_at	339.34998	11.55	26	19.7	9.45	238.5	---	---
1562921_at	11.75	13.95	69.5	20.2	51	152.7	---	---
1565681_s_at	51.9	7.7	7.05	6	8.5	104.5	DIP2 disco-interacting protein 2 homolog C (Drosophila)	DIP2C
1569212_at	23.400002	2.9499998	6.05	3.5	10.35	100.2	scavenger receptor protein family member	LOC619207
1570422_at	11.45	6.5	3.0500002	1.9	0.9	195.1	syntrophin, gamma 2	SNTG2
1570445_a_at	3.05	0.75	0.70000005	0.4	2.7	105.7	hypothetical protein LOC643201	LOC643201
201656_at	435.45	23.1	12.950001	4.8	8.7	402.6	integrin, alpha 6	ITGA6
202011_at	4.45	18.95	11.8	6.7	4.5	791.9	tight junction protein 1 (zona occludens 1)	TJP1
202087_s_at	409.3	7.6499996	20.900002	10.4	3.6000001	308.3	cathepsin L1	CTSL1
202619_s_at	7.5	4.05	3.3	2.5	3.55	225.9	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	PLOD2
202620_s_at	6.9	1.75	7.95	2.2	3.9	496.7	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	PLOD2
203104_at	1484.3999	17.150002	18.25	22.5	20.400002	95.4	colony stimulating factor 1 receptor	CSF1R
203796_s_at	106.8	10.65	1.35	0.6	4.4	60.9	B-cell CLL/lymphoma 7A	BCL7A
203889_at	8.799999	6.65	13.95	2.7	8.849999	370	secretogranin V (7B2 protein)	SCG5
204412_s_at	20.9	3.1	9.65	1.5	117.05	789.6	neurofilament, heavy polypeptide	NEFH
204457_s_at	42.3	10.55	45.75	12.1	34.45	161.5	growth arrest-specific 1	GAS1
205919_at	19.4	14.2	24	16.2	7.75	197.3	hemoglobin, epsilon 1	HBE1
206404_at	215.5	17.7	27.4	28.3	31.150002	163.5	fibroblast growth factor 9 (glia-activating factor)	FGF9
206472_s_at	239.3	35.35	56.75	42.5	42.8	120.2	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	TLE3
206626_x_at	11.5	11	9.1	4.1	2.85	1425.6	synovial sarcoma, X breakpoint 1	SSX1
206627_s_at	3.9499998	4.95	3.1000001	5.2	2.6	576.9	synovial sarcoma, X breakpoint 1	SSX1
206654_s_at	36.8	13.6	57.1	27.5	83.55	125.5	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	POLR3G
207109_at	7.3	3.3500001	3.4	3.6	27.400002	210.9	POU class 2 homeobox 3	POU2F3
207493_x_at	2.15	6.45	6.9	2.5	1.1	697.8	synovial sarcoma, X breakpoint 2	SSX2
207666_x_at	3.9	4.2	7.2000003	9	1.5	233.8	synovial sarcoma, X breakpoint 3	SSX3
210394_x_at	18.85	5.1000004	18	6.1	3.3500001	1075.3	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	SSX4 /// SSX4B
210497_x_at	6.3	1.5999999	9.150001	2.8	2.85	713.9	synovial sarcoma, X breakpoint 2	SSX2
211250_s_at	232.6	32.5	47.65	69.4	51.65	106.4	SH3-domain binding protein 2	SH3BP2
211425_x_at	17.75	13.799999	17.15	5.2	13.049999	781	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	SSX4 /// SSX4B
211670_x_at	7.45	2.25	8.7	8.2	2.45	120.9	synovial sarcoma, X breakpoint 3	SSX3
212224_at	309.45	0.55	1.6	0.7	0.65	85.9	aldehyde dehydrogenase 1 family, member A1	ALDH1A1
212504_at	107.3	18.25	16.75	4.2	5.4	70.5	DIP2 disco-interacting protein 2 homolog C (Drosophila)	DIP2C
212575_at	47.399998	28	87.2	48.7	59.5	104.4	chromosome 19 open reading frame 6	C19orf6
212822_at	208.35	43.3	45.15	50.8	56.350002	185	HEG homolog 1 (zebrafish)	HEG1
213058_at	53.949997	17.55	33.6	22.6	6.2	166.7	tetratricopeptide repeat domain 28	TTC28
213920_at	28.599998	1.7	3.95	1.1	2.05	102.8	cut-like homeobox 2	CUX2
213954_at	348.65	13.35	5.2	8.5	0.85	155.8	family with sequence similarity 169, member A	FAM169A
215146_s_at	44.55	15.849999	25.150002	12.4	14.5	110.6	tetratricopeptide repeat domain 28	TTC28
215177_s_at	152.5	11.2	6.6499996	1.4	5.55	210.8	integrin, alpha 6	ITGA6
215575_at	16.75	9.05	8.95	13	6	117.8	phosphodiesterase 4D interacting protein	PDE4DIP
216360_x_at	71.5	13.599999	76.55	28	57.949997	125.4	ribosomal RNA processing 12 homolog (S. cerevisiae)	RRP12
216471_x_at	5.35	5.4	5.8999996	5.9	3	1026.3	synovial sarcoma, X breakpoint 2	SSX2
218275_at	26.55	27.8	77.649994	32.2	66.850006	100.2	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	SLC25A10
218888_s_at	95.55	11.7	22	6.3	36.199997	351	neuropilin (NRP) and tolloid (TLL)-like 2	NETO2
219257_s_at	96.25	3.4499998	13.5	3.7	25.45	157.8	sphingosine kinase 1	SPHK1
219448_at	119.25	26.150002	69.35	46.3	54.05	134.2	transmembrane protein 70	TMEM70
219489_s_at	35.55	4.3	20.849998	10.5	16.05	115.1	nucleoredoxin	NXN
219874_at	10.75	13.1	23.75	7.2	10.75	113.3	solute carrier family 12 (potassium/chloride transporters), member 8	SLC12A8
220217_x_at	27.15	14.75	16.55	14.1	17.349998	1024	SPANX family, member C	SPANXC
220641_at	11.4	9.5	18.8	16.2	14.95	144.4	NADPH oxidase, EF-hand calcium binding domain 5	NOX5

220922_s_at	3.55	1.95	1.4	1	2.05	1506.4	sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member A2 /// SPANX family, member B1 /// SPANX family, member B2 /// SPANX family, member C /// SPANX family, member F1	SPANXA1 /// SPANXA2 /// SPANXB1 /// SPANXB2 /// SPANXC /// SPANXF1
221884_at	2.95	1.8000001	11.8	1.5	3.55	102	MDS1 and EVI1 complex locus	MECOM
222315_at	250.15	18.650002	49.550003	44.7	97.950005	154.9	---	---
222774_s_at	84.850006	0.7	26.6	0.8	26.449999	389.4	neuropilin (NRP) and tolloid (TLL)-like 2	NETO2
223235_s_at	2.9499998	3.8	4.2	1.1	0.65	132.5	SPARC related modular calcium binding 2	SMOC2
223364_s_at	117.2	30.6	93.25	45	94.7	160.6	DEAH (Asp-Glu-Ala-His) box polypeptide 37	DHX37
223484_at	690.35	0.8	5.05	5.2	2.3	151.4	chromosome 15 open reading frame 48	C15orf48
223551_at	32.1	21	6.1	0.7	6.55	946	protein kinase (cAMP-dependent, catalytic) inhibitor beta	PKIB
223960_s_at	314.15	62.300003	79.850006	28.1	233.35	449.6	chromosome 16 open reading frame 5	C16orf5
224032_x_at	9.55	6.2000003	3.9	3.2	1.8499999	1189	sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member A2 /// SPANX family, member C	SPANXA1 /// SPANXA2 /// SPANXC
224164_at	139.05	31.3	51.350002	25.8	31.199999	135.3	tropomyosin 3	TPM3
225255_at	27.849998	22.1	103.25	43.5	59.300003	104.3	mitochondrial ribosomal protein L35	MRPL35
227168_at	740.2	1.2	2.7	2	137.3	552.7	myocardial infarction associated transcript (non-protein coding)	MIAT
227647_at	690.75	16.8	20.3	17.6	22.7	331.6	potassium voltage-gated channel, Isk-related family, member 3	KCNE3
228547_at	3.95	3.75	12.3	4	6.1	140.7	neurexin 1	NRXN1
228648_at	52.45	12.9	34.25	12.1	49.75	454.6	leucine-rich alpha-2-glycoprotein 1	LRG1
228658_at	1067.3999	13.049999	15.25	1.3	207.15	473.1	myocardial infarction associated transcript (non-protein coding)	MIAT
228977_at	8.05	27.849998	38.85	19.2	17.6	109	hypothetical protein LOC729680	LOC729680
229332_at	6.4500003	23.5	85.8	34.7	73.65	111.7	4-hydroxyphenylpyruvate dioxygenase-like	HPDL
230557_at	41.35	32.4	54.1	49.6	38.7	291.2	X-ray radiation resistance associated 1	XRRA1
231120_x_at	16.6	5.8	0.5	0.1	0.75	142.2	protein kinase (cAMP-dependent, catalytic) inhibitor beta	PKIB
231164_at	30.2	19.7	45.4	20.2	124.75	513.2	ATP-binding cassette, sub-family A (ABC1), member 17 (pseudogene)	ABCA17P
231514_at	26.6	2.65	5.6	4	2	288.7	chromosome 1 open reading frame 94	C1orf94
232010_at	5.75	1.5500001	0.90000004	0.9	0.2	115	follistatin-like 5	FSTL5
232616_at	3.45	10.65	8.95	12.5	137.1	481.3	lectin, galactoside-binding, soluble, 14 pseudogene	LOC100129935
235378_at	63.15	10.95	15.25	27.5	23.3	119.3	---	---
235628_x_at	113.45	45.6	61.75	42	36.45	94.7	---	---
236599_at	32.55	33.3	28.1	28.4	12.95	103.8	---	---
236785_at	2.55	0.85	1.75	1.2	1	151.2	---	---
237666_at	3.4	25.4	52.550003	51.4	24.25	102.7	X-ray radiation resistance associated 1	XRRA1
237807_at	4.35	2.6	2.6	9.6	4.15	207.2	spermatogenesis associated 12	SPATA12
240310_at	36.2	20.55	72.7	38.9	63.600002	77.5	---	---
241704_x_at	124.2	13.65	25.349998	23	19.5	106.7	zinc finger protein 320	ZNF320
242335_at	124.9	23.85	70.8	33	69.8	95.7	solute carrier family 25, member 37	SLC25A37
242346_x_at	42.2	13.8	17.65	20.9	8.25	117.1	---	---
242881_x_at	24.9	5.3500004	9.7	3.4	9.65	168.2	---	---
243383_at	62.8	33.8	56.6	20.6	70.149994	153.9	---	---
33323_r_at	82.1	21	40.7	32.2	28.35	107.4	stratifin	SFN
33767_at	41.6	4.8999996	2.05	2.5	153.1	2268.6	neurofilament, heavy polypeptide	NEFH
37079_at	79.45	15.9	71.75	32.7	44	124.1	nuclear undecaprenyl pyrophosphate synthase 1 pseudogene	YDD19

Table S9. Cell cycle analysis of NK cell lines in the different medium condition

	medium*	G0/G1(%)	S(%)	G2/M(%)
KAI3	medium 1	66.73	20.46	11.92
	medium 2	62.56	25	12.78
	medium 3	60.01	26.47	12.86
SNK10	medium 1	89.49	5.12	5.15
	medium 2	88.75	5.9	5.97
	medium 3	89.52	5.42	5.22
HANK1	medium 1	71.69	12.12	16.51
	medium 2	71.73	10.27	17.39
	medium 3	72.34	11.04	16.88
SNK6	medium 1	59.11	23.55	18.97
	medium 2	65.45	16.96	17.05
	medium 3	63.09	20.11	13.6
NKYS	medium 1	76.07	13.72	9.96
	medium 2	84.85	7.63	6.41
	medium 3	76.37	11.79	9.93

*medium1: Gm+RPMI supplemented with 10% human serum and 700 U/ml IL-2
medium2: AIM-V supplemented with 10% bovine serum and 50 U/ml IL-2
medium3: IMDM supplemented with 10% bovine serum and 100 U/ml IL-2