

**Dataset 3a** Comparison of the expression profile of ZD esophagus at tumor endpoint with the published esophageal profile<sup>‡</sup> at 6 wks of ZD diet without NMBA

**Description of the problem:**

Number of classes: 2

Number of genes used for random variance estimation: 31099

Number of genes that passed filtering criteria: 31099

Type of univariate test used: Two-sample T-test (with random variance model)

Univariate test random variance model parameters:

a= 1.90741 , b= 11.98356 , Kolmogorov-Smirnov statistic= 0.0092

Nominal significance level of each univariate test: 0.001

**Summary of Results:**

Number of genes significant at 0.001 level of the univariate test: **861 (630 up-regulated and 231 down-regulated)**

**Genes that discriminate among classes:**

Sorted by Fold-Change

Class 1: ZD esophagus at 5 wks after the first NMBA dose

Class 2: ZD esophagus (No NMBA treatment) (Gastroenterology. 2009, 136:953-966)<sup>‡</sup> treatment.

\*\*Affymetrix probe ID corresponds to the Rat Genome 230 2.0 Array.

Inflammatory probe sets denoted in Table 1 are highlighted in yellow.

p-value	FDR	Geom mean of intensities in class 1	Geom mean of intensities in class 2	Fold-change*	Affymetrix Probe ID**	Gene symbol	Gene Name
0.00	0.00	18628.90	116.90	159.36	1387125_at	S100a9	S100 calcium binding protein A9
0.00	0.00	1117.33	22.12	50.52	1370371_a_at	Ceacam10	carcinoembryonic antigen-related cell adhesion molecule 10
0.00	0.00	312.04	8.71	35.81	1385107_at	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14
0.00	0.01	407.42	14.28	28.53	1368760_at	Cxcl2	chemokine (C-X-C motif) ligand 2
0.00	0.02	1699.86	63.71	26.68	1377429_at	Lpo	lactoperoxidase
0.00	0.01	1380.17	60.71	22.73	1387963_a_at	Uox	urate oxidase
0.00	0.01	187.81	8.96	20.97	1377264_at	Il17f	interleukin 17F
0.00	0.00	499.78	27.18	18.39	1371016_at	RGD1311300	similar to T cell receptor V delta 6
0.00	0.01	9926.13	575.50	17.25	1373349_at	LOC683295	similar to keratin complex 2, basic, gene 6a
0.00	0.00	293.13	18.04	16.25	1390890_at	NA	NA
0.00	0.00	552.25	35.19	15.69	1389748_at	NA	NA
0.00	0.00	179.59	12.20	14.72	1385519_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.01	816.85	56.12	14.56	1398256_at	Il1b	interleukin 1 beta
0.00	0.01	828.42	61.91	13.38	1374236_at	Lgi2	leucine-rich repeat LGI family, member 2
0.00	0.00	388.12	29.90	12.98	1368000_at	C3	complement component 3
0.00	0.01	372.70	29.06	12.83	1395294_at	NA	NA
0.00	0.01	444.21	34.77	12.78	1387011_at	Lcn2	lipocalin 2
0.00	0.01	493.50	41.04	12.02	1388275_at	Tcrb	T-cell receptor beta chain
0.00	0.00	282.41	23.83	11.85	1391447_at	NA	NA
0.00	0.00	412.53	41.04	10.05	1370924_at	Tcrb	T-cell receptor beta chain
0.00	0.01	345.75	35.16	9.83	1368270_at	Apobec1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1
0.00	0.03	665.38	69.16	9.62	1387134_at	S1fn3	schlafen 3

0.00	0.02	156.40	16.56	9.45	1395076_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.01	386.45	45.09	8.57	1384787_at	Cd3g	CD3 molecule, gamma polypeptide
0.00	0.01	42.17	5.09	8.29	1393791_at	Trat1	T cell receptor associated transmembrane adaptor 1
0.00	0.01	384.94	46.51	8.28	1379791_at	Cd3e	CD3 molecule, epsilon polypeptide
0.00	0.00	300.27	37.21	8.07	1392171_at	Chi3l1	chitinase 3-like 1
0.00	0.01	477.54	59.42	8.04	1377092_at	NA	NA
0.00	0.01	1353.06	169.48	7.98	1373667_at	Ccbl1	cysteine conjugate-beta lyase, cytoplasmic
0.00	0.01	242.45	30.39	7.98	1391979_at	NA	NA
0.00	0.01	320.04	41.78	7.66	1370987_at	Spn	sialophorin
0.00	0.03	1823.05	241.46	7.55	1386922_at	Car2	carbonic anhydrase II
0.00	0.00	137.68	18.25	7.54	1370603_a_at	Ptprc	protein tyrosine phosphatase, receptor type, C
0.00	0.01	220.70	29.87	7.39	1380077_at	NA	NA
0.00	0.02	184.42	24.98	7.38	1375917_at	Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4
0.00	0.03	2164.84	297.64	7.27	1367733_at	Car2	carbonic anhydrase II
0.00	0.01	267.42	36.81	7.27	1382622_at	Cst7	cystatin F (leukocystatin)
0.00	0.02	1026.26	142.62	7.20	1384329_at	Prss22	protease, serine, 22
0.00	0.01	280.84	39.44	7.12	1387316_at	Cxcl1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
0.00	0.01	4595.03	645.64	7.12	1372013_at	Ifitm1	interferon induced transmembrane protein 1
0.00	0.02	255.94	35.99	7.11	1370777_at	Ear11	eosinophil-associated, ribonuclease A family, member 11
0.00	0.00	794.25	112.94	7.03	1369964_at	Coro1a	coronin, actin binding protein 1A
0.00	0.00	298.41	43.57	6.85	1368723_at	Lat	linker for activation of T cells
0.00	0.01	390.87	57.82	6.76	1369029_at	Plscr1	phospholipid scramblase 1
0.00	0.02	1120.46	167.48	6.69	1370056_at	Ly6c	Ly6-C antigen
0.00	0.00	554.15	84.45	6.56	1393140_at	Zc3h12a	zinc finger CCCH type containing 12A
0.00	0.00	374.38	57.28	6.54	1390798_at	Ptprc	protein tyrosine phosphatase, receptor type, C
0.00	0.03	85.28	13.09	6.51	1397900_at	NA	NA
0.00	0.00	149.67	23.47	6.38	1398540_at	Rgs1	regulator of G-protein signaling 1
0.00	0.01	439.13	70.86	6.20	1368482_at	Bcl2a1d	B-cell leukemia/lymphoma 2 related protein A1d
0.00	0.00	628.24	101.71	6.18	1368518_at	Cd53	Cd53 molecule
0.00	0.01	337.23	54.79	6.15	1373513_at	NA	NA
0.00	0.01	507.32	83.03	6.11	1389470_at	Cfb	complement factor B
0.00	0.01	332.58	54.44	6.11	1389092_at	Il2rg	interleukin 2 receptor, gamma
0.00	0.02	336.50	55.32	6.08	1368205_at	Cfi	complement factor I
0.00	0.03	129.94	21.60	6.02	1370097_a_at	Cxcr4	chemokine (C-X-C motif) receptor 4
0.00	0.02	273.58	45.75	5.98	1387472_at	Cd3d	CD3 molecule delta polypeptide
0.00	0.00	309.67	51.85	5.97	1368826_at	Comt	catechol-O-methyltransferase
0.00	0.01	531.08	89.07	5.96	1377671_at	NA	NA
0.00	0.00	299.68	51.09	5.87	1373661_a_at	Cxcr4	chemokine (C-X-C motif) receptor 4
0.00	0.00	1184.39	203.43	5.82	1389210_at	Lcp1	lymphocyte cytosolic protein 1
0.00	0.01	193.84	33.47	5.79	1397167_at	NA	NA
0.00	0.01	154.57	26.86	5.76	1376943_at	NA	NA
0.00	0.00	68.18	11.87	5.74	1383585_s_at	NA	NA
0.00	0.00	484.90	85.19	5.69	1393329_at	NA	NA

0.00	0.00	331.53	58.53	5.66	1393929_at	Ccr6	chemokine (C-C motif) receptor 6
0.00	0.03	1363.82	240.81	5.66	1377185_at	RGD1562622	similar to RIKEN cDNA 6330442E10 gene
0.00	0.01	201.18	35.87	5.61	1368783_at	Icos	inducible T-cell co-stimulator
0.00	0.01	56.53	10.17	5.56	1386052_at	Il7r	interleukin 7 receptor
0.00	0.00	215.21	40.07	5.37	1379766_at	Sla	src-like adaptor
0.00	0.01	267.52	50.87	5.26	1389244_x_at	Cxcr4	chemokine (C-X-C motif) receptor 4
0.00	0.03	558.54	106.84	5.23	1388773_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2
0.00	0.03	234.87	45.07	5.21	1378193_at	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7
0.00	0.01	315.91	61.22	5.16	1394585_at	NA	NA
0.00	0.03	134.09	26.07	5.14	1376840_at	NA	NA
0.00	0.02	116.34	22.62	5.14	1383248_at	Fmo5	flavin containing monooxygenase 5
0.00	0.01	75.10	14.64	5.13	1387687_at	Igsf6	immunoglobulin superfamily, member 6
0.00	0.03	16518.39	3222.06	5.13	1368494_at	S100a8	S100 calcium binding protein A8
0.00	0.01	100.39	19.59	5.12	1389997_at	Cd3e	CD3 molecule, epsilon polypeptide
0.00	0.01	340.19	66.66	5.10	1393347_at	Itgal	integrin alpha L
0.00	0.03	174.69	34.46	5.07	1387111_at	Ddah1	dimethylarginine dimethylaminohydrolase 1
0.00	0.00	1015.08	201.13	5.05	1372585_at	RGD1566254	RGD1566254
0.00	0.01	46.83	9.30	5.04	1386695_at	NA	NA
0.00	0.02	237.24	47.40	5.01	1387946_at	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein
0.00	0.02	662.42	133.55	4.96	1389006_at	NA	NA
0.00	0.00	1621.55	329.45	4.92	1375808_at	Prss27	protease, serine 27
0.00	0.00	436.39	88.88	4.91	1383320_at	Lck	lymphocyte-specific protein tyrosine kinase
0.00	0.01	197.72	40.60	4.87	1368558_s_at	Aif1	allograft inflammatory factor 1
0.00	0.00	35.38	7.28	4.86	1385215_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.02	77.16	15.97	4.83	1397859_x_at	RT1-A2	RT1 class Ia, locus A2
0.00	0.01	78.83	16.55	4.76	1381771_at	NA	NA
0.00	0.01	146.42	31.18	4.70	1384837_at	Cd69	Cd69 molecule
0.00	0.01	54.09	11.61	4.66	1369105_a_at	Pkib	protein kinase inhibitor beta, (cAMP-dependent, catalytic) inhibitor beta
0.00	0.00	253.32	54.98	4.61	1368139_s_at	Alpl	alkaline phosphatase, liver/bone/kidney
0.00	0.01	612.17	132.99	4.60	1372404_at	Rac2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
0.00	0.01	2358.78	516.46	4.57	1370822_at	RT1-Ba	RT1 class II, locus Ba
0.00	0.02	96.07	21.07	4.56	1380230_at	NA	NA
0.00	0.01	1885.91	413.89	4.56	1370383_s_at	RT1-Db1	RT1 class II, locus Db1
0.00	0.02	211.72	47.02	4.50	1368492_at	Ptgds2	prostaglandin D2 synthase 2, hematopoietic
0.00	0.02	369.51	82.43	4.48	1376710_at	NA	NA
0.00	0.03	6189.56	1404.50	4.41	1387995_a_at	Ifitm3	interferon induced transmembrane protein 3
0.00	0.01	640.16	145.65	4.40	1368006_at	Laptm5	lysosomal multispinning membrane protein 5
0.00	0.03	306.66	69.78	4.39	1390687_at	Plek	pleckstrin
0.00	0.02	216.39	50.17	4.31	1368914_at	Runx1	runt related transcription factor 1
0.00	0.01	351.86	81.76	4.30	1385440_at	Hcst	hematopoietic cell signal transducer
0.00	0.01	165.64	38.56	4.30	1382167_at	Sit1	signaling threshold regulating transmembrane adaptor 1

0.00	0.03	272.87	64.12	4.26	1372852_at	Ptprcap	protein tyrosine phosphatase, receptor type, C-associated protein
0.00	0.01	4651.24	1094.14	4.25	1373718_at	Tubb2b	tubulin, beta 2b
0.00	0.02	142.86	33.76	4.23	1368061_at	Kcnh1	potassium voltage-gated channel, subfamily H (eag-related), member 1
0.00	0.01	66.60	15.92	4.18	1370769_a_at	Icos	inducible T-cell co-stimulator
0.00	0.02	59.18	14.22	4.16	1368782_at	Sstr2	somatostatin receptor 2
0.00	0.01	208.78	50.31	4.15	1369190_at	Cd2	Cd2 molecule
0.00	0.01	31.59	7.63	4.14	1394051_at	P2ry10	purinergic receptor P2Y, G-protein coupled 10
0.00	0.02	111.47	27.16	4.10	1379499_at	Ltb	lymphotoxin beta (TNF superfamily, member 3)
0.00	0.01	229.42	56.18	4.08	1370382_at	RT1-Db1	RT1 class II, locus Db1
0.00	0.02	94.56	23.29	4.06	1394264_at	Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5
0.00	0.02	458.68	113.10	4.06	1379344_at	Cybb	cytochrome b-245, beta polypeptide
0.00	0.01	151.62	37.86	4.00	1370090_at	Lcp2	lymphocyte cytosolic protein 2
0.00	0.02	191.69	48.23	3.97	1392444_at	Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5
0.00	0.02	346.99	87.41	3.97	1373006_at	Tmem171	transmembrane protein 171
0.00	0.02	336.56	85.18	3.95	1370186_at	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)
0.00	0.03	88.67	22.46	3.95	1387269_s_at	Plaur	plasminogen activator, urokinase receptor
0.00	0.00	181.72	46.31	3.92	1389678_at	NA	NA
0.00	0.01	83.20	21.41	3.89	1383661_at	NA	NA
0.00	0.01	103.73	26.74	3.88	1384939_at	Il18r1	interleukin 18 receptor 1
0.00	0.01	62.66	16.20	3.87	1393649_at	NA	NA
0.00	0.02	55.16	14.26	3.87	1382507_at	Cd96	CD96 molecule
0.00	0.01	174.54	45.17	3.86	1368555_at	Cd37	CD37 molecule
0.00	0.01	233.14	60.42	3.86	1392082_a_at	Cd7	Cd7 molecule
0.00	0.02	4622.69	1205.11	3.84	1370883_at	H2-Ea	histocompatibility 2, class II antigen E alpha
0.00	0.02	102.60	26.88	3.82	1368412_a_at	Ptpro	protein tyrosine phosphatase, receptor type, O
0.00	0.01	286.38	75.13	3.81	1385832_s_at	Sash3	SAM and SH3 domain containing 3
0.00	0.01	3740.32	990.94	3.77	1370172_at	Sod2	superoxide dismutase 2, mitochondrial
0.00	0.00	226.19	60.26	3.75	1385641_at	NA	NA
0.00	0.02	221.20	59.00	3.75	1384544_at	Pon3	paraoxonase 3
0.00	0.01	134.63	35.92	3.75	1393901_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.02	74.95	20.06	3.74	1368693_at	Fgr	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
0.00	0.02	1363.94	365.31	3.73	1370968_at	Nfkb1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
0.00	0.02	155.00	41.85	3.70	1377994_at	NA	NA
0.00	0.00	798.30	216.37	3.69	1371447_at	Plac8	placenta-specific 8
0.00	0.04	253.62	69.26	3.66	1370173_at	Sod2	superoxide dismutase 2, mitochondrial
0.00	0.01	1340.69	366.33	3.66	1379371_at	NA	NA
0.00	0.02	199.94	55.30	3.62	1373932_at	NA	NA
0.00	0.02	311.90	86.65	3.60	1390866_at	NA	NA
0.00	0.01	3047.79	851.70	3.58	1367846_at	S100a4	S100 calcium-binding protein A4
0.00	0.02	229.82	64.27	3.58	1378633_at	Lpxn	leupaxin
0.00	0.01	260.48	73.43	3.55	1389553_at	Clec4a3	C-type lectin domain family 4, member a3

0.00	0.00	1555.25	439.27	3.54	1383658_at	Laptm5	lysosomal multispanning membrane protein 5
0.00	0.03	177.20	50.62	3.50	1393108_at	NA	NA
0.00	0.03	178.49	51.08	3.49	1382026_at	Arhgap9	Rho GTPase activating protein 9
0.00	0.01	967.31	277.79	3.48	1368655_at	Srgn	serglycin
0.00	0.01	99.70	28.65	3.48	1386410_at	NA	NA
0.00	0.02	74.69	21.52	3.47	1378629_at	Satb1	SATB homeobox 1
0.00	0.01	70.49	20.34	3.47	1394122_at	Rhoh	ras homolog gene family, member H
0.00	0.01	228.53	66.05	3.46	1392722_at	Dapp1	dual adaptor of phosphotyrosine and 3-phosphoinositides
0.00	0.02	101.16	29.38	3.44	1378413_at	NA	NA
0.00	0.00	192.44	55.98	3.44	1378377_at	Dapp1	dual adaptor of phosphotyrosine and 3-phosphoinositides
0.00	0.03	62.65	18.26	3.43	1379626_at	Satb1	SATB homeobox 1
0.00	0.01	4918.22	1435.37	3.43	1367679_at	Cd74	Cd74 molecule, major histocompatibility complex, class II invariant chain
0.00	0.01	871.91	256.68	3.40	1387343_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta
0.00	0.02	117.90	34.79	3.39	1398348_at	NA	NA
0.00	0.01	602.74	178.49	3.38	1374730_at	Tyrobp	Tyro protein tyrosine kinase binding protein
0.00	0.03	188.44	56.18	3.35	1368374_a_at	Ggt1	gamma-glutamyltransferase 1
0.00	0.00	890.10	266.52	3.34	1368490_at	Cd14	CD14 molecule
0.00	0.01	166.14	49.81	3.34	1372200_at	Gpsm3	G-protein signaling modulator 3 (AGS3-like, C. elegans)
0.00	0.03	268.37	80.46	3.34	1368503_at	Gch1	GTP cyclohydrolase 1
0.00	0.02	489.49	147.13	3.33	1379677_at	Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13
0.00	0.02	119.60	36.09	3.31	1389413_at	Evi2a	ecotropic viral integration site 2A
0.00	0.00	305.69	92.35	3.31	1392716_at	NA	NA
0.00	0.02	116.30	35.21	3.30	1382566_at	Il7r	interleukin 7 receptor
0.00	0.03	230.45	69.82	3.30	1382692_at	Clec7a	C-type lectin domain family 7, member a
0.00	0.01	145.57	44.31	3.29	1377195_at	NA	NA
0.00	0.01	76.36	23.26	3.28	1378915_x_at	LOC308990	hypothetical protein LOC308990
0.00	0.03	498.26	152.26	3.27	1374119_at	Elf3	E74-like factor 3
0.00	0.02	395.38	120.87	3.27	1367786_at	Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)
0.00	0.02	96.25	29.45	3.27	1398727_at	NA	NA
0.00	0.01	134.72	41.29	3.26	1390797_at	Lcp2	lymphocyte cytosolic protein 2
0.00	0.01	660.33	202.40	3.26	1370882_at	Hla-dmb	major histocompatibility complex, class II, DM beta
0.00	0.01	1037.73	320.04	3.24	1371659_at	Rhoc	ras homolog gene family, member C
0.00	0.02	477.87	147.64	3.24	1377353_a_at	Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13
0.00	0.02	321.11	99.22	3.24	1376788_at	Dapk1	death associated protein kinase 1
0.00	0.03	121.62	37.84	3.21	1376394_at	Clec9a	C-type lectin domain family 9, member a
0.00	0.03	88.22	27.51	3.21	1392280_at	Tlr2	toll-like receptor 2
0.00	0.02	414.11	129.66	3.19	1374838_at	Sp140	SP140 nuclear body protein
0.00	0.01	124.21	39.13	3.17	1385557_at	NA	NA
0.00	0.03	29.75	9.44	3.15	1377190_at	NA	NA
0.00	0.03	32.86	10.46	3.14	1372702_at	PRP-2	proline-rich protein
0.00	0.02	35.15	11.19	3.14	1387459_at	Pkib	protein kinase inhibitor beta, (cAMP-dependent, catalytic) inhibitor beta

0.00	0.04	49.96	15.94	3.14	1380425_at	Rnasel	ribonuclease L (2@#%&,5@#%&-oligoisoadenylate synthetase-dependent)
0.00	0.02	157.91	50.37	3.14	1393049_at	Myo1g	myosin IG
0.00	0.02	173.90	55.67	3.12	1374157_at	Pde4b	phosphodiesterase 4B, cAMP specific
0.00	0.01	95.18	30.47	3.12	1392794_at	NA	NA
0.00	0.02	816.12	262.45	3.11	1373575_at	Fcer1g	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
0.00	0.01	159.56	51.66	3.09	1369204_at	Hck	hemopoietic cell kinase
0.00	0.02	81.97	26.58	3.08	1390849_at	NA	NA
0.00	0.02	185.99	60.93	3.05	1384968_at	Sh3bp2	SH3-domain binding protein 2
0.00	0.03	313.89	103.08	3.05	1369705_at	Slc6a20	solute carrier family 6 (neurotransmitter transporter), member 20
0.00	0.03	226.63	74.43	3.05	1398350_at	Basp1	brain abundant, membrane attached signal protein 1
0.00	0.02	223.43	74.29	3.01	1368813_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta
0.00	0.01	54.58	18.17	3.00	1398644_at	Plxnc1	plexin C1
0.00	0.02	39.99	13.33	3.00	1381357_at	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
0.00	0.02	127.53	42.52	3.00	1382442_at	Sep-06	septin 6
0.00	0.02	118.06	39.56	2.98	1394673_at	LOC687856	similar to Myeloid cell surface antigen CD33 precursor (Siglec-3)
0.00	0.01	254.14	85.23	2.98	1390946_at	NA	NA
0.00	0.02	1653.67	555.44	2.98	1367632_at	Glul	glutamate-ammonia ligase (glutamine synthetase)
0.00	0.02	261.37	88.22	2.96	1379911_at	Dapk1	death associated protein kinase 1
0.00	0.01	65.71	22.42	2.93	1376327_at	Tnfrsf14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)
0.00	0.03	316.16	107.89	2.93	1368207_at	Fxyd5	FXFD domain-containing ion transport regulator 5
0.00	0.03	204.92	70.11	2.92	1374544_at	MGC112715	platelet receptor Gi24
0.00	0.02	141.75	48.50	2.92	1379381_at	NA	NA
0.00	0.02	142.00	48.60	2.92	1379387_at	NA	NA
0.00	0.02	37.38	12.79	2.92	1396147_at	NA	NA
0.00	0.01	525.57	180.39	2.91	1388131_at	Tubb2b	tubulin, beta 2b
0.00	0.02	48.66	16.78	2.90	1367627_at	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
0.00	0.01	493.73	170.51	2.90	1370219_at	Cyba	cytochrome b-245, alpha polypeptide
0.00	0.03	131.45	45.89	2.86	1367861_at	Evl	Enah/Vasp-like
0.00	0.02	258.86	90.81	2.85	1395836_at	Odz2	odz, odd Oz/ten-m homolog 2 (Drosophila)
0.00	0.03	73.25	25.75	2.84	1398484_at	RGD1308221	similar to TBC1 domain family, member 8 (with GRAM domain); vascular Rab-GAP/TBC-containing
0.00	0.00	240.08	84.48	2.84	1383131_at	Itgb2	integrin beta 2
0.00	0.02	178.04	62.94	2.83	1397096_at	NA	NA
0.00	0.02	129.05	45.73	2.82	1388485_at	Cxcl14	chemokine (C-X-C motif) ligand 14
0.00	0.01	77.47	27.51	2.82	1382663_at	Batf	basic leucine zipper transcription factor, ATF-like
0.00	0.03	930.77	330.65	2.81	1388596_at	Cot11	coactosin-like 1 (Dictyostelium)
0.00	0.01	240.81	86.04	2.80	1374310_at	Ppm1j	protein phosphatase 1J
0.00	0.00	223.91	80.04	2.80	1376766_at	Fmn11	formin-like 1
0.00	0.03	470.60	170.36	2.76	1387450_at	Tgfa	transforming growth factor alpha
0.00	0.03	121.34	44.08	2.75	1370585_a_at	Prkcb	protein kinase C, beta
0.00	0.02	22.18	8.07	2.75	1369290_at	Ccr5	chemokine (C-C motif) receptor 5

0.00	0.02	661.70	241.21	2.74	1376969_at	NA	NA
0.00	0.02	283.02	103.64	2.73	1392107_at	Sbno2	strawberry notch homolog 2 (Drosophila)
0.00	0.02	273.68	100.28	2.73	1368073_at	Irf1	interferon regulatory factor 1
0.00	0.02	72.51	26.65	2.72	1369181_at	Cybb	cytochrome b-245, beta polypeptide
0.00	0.02	842.66	310.15	2.72	1370344_at	Hspa4	heat shock protein 4
0.00	0.03	112.25	41.66	2.69	1378314_at	NA	NA
0.00	0.04	105.71	39.49	2.68	1369294_at	Bst1	bone marrow stromal cell antigen 1
0.00	0.01	340.66	127.74	2.67	1373065_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18
0.00	0.01	99.55	37.35	2.67	1395442_at	NA	NA
0.00	0.02	121.14	45.63	2.65	1392554_a_at	NA	NA
0.00	0.03	337.87	127.62	2.65	1370885_at	Ctsz	cathepsin Z
0.00	0.02	137.71	52.14	2.64	1370265_at	Arrb2	arrestin, beta 2
0.00	0.02	209.75	79.68	2.63	1368521_at	Napsa	napsin A aspartic peptidase
0.00	0.01	64.02	24.38	2.63	1382346_at	NA	NA
0.00	0.02	135.73	51.98	2.61	1367936_at	Stk10	serine/threonine kinase 10
0.00	0.02	17.53	6.73	2.60	1391058_at	RGD1310958	similar to RIKEN cDNA C130090K23
0.00	0.02	52.15	20.07	2.60	1395183_at	NA	NA
0.00	0.03	56.92	21.93	2.60	1387394_at	Il2rb	interleukin 2 receptor, beta
0.00	0.03	171.43	66.45	2.58	1393400_at	Zap70	zeta-chain (TCR) associated protein kinase
0.00	0.01	77.74	30.23	2.57	1368735_a_at	Trpv2	transient receptor potential cation channel, subfamily V, member 2
0.00	0.01	207.59	80.76	2.57	1390529_at	Cd83	CD83 molecule
0.00	0.02	141.50	55.08	2.57	1380537_at	Nckap1l	NCK associated protein 1 like
0.00	0.03	195.83	76.48	2.56	1376624_at	NA	NA
0.00	0.02	177.76	69.55	2.56	1380520_at	NA	NA
0.00	0.03	742.36	291.26	2.55	1376076_at	NA	NA
0.00	0.01	520.45	204.85	2.54	1372691_at	Upp1	uridine phosphorylase 1
0.00	0.00	312.86	123.20	2.54	1381193_at	LOC317456	hypothetical LOC317456
0.00	0.01	323.63	127.89	2.53	1391027_at	NA	NA
0.00	0.03	979.64	387.65	2.53	1373881_at	Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta
0.00	0.02	322.37	127.96	2.52	1370834_at	Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
0.00	0.01	36.22	14.38	2.52	1393926_at	Stap1	signal transducing adaptor family member 1
0.00	0.03	123.40	49.05	2.52	1377286_at	Gimap4	GTPase, IMAP family member 4
0.00	0.01	48.07	19.14	2.51	1370483_at	Cd244	Cd244 molecule, natural killer cell receptor 2B4
0.00	0.02	34.57	13.80	2.50	1373751_at	NA	NA
0.00	0.03	1278.30	510.47	2.50	1392894_at	Fgl2	fibrinogen-like 2
0.00	0.03	46.90	18.83	2.49	1378843_at	NA	NA
0.00	0.02	634.78	256.80	2.47	1373037_at	Ube2l6	ubiquitin-conjugating enzyme E2L 6
0.00	0.02	395.81	160.15	2.47	1373088_at	LOC682888	hypothetical protein LOC682888
0.00	0.03	101.80	41.31	2.46	1380728_at	NA	NA
0.00	0.03	83.92	34.16	2.46	1378617_at	Trerf1	transcriptional regulating factor 1
0.00	0.02	75.03	30.58	2.45	1377023_at	Dusp2	dual specificity phosphatase 2
0.00	0.02	115.30	47.07	2.45	1376259_at	Prkcq	protein kinase C, theta
0.00	0.03	345.11	140.90	2.45	1387030_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
0.00	0.02	145.25	59.51	2.44	1384298_at	Myo1f	myosin IF
0.00	0.03	61.50	25.22	2.44	1374976_a_at	Soat1	sterol O-acyltransferase 1

0.00	0.01	67.26	27.59	2.44	1378418_at	Tfab	TRAF-interacting protein with forkhead-associated domain, family member B
0.00	0.03	231.97	95.84	2.42	1383786_at	Rab32	RAB32, member RAS oncogene family
0.00	0.03	119.83	49.55	2.42	1378443_at	Slamf9	SLAM family member 9
0.00	0.02	84.73	35.12	2.41	1372326_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3
0.00	0.01	148.82	61.88	2.40	1377908_at	NA	NA
0.00	0.02	74.26	31.14	2.38	1384896_at	NA	NA
0.00	0.01	837.15	351.29	2.38	1391719_at	NA	NA
0.00	0.02	199.27	83.64	2.38	1392407_at	NA	NA
0.00	0.03	56.67	23.86	2.38	1390364_at	NA	NA
0.00	0.02	261.79	110.52	2.37	1373504_at	Glpr1	GLI pathogenesis-related 1
0.00	0.03	38.95	16.47	2.36	1384027_a_at	NA	NA
0.00	0.02	166.79	70.58	2.36	1370082_at	Tgfb1	transforming growth factor, beta 1
0.00	0.03	122.07	51.69	2.36	1368008_at	Prom1	prominin 1
0.00	0.03	514.46	217.87	2.36	1368851_at	Ets1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
0.00	0.01	195.28	83.00	2.35	1378700_at	NA	NA
0.00	0.02	152.03	64.84	2.34	1393280_at	Ly86	lymphocyte antigen 86
0.00	0.03	234.13	99.99	2.34	1379295_at	Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
0.00	0.03	220.57	94.42	2.34	1380450_at	Bzrap1	benzodiazapine receptor associated protein 1
0.00	0.00	111.45	47.71	2.34	1385888_at	NA	NA
0.00	0.02	75.72	32.42	2.34	1390556_at	NA	NA
0.00	0.00	48.52	20.80	2.33	1379768_at	NA	NA
0.00	0.02	93.83	40.26	2.33	1382601_at	NA	NA
0.00	0.02	72.81	31.36	2.32	1395301_x_at	LOC685157	similar to paired immunoglobulin-like type 2 receptor beta
0.00	0.01	136.55	58.82	2.32	1387198_at	Inpp5d	inositol polyphosphate-5-phosphatase D
0.00	0.01	282.17	121.98	2.31	1377239_at	Apbb1ip	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein
0.00	0.02	406.21	175.89	2.31	1370348_at	Ninj1	ninjurin 1
0.00	0.03	95.31	41.29	2.31	1373754_at	NA	NA
0.00	0.03	327.00	141.89	2.30	1388673_at	Lsp1	lymphocyte-specific protein 1
0.00	0.01	107.54	46.82	2.30	1382181_at	Pion	pigeon homolog (Drosophila)
0.00	0.03	151.58	66.19	2.29	1384013_at	NA	NA
0.00	0.02	472.68	206.71	2.29	1384507_at	Fam105a	family with sequence similarity 105, member A
0.00	0.02	119.80	52.61	2.28	1377882_at	Flt3	fms-related tyrosine kinase 3
0.00	0.02	46.82	20.61	2.27	1390948_at	Phemx	pan hematopoietic expression
0.00	0.04	247.24	108.87	2.27	1371537_at	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
0.00	0.03	718.19	316.46	2.27	1371727_at	Glb1	galactosidase, beta 1
0.00	0.03	261.55	115.35	2.27	1371468_at	LOC312502	similar to RAB11 family interacting protein 5 (class I) isoform 1
0.00	0.02	1266.64	560.11	2.26	1367925_at	Mvp	major vault protein
0.00	0.01	1291.01	573.64	2.25	1379366_a_at	Bspry	B-box and SPRY domain containing
0.00	0.02	67.09	29.83	2.25	1367919_at	Nup210	nucleoporin 210
0.00	0.03	107.08	47.69	2.25	1379425_at	Dem1	defects in morphology 1 homolog (S. cerevisiae)
0.00	0.03	261.82	117.05	2.24	1392927_at	Pagr4	progesterin and adipoQ receptor family member IV



0.00	0.00	93.70	42.09	2.23	1378914_a_at	LOC308990	hypothetical protein LOC308990
0.00	0.03	88.19	39.83	2.21	1397540_at	NA	NA
0.00	0.02	671.38	303.56	2.21	1377660_at	RGD1309350	similar to transthyretin (4L369)
0.00	0.04	121.93	55.66	2.19	1374537_at	Chsy1	chondroitin sulfate synthase 1
0.00	0.03	699.74	319.44	2.19	1369944_at	Marcks1	MARCKS-like 1
0.00	0.01	143.92	65.72	2.19	1388740_at	Fermt3	fermitin family homolog 3 (Drosophila)
0.00	0.01	192.44	87.92	2.19	1371106_at	Itgb7	integrin, beta 7
0.00	0.02	74.01	33.95	2.18	1393003_at	NA	NA
0.00	0.01	69.79	32.11	2.17	1377153_a_at	Klhl6	kelch-like 6 (Drosophila)
0.00	0.02	202.22	93.10	2.17	1397548_at	Hmha1	histocompatibility (minor) HA-1
0.00	0.02	230.28	106.87	2.15	1389109_at	Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
0.00	0.01	187.71	87.14	2.15	1385723_at	NA	NA
0.00	0.02	75.78	35.35	2.14	1382404_at	NA	NA
0.00	0.02	55.63	25.95	2.14	1377975_at	NA	NA
0.00	0.01	345.01	161.09	2.14	1390553_at	Tmem194b	transmembrane protein 194B
0.00	0.01	307.35	144.05	2.13	1375643_at	Ckap4	cytoskeleton-associated protein 4
0.00	0.04	240.64	112.97	2.13	1385986_at	NA	NA
0.00	0.02	125.04	58.73	2.13	1390287_at	Bin2	bridging integrator 2
0.00	0.02	1571.05	738.49	2.13	1370848_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1
0.00	0.03	172.63	81.29	2.12	1369197_at	Apaf1	apoptotic peptidase activating factor 1
0.00	0.03	76.49	36.04	2.12	1372989_at	Zdhhc14	zinc finger, DHHC-type containing 14
0.00	0.03	87.62	41.41	2.12	1372308_at	NA	NA
0.00	0.01	153.30	72.61	2.11	1380410_at	NA	NA
0.00	0.00	60.47	28.67	2.11	1390694_at	NA	NA
0.00	0.01	97.27	46.17	2.11	1379284_at	Ubash3b	ubiquitin associated and SH3 domain containing, B
0.00	0.03	102.57	48.82	2.10	1398098_at	NA	NA
0.00	0.02	73.97	35.27	2.10	1379698_at	NA	NA
0.00	0.01	21.02	10.02	2.10	1380803_at	NA	NA
0.00	0.01	101.10	48.26	2.10	1377759_at	Bid	BH3 interacting domain death agonist
0.00	0.02	63.94	30.60	2.09	1388026_at	Cd247	Cd247 molecule
0.00	0.02	269.95	129.38	2.09	1383426_at	Pstpip1	proline-serine-threonine phosphatase-interacting protein 1
0.00	0.03	52.22	25.14	2.08	1384090_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O
0.00	0.02	22.05	10.65	2.07	1386482_at	NA	NA
0.00	0.02	45.31	21.89	2.07	1397214_at	NA	NA
0.00	0.02	175.68	84.91	2.07	1376835_at	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
0.00	0.01	1253.05	607.94	2.06	1378133_at	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11
0.00	0.00	143.56	69.88	2.05	1382920_at	Lrrc8a	leucine rich repeat containing 8 family, member A
0.00	0.02	33.28	16.20	2.05	1379150_at	NA	NA
0.00	0.04	38.47	18.73	2.05	1374939_at	Cyfp2	cytoplasmic FMR1 interacting protein 2
0.00	0.03	500.78	243.88	2.05	1388492_at	Tnip1	TNFAIP3 interacting protein 1
0.00	0.03	353.22	172.57	2.05	1381461_at	NA	NA
0.00	0.03	172.46	84.49	2.04	1376627_at	NA	NA
0.00	0.02	499.72	245.25	2.04	1373889_at	RGD1561778	similar to dendritic cell-derived immunoglobulin(Ig)-like receptor 1, DlgR1 - mouse

0.00	0.00	45.53	22.36	2.04	1385336_at	Dok2	docking protein 2
0.00	0.02	3577.21	1761.16	2.03	1374987_at	NA	NA
0.00	0.02	45.91	22.65	2.03	1388282_s_at	Klra5	killer cell lectin-like receptor, subfamily A, member 5
0.00	0.01	20.91	10.41	2.01	1377106_at	NA	NA
0.00	0.01	113.31	56.48	2.01	1384191_at	NA	NA
0.00	0.02	88.66	44.22	2.01	1385046_at	Fam55c	family with sequence similarity 55, member C
0.00	0.03	132.41	66.06	2.00	1385159_at	Nbeal2	neurobeachin-like 2
0.00	0.03	186.78	93.49	2.00	1373631_at	Rap1gap	Rap1 GTPase-activating protein
0.00	0.01	184.89	92.57	2.00	1371256_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18
0.00	0.02	768.66	386.47	1.99	1391743_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
0.00	0.01	251.00	126.35	1.99	1387310_at	Atp2c2	ATPase, Ca++ transporting, type 2C, member 2
0.00	0.02	1026.97	517.32	1.99	1398481_at	NA	NA
0.00	0.02	333.82	168.30	1.98	1367881_at	Sirpa	signal-regulatory protein alpha
0.00	0.03	93.62	47.33	1.98	1391803_at	NA	NA
0.00	0.02	2707.53	1369.70	1.98	1372070_at	Ifi30	interferon gamma inducible protein 30
0.00	0.02	421.66	215.41	1.96	1384944_at	Bcl11b	B-cell CLL/lymphoma 11B (zinc finger protein)
0.00	0.03	73.35	37.49	1.96	1378980_at	RGD1305685	similar to hypothetical protein FLJ13089
0.00	0.03	42.41	21.76	1.95	1369044_a_at	Pde4b	phosphodiesterase 4B, cAMP specific
0.00	0.02	41.84	21.54	1.94	1391741_a_at	NA	NA
0.00	0.03	183.03	94.26	1.94	1385696_at	NA	NA
0.00	0.02	118.29	61.01	1.94	1377116_at	Rnasel	ribonuclease L (2@#%\$&.5@#%\$&-oligoisoadenylate synthetase-dependent)
0.00	0.03	496.95	256.31	1.94	1373611_at	Il17ra	interleukin 17 receptor A
0.00	0.03	257.20	133.04	1.93	1367915_at	Dgat1	diacylglycerol O-acyltransferase homolog 1 (mouse)
0.00	0.02	79.74	41.25	1.93	1376197_at	Tcf7	transcription factor 7, T-cell specific
0.00	0.02	170.52	88.25	1.93	1372135_at	Ptk9l	protein tyrosine kinase 9-like (A6-related protein)
0.00	0.03	80.79	41.90	1.93	1381161_a_at	NA	NA
0.00	0.03	58.45	30.36	1.93	1378447_at	NA	NA
0.00	0.02	370.09	192.86	1.92	1379520_at	NA	NA
0.00	0.03	87.26	45.49	1.92	1373226_at	RGD1308019	similar to hypothetical protein FLJ20245
0.00	0.03	236.62	123.44	1.92	1375989_a_at	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100
0.00	0.01	356.96	186.32	1.92	1377630_at	Tspan13	tetraspanin 13
0.00	0.01	277.95	145.40	1.91	1393183_at	Stard5	StAR-related lipid transfer (START) domain containing 5
0.00	0.03	68.56	35.89	1.91	1368109_at	St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
0.00	0.01	486.38	254.63	1.91	1376040_at	Sipa12	signal-induced proliferation-associated 1 like 2
0.00	0.00	53.76	28.16	1.91	1382597_at	NA	NA
0.00	0.02	308.65	161.71	1.91	1374300_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4
0.00	0.02	679.43	356.31	1.91	1377892_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F
0.00	0.00	401.74	210.98	1.90	1387104_at	Scnn1a	sodium channel, nonvoltage-gated, type I, alpha
0.00	0.02	1277.29	672.78	1.90	1367675_at	Cib1	calcium and integrin binding 1 (calmyrin)

0.00	0.03	104.80	55.25	1.90	1390909_at	NA	NA
0.00	0.02	86.21	45.46	1.90	1369038_at	Itgad	integrin, alpha D
0.00	0.02	155.75	82.30	1.89	1370516_at	Slc15a3	solute carrier family 15, member 3
0.00	0.02	318.79	168.96	1.89	1385919_at	NA	NA
0.00	0.03	82.16	43.60	1.88	1395775_at	NA	NA
0.00	0.02	65.75	34.92	1.88	1375118_at	NA	NA
0.00	0.03	5420.80	2882.55	1.88	1370156_at	Prnp	prion protein
0.00	0.01	109.43	58.46	1.87	1368770_at	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2
0.00	0.02	200.31	107.11	1.87	1382110_at	Cnpy3	canopy 3 homolog (zebrafish)
0.00	0.02	64.07	34.43	1.86	1394805_at	NA	NA
0.00	0.03	195.27	105.21	1.86	1398745_at	NA	NA
0.00	0.02	35.99	19.42	1.85	1385382_at	NA	NA
0.00	0.02	113.73	61.38	1.85	1368251_at	Jak3	Janus kinase 3
0.00	0.03	1278.33	690.63	1.85	1389494_at	Ccdc88b	coiled-coil domain containing 88B
0.00	0.01	234.92	127.10	1.85	1390859_at	N4bp1	Nedd4 binding protein 1
0.00	0.03	59.45	32.20	1.85	1382087_at	NA	NA
0.00	0.03	16.93	9.18	1.84	1392214_at	NA	NA
0.00	0.02	43.00	23.34	1.84	1370617_at	Grb2	growth factor receptor bound protein 2
0.00	0.02	100.85	54.84	1.84	1372427_at	Raver1	ribonucleoprotein, PTB-binding 1
0.00	0.03	488.60	265.84	1.84	1387264_at	Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6
0.00	0.02	176.86	96.39	1.83	1386185_at	NA	NA
0.00	0.03	176.71	96.36	1.83	1397157_at	NA	NA
0.00	0.02	270.00	147.41	1.83	1380521_at	Hcls1	hematopoietic cell specific Lyn substrate 1
0.00	0.02	254.62	139.48	1.83	1372408_at	Gga2	golgi associated, gamma adaptin ear containing, ARF binding protein 2
0.00	0.02	16.68	9.16	1.82	1384035_at	LOC685277	similar to liver-specific bHLH-Zip transcription factor
0.00	0.02	81.24	44.61	1.82	1398330_at	Stxbp1	syntaxin binding protein 1
0.00	0.02	85.24	47.38	1.80	1370469_at	Ptpn7	protein tyrosine phosphatase, non-receptor type 7
0.00	0.03	110.70	61.56	1.80	1377002_at	NA	NA
0.00	0.02	99.79	55.52	1.80	1397781_at	NA	NA
0.00	0.02	658.37	366.56	1.80	1375211_at	Rnaset2	ribonuclease T2
0.00	0.01	277.93	155.14	1.79	1373863_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4
0.00	0.04	190.96	106.78	1.79	1373519_at	NA	NA
0.00	0.03	153.21	85.80	1.79	1368754_at	P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6
0.00	0.03	72.40	40.60	1.78	1382392_at	NA	NA
0.00	0.01	76.95	43.18	1.78	1369387_at	Vav1	vav 1 guanine nucleotide exchange factor
0.00	0.02	111.04	62.31	1.78	1372027_at	NA	NA
0.00	0.03	63.51	35.71	1.78	1380154_at	Immt	inner membrane protein, mitochondrial
0.00	0.01	627.46	352.82	1.78	1389988_at	Kctd2	potassium channel tetramerisation domain containing 2
0.00	0.02	202.23	113.99	1.77	1372921_at	NA	NA
0.00	0.01	81.53	45.98	1.77	1384350_at	Nckap1l	NCK associated protein 1 like
0.00	0.03	195.83	110.50	1.77	1380028_at	Arl4c	ADP-ribosylation factor-like 4C
0.00	0.03	115.31	65.07	1.77	1388742_at	NA	NA
0.00	0.03	121.43	68.71	1.77	1373298_at	NA	NA
0.00	0.03	1227.09	696.06	1.76	1388763_at	LOC690976	similar to Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin)

0.00	0.02	147.56	83.76	1.76	1373031_at	Trim8	tripartite motif-containing 8
0.00	0.01	219.11	124.67	1.76	1373528_at	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide
0.00	0.04	383.06	218.03	1.76	1380851_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F
0.00	0.03	69.00	39.36	1.75	1376675_at	Cd300a	CD300A molecule
0.00	0.01	161.30	92.02	1.75	1368010_at	Ptpn6	protein tyrosine phosphatase, non-receptor type 6
0.00	0.03	337.04	192.80	1.75	1368254_a_at	Sphk1	sphingosine kinase 1
0.00	0.01	386.45	221.92	1.74	1371782_at	Nipsnap3a	nipsnap homolog 3A (C. elegans)
0.00	0.03	63.24	36.38	1.74	1376795_at	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1
0.00	0.03	31.73	18.28	1.74	1398719_at	Cdyl2	chromodomain protein, Y chromosome-like 2
0.00	0.03	162.75	94.02	1.73	1376895_at	Il16	interleukin 16
0.00	0.02	310.18	179.20	1.73	1383618_at	Mrp138	mitochondrial ribosomal protein L38
0.00	0.02	1206.38	697.48	1.73	1368118_at	Bcl10	B-cell CLL/lymphoma 10
0.00	0.02	333.40	193.22	1.73	1376568_at	NA	NA
0.00	0.03	107.64	62.56	1.72	1375020_at	Rin3	Ras and Rab interactor 3
0.00	0.03	275.59	160.69	1.72	1376701_a_at	MGC94282	similar to 5930416119Rik protein
0.00	0.03	231.56	135.33	1.71	1387205_at	H2-M3	histocompatibility 2, M region locus 3
0.00	0.02	482.11	282.04	1.71	1374676_at	NA	NA
0.00	0.03	12.67	7.41	1.71	1382337_at	Stap1	signal transducing adaptor family member 1
0.00	0.01	25.64	15.06	1.70	1382891_at	Usp27x	ubiquitin specific peptidase 27, X-linked
0.00	0.02	366.33	215.22	1.70	1383074_at	Man2a1	mannosidase, alpha, class 2A, member 1
0.00	0.03	53.76	31.59	1.70	1382107_at	NA	NA
0.00	0.01	87.64	51.70	1.70	1375420_at	Tp53i11	tumor protein p53 inducible protein 11
0.00	0.03	135.46	80.11	1.69	1369310_at	Basp1	brain abundant, membrane attached signal protein 1
0.00	0.01	151.57	89.77	1.69	1373928_at	Il17re	interleukin 17 receptor E
0.00	0.02	66.64	39.47	1.69	1374025_at	Nmnat3	nicotinamide nucleotide adenylyltransferase 3
0.00	0.03	46.93	27.85	1.68	1381079_at	Bnc1	basonuclin 1
0.00	0.01	105.60	62.73	1.68	1396623_at	NA	NA
0.00	0.03	89.63	53.58	1.67	1393757_at	N4bp211	NEDD4 binding protein 2-like 1
0.00	0.02	47.20	28.26	1.67	1392335_at	NA	NA
0.00	0.01	112.09	67.35	1.66	1374265_at	NA	NA
0.00	0.03	140.31	84.62	1.66	1381790_at	Map4k4	mitogen-activated protein kinase kinase kinase 4
0.00	0.02	717.19	432.60	1.66	1377821_at	NA	NA
0.00	0.02	261.73	158.22	1.65	1372138_at	Cux1	cut-like homeobox 1
0.00	0.03	34.85	21.09	1.65	1396133_at	Itgb5	integrin, beta 5
0.00	0.03	226.66	137.14	1.65	1376200_at	MGC72974	hypothetical LOC316976
0.00	0.03	103.68	62.78	1.65	1376255_at	Map4k1	mitogen activated protein kinase kinase kinase 1
0.00	0.01	666.38	404.10	1.65	1373150_at	Comtd1	catechol-O-methyltransferase domain containing 1
0.00	0.03	84.08	51.57	1.63	1369483_at	Cd4	Cd4 molecule
0.00	0.03	39.81	24.48	1.63	1397713_at	NA	NA
0.00	0.03	573.77	353.81	1.62	1383152_at	Chid1	chitinase domain containing 1
0.00	0.03	63.00	38.89	1.62	1397102_at	NA	NA
0.00	0.03	205.96	127.27	1.62	1394452_at	NA	NA

0.00	0.02	33.12	20.48	1.62	1379975_at	NA	NA
0.00	0.03	389.32	241.02	1.62	1383863_at	Lmo2	LIM domain only 2
0.00	0.02	1764.02	1092.56	1.61	1371715_at	MGC112883	LOC500651
0.00	0.04	291.13	180.40	1.61	1390000_at	Jmjd3	jumonji domain containing 3
0.00	0.02	73.45	45.54	1.61	1384292_at	Dok1	docking protein 1
0.00	0.02	29.70	18.48	1.61	1380653_at	NA	NA
0.00	0.03	497.34	310.84	1.60	1373852_at	Srd5a3	steroid 5 alpha-reductase 3
0.00	0.01	143.99	90.07	1.60	1377321_at	NA	NA
0.00	0.01	30.50	19.13	1.59	1375370_at	NA	NA
0.00	0.00	177.01	111.05	1.59	1376160_at	Sfrs16	splicing factor, arginine/serine-rich 16
0.00	0.02	1061.64	666.92	1.59	1377103_at	Midn	midnolin
0.00	0.01	338.19	212.78	1.59	1383608_at	Arrdc2	arrestin domain containing 2
0.00	0.01	580.47	365.70	1.59	1371446_at	Mapkapk2	mitogen-activated protein kinase-activated protein kinase 2
0.00	0.02	40.26	25.38	1.59	1386069_at	Sp2	Sp2 transcription factor
0.00	0.03	4788.21	3019.28	1.59	1387766_a_at	Rbp2	retinol binding protein 2, cellular
0.00	0.01	771.53	490.76	1.57	1399157_at	RGD1310358	similar to NNX3
0.00	0.03	250.76	160.10	1.57	1392425_x_at	Luc7l	LUC7-like ( <i>S. cerevisiae</i> )
0.00	0.02	270.29	173.14	1.56	1389347_at	Pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1
0.00	0.03	22.02	14.19	1.55	1383833_at	Fam55b	family with sequence similarity 55, member B
0.00	0.02	158.30	102.04	1.55	1398335_at	Ttyh3	tweety homolog 3 ( <i>Drosophila</i> )
0.00	0.01	290.94	188.15	1.55	1387132_at	Lipe	lipase, hormone sensitive
0.00	0.02	41.09	26.62	1.54	1380469_at	NA	NA
0.00	0.00	146.66	95.09	1.54	1390936_at	Lgi4	leucine-rich repeat LGI family, member 4
0.00	0.03	1231.99	802.00	1.54	1391106_at	NA	NA
0.00	0.03	54.20	35.29	1.54	1397209_at	RGD1565712	similar to Hypothetical protein MGC59495
0.00	0.03	1357.65	884.50	1.53	1388468_at	Cdc42se1	CDC42 small effector 1
0.00	0.02	278.07	181.25	1.53	1372561_at	Smap2	small ArfGAP2
0.00	0.02	355.96	232.21	1.53	1385608_at	NA	NA
0.00	0.02	132.45	86.41	1.53	1383350_at	Slc35c2	solute carrier family 35, member C2
0.00	0.01	136.30	88.99	1.53	1384997_at	Aen	apoptosis enhancing nuclease
0.00	0.02	14.17	9.25	1.53	1380468_a_at	NA	NA
0.00	0.04	58.11	37.99	1.53	1392301_at	Sh3tc1	SH3 domain and tetratricopeptide repeats 1
0.00	0.01	50.14	32.88	1.52	1374320_at	F5	coagulation factor V (proaccelerin, labile factor)
0.00	0.01	229.87	150.87	1.52	1381016_at	NA	NA
0.00	0.03	169.81	111.79	1.52	1369088_at	ErbB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
0.00	0.01	45.42	29.91	1.52	1369552_at	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1
0.00	0.02	296.18	195.26	1.52	1374686_at	Slc30a7	solute carrier family 30 (zinc transporter), member 7
0.00	0.03	12.47	8.22	1.52	1381940_at	NA	NA
0.00	0.02	25.32	16.71	1.52	1395205_at	NA	NA
0.00	0.02	146.40	96.70	1.51	1394047_at	NA	NA
0.00	0.02	88.75	58.64	1.51	1375839_at	NA	NA
0.00	0.03	67.79	44.86	1.51	1379311_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)
0.00	0.03	131.66	87.16	1.51	1385534_at	Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1
0.00	0.03	223.31	148.79	1.50	1372129_at	Tbc1d9b	TBC1 domain family, member 9B

0.00	0.03	38.24	25.52	1.50	1393830_at	Sh2d2a	SH2 domain protein 2A
0.00	0.04	28.50	19.03	1.50	1378549_at	NA	NA
0.00	0.03	57.17	38.24	1.50	1389516_at	NA	NA
0.00	0.02	29.95	20.04	1.49	1387879_a_at	Cugbp2	CUG triplet repeat, RNA binding protein 2
0.00	0.03	137.77	92.27	1.49	1374221_at	Slc29a3	solute carrier family 29 (nucleoside transporters), member 3
0.00	0.02	153.73	103.56	1.48	1382811_at	NA	NA
0.00	0.02	97.28	65.60	1.48	1378982_at	NA	NA
0.00	0.03	14.44	9.74	1.48	1393333_at	NA	NA
0.00	0.02	1379.91	932.64	1.48	1373033_at	Sft2d1	SFT2 domain containing 1
0.00	0.02	91.77	62.30	1.47	1387905_at	Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12
0.00	0.03	472.86	321.29	1.47	1382008_at	RGD1309804	similar to hypothetical protein FLJ11218
0.00	0.02	41.83	28.45	1.47	1382817_at	Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein
0.00	0.03	91.48	62.42	1.47	1378437_at	NA	NA
0.00	0.00	4462.41	3047.89	1.46	1388113_at	Cox8a	cytochrome c oxidase, subunit VIIIa
0.00	0.03	505.37	345.23	1.46	1387066_a_at	Rgs12	regulator of G-protein signaling 12
0.00	0.01	237.14	162.25	1.46	1390154_at	LOC686326	similar to Interferon-alpha/beta receptor beta chain precursor (IFN-alpha-REC) (Type I interferon receptor) (IFN-R) (Interferon alpha/beta receptor-2)
0.00	0.02	37.46	25.71	1.46	1370733_at	Lipogenin	Lipogenin
0.00	0.02	1404.54	964.42	1.46	1373100_at	LOC499779	similar to RIKEN cDNA 2900010J23
0.00	0.03	247.43	169.90	1.46	1372955_at	Stk38l	serine/threonine kinase 38 like
0.00	0.03	180.41	124.10	1.45	1383917_at	Abi3	ABI family, member 3
0.00	0.02	137.62	94.93	1.45	1376839_at	NA	NA
0.00	0.03	223.20	154.27	1.45	1373262_at	RGD1309543	similar to 2310014H01Rik protein
0.00	0.03	511.23	353.35	1.45	1399023_at	Ric8a	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)
0.00	0.02	19.91	13.77	1.45	1385587_at	Mcoln2	mucolin 2
0.00	0.03	19.37	13.41	1.44	1395319_at	NA	NA
0.00	0.02	108.68	75.50	1.44	1379280_at	NA	NA
0.00	0.01	66.42	46.33	1.43	1369214_a_at	Ciita	class II transactivator
0.00	0.03	74.89	52.26	1.43	1377159_at	Tsc22d4	TSC22 domain family, member 4
0.00	0.02	1176.94	823.21	1.43	1367710_at	Psme2	proteasome (prosome, macropain) activator subunit 2
0.00	0.02	9.75	6.83	1.43	1385831_at	Sash3	SAM and SH3 domain containing 3
0.00	0.00	480.78	338.87	1.42	1389530_at	Slc35e1	solute carrier family 35, member E1
0.00	0.02	111.10	78.41	1.42	1371071_at	Gnb4	guanine nucleotide binding protein (G protein), beta polypeptide 4
0.00	0.03	84.85	60.04	1.41	1391112_at	Ggta1	glycoprotein, alpha-galactosyltransferase 1
0.00	0.03	149.98	106.16	1.41	1370049_at	Smpd2	sphingomyelin phosphodiesterase 2, neutral
0.00	0.03	212.42	151.87	1.40	1374068_at	Vps39	vacuolar protein sorting 39 homolog (S. cerevisiae)
0.00	0.01	929.58	665.69	1.40	1370305_at	Yif1	Yip1 interacting factor homolog (S. cerevisiae)
0.00	0.03	30.01	21.50	1.40	1383128_at	Rpl5	ribosomal protein L5
0.00	0.02	2703.64	1936.79	1.40	1398892_at	Npc2	Niemann-Pick disease, type C2
0.00	0.01	338.39	242.85	1.39	1370916_at	Tec	tec protein tyrosine kinase
0.00	0.03	109.49	78.65	1.39	1389219_at	LOC679692	similar to lysophosphatidylglycerol acyltransferase 1
0.00	0.02	1160.74	835.52	1.39	1371880_at	Sp1	Sp1 transcription factor

0.00	0.04	34.48	24.84	1.39	1380064_at	NA	NA
0.00	0.02	400.42	289.17	1.38	1388813_at	Arf2	ADP-ribosylation factor 2
0.00	0.03	535.70	387.14	1.38	1378160_at	Frrs1	ferric-chelate reductase 1
0.00	0.02	1186.24	857.42	1.38	1367922_at	Adam17	ADAM metallopeptidase domain 17
0.00	0.00	195.91	141.68	1.38	1385839_x_at	Tm2d1	TM2 domain containing 1
0.00	0.02	5613.46	4060.63	1.38	1371644_at	Twf1	twinfilin, actin-binding protein, homolog 1 (Drosophila)
0.00	0.02	33.53	24.36	1.38	1382036_at	Tln1	talin 1
0.00	0.02	487.32	354.69	1.37	1383674_at	Tmem219	transmembrane protein 219
0.00	0.03	67.72	49.32	1.37	1382917_at	NA	NA
0.00	0.03	119.31	87.90	1.36	1375015_at	NA	NA
0.00	0.03	138.21	102.14	1.35	1396062_at	NA	NA
0.00	0.03	682.10	504.17	1.35	1375938_at	Ccdc12	coiled-coil domain containing 12
0.00	0.02	372.78	275.58	1.35	1385208_at	RGD1305014	similar to RIKEN cDNA 2310057M21
0.00	0.01	210.73	155.96	1.35	1394460_at	NA	NA
0.00	0.03	267.37	198.03	1.35	1389700_at	NA	NA
0.00	0.00	246.69	182.96	1.35	1380857_at	Pde12	phosphodiesterase 12
0.00	0.01	230.24	171.74	1.34	1375435_at	RGD1311021	hypothetical LOC308765
0.00	0.02	2845.12	2122.92	1.34	1389538_at	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
0.00	0.02	345.43	259.49	1.33	1371681_at	Tox4	TOX high mobility group box family member 4
0.00	0.03	338.04	254.01	1.33	1373542_at	Sphk2	sphingosine kinase 2
0.00	0.03	395.47	298.11	1.33	1376073_at	Sel1l	sel-1 suppressor of lin-12-like (C. elegans)
0.00	0.03	58.63	44.32	1.32	1384948_at	Trps1	trichorhinophalangeal syndrome I homolog (human)
0.00	0.02	1349.63	1025.49	1.32	1398952_at	RGD1564093	similar to RIKEN cDNA 2310036O22
0.00	0.04	515.73	392.21	1.31	1372430_at	RGD1311739	similar to RIKEN cDNA 1700037H04
0.00	0.03	13.38	10.23	1.31	1396217_at	NA	NA
0.00	0.02	16.37	12.53	1.31	1382563_at	RGD1560818	similar to hypothetical protein FLJ38944
0.00	0.02	550.04	423.78	1.30	1369060_a_at	Hdac3	histone deacetylase 3
0.00	0.03	67.99	52.61	1.29	1380241_a_at	Lrp5	low density lipoprotein receptor-related protein 5
0.00	0.03	313.29	242.84	1.29	1374997_at	Map3k11	mitogen-activated protein kinase kinase kinase 11
0.00	0.03	1854.15	1438.99	1.29	1387806_at	Rap1b	RAP1B, member of RAS oncogene family
0.00	0.03	357.03	277.55	1.29	1389571_at	Stat2	signal transducer and activator of transcription 2
0.00	0.02	398.08	309.53	1.29	1372987_at	NA	NA
0.00	0.02	4399.20	3421.06	1.29	1370051_at	Tgm1	transglutaminase 1, K polypeptide
0.00	0.03	144.83	112.99	1.28	1384925_at	NA	NA
0.00	0.04	200.21	156.37	1.28	1390447_at	Stx3	syntaxin 3
0.00	0.02	681.45	533.46	1.28	1390228_at	Aof1	amine oxidase (flavin containing) domain 1
0.00	0.03	685.58	537.41	1.28	1374105_at	Higd1a	HIG1 domain family, member 1A
0.00	0.02	532.41	417.89	1.27	1372853_at	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
0.00	0.03	373.32	293.11	1.27	1387875_at	Ptk2	PTK2 protein tyrosine kinase 2
0.00	0.02	183.02	144.09	1.27	1375045_at	NA	NA
0.00	0.02	1296.48	1027.66	1.26	1368834_at	Camk2d	calcium/calmodulin-dependent protein kinase II delta
0.00	0.03	325.72	259.20	1.26	1367478_at	Htra2	HtrA serine peptidase 2
0.00	0.01	9.62	7.67	1.25	1376540_at	NA	NA

0.00	0.02	604.94	485.72	1.25	1399114_at	Gtf2e2	general transcription factor IIE, polypeptide 2, beta
0.00	0.03	611.30	491.43	1.24	1399049_at	RGD1308917	similar to RIKEN cDNA 1200003C05
0.00	0.03	130.29	105.92	1.23	1375712_at	Thoc7	THO complex 7 homolog (Drosophila)
0.00	0.03	1387.33	1128.64	1.23	1375090_at	NA	NA
0.00	0.03	292.87	238.63	1.23	1370440_at	Slc15a4	solute carrier family 15, member 4
0.00	0.01	921.86	752.91	1.22	1367543_at	LOC685079	similar to Protein SYS1 homolog
0.00	0.02	1074.62	878.84	1.22	1367546_at	Mrp143	mitochondrial ribosomal protein L43
0.00	0.03	2365.92	1949.22	1.21	1371346_at	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
0.00	0.03	436.19	362.17	1.20	1371934_at	Usp21	ubiquitin specific peptidase 21
0.00	0.01	230.85	192.22	1.20	1371733_at	Arl8a	ADP-ribosylation factor-like 8A
0.00	0.03	3341.22	2790.83	1.20	1370250_at	Ube2i	ubiquitin-conjugating enzyme E2I
0.00	0.03	185.07	155.29	1.19	1378041_at	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8
0.00	0.01	428.21	363.91	1.18	1374402_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1
0.00	0.03	277.56	236.06	1.18	1367550_a_at	Tm2d1	TM2 domain containing 1
0.00	0.02	5893.84	5104.64	1.15	1371511_at	Arpc2	actin related protein 2/3 complex, subunit 2
0.00	0.03	172.03	149.92	1.15	1389152_at	Zfyve27	zinc finger, FYVE domain containing 27
0.00	0.03	449.41	399.26	1.13	1374523_at	Pgls	6-phosphogluconolactonase
0.00	0.03	299.54	268.12	1.12	1380309_at	Vps8	vacuolar protein sorting 8 homolog (S. cerevisiae)
0.00	0.03	11622.40	10524.21	1.10	1388449_at	Eef1b2	eukaryotic translation elongation factor 1 beta 2
0.00	0.03	11055.30	10446.83	1.06	1367618_a_at	Gnb211	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
0.00	0.03	46.50	1303.59	0.04	1384236_at	NA	NA
0.00	0.02	371.67	9934.66	0.04	1383203_at	RGD1559748	similar to Palate lung and nasal carcinoma-like protein precursor (Tongue plunc-like protein)
0.00	0.01	37.86	658.70	0.06	1398090_at	LOC687873	similar to kallikrein 5 preproprotein
0.00	0.02	86.60	1128.61	0.08	1394228_at	Tmigd1	transmembrane and immunoglobulin domain containing 1
0.00	0.01	125.64	1465.62	0.09	1373493_at	Slurp1	secreted Ly6/Plaur domain containing 1
0.00	0.03	15.16	157.98	0.10	1397903_at	NA	NA
0.00	0.01	135.41	1173.77	0.12	1372390_at	Apeg3	antisense paternally expressed gene 3
0.00	0.04	88.26	739.68	0.12	1378324_at	Ttc30b	tetratricopeptide repeat domain 30B
0.00	0.00	37.25	260.01	0.14	1382088_at	NA	NA
0.00	0.02	39.24	243.17	0.16	1392943_at	Mboat2	membrane bound O-acyltransferase domain containing 2
0.00	0.02	51.04	306.92	0.17	1382031_at	NA	NA
0.00	0.02	614.94	3166.35	0.19	1368470_at	Ggh	gamma-glutamyl hydrolase
0.00	0.00	1510.68	7661.72	0.20	1381573_at	RGD1562107	similar to class-alpha glutathione S-transferase
0.00	0.03	21.24	103.82	0.20	1371089_at	Yc2	glutathione S-transferase Yc2 subunit
0.00	0.02	65.66	313.35	0.21	1384392_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1
0.00	0.03	175.77	837.31	0.21	1393684_at	Hells	helicase, lymphoid specific
0.00	0.03	389.36	1852.75	0.21	1384180_at	Ifit2	interferon-induced protein with tetratricopeptide repeats 2
0.00	0.02	568.36	2575.90	0.22	1372760_at	NA	NA
0.00	0.01	49.60	216.80	0.23	1379075_at	Mboat2	membrane bound O-acyltransferase domain containing 2
0.00	0.01	86.18	356.79	0.24	1389662_at	Wnk4	WNK lysine deficient protein kinase 4
0.00	0.03	58.65	228.92	0.26	1383894_at	NA	NA



0.00	0.02	778.79	3028.40	0.26	1387156_at	Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2
0.00	0.03	427.72	1654.40	0.26	1374863_at	Rbp7	retinol binding protein 7, cellular
0.00	0.01	948.60	3310.01	0.29	1387022_at	Aldh1a1	aldehyde dehydrogenase 1 family, member A1
0.00	0.03	16.78	57.62	0.29	1369169_at	Slc23a1	solute carrier family 23 (nucleobase transporters), member 1
0.00	0.03	29.79	96.35	0.31	1383164_at	NA	NA
0.00	0.02	129.24	401.88	0.32	1368121_at	Akr7a3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
0.00	0.01	53.42	165.38	0.32	1369179_a_at	Pparg	peroxisome proliferator-activated receptor gamma
0.00	0.02	60.18	182.35	0.33	1387282_at	Hspb8	heat shock protein 8
0.00	0.03	115.75	348.09	0.33	1394290_at	NA	NA
0.00	0.03	232.00	694.18	0.33	1372604_at	RGD1309808	similar to apolipoprotein L2; apolipoprotein L-II
0.00	0.03	81.60	242.59	0.34	1369435_at	Ttpa	tocopherol (alpha) transfer protein
0.00	0.02	59.15	168.84	0.35	1374948_at	Tmem106a	transmembrane protein 106A
0.00	0.02	196.51	539.06	0.36	1388721_at	Hspb8	heat shock protein 8
0.00	0.03	269.30	733.85	0.37	1384993_at	RGD1309847	similar to peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor; peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor protein-1
0.00	0.01	24.96	67.41	0.37	1395052_at	NA	NA
0.00	0.03	857.40	2311.63	0.37	1367702_at	Acadm	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
0.00	0.02	278.99	749.46	0.37	1386075_at	Mina	myc induced nuclear antigen
0.00	0.01	346.42	911.72	0.38	1372449_at	NA	NA
0.00	0.01	192.63	501.49	0.38	1379934_at	NA	NA
0.00	0.02	87.88	225.05	0.39	1375818_at	Lactb	lactamase, beta
0.00	0.02	153.83	392.99	0.39	1381597_at	NA	NA
0.00	0.02	26.15	66.39	0.39	1382775_at	Ryr2	ryanodine receptor 2, cardiac
0.00	0.03	735.18	1818.95	0.40	1368132_at	Tob1	transducer of ErbB-2.1
0.00	0.01	279.89	683.82	0.41	1374176_at	RGD1308059	similar to DNA segment, Chr 4, Brigham & Womens Genetics 0951 expressed
0.00	0.03	305.00	740.67	0.41	1382255_at	NA	NA
0.00	0.01	96.93	231.67	0.42	1397452_at	NA	NA
0.00	0.03	205.49	483.91	0.42	1375990_a_at	NA	NA
0.00	0.03	844.95	1985.86	0.43	1389014_at	Nampt	nicotinamide phosphoribosyltransferase
0.00	0.01	277.35	643.03	0.43	1390819_at	Tef	thyrotrophic embryonic factor
0.00	0.01	49.03	113.62	0.43	1380402_at	NA	NA
0.00	0.03	124.96	289.08	0.43	1398287_at	Plau	plasminogen activator, urokinase
0.00	0.00	118.59	274.28	0.43	1396403_at	RGD1311595	similar to KIAA2026 protein
0.00	0.03	504.57	1163.78	0.43	1389351_at	Lrrfp1	leucine rich repeat (in FLII) interacting protein 1
0.00	0.01	168.75	388.34	0.43	1393634_at	Nrg4	neuregulin 4
0.00	0.03	918.79	2111.64	0.44	1398343_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4
0.00	0.03	59.56	136.77	0.44	1393437_at	NA	NA
0.00	0.02	116.74	264.92	0.44	1387753_s_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3
0.00	0.02	264.90	598.20	0.44	1372103_at	LOC498996	similar to DnaJ (Hsp40) homolog, subfamily A, member 4
0.00	0.00	381.82	860.35	0.44	1383353_at	NA	NA
0.00	0.01	20.05	45.03	0.45	1380465_at	NA	NA

0.00	0.03	21.74	48.43	0.45	1384210_at	Micalcl	MICAL C-terminal like
0.00	0.04	105.90	229.71	0.46	1384263_at	Tmem161b	transmembrane protein 161B
0.00	0.02	1045.41	2263.78	0.46	1372500_at	Tmod3	tropomodulin 3
0.00	0.02	131.12	283.59	0.46	1376411_at	Arl13b	ADP-ribosylation factor-like 13B
0.00	0.03	25.10	53.87	0.47	1393279_at	NA	NA
0.00	0.02	675.06	1434.14	0.47	1373986_at	NA	NA
0.00	0.02	2124.85	4466.96	0.48	1377662_at	Pir	pirin (iron-binding nuclear protein)
0.00	0.03	419.87	874.26	0.48	1367960_at	Arl4a	ADP-ribosylation factor-like 4A
0.00	0.02	336.80	700.07	0.48	1374278_at	RGD1307696	similar to dJ881L22.2 (novel protein)
0.00	0.03	527.28	1092.71	0.48	1398600_at	NA	NA
0.00	0.02	577.11	1192.65	0.48	1384254_at	Otud1	OTU domain containing 1
0.00	0.02	73.20	148.11	0.49	1374073_at	Slc46a1	solute carrier family 46, member 1
0.00	0.03	90.15	182.23	0.49	1391184_at	Rfx2	regulatory factor X, 2 (influences HLA class II expression)
0.00	0.03	29.68	59.31	0.50	1378333_at	NA	NA
0.00	0.03	127.00	253.03	0.50	1377818_at	NA	NA
0.00	0.02	274.36	544.38	0.50	1383573_at	Tshz1	teashirt zinc finger homeobox 1
0.00	0.03	116.20	229.30	0.51	1378987_at	NA	NA
0.00	0.01	617.08	1192.88	0.52	1378679_at	Usp25	ubiquitin specific peptidase 25
0.00	0.01	405.99	780.60	0.52	1381279_at	Ripk2	receptor-interacting serine-threonine kinase 2
0.00	0.02	588.47	1131.06	0.52	1370054_at	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
0.00	0.02	624.00	1197.20	0.52	1372774_at	Coq6	coenzyme Q6 homolog (yeast)
0.00	0.03	122.31	232.77	0.53	1383212_at	NA	NA
0.00	0.03	207.49	392.02	0.53	1380321_at	Mtus1	mitochondrial tumor suppressor 1
0.00	0.03	207.64	390.87	0.53	1384916_at	NA	NA
0.00	0.03	50.92	95.17	0.54	1369919_at	Tef	thyrotrophic embryonic factor
0.00	0.00	100.02	186.85	0.54	1371091_at	Irs2	insulin receptor substrate 2
0.00	0.02	68.65	127.60	0.54	1396275_at	Dusp18	dual specificity phosphatase 18
0.00	0.03	159.79	296.66	0.54	1368115_at	Cldn3	claudin 3
0.00	0.02	4781.11	8870.02	0.54	1398688_at	Spink5	serine peptidase inhibitor, Kazal type 5
0.00	0.03	126.85	234.91	0.54	1372976_at	Abhd14a	abhydrolase domain containing 14A
0.00	0.02	482.13	890.25	0.54	1390508_at	NA	NA
0.00	0.02	34.74	63.84	0.54	1377523_at	LOC686314	similar to dachshund b
0.00	0.01	200.72	368.89	0.54	1372554_at	Tmem131	transmembrane protein 131
0.00	0.00	61.69	113.09	0.55	1376667_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1
0.00	0.02	138.03	251.82	0.55	1392157_at	Plxna2	plexin A2
0.00	0.03	85.08	154.93	0.55	1384570_at	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4
0.00	0.03	118.41	215.26	0.55	1370932_at	Lrp4	low density lipoprotein receptor-related protein 4
0.00	0.02	17.67	31.98	0.55	1382983_at	NA	NA
0.00	0.03	47.78	86.41	0.55	1387672_at	Gnmt	glycine N-methyltransferase
0.00	0.03	61.88	111.81	0.55	1369325_at	Lyst	lysosomal trafficking regulator
0.00	0.01	64.02	114.85	0.56	1386569_at	NA	NA
0.00	0.03	219.25	393.24	0.56	1398409_at	NA	NA
0.00	0.02	17.02	30.47	0.56	1379445_at	NA	NA
0.00	0.03	386.39	688.23	0.56	1377934_at	NA	NA
0.00	0.02	684.87	1207.53	0.57	1390763_at	NA	NA

0.00	0.03	145.31	255.30	0.57	1376863_at	NA	NA
0.00	0.03	235.74	413.17	0.57	1389456_at	NA	NA
0.00	0.02	71.70	125.17	0.57	1398452_at	RGD1559923	similar to chromosome 14 open reading frame 35
0.00	0.01	127.18	221.70	0.57	1389403_at	Bmp7	bone morphogenetic protein 7
0.00	0.02	23.67	41.25	0.57	1378339_at	Fam124a	family with sequence similarity 124A
0.00	0.02	94.31	162.28	0.58	1383149_at	LOC684122	similar to development and differentiation enhancing factor-like 1
0.00	0.02	119.13	204.90	0.58	1390522_at	Fbxl11	F-box and leucine-rich repeat protein 11
0.00	0.03	30.31	51.94	0.58	1368696_at	Fxyd7	FXD domain-containing ion transport regulator 7
0.00	0.03	1031.31	1765.55	0.58	1369968_at	Ptn	pleiotrophin
0.00	0.04	955.99	1632.76	0.59	1370357_at	Slc30a4	solute carrier family 30 (zinc transporter), member 4
0.00	0.02	8667.95	14799.25	0.59	1367577_at	Hspb1	heat shock protein 1
0.00	0.01	375.31	636.65	0.59	1379942_at	Sox2	SRY (sex determining region Y)-box 2
0.00	0.01	410.24	689.06	0.60	1370541_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2
0.00	0.00	839.41	1401.74	0.60	1368702_at	Pawr	PRKC, apoptosis, WT1, regulator
0.00	0.02	127.42	212.63	0.60	1387266_at	Siah1a	seven in absentia 1A
0.00	0.03	1355.75	2259.71	0.60	1369998_at	Arf6	ADP-ribosylation factor 6
0.00	0.01	43.95	73.05	0.60	1380193_at	NA	NA
0.00	0.03	1760.88	2925.65	0.60	1384244_at	Hsd12	hydroxysteroid dehydrogenase like 2
0.00	0.02	38.63	64.08	0.60	1392658_at	Tcea1	transcription elongation factor A (SII) 1
0.00	0.03	169.45	278.92	0.61	1379982_at	NA	NA
0.00	0.03	96.58	158.89	0.61	1382032_at	NA	NA
0.00	0.03	57.12	93.66	0.61	1388456_at	S100a1	S100 calcium binding protein A1
0.00	0.03	98.33	160.89	0.61	1384945_at	Fytd1	forty-two-three domain containing 1
0.00	0.03	1238.93	2022.41	0.61	1375641_at	Arpc5l	actin related protein 2/3 complex, subunit 5-like
0.00	0.01	22.09	36.04	0.61	1381887_x_at	RGD1311595	similar to KIAA2026 protein
0.00	0.03	244.51	394.57	0.62	1387148_at	Gprasp1	G protein-coupled receptor associated sorting protein 1
0.00	0.03	830.63	1340.37	0.62	1376587_at	Fbxo11	F-box protein 11
0.00	0.03	179.85	284.99	0.63	1384172_at	RGD1310474	similar to KIAA0423
0.00	0.02	42.39	66.85	0.63	1379577_at	RGD1559441	similar to MIC2L1
0.00	0.01	650.31	1023.24	0.64	1379226_at	Aim1l	absent in melanoma 1-like
0.00	0.03	15.11	23.62	0.64	1384675_at	Apeg3	antisense paternally expressed gene 3
0.00	0.02	511.39	796.30	0.64	1387784_at	Psm10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10
0.00	0.03	393.27	610.98	0.64	1382309_at	NA	NA
0.00	0.03	30.63	47.52	0.64	1391617_at	NA	NA
0.00	0.01	35.95	55.49	0.65	1381396_s_at	Klf15	Kruppel-like factor 15
0.00	0.02	141.64	218.27	0.65	1369974_at	Vamp2	vesicle-associated membrane protein 2
0.00	0.03	757.49	1164.13	0.65	1373836_at	Fytd1	forty-two-three domain containing 1
0.00	0.02	1195.99	1837.83	0.65	1372091_at	Mid1ip1	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))
0.00	0.03	24.27	37.24	0.65	1397506_at	Fxn	frataxin
0.00	0.02	5848.65	8931.03	0.65	1370235_at	Dbi	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
0.00	0.03	220.69	336.17	0.66	1370974_at	Vps54	vacuolar protein sorting 54 homolog (S. cerevisiae)
0.00	0.02	1565.29	2379.93	0.66	1367619_at	Pgrmc1	progesterone receptor membrane component 1

0.00	0.02	33.01	49.90	0.66	1398196_at	NA	NA
0.00	0.02	90.31	136.36	0.66	1393666_at	NA	NA
0.00	0.02	33.87	51.04	0.66	1389848_at	Arhgap23	Rho GTPase activating protein 23
0.00	0.01	1456.86	2194.05	0.66	1398909_at	LOC301124	hypothetical LOC301124
0.00	0.03	959.65	1444.16	0.66	1391880_at	NA	NA
0.00	0.03	132.79	198.90	0.67	1390990_at	NA	NA
0.00	0.01	16.45	24.63	0.67	1369911_at	Cxcr5	chemokine (C-X-C motif) receptor 5
0.00	0.03	108.82	162.74	0.67	1383737_at	NA	NA
0.00	0.03	28.02	41.73	0.67	1392034_at	NA	NA
0.00	0.02	33.94	50.53	0.67	1380348_at	Wnt9a	wingless-type MMTV integration site family, member 9A
0.00	0.03	505.34	752.27	0.67	1396692_at	RGD1306402	similar to RIKEN cDNA 4933435A13
0.00	0.00	1525.49	2255.88	0.68	1369980_s_at	Mprip	myosin phosphatase Rho interacting protein
0.00	0.03	222.83	326.40	0.68	1386632_at	Tmem55a	transmembrane protein 55A
0.00	0.04	84.13	122.99	0.68	1376779_at	Foxo1	forkhead box O1
0.00	0.03	1588.85	2319.48	0.69	1367824_at	Fnta	farnesyltransferase, CAAX box, alpha
0.00	0.02	657.69	960.11	0.69	1374447_at	Usp9x	ubiquitin specific peptidase 9, X-linked
0.00	0.01	8094.69	11796.71	0.69	1368017_at	Lgals7	lectin, galactoside-binding, soluble, 7
0.00	0.02	11.34	16.52	0.69	1398015_at	NA	NA
0.00	0.02	20.44	29.72	0.69	1375026_at	Calml4	calmodulin-like 4
0.00	0.01	1402.29	2015.96	0.70	1399011_at	Cops6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)
0.00	0.01	427.78	614.52	0.70	1368859_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform
0.00	0.03	248.55	356.51	0.70	1386989_at	S1pr2	sphingosine-1-phosphate receptor 2
0.00	0.02	248.74	356.69	0.70	1382100_at	RGD1309605	similar to RIKEN cDNA 2310047O13
0.00	0.02	276.04	395.52	0.70	1383769_at	NA	NA
0.00	0.03	132.01	189.01	0.70	1389665_at	Habp4	hyaluronan binding protein 4
0.00	0.02	197.82	282.79	0.70	1393170_at	RGD1561431	similar to homeobox-containing transcription factor
0.00	0.02	27.11	38.73	0.70	1387184_at	Axin2	axin2
0.00	0.01	172.50	245.90	0.70	1392985_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)
0.00	0.02	8.71	12.40	0.70	1370513_at	Tpm1	tropomyosin 1, alpha
0.00	0.03	655.72	932.32	0.70	1372741_at	Sccpdh	saccharopine dehydrogenase (putative)
0.00	0.02	137.35	195.14	0.70	1390841_at	NA	NA
0.00	0.03	316.93	449.88	0.70	1372779_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
0.00	0.03	737.11	1039.05	0.71	1377702_at	P2ry5	purinergic receptor P2Y, G-protein coupled, 5
0.00	0.03	133.45	188.07	0.71	1372557_at	Arl6	ADP-ribosylation factor-like 6
0.00	0.03	175.54	247.31	0.71	1397888_at	NA	NA
0.00	0.00	784.45	1103.64	0.71	1380580_at	NA	NA
0.00	0.01	283.47	396.60	0.71	1374696_at	NA	NA
0.00	0.01	626.09	874.48	0.72	1373974_at	Osbp	oxysterol binding protein
0.00	0.03	6.70	9.32	0.72	1396682_at	NA	NA
0.00	0.03	17.21	23.90	0.72	1398266_a_at	Egr2	early growth response 2
0.00	0.02	19.22	26.58	0.72	1389982_at	Lhx1	LIM homeobox 1
0.00	0.02	22.48	31.03	0.72	1397243_at	NA	NA
0.00	0.01	305.34	420.86	0.73	1396170_at	Wbp4	WW domain binding protein 4 (formin binding protein 21)

0.00	0.02	175.82	242.32	0.73	1370330_at	Sipa111	signal-induced proliferation-associated 1 like 1
0.00	0.03	19.54	26.90	0.73	1375499_at	NA	NA
0.00	0.02	2610.29	3571.00	0.73	1371253_at	Etfa	electron-transfer-flavoprotein, alpha polypeptide
0.00	0.02	39.33	53.78	0.73	1375876_at	RGD1308049	similar to RIKEN cDNA 2410004C24
0.00	0.02	102.66	140.27	0.73	1392421_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B
0.00	0.03	414.96	564.00	0.74	1376082_at	Evi1	ecotropic viral integration site 1
0.00	0.03	7.34	9.91	0.74	1397850_at	NA	NA
0.00	0.02	264.76	357.03	0.74	1373643_at	NA	NA
0.00	0.03	524.62	707.23	0.74	1389233_at	Reps1	RALBP1 associated Eps domain containing 1
0.00	0.01	5148.92	6940.09	0.74	1390208_at	Htatip2	HIV-1 tat interactive protein 2, homolog (human)
0.00	0.03	185.23	245.74	0.75	1374553_at	Fam32a	family with sequence similarity 32, member A
0.00	0.01	187.04	246.46	0.76	1374169_at	RGD1310686	similar to chromosome 16 open reading frame 5
0.00	0.03	342.93	450.80	0.76	1372596_at	RGD1311660	similar to RIKEN cDNA 1110007L15
0.00	0.03	72.27	94.78	0.76	1380594_at	Scube1	signal peptide, CUB domain, EGF-like 1
0.00	0.03	15.34	20.08	0.76	1370268_at	Kcna5	potassium voltage-gated channel, shaker-related subfamily, member 5
0.00	0.02	6.69	8.67	0.77	1385127_at	Bmp5	bone morphogenetic protein 5
0.00	0.01	7.32	9.45	0.77	1392290_at	NA	NA
0.00	0.03	1058.52	1363.14	0.78	1372787_at	Utp3	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)
0.00	0.01	1226.05	1575.22	0.78	1375425_at	Ift20	intraflagellar transport 20 homolog (Chlamydomonas)
0.00	0.02	11.02	14.10	0.78	1380657_at	NA	NA
0.00	0.02	7.85	9.97	0.79	1382650_at	NA	NA
0.00	0.03	89.88	114.00	0.79	1397846_at	Cby1	chibby homolog 1 (Drosophila)
0.00	0.02	2931.69	3704.97	0.79	1374513_at	Sep-07	septin 7
0.00	0.03	1377.55	1732.15	0.80	1387915_at	Sels	selenoprotein S
0.00	0.03	745.28	936.25	0.80	1393236_at	Riok3	RIO kinase 3 (yeast)
0.00	0.02	81.53	101.78	0.80	1397411_at	Fgd2	FYVE, RhoGEF and PH domain containing 2
0.00	0.01	4308.73	5314.14	0.81	1398770_at	Rpl36al	ribosomal protein L36a-like
0.00	0.01	1344.61	1649.83	0.81	1388563_at	Gbp1	GC-rich promoter binding protein 1
0.00	0.01	2369.31	2888.52	0.82	1389305_at	Anxa4	annexin A4
0.00	0.03	5.40	6.52	0.83	1381633_at	NA	NA
0.00	0.03	10.48	12.61	0.83	1374966_at	Dcx	doublecortin
0.00	0.03	1205.69	1449.95	0.83	1388761_at	Hdac1	histone deacetylase 1
0.00	0.03	20.67	24.80	0.83	1394777_at	NA	NA
0.00	0.03	778.57	930.28	0.84	1372862_at	Rab22a	RAB22A, member RAS oncogene family
0.00	0.03	3824.57	4530.08	0.84	1372437_at	Skp1	S-phase kinase-associated protein 1
0.00	0.03	8.57	10.13	0.85	1383511_at	NA	NA
0.00	0.03	200.90	237.21	0.85	1395362_at	NA	NA
0.00	0.03	673.99	791.54	0.85	1373505_at	LOC684800	similar to stromal membrane-associated protein 1
0.00	0.03	47.04	54.43	0.86	1373261_at	NA	NA
0.00	0.03	203.52	233.67	0.87	1374201_at	NA	NA

**Dataset 30** Comparison of the expression profile of ZS esophagus at tumor endpoint with the published esophageal profile<sup>‡</sup> at 6 wks of ZS diet

Description of the problem:

Number of classes: 2

Number of genes used for random variance estimation: 31099

Number of genes that passed filtering criteria: 31099

Type of univariate test used: Two-sample T-test (with random variance model)

Univariate test random variance model parameters:

a= 1.90741 , b= 11.98356 , Kolmogorov-Smirnov statistic= 0.0092

Nominal significance level of each univariate test: 0.001

Summary of Results:

Number of genes significant at 0.001 level of the univariate test: 722 (409 up-regulated and 313down-regulated)

Genes that discriminate among classes:

Sorted by Fold-Change

Class 1: ZD esophagus at 5 wks post first NMBA dose

Class 2: ZD esophagus prior to NMBA treatment (Gastroenterology, 2009, 136:953-966)<sup>‡</sup>

\*Fold change represents ZS oesophagus at 5 wks after the first NMBA dose vs ZS esophagus before NMBA treatment.

\*\*Affymetrix probe ID corresponds to the Rat Genome 230 2.0 Array.

Inflammatory probe sets denoted in Table 1 are highlighted in yellow.

p-value	FDR	Geom mean of intensities in class 1	Geom mean of intensities in class 2	Fold-change*	Affymetrix Probe ID**	Gene Symbol	Gene Name
0.00	0.04	5605.53	180.31	31.09	1392402_at	NA	NA
0.00	0.02	7010.23	423.86	16.54	1384721_at	NA	NA
0.00	0.04	654.35	41.75	15.67	1377429_at	Lpo	lactoperoxidase
0.00	0.00	175.38	22.64	7.74	1371016_at	RGD1311300	similar to T cell receptor V delta 6
0.00	0.00	505.60	65.89	7.67	1389748_at	NA	NA
0.00	0.02	498.82	68.78	7.25	1385889_at	RGD1565095	similar to hypothetical protein MGC52110
0.00	0.00	126.47	20.01	6.32	1385519_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.00	158.91	25.54	6.22	1388275_at	Tcrb	T-cell receptor beta chain
0.00	0.02	240.16	46.07	5.21	1380533_at	App	amyloid beta (A4) precursor protein
0.00	0.01	180.03	34.65	5.20	1368482_at	Bcl2a1d	B-cell leukemia/lymphoma 2 related protein A1d
0.00	0.04	180.77	35.36	5.11	1371170_a_at	Il1a	interleukin 1 alpha
0.00	0.04	449.46	88.91	5.06	1370792_at	Mapre1	microtubule-associated protein, RP/EB family, member 1
0.00	0.00	304.03	60.45	5.03	1395294_at	NA	NA
0.00	0.01	399.36	79.80	5.00	1369964_at	Coro1a	coronin, actin binding protein 1A
0.00	0.02	327.97	65.90	4.98	1368518_at	Cd53	Cd53 molecule
0.00	0.00	119.56	24.44	4.89	1391979_at	NA	NA
0.00	0.01	1334.22	276.63	4.82	1370822_at	RT1-Ba	RT1 class II, locus Ba
0.00	0.01	65.94	15.26	4.32	1385925_at	NA	NA
0.00	0.01	1221.38	286.80	4.26	1393474_at	Sult2b1	sulfotransferase family, cytosolic, 2B, member 1
0.00	0.01	274.30	64.64	4.24	1391447_at	NA	NA
0.00	0.01	58.61	13.84	4.23	1395879_at	Ttc39b	tetratricopeptide repeat domain 39B
0.00	0.00	133.45	31.86	4.19	1395076_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.03	748.36	182.20	4.11	1387221_at	Gch1	GTP cyclohydrolase 1
0.00	0.01	134.04	32.73	4.09	1368503_at	Gch1	GTP cyclohydrolase 1
0.00	0.03	244.01	60.86	4.01	1368144_at	Rgs2	regulator of G-protein signaling 2
0.00	0.02	414.93	103.94	3.99	1387629_at	Bspry	B-box and SPRY domain containing

0.00	0.02	260.00	65.46	3.97	1369670_at	Cd200	Cd200 molecule
0.00	0.01	550.71	142.16	3.87	1372585_at	RGD1566254	RGD1566254
0.00	0.04	327.96	86.00	3.81	1369672_at	Alox5ap	arachidonate 5-lipoxygenase activating protein
0.00	0.01	73.22	19.30	3.79	1390890_at	NA	NA
0.00	0.01	27.93	7.50	3.72	1385215_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.03	130.82	35.48	3.69	1370987_at	Spn	sialophorin
0.00	0.04	186.53	50.68	3.68	1367970_at	Pfn2	profilin 2
0.00	0.00	169.72	46.94	3.62	1384787_at	Cd3g	CD3 molecule, gamma polypeptide
0.00	0.03	76.57	21.56	3.55	1369025_at	Cd5	Cd5 molecule
0.00	0.03	99.86	28.29	3.53	1385582_at	Osbp12	oxysterol binding protein-like 2
0.00	0.01	115.56	32.94	3.51	1380728_at	NA	NA
0.00	0.02	95.21	27.28	3.49	1382622_at	Cst7	cystatin F (leukocystatin)
0.00	0.02	322.06	92.43	3.48	1379677_at	Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13
0.00	0.01	698.90	202.07	3.46	1398511_at	Susd2	sushi domain containing 2
0.00	0.01	95.91	27.75	3.46	1397167_at	NA	NA
0.00	0.02	3116.25	902.43	3.45	1370883_at	H2-Ea	histocompatibility 2, class II antigen E alpha
0.00	0.01	184.03	53.82	3.42	1390798_at	Ptpcr	protein tyrosine phosphatase, receptor type, C
0.00	0.01	33.21	9.76	3.40	1369105_a_at	Pkib	protein kinase inhibitor beta, (cAMP-dependent, catalytic) inhibitor beta
0.00	0.04	339.68	99.96	3.40	1387769_a_at	Id3	inhibitor of DNA binding 3
0.00	0.02	97.34	28.72	3.39	1393901_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
0.00	0.01	131.70	39.50	3.33	1375716_at	Ifngr2	interferon gamma receptor 2
0.00	0.01	156.45	47.68	3.28	1370585_a_at	Prkcb	protein kinase C, beta
0.00	0.01	110.39	34.05	3.24	1380077_at	NA	NA
0.00	0.03	176.70	54.61	3.24	1380373_at	Gmps	guanine monphosphate synthetase
0.00	0.03	87.99	27.40	3.21	1381875_at	Nmi	N-myc (and STAT) interactor
0.00	0.01	57.88	18.04	3.21	1368338_at	Cd52	CD52 antigen
0.00	0.01	106.89	33.52	3.19	1379766_at	Sla	src-like adaptor
0.00	0.03	2747.34	870.57	3.16	1388552_at	Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal
0.00	0.02	83.56	26.68	3.13	1387328_at	Cyp2c	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
0.00	0.04	3655.05	1178.25	3.10	1367784_a_at	Clu	clusterin
0.00	0.02	67.84	21.91	3.10	1384837_at	Cd69	Cd69 molecule
0.00	0.02	1508.16	487.34	3.09	1390738_at	Bst2	bone marrow stromal cell antigen 2
0.00	0.01	24.57	8.08	3.04	1386695_at	NA	NA
0.00	0.04	138.91	46.19	3.01	1375627_at	Akirin2	akirin 2
0.00	0.01	131.73	44.02	2.99	1389092_at	Il2rg	interleukin 2 receptor, gamma
0.00	0.01	55.33	18.60	2.97	1370603_a_at	Ptpcr	protein tyrosine phosphatase, receptor type, C
0.00	0.04	279.60	94.01	2.97	1389166_at	Cib2	calcium and integrin binding family member 2
0.00	0.01	151.92	51.16	2.97	1368826_at	Comt	catechol-O-methyltransferase
0.00	0.03	118.58	40.05	2.96	1388246_at	Clu	clusterin
0.00	0.01	84.49	28.59	2.96	1389413_at	Evi2a	ecotropic viral integration site 2A
0.00	0.03	139.35	47.38	2.94	1371090_at	Scamp2	secretory carrier membrane protein 2
0.00	0.03	139.96	48.18	2.90	1390942_at	Peli2	pellino 2
0.00	0.04	108.81	37.47	2.90	1369597_at	Vapb	VAMP (vesicle-associated membrane protein)-associated protein B and C

0.00	0.02	64.50	22.25	2.90	1374236_at	Lgi2	leucine-rich repeat LGI family, member 2
0.00	0.01	86.82	30.43	2.85	1390797_at	Lcp2	lymphocyte cytosolic protein 2
0.00	0.01	39.76	14.02	2.84	1398644_at	Plxnc1	plexin C1
0.00	0.01	215.91	76.35	2.83	1381817_at	NA	NA
0.00	0.01	110.43	39.40	2.80	1379791_at	Cd3e	CD3 molecule, epsilon polypeptide
0.00	0.04	121.76	43.77	2.78	1398256_at	Il1b	interleukin 1 beta
0.00	0.01	65.14	23.42	2.78	1376943_at	NA	NA
0.00	0.01	117.03	42.08	2.78	1369190_at	Cd2	Cd2 molecule
0.00	0.01	149.55	54.39	2.75	1369029_at	Plscr1	phospholipid scramblase 1
0.00	0.02	63.40	23.08	2.75	1369568_at	Stx6	syntaxin 6
0.00	0.01	15.99	5.88	2.72	1393791_at	Trat1	T cell receptor associated transmembrane adaptor 1
0.00	0.03	82.41	30.59	2.69	1389961_at	Sdccag3	serologically defined colon cancer antigen 3
0.00	0.04	269.49	100.24	2.69	1392621_at	Tcf25	transcription factor 25 (basic helix-loop-helix)
0.00	0.01	84.95	31.63	2.69	1368783_at	Icos	inducible T-cell co-stimulator
0.00	0.03	341.90	127.85	2.67	1377905_at	Lsm14a	LSM14A, SCD6 homolog A (S. cerevisiae)
0.00	0.02	62.62	23.51	2.66	1386410_at	NA	NA
0.00	0.04	101.20	38.14	2.65	1374542_at	NA	NA
0.00	0.03	39.78	15.05	2.64	1393649_at	NA	NA
0.00	0.03	31.32	11.86	2.64	1385302_at	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1
0.00	0.02	1046.98	397.70	2.63	1399080_at	LOC688495	hypothetical protein LOC688495
0.00	0.03	78.30	29.86	2.62	1392259_at	Hectd1	HECT domain containing 1
0.00	0.03	359.31	138.02	2.60	1382274_at	Rarres1	retinoic acid receptor responder (tazarotene induced) 1
0.00	0.03	401.18	154.92	2.59	1367652_at	Igfbp3	insulin-like growth factor binding protein 3
0.00	0.04	164.26	63.44	2.59	1394709_at	NA	NA
0.00	0.01	68.32	26.53	2.58	1392794_at	NA	NA
0.00	0.02	41.43	16.15	2.57	1394891_at	RGD1564541	similar to hypothetical protein FLJ22965
0.00	0.02	340.08	132.57	2.57	1372404_at	Rac2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
0.00	0.01	194.34	76.05	2.56	1383320_at	Lck	lymphocyte-specific protein tyrosine kinase
0.00	0.03	43.94	17.23	2.55	1378418_at	Tifab	TRAF-interacting protein with forkhead-associated domain, family member B
0.00	0.02	162.38	63.85	2.54	1368983_at	Hbegf	heparin-binding EGF-like growth factor
0.00	0.03	174.67	68.91	2.53	1393329_at	NA	NA
0.00	0.01	683.69	272.09	2.51	1389210_at	Lcp1	lymphocyte cytosolic protein 1
0.00	0.02	135.08	53.85	2.51	1393347_at	Itgal	integrin alpha L
0.00	0.01	441.59	177.30	2.49	1370882_at	Hla-dmb	major histocompatibility complex, class II, DM beta
0.00	0.01	57.12	23.00	2.48	1395602_at	NA	NA
0.00	0.01	995.04	401.41	2.48	1370383_s_at	RT1-Db1	RT1 class II, locus Db1
0.00	0.03	197.64	80.04	2.47	1378700_at	NA	NA
0.00	0.01	286.04	116.61	2.45	1370056_at	Ly6c	Ly6-C antigen
0.00	0.03	117.31	48.08	2.44	1368776_at	Alox5	arachidonate 5-lipoxygenase
0.00	0.03	314.98	129.23	2.44	1368006_at	Laptm5	lysosomal multispinning membrane protein 5
0.00	0.01	24.71	10.16	2.43	1387459_at	Pkib	protein kinase inhibitor beta, (cAMP-dependent, catalytic) inhibitor beta



0.00	0.02	45.57	18.83	2.42	1390077_at	Tram1	translocation associated membrane protein 1
0.00	0.01	62.94	26.03	2.42	1382566_at	Il7r	interleukin 7 receptor
0.00	0.01	113.55	46.99	2.42	1376624_at	NA	NA
0.00	0.01	294.91	122.54	2.41	1370904_at	Hla-dma	major histocompatibility complex, class II, DM alpha
0.00	0.03	178.46	74.50	2.40	1388773_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2
0.00	0.01	793.30	331.40	2.39	1386860_at	Mfge8	milk fat globule-EGF factor 8 protein
0.00	0.04	129.92	54.39	2.39	1395589_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3
0.00	0.02	47.28	19.82	2.38	1379492_at	NA	NA
0.00	0.01	27.22	11.43	2.38	1378043_at	RGD1563091	similar to OEF2
0.00	0.04	5498.61	2314.57	2.38	1387108_at	Csnk2b	casein kinase 2, beta subunit
0.00	0.03	652.71	276.18	2.36	1374388_at	Efh2	EF-hand domain family, member D2
0.00	0.04	850.74	360.29	2.36	1375259_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2
0.00	0.04	123.51	52.37	2.36	1375130_at	LOC679612	hypothetical protein LOC679612
0.00	0.01	274.42	116.66	2.35	1377671_at	NA	NA
0.00	0.01	83.45	35.53	2.35	1385885_at	NA	NA
0.00	0.03	99.96	42.58	2.35	1377286_at	Gimap4	GTPase, IMAP family member 4
0.00	0.02	36.22	15.43	2.35	1388036_a_at	Milt4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4
0.00	0.01	141.86	60.61	2.34	1382026_at	Arhgap9	Rho GTPase activating protein 9
0.00	0.02	208.80	89.23	2.34	1394292_at	Mrpl37	mitochondrial ribosomal protein L37
0.00	0.04	85.82	36.71	2.34	1369093_at	Reln	reelin
0.00	0.03	17.37	7.44	2.33	1394051_at	P2ry10	purinergic receptor P2Y, G-protein coupled 10
0.00	0.03	49.07	21.05	2.33	1370766_at	Snap29	synaptosomal-associated protein 29
0.00	0.04	74.41	31.95	2.33	1380529_at	NA	NA
0.00	0.01	246.39	106.38	2.32	1375254_at	Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member A1
0.00	0.04	84.61	36.70	2.31	1383577_at	NA	NA
0.00	0.03	48.85	21.19	2.31	1398540_at	Rgs1	regulator of G-protein signaling 1
0.00	0.01	111.64	48.43	2.31	1368723_at	Lat	linker for activation of T cells
0.00	0.03	194.27	84.29	2.30	1370529_a_at	Pld1	phospholipase D1
0.00	0.02	51.70	22.45	2.30	1369331_a_at	Unc13b	unc-13 homolog B (C. elegans)
0.00	0.04	579.07	251.82	2.30	1387074_at	Rgs2	regulator of G-protein signaling 2
0.00	0.02	195.62	85.70	2.28	1394960_at	Sdr42e1	short chain dehydrogenase/reductase family 42E, member 1
0.00	0.04	436.70	191.54	2.28	1368655_at	Srgn	serglycin
0.00	0.04	39.66	17.42	2.28	1387687_at	Igsf6	immunoglobulin superfamily, member 6
0.00	0.01	150.91	66.37	2.27	1370924_at	Tcrb	T-cell receptor beta chain
0.00	0.01	3372.38	1486.58	2.27	1367679_at	Cd74	Cd74 molecule, major histocompatibility complex, class II invariant chain
0.00	0.01	31.73	13.99	2.27	1389859_at	Csnk1a1	casein kinase 1, alpha 1
0.00	0.02	96.16	42.64	2.26	1370090_at	Lcp2	lymphocyte cytosolic protein 2
0.00	0.01	63.58	28.23	2.25	1378314_at	NA	NA
0.00	0.02	69.61	30.97	2.25	1368270_at	Apobec1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1
0.00	0.03	49.49	22.05	2.24	1381771_at	NA	NA
0.00	0.03	50.87	22.71	2.24	1378915_x_at	LOC308990	hypothetical protein LOC308990
0.00	0.02	195.35	87.26	2.24	1376989_at	NA	NA

0.00	0.03	164.32	73.58	2.23	1379568_at	Ifit2	interferon-induced protein with tetratricopeptide repeats 2
0.00	0.01	116.48	52.20	2.23	1378633_at	Lpxn	leupaxin
0.00	0.02	140.05	62.89	2.23	1368422_at	Meox2	mesenchyme homeobox 2
0.00	0.04	31.21	14.02	2.23	1395758_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein
0.00	0.04	283.27	127.28	2.23	1374626_at	Lrg1	leucine-rich alpha-2-glycoprotein 1
0.00	0.04	333.73	149.96	2.23	1370219_at	Cyba	cytochrome b-245, alpha polypeptide
0.00	0.02	19.81	8.91	2.22	1393589_at	Klhl4	kelch-like 4 (Drosophila)
0.00	0.03	256.92	116.21	2.21	1379598_at	NA	NA
0.00	0.04	4003.92	1812.93	2.21	1370952_at	Gstm2	glutathione S-transferase mu 2
0.00	0.03	20.45	9.27	2.21	1375764_at	Chmp2b	chromatin modifying protein 2B
0.00	0.03	23.65	10.81	2.19	1379554_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B@#%&, epsilon isoform
0.00	0.01	145.83	66.77	2.18	1397717_at	Isoc2b	isochorismatase domain containing 2b
0.00	0.02	34.64	15.92	2.18	1380432_at	Cmah	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid hydroxylase) pseudogene
0.00	0.01	93.18	42.87	2.17	1387472_at	Cd3d	CD3 molecule delta polypeptide
0.00	0.01	116.91	53.98	2.17	1372852_at	Ptpncap	protein tyrosine phosphatase, receptor type, C-associated protein
0.00	0.03	529.12	245.31	2.16	1369559_a_at	Cd47	Cd47 molecule
0.00	0.02	207.24	96.12	2.16	1370186_at	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)
0.00	0.02	202.87	94.12	2.16	1378376_at	Chic2	cysteine-rich hydrophobic domain 2
0.00	0.01	1015.25	472.15	2.15	1383658_at	Laptm5	lysosomal multispansing membrane protein 5
0.00	0.01	149.06	69.59	2.14	1386681_at	LOC497934	similar to hypothetical protein FLJ20014
0.00	0.04	160.69	75.03	2.14	1388125_a_at	Klc1	kinesin light chain 1
0.00	0.03	194.22	90.89	2.14	1380617_at	Gimap5	GTPase, IMAP family member 5
0.00	0.02	62.64	29.33	2.14	1384483_at	NA	NA
0.00	0.02	65.38	30.73	2.13	1397604_at	LOC681825	similar to Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1) (VHL-binding protein 1) (VBP-1)
0.00	0.03	19.00	9.00	2.11	1395721_at	Papss2	3@#%&-phosphoadenosine 5@#%&-phosphosulfate synthase 2
0.00	0.03	440.84	209.40	2.11	1394565_at	Copz1	coatamer protein complex, subunit zeta 1
0.00	0.01	1392.25	662.66	2.10	1386996_at	Mrlc2	myosin regulatory light chain MRLC2
0.00	0.01	1027.38	489.34	2.10	1373397_at	Mapre1	microtubule-associated protein, RP/EB family, member 1
0.00	0.01	63.22	30.23	2.09	1369721_at	Strn	striatin, calmodulin binding protein
0.00	0.02	217.96	104.59	2.08	1373963_at	Hdhd3	haloacid dehalogenase-like hydrolase domain containing 3
0.00	0.01	95.94	46.13	2.08	1397866_at	Serpnb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b
0.00	0.03	336.83	162.00	2.08	1379516_at	RGD1559896	similar to RIKEN cDNA 2310022B05
0.00	0.03	198.39	95.48	2.08	1379295_at	Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
0.00	0.03	1019.36	493.36	2.07	1371833_at	Bri3	brain protein I3
0.00	0.02	50.59	24.54	2.06	1395640_at	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)
0.00	0.02	2984.20	1449.73	2.06	1388365_at	Atp6v0d1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1

0.00	0.04	74.61	36.28	2.06	1370571_at	Slco3a1	solute carrier organic anion transporter family, member 3a1
0.00	0.04	337.24	164.15	2.05	1378137_at	Lrrc59	leucine rich repeat containing 59
0.00	0.02	6762.98	3315.00	2.04	1371542_at	Tuba4a	tubulin, alpha 4A
0.00	0.03	94.28	46.31	2.04	1385143_at	RGD1561963	similar to Dedicator of cytokinesis protein 10 (Protein zizimin 3)
0.00	0.03	214.98	105.85	2.03	1390152_at	Tmed7	transmembrane emp24 protein transport domain containing 7
0.00	0.02	2310.46	1139.26	2.03	1372513_at	Rac1	ras-related C3 botulinum toxin substrate 1
0.00	0.01	70.62	34.86	2.03	1394488_at	NA	NA
0.00	0.03	26.76	13.22	2.02	1375717_at	Aes	amino-terminal enhancer of split
0.00	0.04	594.44	293.95	2.02	1367773_at	Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1
0.00	0.02	137.05	67.77	2.02	1369209_at	P34	p34 protein
0.00	0.04	25.47	12.60	2.02	1370769_a_at	Icos	inducible T-cell co-stimulator
0.00	0.02	270.05	134.03	2.01	1373065_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18
0.00	0.03	398.77	198.11	2.01	1376788_at	Dapk1	death associated protein kinase 1
0.00	0.03	247.56	123.05	2.01	1371959_at	Hist2h2aa3	histone cluster 2, H2aa3
0.00	0.01	137.58	68.54	2.01	1395251_at	NA	NA
0.00	0.01	279.39	139.46	2.00	1393883_at	NA	NA
0.00	0.04	1541.72	770.12	2.00	1378059_at	NA	NA
0.00	0.01	54.21	27.11	2.00	1382167_at	Sit1	signaling threshold regulating transmembrane adaptor 1
0.00	0.03	1487.47	746.86	1.99	1387279_at	F11r	F11 receptor
0.00	0.02	29.29	14.71	1.99	1375528_at	Pnpla8	patatin-like phospholipase domain containing 8
0.00	0.04	53.09	26.66	1.99	1379192_at	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)
0.00	0.01	361.28	183.11	1.97	1394842_at	Tmem19	transmembrane protein 19
0.00	0.02	24.89	12.63	1.97	1394833_at	NA	NA
0.00	0.03	96.35	48.98	1.97	1392019_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
0.00	0.02	104.19	53.11	1.96	1390914_at	Fli1	Friend leukemia virus integration 1
0.00	0.03	238.46	121.67	1.96	1370614_s_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)
0.00	0.01	343.31	175.66	1.95	1375216_at	Pvr2	poliovirus receptor-related 2
0.00	0.04	98.80	50.66	1.95	1382813_at	RGD1310810	similar to RIKEN cDNA 4930444A02
0.00	0.04	675.65	346.55	1.95	1370968_at	Nfkb1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
0.00	0.04	207.07	106.42	1.95	1370251_at	Avpi1	arginine vasopressin-induced 1
0.00	0.04	202.55	104.28	1.94	1368645_at	Ptpn1	protein tyrosine phosphatase, non-receptor type 1
0.00	0.03	113.95	58.68	1.94	1389876_at	Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1
0.00	0.01	277.93	143.39	1.94	1393250_at	NA	NA
0.00	0.02	4950.84	2555.19	1.94	1371644_at	Twf1	twinfilin, actin-binding protein, homolog 1 (Drosophila)
0.00	0.01	19.90	10.27	1.94	1368240_a_at	Prkcb	protein kinase C, beta
0.00	0.02	22.45	11.59	1.94	1384104_at	NA	NA
0.00	0.01	280.38	144.84	1.94	1392716_at	NA	NA
0.00	0.02	31.72	16.39	1.94	1383096_at	Aplp2	amyloid beta (A4) precursor-like protein 2
0.00	0.04	45.30	23.46	1.93	1389922_at	Hadh	hydroxyacyl-Coenzyme A dehydrogenase
0.00	0.03	79.44	41.21	1.93	1376977_at	Ptger3	prostaglandin E receptor 3 (subtype EP3)

0.00	0.01	97.67	50.68	1.93	1380537_at	Nckap1l	NCK associated protein 1 like
0.00	0.02	72.43	37.67	1.92	1378914_a_at	LOC308990	hypothetical protein LOC308990
0.00	0.03	108.46	56.45	1.92	1370539_at	Rab8b	RAB8B, member RAS oncogene family
0.00	0.01	109.93	57.27	1.92	1372200_at	Gpsm3	G-protein signaling modulator 3 (AGS3-like, <i>C. elegans</i> )
0.00	0.03	467.06	244.14	1.91	1386954_at	Ak2	adenylate kinase 2
0.00	0.02	946.64	495.69	1.91	1399090_at	Dync1li1	dynein cytoplasmic 1 light intermediate chain 1
0.00	0.02	1562.39	822.89	1.90	1376248_at	Sult2b1	sulfotransferase family, cytosolic, 2B, member 1
0.00	0.01	40.02	21.08	1.90	1397201_at	RGD1310950	similar to KIAA1078 protein
0.00	0.03	406.37	214.26	1.90	1377673_at	NA	NA
0.00	0.03	216.79	114.50	1.89	1368073_at	Irf1	interferon regulatory factor 1
0.00	0.03	1650.26	873.64	1.89	1388120_at	Pdcd6ip	programmed cell death 6 interacting protein
0.00	0.02	30.31	16.09	1.88	1392068_at	NA	NA
0.00	0.02	31.29	16.64	1.88	1398530_at	Gng11	guanine nucleotide binding protein (G protein), gamma 11
0.00	0.01	68.62	36.51	1.88	1392082_a_at	Cd7	Cd7 molecule
0.00	0.03	646.66	344.32	1.88	1391495_at	RGD1311783	similar to RIKEN cDNA 2010012O05
0.00	0.02	99.61	53.09	1.88	1382692_at	Clec7a	C-type lectin domain family 7, member a
0.00	0.02	825.94	440.96	1.87	1368118_at	Bcl10	B-cell CLL/lymphoma 10
0.00	0.01	85.04	45.42	1.87	1387270_at	Hhex	hematopoietically expressed homeobox
0.00	0.04	806.70	431.47	1.87	1371359_at	Mlf2	myeloid leukemia factor 2
0.00	0.02	45.25	24.22	1.87	1397304_at	Igtp	interferon gamma induced GTPase
0.00	0.01	46.28	24.77	1.87	1383638_at	NA	NA
0.00	0.02	19.77	10.58	1.87	1396255_at	Kif16b	kinesin family member 16B
0.00	0.02	96.99	51.94	1.87	1369562_at	Hpcal1	hippocalcin-like 1
0.00	0.04	1608.63	861.91	1.87	1375637_at	RGD1311122	similar to RIKEN cDNA 1110003E01
0.00	0.04	304.72	163.48	1.86	1381119_at	Ttc1	tetratricopeptide repeat domain 1
0.00	0.04	114.00	61.30	1.86	1373863_at	Map4k4	mitogen-activated protein kinase kinase kinase 4
0.00	0.01	88.83	47.80	1.86	1368926_at	Sema4f	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F
0.00	0.03	66.04	35.65	1.85	1372326_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3
0.00	0.02	324.61	175.98	1.84	1372179_at	Hpcal1	hippocalcin-like 1
0.00	0.03	21.84	11.87	1.84	1393926_at	Stap1	signal transducing adaptor family member 1
0.00	0.04	1877.28	1020.36	1.84	1369956_at	Ifngr1	interferon gamma receptor 1
0.00	0.03	21.94	11.93	1.84	1388202_at	RT1-Aw2	RT1 class Ib, locus Aw2
0.00	0.04	52.57	28.62	1.84	1369518_at	Pik3r3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)
0.00	0.02	32.22	17.55	1.84	1397813_at	NA	NA
0.00	0.02	106.19	57.93	1.83	1393049_at	Myo1g	myosin IG
0.00	0.03	54.06	29.56	1.83	1368735_a_at	Trpv2	transient receptor potential cation channel, subfamily V, member 2
0.00	0.03	227.69	124.56	1.83	1391489_at	Irgm	immunity-related GTPase family, M
0.00	0.03	5375.57	2944.54	1.83	1387043_at	Lypd3	Ly6/Plaur domain containing 3
0.00	0.02	1457.92	799.52	1.82	1372247_at	Ddost	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
0.00	0.04	299.46	164.29	1.82	1393015_at	RGD1310587	similar to hypothetical protein FLJ14146
0.00	0.04	59.63	32.80	1.82	1370561_at	A3galt2	alpha 1,3-galactosyltransferase 2

0.00	0.04	706.34	389.65	1.81	1376172_at	Abcg4	ATP-binding cassette, sub-family G (WHITE), member 4
0.00	0.02	474.03	262.65	1.80	1370199_at	Nucb1	nucleobindin 1
0.00	0.02	71.58	39.81	1.80	1373838_at	Fut4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
0.00	0.03	67.19	37.41	1.80	1376710_at	NA	NA
0.00	0.02	180.44	100.47	1.80	1383289_at	Nif31	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)
0.00	0.02	915.48	510.72	1.79	1388386_at	Chmp1a	chromatin modifying protein 1A
0.00	0.02	136.36	76.17	1.79	1374872_at	Rasgrp2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
0.00	0.03	191.24	106.93	1.79	1398425_at	Fam110b	family with sequence similarity 110, member B
0.00	0.02	103.31	57.77	1.79	1391193_at	NA	NA
0.00	0.03	233.74	130.71	1.79	1385919_at	NA	NA
0.00	0.03	103.91	58.32	1.78	1388740_at	Fermt3	fermitin family homolog 3 (Drosophila)
0.00	0.02	675.88	379.84	1.78	1374412_at	Fbxw11	F-box and WD repeat domain containing 11
0.00	0.04	71.03	39.98	1.78	1374355_at	Fam113b	family with sequence similarity 113, member B
0.00	0.02	53.44	30.10	1.78	1397209_at	RGD1565712	similar to Hypothetical protein MGC59495
0.00	0.03	192.32	108.49	1.77	1387205_at	H2-M3	histocompatibility 2, M region locus 3
0.00	0.01	3912.24	2210.06	1.77	1388482_at	Fam129b	family with sequence similarity 129, member B
0.00	0.04	24.91	14.08	1.77	1398528_at	NA	NA
0.00	0.01	141.47	80.00	1.77	1376766_at	Fmn1	formin-like 1
0.00	0.03	44.24	25.03	1.77	1377153_a_at	Klh6	kelch-like 6 (Drosophila)
0.00	0.03	791.99	449.17	1.76	1388551_at	Pcdhgc3	protocadherin gamma subfamily C, 3
0.00	0.02	2790.93	1588.36	1.76	1367907_a_at	Cltb	clathrin, light chain (Lcb)
0.00	0.01	129.86	73.95	1.76	1389698_at	NA	NA
0.00	0.02	790.69	450.35	1.76	1377594_at	Shc1	SHC (Src homology 2 domain containing) transforming protein 1
0.00	0.04	95.03	54.16	1.75	1391671_at	LOC689165	hypothetical protein LOC689165
0.00	0.02	132.03	75.37	1.75	1371285_at	Hoxc4	homeo box C4
0.00	0.02	286.02	163.50	1.75	1385090_at	Rad17	RAD17 homolog (S. pombe)
0.00	0.03	153.84	88.05	1.75	1384943_at	RGD1563888	similar to DNA segment, Chr 16, ERATO Doi 472, expressed
0.00	0.04	126.94	72.66	1.75	1374784_at	Prtfdc1	phosphoribosyl transferase domain containing 1
0.00	0.04	26.37	15.11	1.74	1391214_at	Fam26f	family with sequence similarity 26, member F
0.00	0.04	469.30	269.03	1.74	1383169_at	NA	NA
0.00	0.02	1066.27	612.15	1.74	1367942_at	Acp5	acid phosphatase 5, tartrate resistant
0.00	0.02	344.61	197.91	1.74	1387096_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)
0.00	0.04	37.98	21.84	1.74	1394715_at	Dicer1	dicer 1, ribonuclease type III
0.00	0.04	23.18	13.41	1.73	1380693_at	NA	NA
0.00	0.01	3842.26	2227.77	1.72	1388199_at	Tacstd1	tumor-associated calcium signal transducer 1
0.00	0.04	51.69	29.98	1.72	1386069_at	Sp2	Sp2 transcription factor
0.00	0.03	6929.60	4021.58	1.72	1367578_at	Prdx2	peroxiredoxin 2
0.00	0.03	94.79	55.02	1.72	1379592_at	Slc25a13	solute carrier family 25, member 13 (citrin)
0.00	0.01	737.00	428.59	1.72	1383063_a_at	NA	NA
0.00	0.02	97.62	57.09	1.71	1382587_at	NA	NA

0.00	0.03	63.01	36.90	1.71	1385567_at	Gtf2f1	general transcription factor IIF, polypeptide 1
0.00	0.02	84.03	49.24	1.71	1377882_at	Flt3	fms-related tyrosine kinase 3
0.00	0.04	236.07	138.69	1.70	1390422_at	Pxk	PX domain containing serine/threonine kinase
0.00	0.03	164.59	96.73	1.70	1388561_at	NA	NA
0.00	0.02	2530.86	1488.50	1.70	1371336_at	Hn1	hematological and neurological expressed 1
0.00	0.04	133.87	78.75	1.70	1392722_at	Dapp1	dual adaptor of phosphotyrosine and 3-phosphoinositides
0.00	0.04	243.16	143.06	1.70	1373734_at	Slco3a1	solute carrier organic anion transporter family, member 3a1
0.00	0.03	278.53	164.09	1.70	1387264_at	Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6
0.00	0.02	628.63	370.46	1.70	1371769_at	Scamp2	secretory carrier membrane protein 2
0.00	0.04	36.97	21.79	1.70	1394122_at	Rhoh	ras homolog gene family, member H
0.00	0.02	791.22	467.30	1.69	1370298_at	Znf394	zinc finger protein 394
0.00	0.04	46.83	27.75	1.69	1378929_at	NA	NA
0.00	0.04	16.63	9.85	1.69	1370499_at	Klr1a	killer cell lectin-like receptor subfamily B, member 1A
0.00	0.02	19.13	11.36	1.68	1376872_at	Plxnc1	plexin C1
0.00	0.03	2450.18	1455.62	1.68	1371358_at	Gpsn2	glycoprotein, synaptic 2
0.00	0.01	171.39	102.01	1.68	1368567_at	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3
0.00	0.02	291.54	173.72	1.68	1375645_at	RGD1560286	similar to DNA segment, Chr 4, ERATO Doi 22, expressed
0.00	0.04	234.32	139.76	1.68	1367948_a_at	Kdr	kinase insert domain protein receptor
0.00	0.02	92.56	55.26	1.67	1378149_at	Vps26b	vacuolar protein sorting 26 homolog B (S. pombe)
0.00	0.03	144.55	86.32	1.67	1392292_at	Kctd5	potassium channel tetramerisation domain containing 5
0.00	0.04	136.91	81.79	1.67	1370942_at	Rasa3	RAS p21 protein activator 3
0.00	0.04	44.05	26.32	1.67	1373358_at	Usp8	ubiquitin specific peptidase 8
0.00	0.03	66.41	39.69	1.67	1392767_at	NA	NA
0.00	0.04	1194.25	714.96	1.67	1373501_at	Nek7	NIMA (never in mitosis gene a)-related kinase 7
0.00	0.04	767.66	460.40	1.67	1398918_at	Zfand3	zinc finger, AN1-type domain 3
0.00	0.04	19.37	11.62	1.67	1392862_at	NA	NA
0.00	0.02	613.87	368.84	1.66	1374394_at	Wbp2	WW domain binding protein 2
0.00	0.04	52.54	31.57	1.66	1380245_at	NA	NA
0.00	0.04	1137.83	684.02	1.66	1369996_at	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F
0.00	0.04	247.11	148.81	1.66	1371673_at	Vps72	vacuolar protein sorting 72 homolog (S. cerevisiae)
0.00	0.02	17.50	10.54	1.66	1392671_at	NA	NA
0.00	0.03	410.43	247.45	1.66	1368386_at	Grb2	growth factor receptor bound protein 2
0.00	0.04	493.09	297.45	1.66	1373385_at	NA	NA
0.00	0.02	45.48	27.52	1.65	1388203_x_at	RT1-Aw2	RT1 class Ib, locus Aw2
0.00	0.02	95.15	57.66	1.65	1384337_x_at	Cln3	ceroid-lipofuscinosis, neuronal 3
0.00	0.02	3565.15	2165.86	1.65	1367599_at	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)
0.00	0.02	28.88	17.62	1.64	1379763_at	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)
0.00	0.04	490.44	299.70	1.64	1371389_at	LOC306766	hypothetical LOC306766
0.00	0.02	219.88	134.49	1.63	1394815_at	RGD1559505	similar to RIKEN cDNA 9030409E16
0.00	0.04	46.78	28.64	1.63	1389827_at	Fdx1	ferredoxin 1

0.00	0.02	170.44	104.36	1.63	1369042_at	Pigm	phosphatidylinositol glycan anchor biosynthesis, class M
0.00	0.03	40.55	24.90	1.63	1388940_at	Arhgap25	Rho GTPase activating protein 25
0.00	0.02	223.57	137.61	1.62	1399124_at	RGD1310427	similar to KIAA0090 protein
0.00	0.03	182.73	112.82	1.62	1386346_at	Tmem19	transmembrane protein 19
0.00	0.04	81.87	50.78	1.61	1384191_at	NA	NA
0.00	0.02	124.81	77.63	1.61	1380450_at	Bzrap1	benzodiazapine receptor associated protein 1
0.00	0.03	51.84	32.30	1.61	1393612_a_at	Depdc7	DEP domain containing 7
0.00	0.04	73.95	46.14	1.60	1397411_at	Fgd2	FYVE, RhoGEF and PH domain containing 2
0.00	0.03	103.98	64.89	1.60	1394808_at	Tm9sf4	transmembrane 9 superfamily protein member 4
0.00	0.04	540.55	337.55	1.60	1367767_at	Hmgcl	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase
0.00	0.04	62.30	38.96	1.60	1383493_at	NA	NA
0.00	0.04	60.91	38.16	1.60	1380555_at	Faf2	Fas associated factor family member 2
0.00	0.04	25.21	15.83	1.59	1386311_at	NA	NA
0.00	0.02	1825.73	1146.64	1.59	1371724_at	Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
0.00	0.04	68.93	43.35	1.59	1391091_at	Cyld	cylindromatosis (turban tumor syndrome)
0.00	0.04	140.15	88.20	1.59	1381263_at	NA	NA
0.00	0.04	80.26	50.54	1.59	1377698_at	Cd40	CD40 molecule, TNF receptor superfamily member 5
0.00	0.04	215.78	136.22	1.58	1389729_at	Rilpl2	Rab interacting lysosomal protein-like 2
0.00	0.02	75.06	47.63	1.58	1382917_at	NA	NA
0.00	0.04	79.82	50.67	1.58	1376255_at	Map4k1	mitogen activated protein kinase kinase kinase kinase 1
0.00	0.03	1959.06	1252.16	1.56	1398897_at	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1
0.00	0.04	633.91	405.48	1.56	1372355_at	NA	NA
0.00	0.02	110.66	70.91	1.56	1370772_a_at	Hfe	hemochromatosis
0.00	0.04	115.43	74.27	1.55	1387596_at	F2r1	coagulation factor II (thrombin) receptor-like 1
0.00	0.03	1557.09	1005.11	1.55	1388455_at	Gng10	guanine nucleotide binding protein (G protein), gamma 10
0.00	0.04	95.84	62.14	1.54	1396485_at	Btbd10	BTB (POZ) domain containing 10
0.00	0.02	26.34	17.11	1.54	1368675_at	Chn2	chimerin (chimaerin) 2
0.00	0.04	279.80	182.78	1.53	1399083_at	Abhd11	abhydrolase domain containing 11
0.00	0.03	139.68	91.26	1.53	1390946_at	NA	NA
0.00	0.04	481.16	314.98	1.53	1367621_at	Dapk3	death-associated protein kinase 3
0.00	0.04	15.02	9.90	1.52	1396186_at	NA	NA
0.00	0.02	402.86	265.84	1.52	1398375_at	Mta3	metastasis associated 1 family, member 3
0.00	0.03	2911.16	1921.28	1.52	1367827_at	Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
0.00	0.03	42.26	27.90	1.51	1375543_at	Rnf149	ring finger protein 149
0.00	0.04	58.46	38.64	1.51	1370469_at	Ptpn7	protein tyrosine phosphatase, non-receptor type 7
0.00	0.03	1878.14	1243.56	1.51	1371526_at	Rnf10	ring finger protein 10
0.00	0.04	119.40	79.48	1.50	1371256_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18
0.00	0.03	4775.94	3183.10	1.50	1370888_at	Cox5a	cytochrome c oxidase, subunit Va
0.00	0.03	124.67	83.19	1.50	1368231_at	Stat5a	signal transducer and activator of transcription 5A
0.00	0.04	128.83	85.99	1.50	1390431_at	NA	NA

0.00	0.03	174.23	116.61	1.49	1372034_at	Parp14	poly (ADP-ribose) polymerase family, member 14
0.00	0.04	101.94	68.25	1.49	1383526_at	NA	NA
0.00	0.04	8541.76	5719.32	1.49	1388356_at	S100a16	S100 calcium binding protein A16
0.00	0.04	12.88	8.65	1.49	1392703_at	Tbx4	T-box 4
0.00	0.04	282.69	191.29	1.48	1392203_at	NA	NA
0.00	0.03	38.94	26.36	1.48	1381898_at	NA	NA
0.00	0.04	46.26	31.34	1.48	1393060_at	Adamtsl2	ADAMTS-like 2
0.00	0.04	11.50	7.81	1.47	1396250_at	Coro1c	coronin, actin binding protein 1C
0.00	0.04	1027.22	698.82	1.47	1371502_at	Rbm42	RNA binding motif protein 42
0.00	0.03	26.97	18.38	1.47	1368882_at	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
0.00	0.04	239.35	163.62	1.46	1368295_at	Slco2b1	solute carrier organic anion transporter family, member 2b1
0.00	0.04	44.25	30.48	1.45	1379772_at	Aplnr	apelin receptor
0.00	0.04	10927.59	7527.77	1.45	1369976_at	Dynl1	dynein light chain LC8-type 1
0.00	0.03	45.70	31.59	1.45	1392032_at	Grap	GRB2-related adaptor protein translocase of outer mitochondrial membrane 6 homolog (yeast)
0.00	0.03	1819.26	1263.07	1.44	1371399_at	Tomm6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
0.00	0.04	1236.98	864.42	1.43	1376069_at	Psm11	clathrin, light chain (Lca)
0.00	0.04	4191.72	2944.09	1.42	1386875_a_at	Cita	golgi SNAP receptor complex member 2
0.00	0.04	264.80	186.90	1.42	1375438_at	Gosr2	dpy-19-like 1 (C. elegans)
0.00	0.03	98.74	69.79	1.41	1375174_at	Dpy191	G protein-coupled receptor 182
0.00	0.04	11.76	8.42	1.40	1392664_at	Gpr182	vacuolar protein sorting 52 homolog (S. cerevisiae)
0.00	0.03	15.40	99.25	0.16	1394803_at	Vps52	zinc finger protein 451
0.00	0.01	44.00	145.89	0.30	1394654_at	Zfp451	NA
0.00	0.03	12.31	38.38	0.32	1381553_at	NA	NA
0.00	0.01	15.80	46.90	0.34	1373759_at	NA	NA
0.00	0.01	197.46	581.40	0.34	1380850_at	NA	NA
0.00	0.03	209.81	605.56	0.35	1383697_at	NA	NA
0.00	0.01	165.86	478.66	0.35	1374529_at	NA	NA
0.00	0.02	31.37	88.35	0.36	1397443_at	NA	NA
0.00	0.03	182.90	480.51	0.38	1389503_at	LOC367994	similar to uropod 3B isoform b
0.00	0.03	41.51	108.67	0.38	1379232_at	NA	NA
0.00	0.02	299.83	761.40	0.39	1384916_at	NA	NA
0.00	0.01	238.34	604.85	0.39	1387122_at	Plagl1	pleiomorphic adenoma gene-like 1
0.00	0.02	56.15	138.02	0.41	1368721_at	Ascl2	achaete-scute complex homolog 2 (Drosophila)
0.00	0.04	102.35	249.87	0.41	1385436_at	Tmc4	transmembrane channel-like 4
0.00	0.04	100.37	241.26	0.42	1379656_a_at	NA	NA
0.00	0.03	29.96	71.41	0.42	1369773_at	Bmp3	bone morphogenetic protein 3
0.00	0.03	168.74	399.45	0.42	1377967_at	Cdt1	chromatin licensing and DNA replication factor 1
0.00	0.02	114.48	270.64	0.42	1380472_at	LOC683587	similar to carboxylesterase 5
0.00	0.01	269.66	634.46	0.43	1391051_at	NA	NA
0.00	0.04	103.00	241.80	0.43	1378640_at	Uhrf1	ubiquitin-like with PHD and ring finger domains 1
0.00	0.03	82.49	192.08	0.43	1391170_at	Setd5	SET domain containing 5
0.00	0.01	277.79	644.80	0.43	1376411_at	Arl13b	ADP-ribosylation factor-like 13B
0.00	0.03	46.61	106.65	0.44	1392231_at	Stk4	serine/threonine kinase 4



0.00	0.03	227.69	515.20	0.44	1374775_at	Mki67	antigen identified by monoclonal antibody Ki-67
0.00	0.02	32.68	73.59	0.44	1392954_at	NA	NA
0.00	0.02	155.58	348.11	0.45	1398566_at	NA	NA
0.00	0.01	92.77	207.44	0.45	1382720_at	NA	NA
0.00	0.02	387.07	860.90	0.45	1373118_at	rCG_58914	similar to Protein KIAA1543
0.00	0.01	437.74	966.49	0.45	1398382_at	Nat13	N-acetyltransferase 13
0.00	0.03	245.90	541.40	0.45	1379510_at	NA	NA
0.00	0.01	121.57	267.63	0.45	1383978_at	NA	NA
0.00	0.03	22.88	50.27	0.46	1384542_at	NA	NA
0.00	0.04	52.34	113.58	0.46	1385533_at	NA	NA
0.00	0.02	59.59	128.79	0.46	1378170_at	Aff4	AF4/FMR2 family, member 4
0.00	0.03	124.86	269.11	0.46	1381764_s_at	Rnf126	ring finger protein 126
0.00	0.01	185.31	399.08	0.46	1392111_at	Exosc3	exosome component 3
0.00	0.03	2054.20	4421.12	0.46	1370912_at	Hspa1b	heat shock 70kD protein 1B (mapped)
0.00	0.04	67.62	145.21	0.47	1385132_at	NA	NA
0.00	0.02	382.28	815.26	0.47	1376786_a_at	NA	NA
0.00	0.02	126.82	269.86	0.47	1398521_at	NA	NA
0.00	0.01	216.41	457.60	0.47	1389444_at	Zdhhc20	zinc finger, DHHC-type containing 20
0.00	0.01	159.73	337.52	0.47	1370367_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
0.00	0.02	497.41	1039.67	0.48	1382255_at	NA	NA
0.00	0.03	415.84	868.46	0.48	1383102_at	NA	NA
0.00	0.03	214.67	445.69	0.48	1391063_at	Kif23	kinesin family member 23
0.00	0.01	2870.48	5944.73	0.48	1387022_at	Aldh1a1	aldehyde dehydrogenase 1 family, member A1
0.00	0.03	213.02	440.78	0.48	1374530_at	Fzd7	frizzled homolog 7 (Drosophila)
0.00	0.04	415.71	859.78	0.48	1381925_x_at	Arid1b	AT rich interactive domain 1B (Swi1 like)
0.00	0.01	128.61	263.86	0.49	1383164_at	NA	NA
0.00	0.03	570.49	1163.94	0.49	1373566_at	NA	NA
0.00	0.03	219.84	447.00	0.49	1383675_at	NA	NA
0.00	0.03	157.76	320.13	0.49	1385689_at	NA	NA
0.00	0.01	278.18	564.35	0.49	1373229_at	Lsm12	LSM12 homolog (S. cerevisiae)
0.00	0.01	35.90	72.79	0.49	1369050_at	Pik3c2g	phosphoinositide-3-kinase, class 2, gamma polypeptide
0.00	0.03	32.95	66.31	0.50	1383112_at	Trps1	trichorhinophalangeal syndrome I homolog (human)
0.00	0.02	139.35	280.34	0.50	1382242_at	Zfp451	zinc finger protein 451
0.00	0.02	146.08	293.41	0.50	1389784_at	Pogz	pogo transposable element with ZNF domain
0.00	0.01	109.29	218.79	0.50	1374403_at	Efnb1	ephrin B1
0.00	0.03	320.99	641.84	0.50	1392454_at	Znhit6	zinc finger, HIT type 6
0.00	0.03	32.93	65.68	0.50	1385965_at	Ankhd1-Eif4ebp3	Ankhd1-Eif4ebp3 fusion transcript
0.00	0.01	73.22	144.53	0.51	1388924_at	Angptl4	angiopoietin-like 4
0.00	0.02	249.86	492.87	0.51	1380182_at	RGD1563437	similar to KIAA1217
0.00	0.03	78.80	155.16	0.51	1376842_at	NA	NA
0.00	0.01	345.94	680.54	0.51	1393226_at	NA	NA
0.00	0.04	169.53	329.27	0.51	1374579_at	RGD1560873	similar to RIKEN cDNA E230015L20 gene
0.00	0.02	39.65	76.92	0.52	1384210_at	Micalcl	MICAL C-terminal like
0.00	0.03	71.86	139.16	0.52	1393021_at	NA	NA

0.00	0.01	686.70	1326.23	0.52	1381145_at	NA	NA
0.00	0.03	1396.82	2695.33	0.52	1369968_at	Ptn	pleiotrophin
0.00	0.03	104.01	200.52	0.52	1391486_at	NA	NA
0.00	0.01	51.63	99.50	0.52	1388198_at	Nupl1	nucleoporin like 1
0.00	0.01	175.99	338.53	0.52	1374425_at	Tle1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
0.00	0.02	199.25	382.49	0.52	1379982_at	NA	NA
0.00	0.02	100.27	192.15	0.52	1380431_at	RGD1308772	similar to KIAA0564 protein
0.00	0.04	17.78	34.07	0.52	1375088_at	NA	NA
0.00	0.01	250.84	479.87	0.52	1389072_at	Mtmr4	myotubularin related protein 4
0.00	0.02	793.42	1515.38	0.52	1387917_at	Tor1aip1	torsin A interacting protein 1
0.00	0.02	40.52	77.18	0.52	1390949_at	NA	NA
0.00	0.02	58.23	110.77	0.53	1391059_at	Npw	neuropeptide W
0.00	0.04	162.86	309.21	0.53	1382967_at	Gpr64	G protein-coupled receptor 64
0.00	0.02	27.46	52.12	0.53	1384179_at	NA	NA
0.00	0.02	34.04	64.46	0.53	1391157_at	NA	NA
0.00	0.03	81.41	154.09	0.53	1376917_at	Znf292	zinc finger protein 292
0.00	0.02	107.84	203.12	0.53	1390823_at	Skp2	S-phase kinase-associated protein 2 (p45)
0.00	0.04	518.52	976.50	0.53	1370007_at	Pdia4	protein disulfide isomerase family A, member 4
0.00	0.04	231.15	435.26	0.53	1399140_at	NA	NA
0.00	0.01	287.48	541.29	0.53	1393216_at	Slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1
0.00	0.03	531.58	999.29	0.53	1383573_at	Tshz1	teashirt zinc finger homeobox 1
0.00	0.03	95.59	179.28	0.53	1373249_at	Ubl4	ubiquitin-like 4
0.00	0.02	54.26	101.67	0.53	1373801_at	NA	NA
0.00	0.04	33.75	63.19	0.53	1376747_at	NA	NA
0.00	0.02	488.40	913.34	0.53	1369072_at	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
0.00	0.03	83.37	155.91	0.53	1395503_at	Ears2	glutamyl-tRNA synthetase 2 mitochondrial (putative)
0.00	0.04	99.93	186.78	0.53	1383607_at	NA	NA
0.00	0.01	59.03	110.30	0.54	1378327_at	Dmrt2	doublesex and mab-3 related transcription factor 2
0.00	0.04	853.41	1590.07	0.54	1388453_at	Myadm	myeloid-associated differentiation marker
0.00	0.04	97.74	181.93	0.54	1381687_at	RGD1309077	similar to putative RNA methyltransferase
0.00	0.03	124.60	230.81	0.54	1391445_at	NA	NA
0.00	0.03	140.27	259.81	0.54	1389797_at	NA	NA
0.00	0.03	46.31	85.70	0.54	1394065_at	NA	NA
0.00	0.04	35.61	65.86	0.54	1373802_at	Chm	choroideremia (Rab escort protein 1)
0.00	0.04	88.82	164.04	0.54	1374868_at	NA	NA
0.00	0.03	62.05	114.52	0.54	1390711_at	NA	NA
0.00	0.04	37.66	69.41	0.54	1376847_at	LOC690745	MOCO sulphurase C-terminal domain containing-like
0.00	0.02	272.02	498.41	0.55	1373629_at	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
0.00	0.02	208.21	379.05	0.55	1370979_at	Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
0.00	0.03	1306.40	2377.59	0.55	1370976_at	G3bp1	GTPase activating protein (SH3 domain) binding protein 1
0.00	0.02	328.08	595.41	0.55	1374956_at	Pcm1	pericentriolar material 1
0.00	0.03	135.71	246.18	0.55	1389660_at	Amigo3	adhesion molecule with Ig like domain 3

0.00	0.01	228.41	414.11	0.55	1370974_at	Vps54	vacuolar protein sorting 54 homolog ( <i>S. cerevisiae</i> )
0.00	0.03	415.20	752.46	0.55	1376634_a_at	LOC690728	similar to Protein C12orf11 (Sarcoma antigen NY-SAR-95)
0.00	0.02	577.93	1046.85	0.55	1379336_at	NA	NA
0.00	0.03	301.13	544.70	0.55	1368709_at	Fut1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase)
0.00	0.04	1033.90	1863.60	0.55	1367923_at	Acsbg1	acyl-CoA synthetase bubblegum family member 1
0.00	0.03	92.93	167.43	0.56	1385261_s_at	NA	NA
0.00	0.04	99.68	179.14	0.56	1374359_at	Ccne2	cyclin E2
0.00	0.02	26.69	47.92	0.56	1388539_at	Pkp2	plakophilin 2
0.00	0.02	221.97	398.39	0.56	1384439_at	NA	NA
0.00	0.04	47.99	86.03	0.56	1397915_at	NA	NA
0.00	0.03	204.57	366.58	0.56	1397301_at	NA	NA
0.00	0.01	94.47	168.63	0.56	1373569_at	NA	NA
0.00	0.02	469.49	837.53	0.56	1374036_at	Mcm2	minichromosome maintenance complex component 2
0.00	0.02	1652.75	2948.12	0.56	1373499_at	Gas5	growth arrest specific 5
0.00	0.03	410.39	732.02	0.56	1373557_at	Mcm4	minichromosome maintenance complex component 4
0.00	0.02	1415.29	2522.15	0.56	1377016_at	Creld2	cysteine-rich with EGF-like domains 2
0.00	0.03	519.39	924.76	0.56	1390489_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein
0.00	0.04	96.19	171.24	0.56	1391995_at	Trim37	tripartite motif-containing 37
0.00	0.04	349.22	620.87	0.56	1382521_at	Gls	glutaminase
0.00	0.03	177.90	315.14	0.56	1393256_at	Sephs1	selenophosphate synthetase 1
0.00	0.02	31.64	55.81	0.57	1370997_at	Homer1	homer homolog 1 ( <i>Drosophila</i> )
0.00	0.03	113.76	200.54	0.57	1393459_at	Fmr1	fragile X mental retardation 1
0.00	0.02	31.71	55.88	0.57	1377444_at	NA	NA
0.00	0.02	349.03	613.92	0.57	1378637_at	Nfx1	nuclear transcription factor, X-box binding 1
0.00	0.02	90.48	158.99	0.57	1384144_at	Nxn	nucleoredoxin
0.00	0.03	181.20	318.29	0.57	1389127_at	NA	NA
0.00	0.04	221.01	387.91	0.57	1390468_at	NA	NA
0.00	0.02	120.61	211.54	0.57	1380118_at	RGD1562252	similar to hypothetical gene supported by AK085276
0.00	0.01	97.44	170.88	0.57	1393465_at	NA	NA
0.00	0.03	428.44	750.84	0.57	1372626_at	Tpd5211	tumor protein D52-like 1
0.00	0.03	441.45	772.48	0.57	1367505_at	Znf644	zinc finger protein 644
0.00	0.02	144.13	250.61	0.58	1370663_at	Wee1	wee 1 homolog ( <i>S. pombe</i> )
0.00	0.02	21.56	37.38	0.58	1374977_at	NA	NA
0.00	0.02	192.14	333.08	0.58	1377004_at	NA	NA
0.00	0.03	73.35	126.88	0.58	1376779_at	Foxo1	forkhead box O1
0.00	0.02	148.68	257.16	0.58	1385043_at	Inadl	InaD-like ( <i>Drosophila</i> )
0.00	0.01	103.03	177.98	0.58	1383642_at	NA	NA
0.00	0.03	79.35	137.07	0.58	1383522_at	Utx	ubiquitously transcribed tetratricopeptide repeat, X chromosome
0.00	0.01	220.10	379.72	0.58	1391286_at	NA	NA
0.00	0.02	494.97	853.85	0.58	1372236_at	Nod1	nucleotide-binding oligomerization domain containing 1
0.00	0.02	136.13	234.62	0.58	1376947_at	Rbbp6	retinoblastoma binding protein 6
0.00	0.02	92.17	158.56	0.58	1391161_at	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)
0.00	0.02	74.27	127.75	0.58	1377417_at	LOC363328	similar to TICAM-1

0.00	0.04	68.35	117.54	0.58	1387162_at	Tpsab1	trypsin alpha/beta 1
0.00	0.04	420.97	723.21	0.58	1373250_at	Anln	anillin, actin binding protein
0.00	0.02	61.34	105.37	0.58	1395285_at	NA	NA
0.00	0.03	159.88	274.57	0.58	1378334_a_at	NA	NA
0.00	0.04	61.88	106.08	0.58	1377418_at	NA	NA
0.00	0.02	85.59	146.52	0.58	1378081_at	NA	NA
0.00	0.03	140.79	241.01	0.58	1393365_at	Chd1	chromodomain helicase DNA binding protein 1
0.00	0.04	199.47	341.30	0.58	1383660_at	NA	NA
0.00	0.02	45.31	77.12	0.59	1385151_at	NA	NA
0.00	0.04	89.05	151.21	0.59	1376026_at	Donson	downstream neighbor of SON
0.00	0.02	2474.10	4196.74	0.59	1385759_at	Serpib10	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10
0.00	0.01	17.04	28.89	0.59	1370643_a_at	Kalrn	kalirin, RhoGEF kinase
0.00	0.01	463.31	784.62	0.59	1371685_at	Kbtbd2	kelch repeat and BTB (POZ) domain containing 2
0.00	0.04	80.18	135.79	0.59	1383931_at	NA	NA
0.00	0.03	308.58	522.18	0.59	1392452_at	Phf14	PHD finger protein 14
0.00	0.02	252.18	426.18	0.59	1377670_at	Pcf11	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)
0.00	0.03	273.82	462.61	0.59	1384172_at	RGD1310474	similar to KIAA0423
0.00	0.03	283.41	478.67	0.59	1371582_at	Ilf2	interleukin enhancer binding factor 2
0.00	0.04	188.84	318.69	0.59	1393972_at	Mtf2	metal response element binding transcription factor 2
0.00	0.04	19.42	32.76	0.59	1375046_at	Nacad	NAC alpha domain containing
0.00	0.03	168.47	284.12	0.59	1392157_at	Plxna2	plexin A2
0.00	0.01	451.97	761.13	0.59	1374702_at	NA	NA
0.00	0.04	191.34	321.79	0.59	1383083_at	Banp	Btg3 associated nuclear protein
0.00	0.04	69.56	116.91	0.60	1392552_at	Gatad2b	GATA zinc finger domain containing 2B
0.00	0.02	109.66	183.47	0.60	1379217_at	Acvr1	activin A receptor, type I
0.00	0.02	454.89	759.74	0.60	1381981_at	NA	NA
0.00	0.02	319.20	532.72	0.60	1384246_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
0.00	0.03	420.23	701.28	0.60	1388656_at	NA	NA
0.00	0.02	20.79	34.53	0.60	1389160_at	Eraf	erythroid associated factor
0.00	0.02	2278.55	3777.84	0.60	1389301_at	Mbnl2	muscleblind-like 2
0.00	0.02	307.97	510.55	0.60	1383929_at	NA	NA
0.00	0.04	122.58	202.62	0.60	1397918_at	NA	NA
0.00	0.02	262.76	433.54	0.61	1393047_at	Rnf217	ring finger protein 217
0.00	0.04	187.03	308.10	0.61	1374794_at	Kif15	kinesin family member 15
0.00	0.02	542.20	890.72	0.61	1377577_at	Gmps	guanine monophosphate synthetase
0.00	0.02	150.67	247.38	0.61	1375948_at	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)
0.00	0.02	13.24	21.73	0.61	1391258_at	NA	NA
0.00	0.03	10.51	17.25	0.61	1396980_at	NA	NA
0.00	0.04	362.86	595.15	0.61	1372432_at	Prpf3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)
0.00	0.03	544.48	892.64	0.61	1376687_at	Usp1	ubiquitin specific peptidase 1
0.00	0.04	25.17	41.23	0.61	1374880_at	NA	NA
0.00	0.03	12.31	20.14	0.61	1396800_at	NA	NA
0.00	0.03	30.10	49.24	0.61	1378174_at	NA	NA
0.00	0.02	194.88	318.41	0.61	1377835_at	Dock8	dedicator of cytokinesis 8

0.00	0.02	161.40	263.31	0.61	1391682_at	NA	NA
0.00	0.02	315.08	514.02	0.61	1374696_at	NA	NA
0.00	0.04	718.54	1170.76	0.61	1389153_at	Serbp1	Serpine1 mRNA binding protein 1
0.00	0.03	1794.19	2920.58	0.61	1370189_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
0.00	0.04	787.01	1280.78	0.61	1371586_at	Mrpl48	mitochondrial ribosomal protein L48
0.00	0.04	198.47	322.93	0.61	1379525_at	Crls1	cardiolipin synthase 1
0.00	0.03	22.68	36.89	0.61	1372598_at	RGD1309651	similar to 1190005I06Rik protein
0.00	0.04	23.66	38.48	0.61	1395211_s_at	NA	NA
0.00	0.04	34.32	55.80	0.61	1387558_at	Trpv4	transient receptor potential cation channel, subfamily V, member 4
0.00	0.04	520.06	844.91	0.62	1379942_at	Sox2	SRY (sex determining region Y)-box 2
0.00	0.03	1328.91	2157.42	0.62	1393643_at	Rcn1	reticulocalbin 1, EF-hand calcium binding domain
0.00	0.03	211.65	343.06	0.62	1372396_at	RGD1308026	similar to 2310047B19Rik protein
0.00	0.02	29.57	47.88	0.62	1386266_at	NA	NA
0.00	0.02	1846.26	2989.29	0.62	1392543_at	Rbbp4	retinoblastoma binding protein 4
0.00	0.02	441.64	713.25	0.62	1375845_at	Aig1	androgen-induced 1
0.00	0.04	392.37	632.02	0.62	1372117_at	Mtmt10	myotubularin related protein 10
0.00	0.04	228.37	367.79	0.62	1384314_at	Mtif2	mitochondrial translational initiation factor 2
0.00	0.03	199.20	320.46	0.62	1375863_a_at	NA	NA
0.00	0.03	168.10	270.05	0.62	1392470_at	NIPBL	Nipped-B homolog (Drosophila)
0.00	0.03	208.96	335.51	0.62	1378222_at	NA	NA
0.00	0.04	359.21	576.55	0.62	1383606_at	Tc2n	tandem C2 domains, nuclear
0.00	0.03	587.60	941.40	0.62	1392983_at	Psmc12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
0.00	0.02	564.28	904.02	0.62	1385883_at	Zbtb11	zinc finger and BTB domain containing 11
0.00	0.04	1395.12	2232.08	0.63	1388783_at	Hmgb1	high mobility group box 1
0.00	0.03	74.65	119.36	0.63	1377899_at	RGD1304982	similar to RIKEN cDNA 2810025M15
0.00	0.03	145.66	232.78	0.63	1388462_at	Sbk1	SH3-binding domain kinase 1
0.00	0.04	632.82	1010.97	0.63	1393345_at	NA	NA
0.00	0.01	148.47	236.88	0.63	1378373_at	NA	NA
0.00	0.03	398.94	636.14	0.63	1370899_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
0.00	0.04	517.06	824.00	0.63	1374273_at	NA	NA
0.00	0.03	1222.75	1948.29	0.63	1398622_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)
0.00	0.04	136.15	216.90	0.63	1393815_at	Narg2	NMDA receptor regulated 2
0.00	0.04	77.10	122.61	0.63	1381252_at	NA	NA
0.00	0.02	236.00	374.47	0.63	1374150_at	NA	NA
0.00	0.02	29.68	46.99	0.63	1378596_at	NA	NA
0.00	0.03	39.53	62.36	0.63	1392729_at	NA	NA
0.00	0.04	55.17	86.85	0.64	1379001_at	NA	NA
0.00	0.03	107.50	169.22	0.64	1396472_at	NA	NA
0.00	0.02	724.00	1138.70	0.64	1373479_at	Ppp3ca	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform
0.00	0.03	870.85	1368.82	0.64	1373021_at	NA	NA
0.00	0.02	163.31	256.12	0.64	1398396_at	NA	NA
0.00	0.02	896.77	1405.90	0.64	1374438_at	Otud4	OTU domain containing 4
0.00	0.04	36.73	57.57	0.64	1376526_at	NA	NA
0.00	0.04	67.45	105.71	0.64	1398437_at	NA	NA

0.00	0.03	109.60	171.60	0.64	1392131_at	NA	NA
0.00	0.03	30.76	48.16	0.64	1395896_at	NA	NA
0.00	0.02	256.05	400.83	0.64	1377202_at	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)
0.00	0.03	284.22	444.26	0.64	1372779_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
0.00	0.03	238.49	372.69	0.64	1376864_at	Ccar1	cell division cycle and apoptosis regulator 1
0.00	0.04	181.52	283.20	0.64	1382461_at	Prmt7	protein arginine methyltransferase 7
0.00	0.03	352.47	549.44	0.64	1399156_at	Arid2	AT rich interactive domain 2 (Arid-rfx like)
0.00	0.02	366.86	571.54	0.64	1372785_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)
0.00	0.03	111.74	173.96	0.64	1381902_at	Znf292	zinc finger protein 292
0.00	0.04	151.91	236.43	0.64	1374854_at	Pinx1	PIN2-interacting protein 1
0.00	0.02	315.40	490.65	0.64	1383383_at	NA	NA
0.00	0.03	801.63	1245.43	0.64	1367527_at	NA	NA
0.00	0.02	103.06	159.63	0.65	1390615_at	Kpna1	karyopherin (importin) alpha 1
0.00	0.03	81.54	126.05	0.65	1384937_at	Rbak	RB-associated KRAB zinc finger
0.00	0.04	223.19	343.67	0.65	1378691_at	NA	NA
0.00	0.03	151.81	233.68	0.65	1389716_at	LOC691918	similar to Centrosomal protein of 27 kDa (Cep27 protein)
0.00	0.04	318.33	488.30	0.65	1372120_at	Uba5	ubiquitin-like modifier activating enzyme 5
0.00	0.03	782.11	1198.34	0.65	1398389_at	NA	NA
0.00	0.04	125.04	191.35	0.65	1389757_at	RGD1310159	similar to acetyl-coA dehydrogenase - related (111.6 kD) (5G231)
0.00	0.04	855.20	1308.48	0.65	1389277_at	RGD1306148	similar to KIAA0368
0.00	0.04	2758.72	4215.85	0.65	1367706_at	Vdac1	voltage-dependent anion channel 1
0.00	0.03	500.06	763.92	0.65	1391474_at	Med14	mediator complex subunit 14
0.00	0.03	834.40	1274.57	0.65	1373862_at	Tmed7	transmembrane emp24 protein transport domain containing 7
0.00	0.02	515.20	786.34	0.66	1376010_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
0.00	0.03	3000.81	4576.94	0.66	1370283_at	Hspa5	heat shock protein 5
0.00	0.03	12.53	19.11	0.66	1378270_at	Ppp1r3d	protein phosphatase 1, regulatory subunit 3D
0.00	0.03	451.79	686.22	0.66	1383093_at	NA	NA
0.00	0.04	2230.56	3381.27	0.66	1370170_at	Hnrmpu	heterogeneous nuclear ribonucleoprotein U
0.00	0.03	153.83	233.17	0.66	1372836_at	NA	NA
0.00	0.03	30.17	45.67	0.66	1391681_at	Ccne2	cyclin E2
0.00	0.03	154.03	232.43	0.66	1377380_at	NA	NA
0.00	0.04	231.27	348.99	0.66	1372367_at	Grif1	glucocorticoid receptor DNA binding factor 1
0.00	0.03	111.08	167.52	0.66	1393492_at	NA	NA
0.00	0.04	72.80	109.67	0.66	1384479_at	Galnt3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)
0.00	0.04	60.15	90.58	0.66	1380997_at	Ccnj	cyclin J
0.00	0.03	172.11	258.81	0.66	1392546_at	NA	NA
0.00	0.03	99.00	148.86	0.67	1382875_at	Fam120b	family with sequence similarity 120B
0.00	0.04	86.66	130.20	0.67	1392920_at	Pdia3	protein disulfide isomerase family A, member 3
0.00	0.04	1373.25	2061.45	0.67	1372259_at	Dek	DEK oncogene
0.00	0.04	254.47	380.97	0.67	1388194_at	Dlat	dihydroipoamide S-acetyltransferase

0.00	0.04	196.77	294.47	0.67	1389527_at	LOC378467	promethin
							similar to Putative RNA-binding protein 15 (RNA-binding motif protein 15) (One-twenty two protein)
0.00	0.04	421.01	627.86	0.67	1390576_at	LOC684233	
0.00	0.04	154.23	229.96	0.67	1380692_at	Rbl1	retinoblastoma-like 1 (p107)
0.00	0.03	59.51	88.70	0.67	1374634_at	Pih1d2	PIH1 domain containing 2
0.00	0.03	21.32	31.77	0.67	1398211_at	NA	NA
0.00	0.04	250.60	372.03	0.67	1382126_at	Ncor1	nuclear receptor co-repressor 1
0.00	0.04	86.71	128.61	0.67	1386217_at	RGD1310474	similar to KIAA0423
0.00	0.03	1016.05	1504.16	0.68	1399046_at	Top1	topoisomerase (DNA) I
0.00	0.03	255.30	377.80	0.68	1375941_at	Baiap21	BAI1-associated protein 2-like 1
0.00	0.04	295.04	436.40	0.68	1389361_at	Cluap1	clusterin associated protein 1
0.00	0.03	1381.75	2032.97	0.68	1372878_at	Zfr	zinc finger RNA binding protein
							inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
0.00	0.03	319.45	469.52	0.68	1387115_at	lkbkap	
0.00	0.03	21.47	31.51	0.68	1398192_at	NA	NA
							similar to dJ202D23.2 (novel protein similar to C21ORF5 (KIAA0933))
0.00	0.04	134.07	196.56	0.68	1392495_at	RGD1305534	
0.00	0.04	863.38	1265.33	0.68	1376722_at	Nup205	nucleoporin 205
0.00	0.04	129.72	189.94	0.68	1393230_s_at	RGD1308772	similar to KIAA0564 protein
							Bartter syndrome, infantile, with sensorineural deafness (Barttin)
0.00	0.04	17.61	25.65	0.69	1393209_at	Bsnd	
0.00	0.04	84.27	122.70	0.69	1384901_at	NA	NA
							nuclear protein, ataxia-telangiectasia locus
0.00	0.04	67.31	98.01	0.69	1391866_at	Npat	
0.00	0.04	12.68	18.40	0.69	1370515_x_at	Syt7	synaptotagmin VII
0.00	0.03	82.05	118.58	0.69	1384238_at	Ttyh2	tweety homolog 2 (Drosophila)
0.00	0.04	418.73	601.05	0.70	1388737_at	Pbrm1	polybromo 1
0.00	0.04	86.24	123.52	0.70	1379305_at	Vps13d	vacuolar protein sorting 13D (yeast)
							methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
0.00	0.04	645.62	922.20	0.70	1368181_at	Mthfd1	
0.00	0.04	756.13	1077.17	0.70	1389287_at	NA	NA
0.00	0.04	98.68	140.06	0.70	1377612_at	Narg1	NMDA receptor regulated 1
							potassium voltage-gated channel, shaker-related subfamily, member 5
0.00	0.04	14.91	21.05	0.71	1370268_at	Kcna5	
0.00	0.04	52.56	74.12	0.71	1368309_at	Txnrd2	thioredoxin reductase 2
0.00	0.04	156.60	219.71	0.71	1377807_a_at	lqwd1	IQ motif and WD repeats 1
							potassium inwardly-rectifying channel, subfamily J, member 3
0.00	0.04	14.78	20.73	0.71	1369742_at	Kcnj3	
							similar to Der1-like domain family, member 2
0.00	0.04	194.77	271.44	0.72	1377763_at	LOC687738	
							splicing factor, arginine/serine-rich 2, interacting protein
0.00	0.04	408.83	563.09	0.73	1374154_at	Sfrs2ip	
0.00	0.04	904.56	1238.10	0.73	1374286_at	NA	NA