

List of differentially expressed genes at 3 moths after infeciton (RMA & PLIER)

Probe Set ID	Gene Symbol	Gene Description	FC ([High] vs [Control])	FC ([Low] vs [Control])	FC ([High] vs [Low])	p (Corrected value)	p Value
Bt.23348.1.S1_a_at	ZYX	zyxin	-1.312746	1.1813085	-1.550758	0.024013	0.00219411
Bt.12664.1.A1_at	ZMYM5	zinc finger, MYM-t	1.1537579	-1.3304294	1.5349935	0.05222191	0.02812233
Bt.14314.1.S1_at	ZMI22	zinc finger, MIZ-ty	1.0843874	-1.4305514	1.551272	0.028171103	0.00608922
Bt.923.1.A1_at	ZCCHC3	zinc finger, CCHC d	1.08294	-1.110482	1.2025853	0.040293388	0.01748752
Bt.23631.1.S1_at	ZNF281	zinc finger protein	1.2193459	-1.0250973	1.2499483	0.034804247	0.01283321
Bt.24587.1.A1_at	ZNF219	zinc finger protein	-2.4458508	-1.2069192	-2.026524	0.019877227	7.59E-05
Bt.27093.1.S1_at	ZNF189	zinc finger protein	1.0824374	-1.0853145	1.174785	0.08010229	0.05606584
Bt.2478.1.S1_at	ZC3H12A	zinc finger CCCH-t	1.0634362	-1.5769081	1.676941	0.029030783	0.00772431
Bt.3604.1.A1_at	ZBTB10	zinc finger and BTB	1.1171721	-1.1035496	1.2328548	0.02901493	0.00750713
Bt.10005.1.S1_at	YIPF5	Yip1 domain famil	1.1024584	-1.1609993	1.2799535	0.06620577	0.04239041
Bt.7619.2.S1_at	XKR8	XK, Kell blood grou	1.0431889	1.2075557	-1.1575619	0.049799785	0.02621968
Bt.2525.1.S1_at	XRCC1	X-ray repair compl	-1.2240465	1.1701528	-1.4323213	0.025713624	0.00410691
Bt.24234.1.S1_at	WAC	WW domain conta	1.0876786	-1.0673612	1.1609459	0.060344376	0.03619542
Bt.28699.1.S1_at	WASL	Wiskott-Aldrich sy	1.0838768	-1.2995358	1.4085368	0.025610251	0.0040723
Bt.4017.1.S1_at	WDR54	WD repeat domain	1.0986885	-1.154257	1.2681688	0.0351668	0.01351996
Bt.6782.1.A1_at	WDR43	WD repeat domain	-1.0127398	-1.1537099	1.1391968	0.052423984	0.02830592
Bt.21128.1.S1_at	VTA1	Vps20-associated	1.0596601	-1.2074454	1.2794815	0.09573271	0.007117372
Bt.8897.1.S1_at	LPLUNC1	von Ebner minor s	1.0928513	1.1738304	-1.0740988	0.082729734	0.05846624
Bt.25408.2.S1_at	VCL	vinculin	1.101106	1.4262034	-1.2952462	0.032487586	0.01078299
Bt.17079.1.S1_a_at	VGLL4	vestigial like 4 (Dro	1.3014108	-1.2371124	1.6099916	0.0411942	0.01835783
Bt.22197.1.S1_at	VEGFA	vascular endotheli	1.1094266	-1.2837551	1.424232	0.027768422	0.00558429
Bt.5527.2.S1_a_at	VEGFA	vascular endotheli	1.3087344	-1.2056749	1.577908	0.03079631	0.0093586
Bt.26765.1.S1_at	VPS8	vacuolar protein s	-1.2343963	-1.3975359	1.1321615	0.09994169	0.07507987
Bt.16785.1.A1_at	VPS37B	vacuolar protein s	-1.020123	1.2088845	-1.2322109	0.027768422	0.00567124
Bt.17824.1.S1_at	VPS36	vacuolar protein s	1.042147	-1.3496815	1.4065666	0.019877227	6.64E-05
Bt.12032.1.S1_at	RELB	v-rel reticuloendot	1.1368499	1.3029972	-1.1461471	0.037121274	0.01508462
Bt.12639.1.S1_at	RALA	v-ral simian leuko	1.0853875	-1.2530656	1.3600616	0.03030335	0.0085657
Bt.8894.1.S1_at	MAFK	v-maf musculoapo	-1.0172421	-1.3102947	1.2880855	0.04219014	0.01949066
Bt.11631.1.A1_at	MAFF	v-maf musculoapo	-1.0856817	-1.2982575	1.1957994	0.04547607	0.02201492
Bt.18638.1.S1_at	MAFF	v-maf musculoapo	1.1739204	-1.3842062	1.6249479	0.027768422	0.00551602
Bt.337.1.S1_at	UPK1A	uroplakin 1A	-1.201452	1.1839315	-1.4224367	0.09839859	0.07360038
Bt.26901.2.S1_a_at	UPB1	Ureidopropionase	1.1048585	1.3968009	-1.2642351	0.027768422	0.00574152
Bt.18207.2.S1_at	UQCRC1	UQCRC1 protein	1.2116141	1.3079423	-1.079504	0.03348652	0.01178536
Bt.1252.1.S1_at	LOC100847751	Uncharacterised L	1.0311464	-1.2599626	1.299206	0.061472975	0.03740326
Bt.24504.1.A1_at	GALNT12	UDP-N-acetyl-alf	1.0634353	-1.5790925	1.6792626	0.028583735	0.00636294
Bt.5538.1.S1_at	UGDH	UDP-glucose 6-def	1.0863973	-1.1768352	1.2785106	0.058394387	0.03388112
Bt.4245.3.S1_at	UBE2W	ubiquitin-conjugat	1.221755	-1.0403076	1.2710011	0.04711235	0.02363941
Bt.24878.1.A1_at	UBE2O	ubiquitin-conjugat	-1.3926576	-1.9550242	1.4038082	0.045480996	0.02217535
Bt.3455.1.S1_at	UBE2I	ubiquitin-conjugat	1.0477207	-1.1269993	1.1807804	0.051180247	0.02734436
Bt.7631.1.S1_at	USP5	ubiquitin specific p	-1.0262587	1.2146035	-1.2464975	0.04096433	0.01812274
Bt.5184.2.S1_at	USP12	ubiquitin specific p	-1.1206006	-1.4839226	1.3242209	0.024048876	0.00250347
Bt.11925.2.S1_a_at	UBAP1	Ubiquitin associat	1.2152978	-1.2293504	1.4940269	0.043822575	0.02081025
Bt.13194.1.A1_at	TNFAIP6	tumor necrosis fac	-1.0869803	-1.2828515	1.1801975	0.03473701	0.01276554
Bt.26837.1.S1_at	TNFAIP6	tumor necrosis fac	1.0454651	-1.1316235	1.1830729	0.02901493	0.00722889
Bt.10121.1.A1_at	TUFT1	tuftelin 1	-1.1286043	-1.3746997	1.2180529	0.032539457	0.01093618
Bt.23960.1.S1_at	TSFM	Ts translation elon	1.0649819	-1.3390949	1.4261119	0.022891732	9.18E-04
Bt.9589.1.S1_at	TPM4	tropomyosin 4	-1.1527637	-1.1346372	-1.0159756	0.07020405	0.04633964
Bt.4560.1.S1_at	TKDP1	trophoblast Kunitz	1.1865766	1.7316489	-1.4593654	0.024013	0.00178367
Bt.5608.1.A1_at	TRNT1	tRNA nucleotidyl t	1.1115991	1.3498275	-1.2143115	0.06238867	0.03849138
Bt.5644.1.S1_at	TRIM13	tripartite motif-co	1.1788636	-1.11224	1.3111794	0.024013	0.00136479
Bt.24542.1.S1_at	TMEM88	transmembrane pr	-1.0748706	1.1179811	-1.201685	0.034428954	0.01253068
Bt.8848.1.S1_at	TMEM106C	transmembrane pr	1.1326925	-1.2076939	1.3679458	0.02537716	0.0399218
Bt.2128.1.S1_at	TM4SF1	transmembrane 4	1.0686474	-1.0627562	1.1357116	0.0498451	0.02641966
Bt.9033.2.S1_at	TRAM1	translocation asso	1.0877334	-1.0294175	1.1197317	0.08010229	0.05609991
Bt.1523.1.S1_at	TOMM40	translocase of out	1.1200352	1.1150899	1.0044348	0.054938056	0.0308155
Bt.3019.1.S1_at	LOC781496 /// TNP2	transition protein	-1.0401373	1.1348562	-1.1804063	0.037895907	0.01556009
Bt.5401.1.S1_at	TGM2	transglutaminase 2	-1.6406403	-1.4984895	-1.0948627	0.07863341	0.05465901
Bt.12225.1.S1_at	TFRC	transferrin recepto	1.1308227	-1.4746407	1.6675571	0.024766458	0.00377536
Bt.13218.2.S1_at	TFCP2	transcription facto	1.1016598	-1.1155008	1.2289023	0.051414404	0.0275058
Bt.13833.1.S1_at	TFCP2	transcription facto	-1.0152949	-1.2185657	1.2002087	0.04035124	0.01770892
Bt.19522.2.S1_at	TFB1M	transcription facto	1.1139874	-1.1283884	1.2570105	0.04033661	0.01765243
Bt.4616.1.S1_at	TFB1M	transcription facto	1.1288637	-1.3097166	1.4784915	0.06538909	0.04142243
Bt.24593.1.S1_at	TCEB3	transcription elong	-1.2047759	-1.1295063	-1.0666393	0.07185469	0.04798776
Bt.5754.1.S1_at	TIFA	TRAF-interacting p	1.113101	-1.1539565	1.2844703	0.025753139	0.00418938
Bt.20001.2.S1_at	TANK	TRAF family memb	1.0889289	1.5221874	-1.3978758	0.028265815	0.00615256
Bt.17641.1.A1_at	TP53RK	TP53 regulating kin	1.0489483	-1.2065583	1.2656173	0.060344376	0.03620098
Bt.6805.2.S1_at	TP53RK	TP53 regulating kin	1.0252875	-1.1948982	1.2251143	0.077641584	0.05364079
Bt.15703.1.S1_at	TOPORS	topoisomerase I be	1.197831	-1.1087569	1.3281034	0.022891732	4.72E-04
Bt.21886.1.S1_at	TLR7	toll-like receptor 7	1.1236278	-1.0277219	1.1547769	0.08744006	0.06329396
Bt.24417.1.A1_at	TNIP1	TNFAIP3 interactin	-1.1871926	-1.2156736	1.0239902	0.06048709	0.03651687
Bt.29922.1.S1_at	TNIP1	TNFAIP3 interactin	1.1704396	-1.2935766	1.5140533	0.025753139	0.00422242
Bt.9012.1.S1_at	TNIP1	TNFAIP3 interactin	1.0461316	1.3256385	-1.2671814	0.029312633	0.00791338

Bt.24396.1.S1_at	TRAF3	TNF receptor-asso	1.1682677	1.3830167	-1.1838183	0.07830902	0.05434591
Bt.13498.1.S1_at	TRAF1	TNF receptor-asso	1.1004375	-1.3048925	1.4359527	0.027768422	0.00529268
Bt.25963.1.A1_at	TFPI2	tissue factor pathw	1.1234291	-1.1773914	1.3227159	0.063047404	0.03625109
Bt.632.1.S1_s_at	TIMP1	TIMP metallopt	-1.1633977	1.0012199	-1.1648169	0.037231397	0.01518199
Bt.19522.1.S1_at	TRHR	thyrotropin-releas	1.0895759	-1.0315801	1.1239848	0.058520373	0.03403694
Bt.29964.1.S1_at	TRIP10	thyroid hormone r	1.045511	-1.47485	1.5419719	0.024142498	0.00264171
Bt.3106.1.S1_at	TTC5	tetratricopeptide r	1.0574112	-1.2764385	1.3497204	0.03878532	0.01616919
Bt.4357.1.S1_at	TSPAN7	tetraspanin 7	-1.9022764	-1.9234401	1.0111254	0.04200343	0.01932455
Bt.9586.1.A1_at	TSPAN13	tetraspanin 13	-1.033376	-1.3103021	1.267982	0.025828011	0.00438132
Bt.12818.3.S1_a_at	LOC784849 /// LOC78	Testis-specific Y-er	-1.0643632	1.207662	-1.285391	0.062562965	0.03873156
Bt.25221.1.A1_at	TBC1D4	TBC1 domain fami	1.0795164	-1.5581473	1.6820455	0.024013	0.00161472
Bt.11731.1.S1_at	TAF7	TAF7 RNA polymet	1.1088166	-1.1005591	1.2203182	0.060198102	0.03577852
Bt.9052.2.S1_at	TAF6	TAF6 RNA polymet	-1.0503998	1.0718211	-1.1258407	0.09663427	0.07211717
Bt.21133.1.S1_at	TAC3	tachykinin 3	-1.0325521	-1.3737208	1.330413	0.058141094	0.03361616
Bt.29765.1.S1_at	LOC505349	T-cell receptor bet	-1.07875	-1.1588203	1.0742251	0.09416667	0.06967668
Bt.13003.15.A1_x_at	TCRA	T cell receptor, alp	1.0804638	1.3624756	-1.2610099	0.02901493	0.00753378
Bt.14092.1.S1_at	SDC4	Syndecan 4	1.181377	-1.314611	1.5530512	0.033165496	0.0116255
Bt.4847.1.S1_at	SV2A	synaptic vesicle gly	-1.0587666	1.4075989	-1.4903187	0.019877227	5.08E-05
Bt.29876.1.A1_at	SFTPA1B	surfactant protein	1.1362562	1.6483594	-1.4506935	0.041676935	0.0188825
Bt.754.1.S1_at	SUZ12	suppressor of zest	-1.3675431	-1.409716	1.0308385	0.03878532	0.01622679
Bt.6167.1.S1_at	SOD2	superoxide dismut	1.1114634	1.295255	-1.1653599	0.06655566	0.04284961
Bt.10575.1.S1_at	SAE1	SUMO1 activating	1.0420696	-1.1120833	1.1588681	0.033475503	0.01175783
Bt.13906.1.S1_at	SRXN1	sulfiredoxin 1	-1.7095217	-1.7693628	1.0350046	0.07325883	0.04928792
Bt.23260.1.S1_at	SUCLG2	succinate-CoA liga	1.0546284	-1.1287752	1.1904384	0.055240024	0.0314263
Bt.27694.1.S1_at	SRD5A1	steroid-5-alpha-re	-1.4115076	-1.8981714	1.344783	0.031530906	0.01002295
Bt.12649.1.S1_at	SNN	Stannin	1.1474856	-1.1776825	1.3513738	0.04567432	0.0223528
Bt.29787.1.S1_s_at	ST6GAL1	ST6 beta-galactosa	1.3917089	1.5017776	-1.0790889	0.045217033	0.02179365
Bt.21064.1.S1_at	SART1	squamous cell carc	-1.1228874	1.1369687	-1.2766879	0.02901493	0.00759469
Bt.16143.1.S1_at	SPTY2D1	SPT2, Suppressor o	1.1420832	-1.1950705	1.36487	0.056312043	0.03219537
Bt.6803.1.A1_at	SPRED1	sprouty-related, E	-1.9274929	-1.8081555	-1.0659995	0.08776141	0.06363478
Bt.8039.2.S1_a_at	SPRY4	Sprouty homolog 4	1.1258816	-1.4841912	1.6710234	0.06668915	0.04310224
Bt.27563.1.A1_at	SPRY2	sprouty homolog 2	1.1059321	-1.4539667	1.6079886	0.024013	0.00157516
Bt.28518.1.S1_s_at	LOC404103 /// PTI	spleen trypsin inhi	-1.5388857	-1.2518246	-1.2293142	0.050006375	0.02661117
Bt.25983.1.A1_at	SPSB2	splA/ryanodine rec	-1.0055368	1.3941296	-1.4018487	0.02901493	0.00708938
Bt.28673.1.A1_at	SPSB2	splA/ryanodine rec	1.0491294	1.4416066	-1.3740981	0.022891732	7.69E-04
Bt.5587.1.S1_at	SGPP1	sphingosine-1-pho	1.2510275	-1.0637723	1.3308085	0.024013	0.00190907
Bt.14326.1.S1_at	SMS	spermine synthase	-1.0027908	-1.3479642	1.3442129	0.036639847	0.01447468
Bt.9062.1.S1_at	SMOC1	SPARC related mo	1.0431056	1.5434558	-1.4796735	0.025828011	0.00444373
Bt.10108.1.S1_at	SRI	Sorcin	-1.0730367	-1.2915621	1.2036515	0.02901493	0.0068415
Bt.464.1.S1_at	SSTR2	somatostatin rece	-1.0272077	1.1330868	-1.1639155	0.022891732	0.00101921
Bt.15990.1.S1_at	SLC8A1	solute carrier fami	1.1024485	-1.0129539	1.1167295	0.04920927	0.02552622
Bt.23472.1.S1_at	SLC7A5	solute carrier fami	1.144613	-1.1278241	1.2909222	0.053989284	0.02987534
Bt.27873.1.S1_at	SLC46A2	solute carrier fami	-1.0589025	1.1573737	-1.2255459	0.09493333	0.07031105
Bt.22090.1.S1_at	SLC39A2	solute carrier fami	1.1001232	-1.1871912	1.3060565	0.05614424	0.03205975
Bt.26889.1.S1_at	SLC33A1	solute carrier fami	1.0679692	-1.2016339	1.2833081	0.033165394	0.01160152
Bt.13332.1.S1_at	SLC25A46	Solute carrier fami	1.0637405	-1.0831393	1.1521791	0.028761048	0.00654358
Bt.19023.1.S1_at	SLC25A19	solute carrier fami	-1.2179339	-1.4790092	1.214359	0.08558816	0.06121217
Bt.5711.2.S1_at	SLC25A19	solute carrier fami	-1.3511401	-1.3585716	1.0055002	0.08681225	0.06242649
Bt.1280.2.S1_a_at	SLC25A11	solute carrier fami	1.1083628	-1.1247672	1.2466502	0.031449206	0.00984594
Bt.29365.1.A1_at	SLC2A6	solute carrier fami	1.0094513	1.178889	-1.1678512	0.03635977	0.01428776
Bt.20569.3.S1_at	SLC11A2	solute carrier fami	1.0456156	-1.4985201	1.5668759	0.024013	0.00234381
Bt.24847.1.S1_at	SNAI1	snail homolog 1 (D	-1.0453944	-1.4308203	1.3686894	0.0969858	0.07482678
Bt.8841.1.A1_at	SMAP	small acidic protei	-1.0105853	-1.1717868	1.159513	0.059017222	0.03458998
Bt.20449.1.S1_at	SLMO2	slowmo homolog 2	1.0528502	-1.3009046	1.3696578	0.036972128	0.0149195
Bt.28989.1.S1_at	SKIL	SKI-like oncogene	-1.0494062	-1.3548005	1.2910163	0.028761048	0.00649347
Bt.9579.2.S1_at	SIRT1	Sirtuin (silent mati	-1.1052902	1.0945485	-1.2097936	0.039713833	0.01689592
Bt.7092.1.S1_at	SIN3A	SIN3 homolog A, t	-1.0630242	-1.4327228	1.3477801	0.041296616	0.01856159
Bt.9213.2.S1_at	LOC531674	similar to Zinc fing	1.2594651	-1.4306909	1.8019053	0.025828011	0.00458525
Bt.22509.1.S1_at	LOC512915	similar to zinc fing	1.092124	-1.2474896	1.3624133	0.040756784	0.01797331
Bt.28576.1.S1_at	LOC512915	Similar to zinc fing	1.1893405	-1.4340607	1.7055864	0.04973036	0.02608098
Bt.27403.1.S1_at	LOC540987	similar to Unchara	1.1019936	-1.2479275	1.3752081	0.024013	0.00126796
Bt.27003.2.S1_at	LOC100140797	similar to Unchara	-1.0006204	1.2996526	-1.3004589	0.024013	0.00237235
Bt.5871.1.S1_at	LOC100138908 /// UG	similar to UDP gluc	-1.0385884	1.2723771	-1.3214762	0.022891732	5.77E-04
Bt.21131.1.A1_at	LOC528994	similar to transme	-1.0457803	-1.2860566	1.2297579	0.046260826	0.02290455
Bt.9870.2.A1_at	PWWP2A	similar to PWWP d	1.0795568	-1.7294122	1.8669986	0.024013	0.00143151
Bt.8609.1.S1_s_at	TOB1	similar to Protein 1	-1.0257518	-1.2584584	1.2268643	0.031530906	0.00998613
Bt.24253.2.S1_at	OTUD4	similar to OTU dor	1.1867636	-1.1320761	1.3435068	0.025498856	0.00403657
Bt.24696.2.S1_at	OTUD4	similar to OTU dor	-1.0550667	-1.3872312	1.3148279	0.032790463	0.0111676
Bt.29334.1.A1_at	N4BP1	similar to Nedd4 b	1.1825522	-1.2794012	1.5129588	0.031530906	0.01007282
Bt.22027.2.S1_at	LOC100138572	similar to N-acetyl	1.2007128	1.2332089	-1.027064	0.031449206	0.0098273
Bt.9554.1.A1_at	LOC509006	Similar to Mhc clas	1.0362997	1.6339248	-1.5766914	0.024142498	0.00268544
Bt.14157.3.S1_at	LOC100140276	similar to jumonji c	1.0458788	-1.3393998	1.4008497	0.02901493	0.00684165
Bt.3254.1.A1_at	LOC100140276	similar to jumonji c	-1.1223044	-1.2750235	1.1360763	0.022891732	9.75E-04
Bt.19105.1.A1_at	LOC782799	Similar to intercell	1.1337298	-1.1104423	1.2589414	0.07651567	0.05237065
Bt.22396.1.S1_at	LOC100139648 /// LO	similar to hepatoc	1.0595676	1.278251	-1.2063894	0.05404766	0.02994584

Bt.28676.1.A1_at	LOC529052	similar to F55A4.8	1.088412	-1.1981889	1.3041232	0.052423984	0.0283616
Bt.10146.1.S1_at	LOC788125	Similar to E3 ubiq	-1.0325761	-1.2425199	1.2033203	0.025878632	0.00463115
Bt.18643.2.S1_at	LOC782359	similar to BCL2 bin	-1.0824589	-1.2882714	1.1901344	0.06163837	0.03767999
Bt.28037.1.S1_at	LOC407195	similar to alpha-tu	1.0481946	-1.8837982	1.9745872	0.022891732	6.43E-04
Bt.24594.1.A1_at	SLAMF1	signaling lymphoc	-1.0688032	1.2305429	-1.3152082	0.024766458	0.00384251
Bt.22137.1.A1_at	SIRPA	signal-regulatory p	-1.0510509	-1.2854378	1.2230024	0.032914232	0.01123504
Bt.26358.1.S1_at	STAM	signal transducing	1.0451106	-1.4154034	1.4792529	0.029807545	0.00821484
Bt.26911.2.S1_at	SESN2	sestrin 2	-1.1807393	1.7228365	-2.0342207	0.07020697	0.04639962
Bt.7709.1.S1_at	SESN2	sestrin 2	-1.062143	-1.2512933	1.1780837	0.006459689	4.57E-06
Bt.29146.1.S1_at	SAA3	serum amyloid A 3	1.2340192	1.3276607	-1.0758834	0.059015814	0.03440851
Bt.6275.1.S1_at	SAA3	serum amyloid A 3	1.0684133	-1.242043	1.3270153	0.025828011	0.00457918
Bt.11589.1.A1_at	SERPIND1	serpin peptidase in	-1.0315311	1.2405193	-1.2796342	0.040293388	0.01755131
Bt.19559.1.S1_at	SERPINB1	serpin peptidase in	1.1946303	-1.1941663	1.4265872	0.024570785	0.00324505
Bt.5362.1.S1_at	SERPINA3-1	serpin peptidase in	1.1678171	1.3810554	-1.1825956	0.032781206	0.01111943
Bt.4741.1.S1_at	SRSF3	serine/arginine-ric	1.056344	-1.0452144	1.1041061	0.08823464	0.06416498
Bt.6289.1.S1_at	SPTLC1	serine palmitoyltra	-1.016584	-1.341883	1.3199921	0.027768422	0.00582843
Bt.20115.2.S1_at	SQSTM1	sequestosome 1	1.2574667	-1.0821596	1.3607796	0.022891732	4.64E-04
Bt.4766.1.S1_at	SEP2	septin 2	1.0373725	-1.2058908	1.2509578	0.033150923	0.01142491
Bt.4766.1.S1_at	SEP2	septin 2	1.0373727	-1.2058903	1.2509576	0.033150923	0.01142506
Bt.3240.1.S1_at	SELT	selenoprotein T	1.0367572	-1.1528006	1.1951743	0.04096433	0.0181024
Bt.20472.1.S1_at	SEC11C	SEC11 homolog C	1.2576557	-1.2361195	1.5546128	0.09839859	0.07364248
Bt.10037.1.S1_at	SCO1	SCO cytochrome o	1.0740823	-1.2244647	1.3151758	0.042790655	0.01994619
Bt.19894.1.S1_at	SAFB2	scaffold attachme	-1.0813644	-1.4750766	1.3640884	0.02901493	0.00744287
Bt.28280.2.S1_at	SAFB2	scaffold attachme	1.0189141	-1.475375	1.5032804	0.03079631	0.00929814
Bt.6442.1.S1_at	LOC100336949 /// LO	sarcomeric tropon	-1.1796635	-1.5337064	1.300122	0.063427314	0.03951204
Bt.22620.1.S1_at	SAMSN1	SAM domain, SH3	1.2610118	-1.8089958	2.2811651	0.024048876	0.00248833
Bt.1915.1.S1_at	SAV1	salvador homolog	1.2039729	-1.0732602	1.2921762	0.022891732	1.64E-04
Bt.11666.3.S1_a_at	RBM43	RNA binding motif	1.1275886	1.3066676	-1.1588159	0.024013	0.00193076
Bt.13991.2.S1_at	RYBP	RING1 and YY1 bin	-1.0524584	1.2158012	-1.2795802	0.024766458	0.00374246
Bt.17063.1.S1_at	RYBP	RING1 and YY1 bin	1.2081473	-1.2657804	1.5292491	0.032781206	0.01112013
Bt.3448.1.S1_at	RYBP	RING1 and YY1 bin	1.1677767	-1.3132497	1.5335824	0.05149784	0.02762322
Bt.16125.1.A1_at	RNFT1	ring finger protein	1.1357195	-1.2367384	1.4045879	0.059017222	0.0345234
Bt.16125.1.A1_s_at	RNFT1	ring finger protein	1.1191678	-1.2618895	1.412266	0.030786525	0.00902926
Bt.21145.1.A1_at	RNF219	ring finger protein	-1.005265	-1.534314	1.5262781	0.02901493	0.00674862
Bt.21482.2.S1_at	RNF19B	ring finger protein	-1.0266603	1.2045794	-1.2366939	0.024013	0.00236465
Bt.19247.2.S1_at	RNF19A	ring finger protein	1.0062635	1.223744	-1.2161269	0.024013	0.00140664
Bt.25995.1.S1_at	RNF19A	ring finger protein	-1.153281	-1.1269652	-1.0233511	0.04227832	0.01957053
Bt.21995.1.S1_at	RNF123	Ring finger protein	1.0332505	1.4191887	-1.3735186	0.031308834	0.00971348
Bt.1938.1.S1_at	RSPRY1	ring finger and SP	-2.0724707	-2.2158363	1.0691762	0.024013	0.00241072
Bt.8555.2.S1_at	LOC505941	ribosome binding	1.1249348	1.4510857	-1.2899287	0.024013	0.00239321
Bt.2451.2.A1_at	RRP9	ribosomal RNA pro	1.2161409	-1.6273515	1.9790888	0.028753668	0.00646196
Bt.5646.1.S1_at	RRP9	ribosomal RNA pro	1.1021872	-1.1511436	1.2687757	0.041864008	0.01921833
Bt.15993.1.S1_s_at	RPLP0	ribosomal protein,	1.1010344	-1.0603572	1.1674898	0.027768422	0.00534778
Bt.5334.1.S1_at	RPSA	ribosomal protein	1.0547787	-1.1480185	1.2109054	0.019877227	4.14E-05
Bt.7863.1.S1_at	RPS3	ribosomal protein	1.0781014	-1.1192806	1.206698	0.022891732	1.73E-04
Bt.28100.1.S1_at	RPS23	ribosomal protein	1.1340679	-1.1385593	1.2912036	0.03950549	0.01663977
Bt.3077.1.S1_at	RPS19BP1	ribosomal protein	1.1905884	-1.1034724	1.3137815	0.05500966	0.03103139
Bt.4832.1.S1_at	RPS15	ribosomal protein	1.0605533	-1.1542583	1.2241523	0.044163227	0.02103605
Bt.4241.1.S1_at	RPS14	ribosomal protein	1.0735271	-1.0942911	1.174751	0.027768422	0.00516485
Bt.1269.1.S1_a_at	RPS12	ribosomal protein	1.0485462	-1.1587832	1.2150377	0.03878532	0.01617631
Bt.3626.1.S1_at	RPS11	ribosomal protein	1.0668167	-1.0910362	1.1639357	0.06984436	0.04600306
Bt.3921.1.S1_at	RPS10	ribosomal protein	1.0600715	-1.0365474	1.0988144	0.046260826	0.02291791
Bt.14228.1.S1_at	RPL36	ribosomal protein	1.1147062	-1.1040523	1.2306939	0.03410501	0.01221996
Bt.4406.1.S1_at	RPL35	ribosomal protein	1.0724051	-1.0864165	1.1650785	0.06590075	0.04210196
Bt.22568.1.S1_at	RPL29	ribosomal protein	1.1090106	-1.0275147	1.1395247	0.027768422	0.0055453
Bt.1226.1.S1_a_at	RPL28	ribosomal protein L2	1.1008149	-1.0867684	1.1963309	0.040293388	0.01736935
Bt.5211.1.S2_at	RPL21	ribosomal protein	1.1152962	-1.2681375	1.414349	0.07503731	0.05112083
Bt.23191.1.S1_at	RPL19	ribosomal protein	1.0484463	-1.1390667	1.1942503	0.03499949	0.01320581
Bt.4012.1.S1_at	RPL18A	ribosomal protein	1.0605772	-1.1121409	1.1795112	0.04379717	0.02070693
Bt.23317.1.S1_at	RPL13	ribosomal protein	1.0695782	-1.1184766	1.1962981	0.02901493	0.00755854
Bt.2534.1.S1_at	RSL24D1	ribosomal L24 don	1.0374844	-1.121739	1.1637868	0.08338141	0.05928035
Bt.18598.1.S1_at	ARHGAP5	Rho GTPase activa	1.0050452	1.3671339	-1.360271	0.024013	0.00190876
Bt.2458.1.S1_at	ARHGDI1	Rho GDP dissociat	1.1061405	-1.3052202	1.443757	0.027768422	0.00561838
Bt.21876.1.A1_at	RND1	Rho family GTPase	1.0498668	1.3195313	-1.256856	0.026534216	0.00478178
Bt.22516.1.A1_at	RDH14	retinol dehydrogen	1.1528794	-1.122486	1.2940909	0.060344376	0.03620663
Bt.1286.1.S1_a_at	RARRES2	retinoic acid recep	1.1463319	1.2960849	-1.1306366	0.05222191	0.02811223
Bt.15948.1.S1_at	RB1	retinoblastoma 1	1.0687746	-1.3273298	1.4186163	0.022891732	7.18E-04
Bt.17081.2.S1_at	RFX5	regulatory factor X	1.0993832	-1.1834124	1.3010238	0.024013	0.00125494
Bt.28075.1.S1_at	RFX2	regulatory factor X	1.0736157	1.3205279	-1.2299819	0.024570785	0.00334124
Bt.2657.1.S1_a_at	RGS20	regulator of G-pro	-1.293061	-1.0702038	-1.2082381	0.047587253	0.02438216
Bt.26533.1.S1_at	RGS2	regulator of G-pro	-2.384517	-1.9539434	-1.2203614	0.025828011	0.00441953
Bt.23286.1.A1_at	RCAN1	regulator of calcin	1.0355575	-1.5540665	1.6093253	0.032171734	0.01043592
Bt.24907.1.A1_at	RIPK2	receptor-interactin	-1.0599014	-1.3447151	1.2687172	0.024570785	0.00345075
Bt.13840.1.S1_at	REEP5	receptor accessory	1.1262372	-1.0628822	1.1970572	0.0935433	0.06914932
Bt.24414.1.S1_at	RASAL2	RAS protein activa	1.0122256	1.2056255	-1.1910641	0.024570785	0.00327114

Bt.3947.1.S1_at	RHOC	ras homolog gene	1.1049331	-1.1609646	1.2827883	0.03250993	0.01082133
Bt.24735.1.A1_at	RASSF5	Ras association (Ra	1.1249201	-1.1112918	1.2501144	0.07863341	0.05468218
Bt.28131.1.S1_at	RASSF5	Ras association (Ra	-1.0006669	-1.2264799	1.2263979	0.04298775	0.02012846
Bt.864.2.S1_a_at	RALGDS	ral guanine nucleo	-1.2514198	-1.8334272	1.4650776	0.024013	0.00177983
Bt.15668.1.S1_at	RAD21	RAD21 homolog (S	1.0100518	-1.2120186	1.2242016	0.022891732	7.93E-04
Bt.10397.2.S1_at	RAB9A	RAB9A, member R	-1.1182021	-1.4535869	1.2999322	0.03136388	0.00977489
Bt.6358.1.S1_at	RAB9A	RAB9A, member R	1.0626501	-1.2279409	1.3048716	0.03499949	0.01322566
Bt.2362.1.S1_at	RAB3A	RAB3A, member R	1.1507801	1.2514508	-1.0874804	0.055018004	0.03114056
Bt.24636.1.A1_at	RAB3A	RAB3A, member R	1.0572755	1.2315127	-1.1647983	0.052105825	0.02798617
Bt.2757.1.S1_at	RAB2A	RAB2A, member R	1.075472	-1.2514857	1.3459377	0.038198154	0.01575939
Bt.12771.1.S1_at	RAB27B	RAB27B, member	-1.1516825	-1.3307823	1.1555115	0.0866939	0.06224806
Bt.25005.1.S1_at	RAB27B	RAB27B, member	-1.2849394	-1.705225	1.3270859	0.046462327	0.02316668
Bt.23143.1.A1_at	RAB12	RAB12, member R	1.0781882	-1.1948088	1.2882289	0.02901493	0.00746715
Bt.8643.2.S1_at	RILPL2	Rab interacting lys	1.1150794	-1.4228634	1.5866057	0.062433682	0.0386074
Bt.5491.1.S1_at	RABAC1	Rab acceptor 1 (pr	1.2254229	1.0947824	1.1193302	0.024013	0.00163593
Bt.11058.1.A1_at	PDP1	pyruvate dehydrog	1.2006571	-1.1437168	1.3732119	0.061207205	0.03715688
Bt.22066.2.S1_at	PCP4L1	Purkinje cell prote	1.0068047	-1.2271787	1.2355294	0.06973509	0.04573264
Bt.8679.2.S1_at	PCP4L1	Purkinje cell prote	-1.0145899	-1.3178607	1.2989097	0.07882939	0.05492988
Bt.25498.1.S1_at	P2RY13	purinergic recepto	-1.0608218	1.2340561	-1.3091136	0.04367994	0.02062064
Bt.12574.2.S1_at	P2RY1	purinergic recepto	1.109802	-1.0960193	1.2163644	0.03507604	0.01331368
Bt.23616.1.S1_at	PCBD1	pterin-4 alpha-carb	1.1831927	-1.0442021	1.2354923	0.08494564	0.06057255
Bt.5455.1.S1_at	PRPF40B	PRP40 pre-mRNA f	1.017466	1.245652	-1.2242689	0.0351668	0.01348215
Bt.10986.1.S1_at	PTPRS	protein tyrosine ph	1.051494	1.299458	-1.2358208	0.029807545	0.00823421
Bt.13706.2.S1_at	PTPN1	protein tyrosine ph	1.0008247	-1.2948102	1.295878	0.054938056	0.03075308
Bt.18951.1.S1_at	PTPN1	Protein tyrosine ph	1.0559641	-1.2199041	1.2881747	0.087049775	0.06281118
Bt.24291.1.S1_at	PTP4A1	Protein tyrosine ph	1.0781056	-1.1781529	1.2701732	0.046462327	0.02315272
Bt.5004.1.S1_at	PPM1B	protein phosphata	1.0946128	-1.1744809	1.2856019	0.027768422	0.00566403
Bt.10207.1.S1_at	PPP2CB	protein phosphata	1.1077448	-1.4168901	1.5695527	0.03499949	0.01320982
Bt.22.1.S1_at	PPP1R8	protein phosphata	1.0932962	-1.1401718	1.2465453	0.055018004	0.03114447
Bt.29961.1.A1_at	PPP1R3D	protein phosphata	-1.0651704	1.1894324	-1.2669481	0.024766458	0.00382144
Bt.21824.1.A1_at	PPP1R3B	protein phosphata	1.1121391	-1.2593892	1.4006159	0.027862236	0.00587345
Bt.9954.1.S1_at	PPP1CB	protein phosphata	1.0528022	-1.1258849	1.1853341	0.043822575	0.02080733
Bt.10903.1.S1_at	PRKAR1A	Protein kinase, cA	1.0533454	-1.1838343	1.2469864	0.032539457	0.01094614
Bt.10903.2.S1_at	PRKAR1A	Protein kinase, cA	-1.1814382	-1.4727329	1.2465594	0.060432903	0.03638787
Bt.13229.1.S1_at	PRKAG2	protein kinase, AM	-1.3308029	-1.5875715	1.1929426	0.0411942	0.01834292
Bt.18951.2.S1_at	PRKCD	protein kinase C, d	1.2130498	-1.3500501	1.6376781	0.03030335	0.00858773
Bt.526.1.S1_at	PROCR	protein C receptor	-3.3287203	-1.8958752	-1.7557697	0.042987745	0.02014196
Bt.2575.1.S1_at	PSME1	proteasome (proso	1.038285	-1.0753024	1.1164703	0.033487722	0.01190412
Bt.3158.1.S1_at	PSMD3	proteasome (proso	-1.1079422	-1.3898264	1.2544214	0.08177954	0.05750575
Bt.15807.1.S1_at	PTGS2	prostaglandin-end	1.1833483	-1.232436	1.4584011	0.027768422	0.00544107
Bt.21602.1.S1_at	PTGS2	Prostaglandin-end	-1.0648292	1.1803619	-1.2568837	0.047509477	0.02427516
Bt.28876.1.S1_at	PTGS2	Prostaglandin-end	1.1780816	-1.1373403	1.3398798	0.031930793	0.0103352
Bt.20560.1.S1_at	PTGER4	prostaglandin E re	-1.0690656	-1.175396	1.0994611	0.024766458	0.00359163
Bt.2337.1.A1_at	PSTPIP2	proline-serine-thre	1.0896386	-1.4957157	1.6297896	0.024570785	0.00332137
Bt.13795.1.S1_at	PNRC1	proline-rich nuclea	-1.1073892	-1.4282176	1.2897161	0.07340301	0.04966276
Bt.21084.1.S1_at	PNRC1	proline-rich nuclea	1.14946	-1.1514223	1.3235139	0.07289889	0.0488912
Bt.8870.3.S1_at	PNRC1	proline-rich nuclea	-1.0071371	-1.2951047	1.2859269	0.047813945	0.02456589
Bt.1455.1.S1_at	PRDM1	PR domain contain	1.1342682	-1.2024986	1.3639557	0.022891732	4.14E-04
Bt.17536.1.S1_at	PRDM1	PR domain contain	1.0949733	-1.1533056	1.262839	0.059017222	0.03478481
Bt.19102.1.S1_at	PRDM1	PR domain contain	1.0682435	-1.2995116	1.3881948	0.03079631	0.0092207
Bt.28417.1.S1_at	PRDM1	PR domain contain	1.0885086	-1.2678869	1.3801057	0.028583735	0.00638336
Bt.25850.1.S1_at	KCNJ2	potassium inwardl	-1.1779641	1.2643024	-1.4893029	0.024013	0.00180433
Bt.16256.1.A1_at	KCTD9	potassium channe	-1.1164397	-1.4101774	1.2631023	0.024013	0.00238265
Bt.2453.1.S1_at	POLR2H	polymerase (RNA)	1.1617262	-1.191174	1.383818	0.046648815	0.02334089
Bt.26515.2.S1_at	POLB	polymerase (DNA)	-1.0354543	1.1493064	-1.1900543	0.028583735	0.00637462
Bt.20188.2.S1_at	POLK	polymerase (DNA)	1.022229	1.2961648	-1.2679789	0.041676935	0.01892903
Bt.5360.1.S1_a_at	PAPOLA	poly(A) polymeras	1.0512542	1.4809393	-1.4087358	0.060432903	0.03636762
Bt.24258.2.S1_at	PARP1	poly (ADP-ribose)	1.1670616	-1.2154287	1.4184802	0.05500966	0.03098743
Bt.27380.1.A1_at	PLK2	polo-like kinase 2	1.0734847	-1.3966444	1.4992763	0.034339253	0.01247376
Bt.20333.1.S1_at	POC1B	POC1 centriolar pr	1.1393502	-1.6320784	1.8595089	0.032178592	0.01054497
Bt.27882.1.S1_at	PHLDA1	Pleckstrin homolo	1.152428	1.2220228	-1.0603898	0.05500966	0.03106199
Bt.16996.1.A1_at	PLEK	pleckstrin	-1.0298958	1.1298528	-1.1636306	0.05462432	0.03049697
Bt.25340.1.A1_at	PLEK	pleckstrin	1.1156492	1.240788	-1.1121669	0.0675663	0.04383453
Bt.29877.1.A1_at	PDGFRA	platelet-derived gr	1.1441463	1.479643	-1.2932287	0.03429107	0.01233509
Bt.22564.2.S1_at	PIM1	pim-1 oncogene	1.1108338	-1.2619022	1.4017636	0.046462327	0.02321475
Bt.13713.1.A1_at	PHAX	phosphorylated ac	1.0620279	-1.3387879	1.42183	0.024570785	0.0030521
Bt.4552.1.S1_a_at	PLCB4	phospholipase C, b	1.0358713	-1.1353027	1.1760274	0.06336082	0.03940461
Bt.27444.1.A1_at	PLB1	phospholipase B1	1.1209329	1.2695607	-1.1325929	0.041676935	0.01893871
Bt.24901.1.A1_at	PIK3R1	phosphoinositide-	1.0506017	-1.3241786	1.3911842	0.041799407	0.01905344
Bt.19988.1.A1_at	PIK3IP1	phosphoinositide-	1.002957	-1.4415504	1.4458131	0.07034051	0.04657884
Bt.27256.1.S1_at	PDE4B	phosphodiesterase	-1.2183168	-1.3287387	1.0906348	0.07194177	0.04809676
Bt.3992.1.S1_at	PISD	phosphatidylserine	-1.2567308	-1.3916383	1.107348	0.09001543	0.06571444
Bt.3288.1.A1_at	PIGY	phosphatidylinosit	1.1848452	-1.020731	1.2094082	0.06984436	0.04596127
Bt.28041.1.S1_at	PIGW	phosphatidylinosit	-1.0217241	-1.4503202	1.4194832	0.024142498	0.0025624
Bt.19656.1.S1_at	PIGH	phosphatidylinosit	1.1476932	-1.1085202	1.2722411	0.058114108	0.03355422

Bt.5754.3.S1_at	PIGH	phosphatidylinosit	1.0513569	-1.2029196	1.2646979	0.07139212	0.04741882
Bt.27042.1.S1_at	PHF13	PHD finger protein	1.0054076	-1.2230799	1.2296938	0.05935854	0.03515368
Bt.23564.1.A1_at	PHF10	PHD finger protein	1.0994053	-1.2053617	1.325181	0.053438853	0.02945746
Bt.13264.1.S1_at	PPARD	peroxisome prolife	-1.1691178	1.1407263	-1.3336434	0.03079631	0.00916829
Bt.12803.1.S1_at	PPARA	peroxisome prolife	1.0394444	1.2198509	-1.1735605	0.03864421	0.01604746
Bt.24155.1.A1_at	PEX5	peroxisomal bioge	1.0426066	-1.238699	1.2914758	0.034708954	0.01273071
Bt.23704.1.A1_at	PEX2	peroxisomal bioge	1.0959069	-1.2348286	1.3532572	0.07343031	0.04955535
Bt.20771.1.A1_at	PEX1	peroxisomal bioge	1.0242695	-1.5140306	1.5507753	0.031873036	0.01029398
Bt.4476.1.S1_at	PRDX3	peroxiredoxin 3	1.0531571	-1.1342177	1.1945094	0.029312633	0.00788332
Bt.16061.1.S1_at	PELI1	pellino homolog 1	1.0572273	-1.427152	1.508824	0.028367294	0.00625484
Bt.4582.3.S1_at	PELI1	pellino homolog 1	1.106551	1.2288328	-1.1105071	0.028171103	0.00604664
Bt.9269.2.S1_at	PELI1	pellino homolog 1	1.118004	-1.436841	1.6063939	0.027768422	0.00534761
Bt.20233.1.S1_at	PCID2	PCI domain contai	-1.0140337	-1.244245	1.2270254	0.025828011	0.00457606
Bt.2634.1.S1_at	PPDPF	pancreatic progen	1.097056	-1.1539378	1.2659345	0.02901493	0.00764442
Bt.15817.2.S1_a_at	PPY	pancreatic polypep	1.2126682	-1.0127981	1.2281879	0.07325883	0.04924156
Bt.9991.1.S1_at	PLDN	pallidin homolog (1.1144981	-1.096657	1.2222222	0.04127434	0.01846407
Bt.26506.2.A1_at	LOC100138271	oviductin-like	-1.0243809	1.3247136	-1.3570113	0.037527665	0.01538236
Bt.20514.1.S1_at	OPTN	optineurin	1.0056981	-1.393389	1.4013287	0.02537716	0.00396988
Bt.28680.1.S1_at	OPTN	optineurin	-1.0613974	-1.317498	1.2412862	0.024766458	0.00361423
Bt.9163.2.S1_at	OPTN	optineurin	1.2041079	-1.1474966	1.3817097	0.03499949	0.01325776
Bt.21469.1.S1_at	OSM	oncostatin M	1.1135044	-1.3416018	1.4938796	0.031097824	0.00958905
Bt.5653.1.A1_at	OCRL	oculocerebrorenal	1.1033839	-1.26531	1.3961227	0.041864008	0.01916574
Bt.17812.1.S1_at	NUPL1	nucleoporin like 1	1.0470262	-1.1576049	1.2120427	0.030210163	0.00847593
Bt.5892.1.S1_at	NR4A1	nuclear receptor s	-1.7445194	-1.2206244	-1.4292023	0.0472649	0.02395666
Bt.14193.1.A1_at	NUPR1	nuclear protein, tr	-1.017286	-1.1654503	1.1456467	0.04742311	0.02412178
Bt.9603.2.S1_at	NUFIP1	nuclear fragile X m	1.0094534	-1.2348857	1.2465595	0.034339253	0.01246437
Bt.19071.1.S1_at	NFKBIZ	nuclear factor of k	1.0314678	-1.3446863	1.3870007	0.027768422	0.00576064
Bt.26277.1.A1_at	NFKBIZ	nuclear factor of k	-1.1689498	-1.0978955	-1.0647187	0.034472622	0.01257093
Bt.11044.1.S1_at	NFKBIE	nuclear factor of k	-1.0580052	1.2575337	-1.3304772	0.039895326	0.01700133
Bt.23624.1.S1_at	NFKBIE	nuclear factor of k	-1.6297636	-1.1177777	-1.458039	0.034805436	0.0129142
Bt.27256.1.S1_a_at	NFKBIE	nuclear factor of k	-1.0921941	-1.3884289	1.2711229	0.05810597	0.03350846
Bt.27320.1.A1_at	NFKBIE	Nuclear factor of k	1.148033	-1.2542267	1.4398936	0.024013	0.00158196
Bt.23626.1.S1_at	NFKBID	nuclear factor of k	1.0152879	-1.7038658	1.7299144	0.029807545	0.00829373
Bt.13199.1.S1_at	NFKBIB	nuclear factor of k	1.0625775	-1.2978864	1.379105	0.030698093	0.00891655
Bt.7310.1.S1_at	NFKBIB	Nuclear factor of k	1.0597293	1.2496239	-1.1791916	0.031530906	0.0101612
Bt.9425.2.S1_at	NFKBIA	nuclear factor of k	1.0465326	1.2456932	-1.1903051	0.025828011	0.00453515
Bt.27040.1.A1_at	NFKB2	nuclear factor of k	1.2305111	-1.2058955	1.4838678	0.023475172	0.00108019
Bt.23067.1.S1_at	NFKB1	nuclear factor of k	-1.4148072	-1.1499267	-1.2303456	0.057406735	0.03290238
Bt.28989.2.S1_at	NFATC1	Nuclear factor of a	-1.012875	-1.2656803	1.2495918	0.022891732	2.04E-04
Bt.23295.1.S1_at	NAF1	nuclear assembly f	1.137162	-1.4621888	1.6627456	0.022891732	5.13E-04
Bt.26786.1.S1_at	NOTCH1	Notch homolog 1,	-1.1109861	-1.2520348	1.1269581	0.090454556	0.06635465
Bt.6667.1.S1_at	NSMCE4A	non-SMC element	1.0928215	-1.1338995	1.2391496	0.04936249	0.02567547
Bt.8566.1.S1_at	NCAPD3	non-SMC condens	1.1205992	-1.0231736	1.1465673	0.024570785	0.00300976
Bt.4662.1.S1_at	NOS3	nitric oxide syntha	1.0124432	1.2052093	-1.190397	0.027768422	0.0053903
Bt.11631.2.S1_at	NOS2	nitric oxide syntha	-1.0886431	-1.4012469	1.2871499	0.07139212	0.04750152
Bt.16782.1.S1_at	NOS2	nitric oxide syntha	1.0403751	1.1763896	-1.130736	0.07343031	0.04960739
Bt.26872.1.S1_at	NIPSNAP3A	nipsnap homolog 3	1.129907	-1.2458806	1.4077293	0.024013	0.0022021
Bt.17970.1.S1_at	NEK3	NIMA (never in mi	-1.0243152	-1.4487815	1.4143901	0.02901493	0.0073375
Bt.16206.2.S1_at	NCF1	neutrophil cytosol	-1.0361248	-1.4470338	1.3965825	0.019877227	8.43E-05
Bt.12206.1.S1_x_at	BNBD-9-LIKE /// DEFB	neutrophil beta-de	-1.6278317	-2.788813	1.7132072	0.06633863	0.04252236
Bt.29138.1.S1_at	NMB	neuromedin B	-1.062485	-1.3889697	1.3072841	0.07139212	0.04762838
Bt.23143.2.S1_at	NGB	neuroglobin	-1.0571729	-1.37726	1.3027766	0.024013	0.00224988
Bt.19400.1.A1_at	NGFR	nerve growth facto	1.0780537	-1.408353	1.5182801	0.052385613	0.02824751
Bt.10029.2.S1_at	NYREN18	NEDD8 ultimate b	-1.0537274	-1.604711	1.5228902	0.024013	0.00190966
Bt.1542.1.S1_at	N4BP3_Hsa	Nedd4 binding pro	1.025177	-1.2455198	1.2768782	0.045694474	0.02245131
Bt.12261.1.A1_at	NCK1	NCK adaptor prote	1.0537966	-1.326549	1.397913	0.022891732	5.57E-04
Bt.4102.2.S1_a_at	NPPC	natriuretic peptide	-1.0649009	1.2740426	-1.356729	0.02901493	0.00698758
Bt.17824.2.A1_at	NPPA	natriuretic peptide	1.1187372	-1.1361208	1.2710207	0.053438853	0.02928641
BtAffx.1.9.S1_at	NPPA	natriuretic peptide	-1.0093884	1.1250722	-1.1356349	0.06558902	0.0417174
Bt.893.1.S1_at	NDUFB6	NADH dehydrogen	1.075428	-1.3277339	1.4278822	0.024048876	0.00250972
Bt.27817.1.S1_at	NDUFB4	NADH dehydrogen	1.0487094	-1.1470976	1.2029719	0.036972128	0.01490985
Bt.28306.1.A1_at	NAT12	N-acetyltransferas	1.0745915	-1.1521139	1.2380519	0.024142498	0.00256179
Bt.9272.1.A1_at	NAT10	N-acetyltransferas	-1.1506974	-1.4314156	1.2439548	0.09008519	0.0658927
Bt.23815.1.S1_at	MTMR6	myotubularin relat	1.0691895	-1.1868819	1.2690018	0.029807545	0.00829977
Bt.1128.1.S1_at	LOC516866	myosin light chain	-1.0459725	1.2193911	-1.2754495	0.09207128	0.06793103
Bt.18724.1.S1_at	MYCBP	MYC binding prote	1.1202213	-1.1866646	1.329327	0.024013	0.00185161
Bt.11041.1.S1_at	MADCAM1	mucosal vascular a	1.0285945	-1.4701914	1.5122308	0.065542854	0.04164171
Bt.9044.1.S1_at	MADCAM1	mucosal vascular a	-1.1320643	1.1623988	-1.3159102	0.06168527	0.03778932
Bt.21293.1.A1_at	MOBKLC2	MOB1, Mps One B	1.0678717	1.287038	-1.2052366	0.032256693	0.01062305
Bt.12986.1.S1_at	MAD2 /// MAD2L1	mitotic checkpoint	-1.1186472	-1.8613433	1.6639234	0.02901493	0.00760712
Bt.24479.1.S1_at	MAPKAPK2	mitogen-activated	-1.0283303	1.2357928	-1.2708031	0.033487722	0.01188501
Bt.26310.1.A1_at	MAP3K8	mitogen-activated	1.0546982	-1.3693293	1.4442292	0.04058254	0.01783911
Bt.4091.2.S1_at	MAP3K14	Mitogen-activated	1.1186513	1.2709545	-1.1361489	0.07871318	0.05479327
Bt.14040.2.A1_at	MAP2K4	Mitogen-activated	1.1574202	-1.3044078	1.5097479	0.038198154	0.01576518
Bt.21843.1.A1_at	MRM1	mitochondrial rRN	1.0799704	-1.3051481	1.4095213	0.024570785	0.00329583

Bt.1674.1.A1_at	MRPS34	Mitochondrial ribo	1.1828711	1.2029513	-1.0169759	0.06783509	0.04420068
Bt.13610.1.A1_at	MRPS31	mitochondrial ribo	1.0793355	-1.303531	1.4069474	0.027862236	0.0058875
Bt.9280.1.S1_at	MRPL53	mitochondrial ribo	1.055734	-1.0477626	1.1061587	0.060518015	0.03665296
Bt.853.1.S1_at	MRPL45	mitochondrial ribo	1.0328641	-1.2149763	1.2549055	0.060518015	0.03663738
Bt.8545.1.S1_at	MRPL43	mitochondrial ribo	1.1328714	-1.2110656	1.3719816	0.034805436	0.01296287
Bt.20487.1.S1_at	MRPL28	mitochondrial ribo	1.0263437	-1.2847638	1.3186094	0.031530906	0.01011794
Bt.25014.1.A1_at	MIOS	missing oocyte, m	1.2130454	1.1234838	1.0797178	0.08558816	0.06115357
Bt.14098.1.S1_at	MAPRE2	microtubule-associ	-1.4019378	-1.0214703	-1.3724704	0.0411942	0.01833957
Bt.3927.1.S1_at	MFAP3	microfibrillar-asso	1.0439396	-1.280022	1.3362656	0.022891732	3.10E-04
Bt.7003.1.S1_at	MVD	mevalonate (diph	1.1546444	-1.199108	1.3845433	0.0443601	0.02122388
Bt.22464.1.A1_at	METTL2B	methyltransferase	1.0722094	-1.1672945	1.251584	0.0472649	0.02385523
Bt.12669.1.A1_at	METTL14	methyltransferase	1.0788622	-1.16787	1.2599708	0.03499949	0.0132331
Bt.7169.1.S1_at	MUT	methylmalonyl Co	1.081724	-1.0904589	1.1795756	0.032539457	0.0109096
Bt.8671.1.S1_at	MBLAC2	metallo-beta-lacta	1.1090703	-1.439048	1.5960054	0.027768422	0.00582597
Bt.12739.1.S1_at	MARCH2	membrane-associ	-1.4686968	1.047811	-1.5389167	0.04162844	0.01882057
Bt.17368.2.S1_at	MEMO1	mediator of cell m	1.260598	-1.0665284	1.3444636	0.055109352	0.03131302
Bt.23806.1.A1_at	MEMO1	mediator of cell m	1.1349736	-1.6054366	1.8221282	0.024013	0.00238453
Bt.23964.1.S1_at	MED24	mediator complex	-1.1142709	1.1704049	-1.3041481	0.030879559	0.00942754
Bt.25834.1.A1_at	MELK	maternal embryon	-1.0421475	-1.2679418	1.2166625	0.0351668	0.01344512
Bt.19038.1.A1_at	MARCKSL1	MARCKS-like 1	1.015032	-1.6460305	1.6707737	0.03079631	0.00929579
Bt.9136.1.S1_at	LOC790576	mannosyl (alpha-1	1.1091107	-1.0427276	1.1565002	0.042790655	0.01988735
Bt.14049.1.A1_at	MANEA	mannosidase, end	1.2940911	-1.1373277	1.4718056	0.024766458	0.0036813
Bt.15687.1.S1_at	MCTS1	malignant T cell ar	1.1259788	-1.1969175	1.3477039	0.024013	0.00159369
Bt.9940.1.S1_at	MCTS1	malignant T cell ar	1.0225606	-1.4087312	1.4405131	0.022891732	3.37E-04
Bt.25270.1.A1_a_at	BOLA-DMB	major histocompa	-1.142038	1.1602901	-1.3250954	0.02901493	0.00681056
Bt.22014.1.S1_at	LOXL4	lysyl oxidase-like 4	-1.2223458	-1.3961669	1.1422029	0.04973036	0.02608754
Bt.21360.1.S1_at	LYRM5	LYR motif containi	1.2540807	1.1911073	1.0528696	0.05500966	0.03105958
Bt.13143.1.A1_at	LIPE	lipase, hormone-se	-1.1250482	1.0520225	-1.1835759	0.053438853	0.02939713
Bt.3942.1.S1_at	LMF2	lipase maturation	1.0169462	1.318933	-1.2969545	0.024048876	0.00245932
Bt.8606.1.S1_a_at	LIN37	lin-37 homolog (C.	-1.0539612	1.2061185	-1.271202	0.02901493	0.00738462
Bt.26286.1.A1_at	LIG4	ligase IV, DNA, AT	-1.067116	1.1695809	-1.2480786	0.05604093	0.03196115
Bt.7959.1.A1_at	LIG4	ligase IV, DNA, AT	1.0855716	-1.1900135	1.2918448	0.06984436	0.04600349
Bt.12690.2.S1_at	LGR4	leucine-rich repea	1.22375	1.3599807	-1.1113224	0.037026286	0.01501985
Bt.20651.1.S1_at	LRRC33	leucine rich repea	1.1128354	-1.5903304	1.769776	0.02901493	0.00682799
Bt.7183.1.S1_at	LAMB2	laminin, beta 2 (la	1.1530381	1.2287064	-1.0656251	0.04517718	0.02174252
Bt.21213.1.S1_at	LMNA	lamin A/C	1.1990746	-1.4078856	1.6881597	0.027768422	0.00544899
Bt.26667.1.S1_at	LASS5	LAG1 homolog, ce	-1.0784768	-1.2442424	1.1537035	0.06538909	0.0414516
Bt.3719.1.S1_at	LAGE3	L antigen family, n	1.1247054	-1.135045	1.2765914	0.024013	0.00207047
Bt.24824.1.S1_at	KLF5	Kruppel-like factor	1.0580846	1.236285	-1.1684179	0.030475466	0.0087442
Bt.27232.1.S1_at	KLF5	Kruppel-like factor	1.0201951	-1.2166322	1.2412024	0.061540138	0.03750089
Bt.27315.1.S1_a_at	KRIT1	KRIT1, ankyrin rep	1.0484377	-1.1910573	1.2487494	0.036972128	0.01472889
Bt.27868.1.S1_at	LOC781667	kin of IRRE like	-1.0888188	1.2158226	-1.3238105	0.024013	0.00122647
Bt.28009.1.S1_at	KRT8	keratin 8	-1.017504	1.2873647	-1.3098987	0.03316394	0.01158614
Bt.23647.1.A1_a_at	KLHL8	kelch-like 8 (Dros	1.0151585	-1.1712329	1.1889871	0.06429198	0.04039263
Bt.2426.2.S1_at	KLHL8	Kelch-like 8 (Dros	1.2674911	-1.6501017	2.0914888	0.033150923	0.01140711
Bt.15783.1.S1_at	KATNA1	katanin p60 (ATPa	1.0372765	-1.148987	1.1918173	0.029446576	0.00797035
Bt.28114.1.S1_at	KLK1	kallikrein 1	1.1289964	1.2361072	-1.0948726	0.07272725	0.04872469
Bt.20427.1.S1_at	JUP	Junction plakoglob	-1.0494815	-1.2807868	1.2203995	0.036972128	0.01486929
Bt.21542.1.S1_at	JUNB	jun B proto-oncog	1.0835648	-1.1305946	1.2250725	0.024013	0.00180757
Bt.13248.2.S1_at	JAG1	jagged 1 (Alagille s	-1.1219006	-1.2868773	1.1470511	0.059017222	0.03463278
Bt.13324.2.S1_a_at	IDH3B	isocitrate dehydro	-1.058015	-1.3336484	1.2605193	0.030352592	0.00865916
Bt.3898.1.S1_at	IDH3A	isocitrate dehydro	1.0168006	-1.4545373	1.4789743	0.022891732	9.89E-04
Bt.25395.1.A1_at	IFFO1	intermediate filam	-1.0128213	-1.2612106	1.2452449	0.046259154	0.022819
Bt.4743.2.S1_at	IL8	interleukin 8	-1.0864727	1.2973231	-1.4095062	0.024142498	0.00281169
Bt.28639.1.S1_at	IL6	interleukin 6 (inter	1.0680652	-1.2135959	1.2961996	0.03635977	0.01431096
Bt.12772.1.S1_at	IL17A	interleukin 17A	1.0912979	1.4729056	-1.3496825	0.024570785	0.00309471
Bt.1673.2.S1_at	IL17RC	interleukin 17 rece	1.094833	1.3079075	-1.1946182	0.053438853	0.02932562
Bt.24532.1.A1_at	IL17RB	interleukin 17 rece	-1.0516573	1.5164632	-1.5947996	0.031283624	0.00968355
Bt.28600.1.S1_at	IL15	interleukin 15	1.0329522	-1.130436	1.1676863	0.024766458	0.00385062
Bt.6964.2.A1_at	IL12B	interleukin 12B (na	1.0034225	-1.2474346	1.251704	0.024013	0.00160084
Bt.28527.1.A1_at	IL10	interleukin 10	1.0619788	-1.3835285	1.4692779	0.024013	0.00135891
Bt.28480.1.S1_at	IL1RN	interleukin 1 recep	-1.0023706	-1.2842442	1.2812068	0.027768422	0.00580412
Bt.9657.1.S1_at	IFNB1	interferon, beta 1,	1.2523599	-1.1611632	1.4541942	0.025878632	0.00464535
Bt.9664.1.A1_at	IRF1	interferon regulato	-1.0252603	-1.2670864	1.2358679	0.068445325	0.04469504
Bt.4251.2.A1_at	IFNGR2	interferon gamma	1.3417035	1.0275526	1.3057274	0.022891732	7.43E-04
Bt.16052.1.S1_at	ICAM1	intercellular adhes	1.1591034	-1.1283126	1.307831	0.024013	0.00133668
Bt.9101.1.S1_at	ITGAV	integrin, alpha V (v	1.0630097	-1.2550033	1.3340808	0.033150923	0.01144549
Bt.1387.1.A1_at	ITGA5	integrin, alpha 5 (f	1.1116632	-1.2020855	1.3363142	0.0741117	0.05017598
Bt.11406.1.A1_at	INTS9	integrator comple	1.1233817	-1.1403911	1.2810946	0.031530906	0.00995098
Bt.4271.2.S1_at	INTS6	integrator comple	1.0356876	-1.2524714	1.2971691	0.022891732	7.87E-04
Bt.9399.1.S1_at	INTS6	integrator comple	1.0380901	-1.3493729	1.4007707	0.03316394	0.01152517
Bt.13540.1.S1_at	INSIG1	insulin induced ge	-1.0990214	-1.426045	1.2975589	0.032539457	0.01092447
Bt.15533.1.A1_at	INPP5B	Inositol polyphosp	1.0721141	1.2268447	-1.1443229	0.09520125	0.07059466
Bt.24389.1.S1_at	INPP5B	inositol polyphosp	-1.0460643	1.567617	-1.6398281	0.022891732	8.80E-04
Bt.18081.2.S1_at	IPMK	Inositol polyphosp	-1.0498838	1.3112652	-1.3766762	0.022891732	0.00100375

Bt.9542.1.S1_at	INHBB	inhibin, beta B	-1.0381165	1.1693611	-1.2139331	0.07089913	0.04699886
Bt.29777.1.S1_at	IGLL1 /// LOC404062	immunoglobulin li	-1.0642239	1.3676175	-1.4554513	0.06668915	0.04312374
Bt.21368.1.S1_s_at	IGL@ /// IGLL1	immunoglobulin li	1.3002291	1.9918663	-1.5320272	0.032178592	0.01055185
Bt.12490.1.S1_at	IGHG1	immunoglobulin h	1.0456483	2.121339	-2.0287309	0.03624472	0.01413928
Bt.20595.1.S1_at	IER3	immediate early re	1.1140356	-1.1768264	1.3110263	0.02901493	0.00732951
Bt.5165.1.S1_at	ICT1	immature colon ca	1.0854769	-1.2103968	1.3138576	0.027157558	0.00497089
Bt.28166.1.A1_at	MGC137894	hypothetical prote	1.0722197	-1.3111907	1.4058846	0.07523109	0.05139287
Bt.20859.1.S1_at	MGC137255	Hypothetical prote	1.0479288	1.1949579	-1.1403043	0.034805436	0.01295974
Bt.11914.1.A1_at	LOC100335716	hypothetical prote	1.0853295	-1.3317124	1.4453467	0.022891732	6.94E-04
Bt.11051.2.S1_a_at	LOC100300734	hypothetical prote	1.0795856	1.3515073	-1.251876	0.0498451	0.02634021
Bt.18219.1.A1_at	LOC784866	hypothetical LOC7	-1.0949397	-1.4389217	1.314156	0.032178592	0.01053777
Bt.4546.1.S1_at	HSD11B2	hydroxysteroid (1)	-1.0197666	1.3515779	-1.378294	0.021954779	1.09E-04
Bt.4760.1.S1_at	HSD3B1	hydroxy-delta-5-st	-1.0215111	1.161703	-1.1866925	0.02806260	0.00594954
Bt.14124.2.S1_at	HYAL2	hyaluronoglycosar	1.0188346	-1.4217044	1.4484816	0.074613065	0.05067361
Bt.17769.1.S1_at	HYAL2	Hyaluronoglycosar	1.0991848	-1.2953416	1.4238198	0.061783127	0.03793986
Bt.21147.2.S1_a_at	HYAL2	Hyaluronoglycosar	1.0504478	1.2984302	-1.236073	0.022891732	6.56E-04
Bt.20073.2.S1_at	HYAL1	hyaluronoglycosar	1.0286514	-1.3637516	1.402825	0.024142498	0.00261578
Bt.29861.1.S1_at	hare	hyaluronan recept	1.248184	1.3844647	-1.1091832	0.04454344	0.02134308
Bt.20020.1.S1_at	HABP4	hyaluronan bindin	1.1292585	-1.3233969	1.4944571	0.04567432	0.02235758
Bt.13243.1.S1_a_at	HCFC1R1	host cell factor C1	1.1596569	1.5359299	-1.3244693	0.024013	0.00161716
Bt.27615.1.A1_at	HNRNPF	heterogeneous nu	1.0105338	-1.2018965	1.214557	0.03079631	0.00933782
Bt.23277.1.A1_at	HNRPDL	heterogeneous nu	-1.1363245	-1.4579833	1.2830694	0.02901493	0.00768947
Bt.23277.3.S1_a_at	HNRPDL	heterogeneous nu	-1.1598	-1.3751497	1.1856784	0.045480996	0.02217801
Bt.23380.2.S1_at	HNRNPA1	heterogeneous nu	1.0046909	-1.1047275	1.1099095	0.0586449	0.03415081
Bt.4705.1.S1_at	HDGF	hepatoma-derived	1.0792916	-1.0967628	1.1837269	0.040293388	0.01731503
Bt.16061.2.S1_at	HEBP2	heme binding prot	1.110157	-1.2402916	1.3769184	0.04162844	0.01882841
Bt.19519.1.S1_at	HLTF	helicase-like trans	1.1766815	-1.0709826	1.262053	0.063427314	0.03954515
Bt.23179.1.S2_at	HSP90AA1	heat shock protein	-1.0591213	-1.167187	1.1020333	0.02901493	0.0066636
Bt.15888.1.A1_at	HSPA1A	heat shock 70kDa	1.0106859	-1.5090175	1.5251426	0.025828011	0.00431897
Bt.24270.1.S1_at	HSPD1	heat shock 60kDa	-1.0102025	-1.1623522	1.1506131	0.022891732	5.88E-04
Bt.27215.1.S1_at	HSPB2	heat shock 27kDa	1.0495689	-1.2398605	1.3013191	0.039045814	0.01639096
Bt.13003.11.S1_at	LOC100335904	hCG1793998-like	-1.2190292	1.0898942	-1.3286128	0.024142498	0.00277166
Bt.17611.1.A1_at	HDHD3	haloacid dehaloge	1.0717942	-1.463989	1.5690949	0.024013	0.00184819
Bt.28185.1.S1_at	HDHD1	haloacid dehaloge	-1.0001178	-1.3844209	1.3842579	0.027768422	0.00525247
Bt.28596.1.S1_at	GIMAP6	GTPase, IMAP fam	1.1650678	1.2439378	-1.0676956	0.024013	0.00215255
Bt.27314.1.A1_at	GCH1	GTP cyclohydrolas	1.0996157	-1.1564193	1.2716168	0.040293388	0.0174061
Bt.27812.1.S1_at	GEM	GTP binding prote	-1.0281217	1.2073232	-1.2412752	0.028367294	0.00622661
Bt.9408.1.S1_at	GTPBP4	GTP binding prote	-1.0207638	-1.4050353	1.376455	0.024766458	0.00375511
Bt.29962.3.S1_at	GRASP	GRP1 (general rece	1.1021641	1.2763126	-1.1580058	0.027363818	0.00504732
Bt.28132.1.S1_at	GHRH	growth hormone r	1.1555738	1.3419647	-1.1612973	0.032539457	0.01093356
Bt.29849.1.A1_at	GDF6	growth differentia	1.0194684	1.6381754	-1.6068918	0.027285432	0.00501358
Bt.21347.1.A1_at	GZMB /// LOC100125	granzyme B (granz	1.0661306	1.2866001	-1.206794	0.02901493	0.00762049
Bt.18123.1.A1_at	GORAB	golgin, RAB6-inter	-1.1005092	-1.4175433	1.2880796	0.04742311	0.02419752
Bt.20280.1.S1_at	GYLTL1B	glycosyltransferas	1.1549913	1.2576965	-1.088923	0.028367294	0.00619757
Bt.20778.1.S1_at	GYPC	glycophorin C (Ger	1.234384	1.5146174	-1.227023	0.045079704	0.02163264
Bt.9873.2.S1_at	GPX3	glutathione peroxi	-1.0143466	-1.2666969	1.2487812	0.024013	0.00211974
Bt.8142.1.S1_at	GHRL	ghrelin/obestatin	-1.1748245	1.249132	-1.4675108	0.024013	0.00138695
Bt.22350.1.A1_at	GMCL1	germ cell-less hom	1.099155	-1.2870606	1.414679	0.024570785	0.00339045
Bt.28268.1.A1_at	GTF3C1	General transcript	1.3068829	1.2827182	1.0188388	0.027768422	0.00574634
Bt.23498.2.S1_at	GJA1	gap junction prote	1.0355576	1.4058002	-1.3575296	0.027768422	0.00528173
Bt.16092.1.S1_at	GGCX	gamma-glutamyl c	-1.0235974	-1.4461731	1.4128339	0.03730011	0.01523637
Bt.26885.1.S1_at	GPR88	G protein-coupled	-1.0852848	-1.2381878	1.1408875	0.055976734	0.03188498
Bt.21134.1.S1_at	GPR65	G protein-coupled	1.2109053	1.0024687	1.2079234	0.024013	0.00183525
Bt.25474.1.S1_at	GPR162	G protein-coupled	1.0448766	1.2756112	-1.2208247	0.03607441	0.01404271
Bt.25474.1.S1_at	GPR162	G protein-coupled	1.0448767	1.2756112	-1.2208246	0.036074318	0.01404273
Bt.27255.1.S1_at	GPR155	G protein-coupled	1.0350763	-1.5314618	1.5851798	0.030912247	0.00945937
Bt.182.1.S1_at	FXD2	FXD domain cont	-1.1034386	1.0339093	-1.1408554	0.033487722	0.01180957
Bt.2587.2.S1_a_at	FH	fumarate hydratase	1.0811723	-1.2512681	1.3528364	0.032761794	0.01106724
Bt.5760.1.S1_at	FTSJ3	FtsJ homolog 3 (E.	-1.2228901	-1.32548	1.0838913	0.024013	0.00242205
Bt.14137.2.S1_a_at	FOSL1	FOS-like antigen 1	-1.081653	1.2828892	-1.387641	0.040686555	0.01791359
Bt.25923.1.S1_at	LOC100336530	formin binding pro	-1.4609846	1.0700649	-1.5633482	0.032178592	0.01050251
Bt.22310.1.S1_at	FOXP3	Forkhead box P3	-1.3574748	-1.3797922	1.0164404	0.06048709	0.00654874
Bt.24660.3.A1_a_at	FLYWCH2	FLYWCH family me	-1.0610774	1.3101282	-1.3901474	0.024013	0.00163305
Bt.20548.1.S1_at	FGFR3	fibroblast growth f	-1.2696376	-1.526588	1.2023809	0.022891732	7.69E-04
Bt.15832.1.A1_at	FECH	ferrochelataase	-1.0303613	-1.672837	1.6235441	0.028171103	0.00606955
Bt.1573.2.S1_a_at	FDX1	ferredoxin 1	1.1607224	-1.1020843	1.2792139	0.033626564	0.01197724
Bt.26724.1.A1_at	FOS	FBJ murine osteos	1.001851	1.2169875	-1.214739	0.06308252	0.03909779
Bt.9929.1.A1_at	FOS	FBJ murine osteos	1.0979004	-1.1822107	1.2979496	0.0351668	0.01342326
Bt.7257.1.S1_at	FASTKD5	FAST kinase doma	1.095069	-1.1989347	1.3129163	0.0472649	0.02394446
Bt.24844.1.S1_at	FSCN1	fascin homolog 1,	-1.1302717	1.1381372	-1.2864041	0.08541716	0.06096914
Bt.8533.3.A1_a_at	FSCN1	fascin homolog 1,	1.1147609	1.258515	-1.1289551	0.049705237	0.02599426
Bt.745.1.S1_at	FAM96A	family with sequen	1.1511836	-1.0426476	1.2002788	0.036972128	0.01472906
Bt.9108.1.S1_at	FAM107B	family with sequen	1.5847368	-1.089927	1.7272475	0.027768422	0.0053102
Bt.20525.1.S1_at	FBXO2	F-box protein 2	1.1192713	1.2633225	-1.1287009	0.040293388	0.01745135
Bt.23190.3.A1_a_at	AU018091_Mmu	expressed sequenc	1.0391374	1.3761125	-1.3242835	0.024570785	0.00340664

Bt.8128.1.S1_at	ETAA1	Ewing tumor-assoc	-1.0298457	-1.3355778	1.2968718	0.024013	0.00183352
Bt.28157.1.S1_at	ESR1	estrogen receptor	1.2746375	1.3182013	-1.0341774	0.04033661	0.01767399
Bt.29963.1.S1_at	EBI3	Epstein-Barr virus	1.0060785	1.2634571	-1.2558235	0.02901493	0.00767882
Bt.1350.1.S1_at	ECT2	epithelial cell trans	1.0394579	-1.2363486	1.2851323	0.025828011	0.00448637
Bt.3007.3.S1_a_at	ECT2	epithelial cell trans	1.0622133	-1.3642708	1.4491466	0.024766458	0.00384918
Bt.11769.1.A1_at	EID3	EP300 interacting	-1.0650723	-1.3407714	1.2588549	0.03626372	0.01417232
Bt.11402.1.A1_at	EDN1	endothelin 1	-1.1377195	-1.8495759	1.6256871	0.02901493	0.00686156
Bt.3458.1.S1_at	EGLN2	egl nine homolog 2	-1.0301559	-1.2371861	1.2009698	0.079790294	0.05571223
Bt.26908.1.A1_a_at	ENC1	ectodermal-neural	1.0126121	-1.6643014	1.6852919	0.024737129	0.00352124
Bt.17618.1.S1_at	DNM1L	dynamin 1-like	1.0215284	-1.3104088	1.3386198	0.027157558	0.00496134
Bt.17183.1.A1_at	DUSP7	dual specificity ph	1.0848587	1.3566712	-1.2505512	0.08236164	0.05803149
Bt.13592.1.A1_at	DUSP16	dual specificity ph	1.0549586	-1.183428	1.2484676	0.030352592	0.00865598
Bt.28123.1.S1_at	DAPP1	dual adaptor of ph	1.0071675	-1.2120546	1.2207419	0.04022706	0.01722799
Bt.10851.1.S1_at	DPH3	DPH3, KTI11 hom	1.2141088	1.39117	-1.1458364	0.065615065	0.04182671
Bt.26494.1.S1_at	DONSON	downstream neigh	-1.16819	-1.5397745	1.3180857	0.049795598	0.02618228
Bt.24540.1.S1_at	DPM3	dolichyl-phosphate	1.136204	1.1659244	-1.0261576	0.050006375	0.02659659
Bt.28640.1.A1_at	DDIT4	DNA-damage-indu	1.2417666	-1.3240348	1.6441423	0.022891732	3.98E-04
Bt.20213.1.S1_at	DIXDC1	DIX domain contai	1.0727723	-1.1644478	1.2491872	0.05325158	0.02901552
Bt.22078.1.S1_at	DPYSL5	dihydropyrimidina	1.134933	-1.2793763	1.4520062	0.028583735	0.00633061
Bt.23550.1.S1_at	DGAT2	diacylglycerol O-ac	-1.5035712	-1.630555	1.0844549	0.077358104	0.05330329
Bt.13370.3.S1_at	DENND5A	DENN/MADD dom	-1.013435	-1.3623583	1.3442976	0.02901493	0.00730013
Bt.21985.1.S1_at	DLC1	deleted in liver car	1.0297567	-1.3190126	1.3582622	0.024766458	0.00380486
Bt.13752.1.S1_at	DEDD	death effector dor	1.2505199	-1.3410302	1.676985	0.04752833	0.02431838
Bt.16662.1.S1_at	DEDD	death effector dor	-1.0768688	1.2101946	-1.3032207	0.054938056	0.03082743
Bt.13425.1.A1_at	DDX20	DEAD (Asp-Glu-Ala	1.053767	-1.0859132	1.1442995	0.036298547	0.01421159
Bt.29.1.S1_at	DBHD1	DDHD domain con	1.122197	-1.1230695	1.2603054	0.06371558	0.03989253
Bt.29346.1.S1_at	DCAF4	DDB1 and CUL4 as	1.0597994	-1.170501	1.2404963	0.0472649	0.02398252
Bt.13081.1.A1_at	CYP1A1	cytochrome P450,	1.0722394	1.341198	-1.2508382	0.06668915	0.04312408
Bt.28261.1.S1_at	COX6C /// MGC14871	cytochrome c oxid	-1.0623932	-1.4630021	1.3770816	0.02901493	0.00694204
Bt.5064.1.S1_a_at	CNGB1	cyclic nucleotide g	1.1311983	1.2598	-1.1136863	0.04540309	0.0219475
Bt.4511.1.S1_at	CTPS	CTP synthase	-1.0495894	-1.2983159	1.2369751	0.036995005	0.01498102
Bt.20846.1.A1_at	CTDSPL	CTD (carboxy-term	1.0383841	1.2472553	-1.2011502	0.034804247	0.01286712
Bt.2262.1.S1_at	CSRP2	CSRP2 binding pro	-1.0386491	-1.3401258	1.2902585	0.029080318	0.00776845
Bt.3220.1.S1_at	CRYL1	crystallin, lambda	1.0182836	-1.2073525	1.2294273	0.053086203	0.02885038
Bt.1647.1.S1_at	CRYGS	crystallin, gamma	1.1253303	1.3298831	-1.1817713	0.032178592	0.01050161
Bt.21479.1.A1_at	CRNKL1	crooked neck pre-	1.3054217	-1.2246907	1.5987378	0.03079631	0.00919414
Bt.28101.1.S1_at	CFDP2	craniofacial devel	-1.1302574	-1.4819845	1.311192	0.099456415	0.07450445
Bt.8949.1.S1_at	CHUK	conserved helix-lo	1.1262633	-1.188111	1.3381257	0.024013	0.00235988
Bt.27852.1.A1_at	CFB	complement facto	1.1215283	-1.235396	1.3855315	0.030879559	0.00941025
Bt.17728.2.A1_a_at	C8G	complement comp	1.1560302	1.4881694	-1.2873102	0.07139212	0.04760662
Bt.4507.1.S1_at	C4A	complement comp	1.3243521	1.3194101	1.0037457	0.033150923	0.0114564
Bt.16082.1.S1_at	C1QBP	complement comp	1.0056458	-1.2079897	1.2148097	0.058056306	0.03343879
Bt.27257.1.S1_at	CSF3	colony stimulating	1.171673	-1.1565738	1.3551263	0.08681225	0.06245574
Bt.4660.1.S1_at	CSF3	colony stimulating	1.1080476	1.3403182	-1.2096215	0.06168527	0.03779585
Bt.25171.1.A1_at	COL13A1	collagen, type XIII,	1.119673	-1.3218285	1.4800156	0.027768422	0.00543723
Bt.4956.1.S1_at	COL11A1	collagen, type XI, a	1.025069	1.5476866	-1.5098364	0.03079631	0.00928573
Bt.13030.1.A1_at	COL2A1	collagen, type II, a	1.1069392	1.3216166	-1.1939379	0.04025451	0.01726819
Bt.13030.2.S1_at	COL2A1	collagen, type II, a	1.0268463	1.3556072	-1.3201658	0.024570785	0.00328434
Bt.9197.1.S1_at	CCDC28A	coiled-coil domain	1.1092129	-1.1230901	1.245746	0.08579262	0.06147966
Bt.28626.1.S1_at	CCDC22	coiled-coil domain	1.3570863	-1.3757696	1.8670381	0.0351668	0.01348656
Bt.25342.1.A1_at	CCDC132	coiled-coil domain	1.1205611	-1.2873085	1.4425077	0.022891732	8.41E-04
Bt.17441.1.A1_at	COQ10A	coenzyme Q10 hom	1.10519	-1.2334272	1.3631715	0.029707072	0.00809944
Bt.22486.1.S1_at	COPB1	coatamer protein	-1.0185264	-1.0888386	1.0690331	0.054460157	0.03026824
Bt.13106.1.A1_at	F9	coagulation factor	1.0151155	1.3456911	-1.3256531	0.022891732	5.60E-04
Bt.20954.1.S1_at	CLUAP1	clusterin associate	1.1301984	-1.277294	1.4435955	0.02901493	0.00698942
Bt.12504.1.S1_at	CLU	Clusterin	-1.9695933	-1.1895244	-1.6557821	0.02901493	0.00751888
Bt.12177.1.S1_at	CLDN4	claudin 4	1.0327471	1.3259937	-1.283948	0.060288828	0.03591766
Bt.7639.1.S1_at	CLDN4	claudin 4	1.025448	-1.276219	1.308696	0.042790655	0.0199087
Bt.20140.1.S1_at	CLDN1	claudin 1	1.0409123	-1.4140944	1.4719483	0.06783509	0.04416587
Bt.20391.1.A1_at	CLDN1	claudin 1	-1.0306299	-1.6562512	1.6070281	0.024570785	0.00344339
Bt.20114.1.S1_at	C25H7ORF47	chromosome 7 op	1.1791781	-1.1811514	1.3927878	0.02901493	0.00685556
Bt.9603.1.A1_at	C9H6ORF203	chromosome 6 op	1.0676675	-1.1540802	1.2321738	0.076685	0.05256851
Bt.10018.1.S1_at	C7H5ORF15	chromosome 5 op	1.0676248	-1.1151098	1.190519	0.036972128	0.01485002
Bt.13402.1.S1_at	C13H20orf30	chromosome 20 o	1.0801699	-1.1131903	1.2024348	0.027084686	0.00491927
Bt.3865.3.S1_a_at	C25H16orf14	chromosome 16 o	1.0523196	-1.2399939	1.3048699	0.06521136	0.04115459
Bt.23489.1.S1_at	C15orf39 Hsa	chromosome 15 o	1.0203115	1.2379055	-1.2132623	0.0498451	0.0264174
Bt.26522.1.A1_at	C10H14orf37	chromosome 14 o	1.1917511	-1.1566774	1.3784715	0.025753139	0.00415036
Bt.25093.2.S1_at	C12H13orf27	chromosome 13 o	-1.0816988	1.3152229	-1.4226749	0.024013	0.00182874
Bt.22709.2.S1_at	C12orf39 Hsa	chromosome 12 o	1.1465914	-1.4917815	1.7104639	0.024013	0.00227805
Bt.2391.1.S1_at	C16H1ORF55	chromosome 1 op	1.0702565	-1.2438669	1.3312566	0.06048709	0.03649117
Bt.26176.2.S1_at	C16H1ORF55	chromosome 1 op	1.1834812	1.2900643	-1.090059	0.044219714	0.02112546
Bt.27875.1.A1_at	C1orf51 Hsa	chromosome 1 op	-1.1319174	-1.4243389	1.2583418	0.043638464	0.02057022
Bt.7654.1.S1_at	C3H1orf43	chromosome 1 op	1.072388	-1.1346633	1.2167994	0.06973509	0.04578367
Bt.23501.1.S1_at	C16H1orf174	chromosome 1 op	1.1639779	-1.1155643	1.2984922	0.046260826	0.02285892
Bt.26587.2.S1_at	CH25H	cholesterol 25-hyd	-1.0204909	1.1751803	-1.1992608	0.03079631	0.00917699

Bt.2513.2.S1_at	CXCL3	Chemokine (C-X-C	1.06916	-1.1369627	1.2155949	0.07679861	0.05270067
Bt.20465.1.S1_at	CXCL2	chemokine (C-X-C	1.0803668	-1.3457812	1.4539374	0.022891732	9.76E-04
Bt.26964.1.S1_at	CCL5	chemokine (C-C m	1.1041877	-1.178647	1.3014477	0.024013	0.00182855
Bt.18025.1.S1_at	CCL3	chemokine (C-C m	1.1644697	-1.2827843	1.4937634	0.0472649	0.02395866
Bt.9609.1.S1_a_at	CCL3	chemokine (C-C m	1.0764062	-1.3485868	1.4516273	0.027768422	0.00546249
Bt.9974.1.S1_a_at	CCL3	chemokine (C-C m	-1.0248569	1.2865101	-1.3184887	0.054512743	0.03039615
Bt.8421.1.A1_at	CCL2	chemokine (C-C m	-1.1089511	-1.4666048	1.3225154	0.03878532	0.01621029
Bt.9246.1.A1_at	CCL2	chemokine (C-C m	1.0126576	-1.1268035	1.1410662	0.054460157	0.03032834
Bt.24448.1.A1_at	CEP120	centrosomal prote	1.0115116	-1.1990564	1.2128594	0.080929756	0.05679382
Bt.13873.2.S1_at	CDC37L1	cell division cycle	1.0255789	-1.258467	1.2906572	0.050666563	0.0270341
Bt.26864.2.S1_at	CDC2L2	cell division cycle	-1.0562409	1.2008982	-1.2684377	0.059064664	0.03489615
Bt.27247.1.A1_at	CDC42EP4	CDC42 effector pro	-1.1057823	1.509588	-1.6692756	0.09008519	0.0658913
Bt.19398.1.A1_at	CDC42EP3	CDC42 effector pro	-1.0037092	-1.3992822	1.3941112	0.06783509	0.04411613
Bt.24912.1.A1_at	CD83	CD83 molecule	-1.0530006	-1.2691296	1.2052506	0.095359795	0.07082908
Bt.8247.2.S1_at	CD83	CD83 molecule	1.0952446	1.2611855	-1.1515102	0.05641992	0.03229692
Bt.16126.1.S1_at	CD72	CD72 molecule	-1.014873	-1.2421727	1.2239686	0.031530906	0.00992559
Bt.16439.1.S1_at	CD40	CD40 molecule, TN	1.1618257	1.1970245	-1.0302962	0.064664565	0.04076381
Bt.11331.1.A1_at	CD33	CD33 molecule	-1.0586838	1.3745424	-1.4552057	0.024013	0.00122094
Bt.9141.2.S1_at	CNOT3	CCR4-NOT transcri	1.0313398	1.3450407	-1.3041685	0.025828011	0.0045198
Bt.9768.1.S1_at	CCR4L	CCR4 carbon cata	1.2306885	-1.6785381	2.0657575	0.07521876	0.0512976
Bt.9541.1.S1_at	CNBP	CCHC-type zinc fin	-1.0332863	-1.2046766	1.1658691	0.042984866	0.02007986
Bt.10006.2.S1_at	CEBPD	CCAAT/enhancer b	1.0023762	-1.393022	1.3963319	0.036382113	0.01434715
Bt.1037.1.S1_at	CEBPD	CCAAT/enhancer b	-1.539023	-1.2718848	-1.2100334	0.0498451	0.02636991
Bt.28175.1.S1_at	CEBPD	CCAAT/enhancer b	1.0980603	1.2949595	-1.1793156	0.022891732	4.49E-04
Bt.19687.1.A1_at	CEBPA	CCAAT/enhancer b	1.010032	-1.3731548	1.3869303	0.027768422	0.0056797
Bt.900.1.S1_at	CITED2	Cbp/p300-interact	1.1065518	1.2055645	-1.0894787	0.07724839	0.05313013
Bt.11032.1.S1_at	CAMP	cathelicidin antimi	1.3185285	1.3445178	-1.0197109	0.06783509	0.04410766
Bt.4259.1.S1_at	CATHL2	cathelicidin 2	1.0644403	1.5546315	-1.4605155	0.030777313	0.00899156
Bt.6599.2.S1_at	CASP4	caspase 4, apopto	1.1641753	1.3821051	-1.1871969	0.06336082	0.03936136
Bt.9391.2.S1_at	CASP4	caspase 4, apopto	1.0726724	-1.2150439	1.303344	0.06212847	0.03827221
Bt.14054.1.A1_at	CFLAR	CASP8 and FADD- <i>i</i>	-1.1056798	-1.7639033	1.5953112	0.028761048	0.00652046
Bt.8694.2.S1_at	CASKIN2	CASK interacting p	1.0527594	1.3249202	-1.2585213	0.07770535	0.0538582
Bt.1408.1.S1_at	CSNK2A2	casein kinase 2, al	1.1545354	-1.0523896	1.2150211	0.024570785	0.00345724
Bt.5381.2.A1_at	CSN2	casein beta	1.0944673	1.6911889	-1.5452164	0.022891732	5.69E-04
Bt.5381.2.S1_x_at	CSN2	casein beta	1.1357101	1.9932283	-1.7550502	0.025828011	0.00448404
Bt.4599.1.S1_at	CROT	carnitine O-octano	-1.558073	-2.5029626	1.6064476	0.02901493	0.00731525
Bt.14213.1.A1_at	CES2	carboxylesterase 2	1.0952419	1.4316639	-1.3071668	0.0472649	0.02382778
Bt.22496.1.S1_at	CBR3	carbonyl reductase	1.1862917	-1.248469	1.4810485	0.031097824	0.00960406
Bt.6398.1.S1_at	CA5B	carbonic anhydras	-1.0074487	-1.3931468	1.3828464	0.03607441	0.01402778
Bt.1390.2.S1_at	CREB1	cAMP responsive e	1.1796391	-1.3261985	1.5644356	0.028171103	0.00603715
Bt.27828.1.S1_at	CLMN	calmin (calponin-li	1.0784311	1.3261743	-1.2297255	0.024570785	0.00299615
Bt.355.1.S1_at	CALD1	Caldesmon 1	-1.1237463	1.3684198	-1.5377567	0.028171103	0.00609213
Bt.13563.1.A1_at	CAMLG	calcium modulatin	1.0794892	-1.1994718	1.2948169	0.0672912	0.0435884
Bt.13100.1.S1_at	CACNB4	calcium channel, v	1.1011122	1.440342	-1.308079	0.022891732	9.92E-04
Bt.7540.1.S1_at	CACNB1	calcium channel, v	1.1396945	1.4167725	-1.243116	0.027768422	0.00563681
Bt.12516.1.S1_at	CABP4	calcium binding pr	1.0315869	1.3143536	-1.2741084	0.024766458	0.00367927
Bt.25433.1.S1_at	C1GALT1C1	C1GALT1-specific d	1.0324199	-1.353152	1.397021	0.024013	0.00190538
Bt.16738.1.A1_at	CLEC4E	C-type lectin doma	-1.1720748	1.0337995	-1.2116903	0.053438853	0.02941474
Bt.27112.1.S1_at	CLEC4E	C-type lectin doma	1.0659682	-1.4407977	1.5358444	0.041391153	0.01866258
Bt.1366.1.S1_at	CLEC3B	C-type lectin doma	1.2879541	1.2796249	1.0065091	0.027768422	0.00537303
Bt.28402.1.A1_at	BTG3	BTG family, memb	-1.033445	1.1928769	-1.2338463	0.022891732	3.57E-04
Bt.1756.1.S1_at	BTG2	BTG family, memb	-1.1087658	1.2947648	-1.435591	0.057961367	0.03334315
Bt.22695.1.S1_at	BRD4	bromodomain con	-1.20292	-1.2482045	1.0376455	0.066560365	0.04289968
Bt.28471.1.S1_at	BAZ1A	bromodomain adja	1.144701	-1.1750468	1.3450773	0.024013	0.00200466
Bt.19850.2.S1_at	BDKRB2	bradykinin recept	1.3710206	-1.081643	1.4829547	0.02901493	0.00758342
Bt.21902.1.S1_at	BDKRB2	bradykinin recept	-1.0615395	-1.389507	1.3089546	0.041232325	0.01841614
Bt.6000.1.A1_at	BCL2A1	BCL2-related prote	-1.5542371	-1.4856764	-1.0461478	0.045480996	0.02213872
Bt.27074.1.A1_at	BAX	BCL2-associated X	-1.114045	1.1690214	-1.3023424	0.049018808	0.0253235
Bt.28059.1.S1_at	BATF	basic leucine zippe	-1.4134078	-1.413244	-1.0001159	0.059017222	0.03482642
Bt.7353.1.S1_at	BATF	basic leucine zippe	1.2325063	-1.2230947	1.5074719	0.024766458	0.0037237
Bt.27943.1.S1_at	BIRC3	baculoviral IAP rep	1.0301236	1.2857567	-1.2481577	0.026862508	0.00485993
Bt.6225.1.S1_at	BIRC3	baculoviral IAP rep	1.0946491	-1.0157095	1.1118455	0.07770535	0.05387205
Bt.20629.2.S1_at	BCL3	B-cell CLL/lympho	1.243487	-1.3052803	1.623099	0.033978608	0.01214076
Bt.22612.2.S1_at	BCL3	B-cell CLL/lympho	1.1471497	-1.424408	1.6340092	0.08867458	0.06461024
Bt.20513.3.S1_a_at	AXIN2	axin 2	-1.0001081	1.5199975	-1.5201617	0.024013	0.00193757
Bt.20898.1.S1_at	AMFR	autocrine motility	-1.0009761	-1.373621	1.3722814	0.025828011	0.00450287
Bt.21223.1.S1_at	ATP1A1	ATPase, Na ⁺ /K ⁺ tr	-1.3386834	-1.4244753	1.0640868	0.049705237	0.02598919
Bt.14987.1.A1_at	ATP6AP2	ATPase, H ⁺ transp	1.0261327	-1.1552596	1.1854496	0.085699916	0.06135266
Bt.20352.1.S1_at	ATP8A1	ATPase, aminopho	1.068914	1.3174765	-1.2325374	0.024766458	0.00381427
Bt.27194.1.S1_at	AGTPBP1	ATP/GTP binding p	1.0186231	-1.1939508	1.2161859	0.053372838	0.02919475
Bt.27829.1.A1_at	ATG4B	ATG4 autophagy r	1.1851796	-1.1630036	1.3783681	0.077641584	0.05366323
Bt.2869.1.A1_at	ATG4B	ATG4 autophagy r	1.0730076	-1.1760646	1.2619262	0.032487586	0.01075422
Bt.24353.1.S1_at	ARID5A	AT rich interactive	-1.0345825	-1.5198791	1.4690748	0.04004019	0.01709903
Bt.27081.1.S1_at	AIP	aryl hydrocarbon r	1.0660459	-1.3751374	1.4659597	0.024013	0.00236201
Bt.14075.1.S1_at	ARRDC2	arrestin domain co	1.2122176	1.0993392	1.1026783	0.03009883	0.00842342

Bt.22490.2.S1_at	ARRDC2	arrestin domain co	1.0775682	-1.3529124	1.4578555	0.03507604	0.01333633
Bt.4628.2.S1_a_at	ARRDC1	arrestin domain co	-1.0049043	1.3831263	-1.3899095	0.036972128	0.01469308
Bt.494.1.S1_at	ARR3	arrestin 3, retinal (1.1484691	1.7087383	-1.4878399	0.082946576	0.05867811
Bt.23649.1.A1_at	ARG2	Arginase, type II	1.0101656	-1.15915	1.1709334	0.034339253	0.01242054
Bt.9491.1.S1_at	ARG2	arginase, type II	1.1195989	-1.0766144	1.2053761	0.09013659	0.06599399
Bt.5481.1.S1_at	AGAP3	ArfGAP with GTPa	1.0597208	1.3226498	-1.2481117	0.04973036	0.02611283
Bt.11733.1.S1_at	AATK	apoptosis-associat	1.2143073	1.2337791	-1.0160352	0.029707072	0.00810384
Bt.14565.1.A1_at	AATK	apoptosis-associat	1.1858504	1.4988378	-1.263935	0.043956228	0.02090639
Bt.21280.1.A1_at	APOA2	apolipoprotein A-I	1.0745403	-1.4076047	1.512528	0.053438853	0.02943642
Bt.5026.1.S1_at	ANXA8L1	Annexin 8-Like 1	-1.2985655	-1.0384938	-1.2504318	0.02901493	0.00711408
Bt.21130.2.S1_at	ANKRD33B	ankyrin repeat dor	1.2203885	1.4383148	-1.1785712	0.025828011	0.00441276
Bt.4265.1.S1_at	ANKRD33B	ankyrin repeat dor	-1.084939	-1.5148932	1.3962935	0.061957367	0.03809393
Bt.21855.1.S1_at	APPBP2	amyloid beta prec	1.243765	-1.0994928	1.3675107	0.03459086	0.0126385
Bt.8570.1.A1_at	AES	amino-terminal en	1.201715	-1.1485411	1.3802191	0.065615065	0.04180734
Bt.4177.1.S1_at	AOC3	amine oxidase, co	-1.2528304	1.0200468	-1.2779458	0.07476502	0.05082965
Bt.10085.1.A1_at	AEBP2	AE binding protein	-1.0498278	1.1852589	-1.2443177	0.06405255	0.04015167
Bt.318.1.S1_at	ADRB3	adrenergic, beta-3	-1.0025127	1.200971	-1.2039886	0.039706826	0.01683682
Bt.24924.1.S1_at	ADRB2	adrenergic, beta-2	-1.3897963	-1.7990648	1.294481	0.08823464	0.06416048
Bt.2581.1.S1_at	ADPGK	ADP-dependent gl	1.0503148	-1.2897316	1.3546243	0.04567432	0.02236912
Bt.29281.1.S1_at	AP1M2	adaptor-related pr	-1.0469544	1.44191	-1.509614	0.024570785	0.00337381
Bt.14048.1.A1_at	ACOT13	acyl-CoA thioester	1.1776707	-1.1142633	1.3122352	0.02901493	0.03362052
Bt.15996.1.S2_at	ACSS1	acyl-CoA syntheta	1.0989279	-1.274705	1.4008089	0.06370892	0.03980119
Bt.24292.1.S1_at	ACOX1	acyl-CoA oxidase 1	-1.0941272	-1.3097118	1.1970379	0.02901493	0.00766478
Bt.5966.1.A1_at	ACADM	acyl-CoA dehydrog	1.1298869	-1.2273359	1.3867507	0.04688844	0.02349393
Bt.401.1.S2_at	ACBD5	acyl-CoA binding d	1.0751575	-1.2412801	1.3345716	0.022891732	7.14E-04
Bt.6860.1.A1_at	ATF1	activating transcri	1.1768854	-1.0933434	1.2867398	0.029807545	0.00823792
Bt.20275.1.S1_at	ARPC5L	actin related prote	1.0844167	-1.1501958	1.2472917	0.07272725	0.04871598
Bt.3310.1.S1_at	ACR	acrosin	-1.1075543	-1.7106814	1.5445576	0.0351668	0.01350284
Bt.21989.1.A1_at	ASCL2	Achaete-scute con	-1.0497566	1.3544596	-1.4218532	0.0832985	0.05916254
Bt.5911.2.S1_at	S68402	Accession S68402	-1.0516521	-1.2317408	1.1712437	0.023475172	0.00109496
Bt.7901.3.S1_at	S68402	Accession S68402	1.1445262	-1.2002239	1.3736879	0.03885797	0.01628465
Bt.29829.1.S1_at	Z86039.1	Accession No Z860	-1.1503882	1.1257899	-1.2950956	0.043822575	0.02081185
Bt.29700.1.A1_at	U49775.1	Accession No U497	1.0816625	1.1773187	-1.0884343	0.06652952	0.04275243
Bt.29800.1.A1_at	U32253	Accession No U322	-1.1324292	1.1010077	-1.2468133	0.07005323	0.04619057
Bt.29800.1.A1_x_at	U32253	Accession No U322	-1.2345924	-1.05948	-1.1652814	0.058141094	0.03367804
Bt.28026.1.A1_at	U30308.1	Accession No U303	-1.1579325	1.2197204	-1.4123539	0.036972128	0.01486832
Bt.29845.1.A1_at	U11629	Accession No U116	1.0567768	1.3879268	-1.3133584	0.024013	0.00146745
Bt.10232.1.A1_at	CK983156	Accession No CK98	-1.0625074	-1.3176029	1.2400882	0.082524456	0.05826285
Bt.2325.1.S1_at	CK983098	Accession No CK98	1.128013	-1.1888837	1.3410763	0.02901493	0.00751319
Bt.11910.1.S1_at	CK981924	Accession No CK98	1.0760818	-1.1088841	1.1932501	0.0472649	0.02398318
Bt.24538.1.S1_at	CK980553	Accession No CK98	1.1318667	-1.0144757	1.1482512	0.042790655	0.01995889
Bt.11500.1.A1_at	CK979767	Accession No CK97	1.1875322	-1.2868339	1.5281568	0.024142498	0.00261058
Bt.13665.1.A1_at	CK978616	Accession No CK97	1.024874	-1.2116368	1.2417749	0.041296616	0.01855972
Bt.11932.1.S1_at	CK976069	Accession No CK97	1.0574328	-1.0256279	1.0845325	0.059017222	0.03464296
Bt.6810.1.A1_at	CK973638	Accession No CK97	1.081614	-1.3684967	1.4801852	0.031050848	0.00954567
Bt.14093.1.S1_at	CK973168	Accession No CK97	1.0134058	1.3382566	-1.3205535	0.09622638	0.07167675
Bt.18023.1.S1_at	CK972079	Accession No CK97	1.143266	-1.0691497	1.2223226	0.05149784	0.02759621
Bt.28648.1.S1_at	CK971411	Accession No CK97	-1.1919639	-1.7272593	1.4490869	0.03030335	0.00857246
Bt.4270.1.S1_at	CK970036	Accession No CK97	-1.0336477	-1.173356	1.1351606	0.036972128	0.01482488
Bt.20063.1.S1_at	CK968078	Accession No CK96	1.1581928	-1.2926445	1.4971315	0.032761794	0.01105584
Bt.15631.1.S1_at	CK966456	Accession No CK96	-1.0974088	-1.7086676	1.5570021	0.033487722	0.0118988
Bt.21097.1.S1_at	CK966370	Accession No CK96	1.02774	-1.283692	1.3193016	0.024013	0.00236261
Bt.842.1.A1_at	CK964339	Accession No CK96	1.0368712	-1.2162831	1.261129	0.052423984	0.02837934
Bt.12359.1.S1_at	CK962217	Accession No CK96	1.0561851	-1.0686837	1.1287278	0.031530906	0.00999404
Bt.12220.1.S1_a_at	CK961206	Accession No CK96	-1.030583	-1.3411018	1.301304	0.041864008	0.01919741
Bt.60.2.A1_at	CK959706	Accession No CK95	1.0780343	-1.1262319	1.2141167	0.024013	0.00240956
Bt.13881.1.S1_at	CK954256	Accession No CK95	1.1819426	-1.1787488	1.3932136	0.06461285	0.04068555
Bt.2670.1.S1_at	CK943460	Accession No CK94	-1.0667297	1.1457406	-1.2221954	0.04786793	0.02465576
Bt.21963.1.S1_at	CK942758	Accession No CK94	-1.3554853	1.0335332	-1.4009391	0.030777313	0.00896322
Bt.7784.1.S1_at	CK941839	Accession No CK94	-1.0186502	1.2582483	-1.2817149	0.053131852	0.02891274
Bt.4686.1.S1_at	CK847421	Accession No CK84	1.0557436	-1.1764368	1.2420155	0.024013	0.00242676
Bt.17306.1.S1_at	CK816719	Accession No CK81	1.1023638	1.3400093	-1.2155781	0.024737129	0.00353138
Bt.26409.1.A1_at	CK779587	Accession No CK77	1.0491828	1.2477953	-1.1893022	0.09145446	0.06741131
Bt.22018.1.A1_at	CK775088	Accession No CK77	1.1678299	-1.2008336	1.4023693	0.022891732	1.95E-04
Bt.12809.1.S1_at	CK773854	Accession No CK77	-1.0015168	1.2603484	-1.2622601	0.0933504	0.06894076
Bt.14283.1.A1_at	CK773057	Accession No CK77	1.0663761	-1.3864734	1.4785019	0.030480286	0.00880556
Bt.16471.1.S1_at	CK770978	Accession No CK77	-1.0769739	-1.4220604	1.3204223	0.031530906	0.01013534
Bt.25361.1.A1_at	CK726729	Accession No CK72	-1.0290457	1.2251772	-1.2607633	0.06973509	0.04566587
Bt.17350.1.A1_at	CB461800	Accession No CB46	-1.1536247	-1.4888545	1.2905884	0.06212847	0.03828694
Bt.1922.1.S1_at	CB458617	Accession No CB45	-1.550503	-1.4234605	-1.0892491	0.091045685	0.06697252
Bt.2706.1.S1_at	CB456865	Accession No CB45	-1.052826	-1.2691711	1.2054899	0.039568648	0.01671546
Bt.17645.1.A1_at	CB456195	Accession No CB45	-1.0988828	-1.4146253	1.2873305	0.028761048	0.00654492
Bt.1824.1.S1_at	CB452353	Accession No CB45	1.0703281	-1.2552035	1.3434795	0.07523109	0.05141234
Bt.1434.1.S1_at	CB445636	Accession No CB44	1.1173599	-1.1906593	1.3303949	0.022891732	8.45E-04
Bt.18336.1.A1_at	CB442916	Accession No CB44	1.1386696	-1.0751495	1.2242401	0.041147	0.01823263

Bt.22403.1.S1_at	CB441530	Accession No CB44	1.0055794	-1.5906556	1.5995305	0.03316394	0.01154606
Bt.9511.1.S1_at	CB436550	Accession No CB436550		-1.0452285	1.2198528	0.07724839	0.0531731
Bt.21865.1.A1_at	CB434195	Accession No CB43	1.0810544	1.1515908	-1.0652477	0.06634728	0.04257479
Bt.16984.1.S1_at	CB432850	Accession No CB43	1.0798424	1.3795072	-1.2775079	0.032790463	0.01116961
Bt.16739.1.A1_at	CB427148	Accession No CB42	-1.0673926	-1.2988139	1.21681	0.025828011	0.00454777
Bt.16078.1.A1_s_at	BP108985	Accession No BP10	1.1522678	-1.2169259	1.4022245	0.024570785	0.00310294
Bt.29776.1.A1_at	AJ012809	Accession No AJ01	1.2139413	1.2689196	-1.045289	0.038569864	0.01594584
Bt.29727.1.A1_at	AF015503.1	Accession No AF01	1.0093138	1.3592203	-1.3466777	0.059017222	0.03477118
Bt.18571.1.S1_at	CK982730	Accession CK9827	-1.1912564	1.0659629	-1.2698352	0.025753139	0.00419726
Bt.11154.1.S1_at	CK982422	Accession CK9824	1.0686746	-1.2366122	1.321536	0.045694474	0.02247587
Bt.27206.1.A1_at	CK980302	Accession CK9803	1.2187331	1.2204316	-1.0013937	0.02901493	0.00728374
Bt.21196.1.S1_at	CK975559	Accession CK9755	1.1985532	-1.0788484	1.2930572	0.034339253	0.01238057
Bt.17151.1.S1_at	CK974498	Accession CK9744	-1.107005	-1.227665	1.1089967	0.045817506	0.02256876
Bt.25823.1.A1_at	CK973132	Accession CK9731	-1.2622876	-1.380351	1.0935313	0.04219014	0.01949989
Bt.3364.2.S1_at	CK968180	Accession CK9681	1.0149236	1.2126328	-1.194802	0.05254975	0.02848456
Bt.17361.1.A1_at	CK967661	Accession CK9676	-1.0043452	-1.3074502	1.3017936	0.022891732	7.67E-04
Bt.23653.1.S1_at	CK964062	Accession CK9640	1.0993797	-1.1022699	1.2118132	0.024013	0.00159137
Bt.3458.2.S1_at	CK962939	Accession CK9629	-1.0465828	-1.3263049	1.2672718	0.024570785	0.00313946
Bt.28179.1.S1_at	CK955216	Accession CK9552	-1.0153095	-1.4342347	1.4126085	0.025828011	0.00447651
Bt.8597.2.S1_at	CK955069	Accession CK9550	1.0207837	1.281608	-1.2555139	0.024766458	0.00384669
Bt.29900.1.S1_at	CK952663	Accession CK9526	-1.1370134	-1.6327943	1.2930572	0.0472649	0.0238057
Bt.6588.1.S1_at	CK952663	Accession CK9526	1.0282829	-1.2430471	1.2782041	0.02901493	0.00756033
Bt.6157.1.S1_at	CK952523	Accession CK9525	1.1027806	-1.2497863	1.37824	0.024570785	0.0034729
Bt.20227.1.S1_at	CK951297	Accession CK9512	-1.1079266	-1.5653954	1.4129052	0.07139212	0.04753425
Bt.12257.1.S1_at	CK949319	Accession CK9493	1.0729975	-1.4882534	1.5968922	0.024570785	0.00307613
Bt.18420.1.S1_at	CK946845	Accession CK9468	1.1722693	1.3188722	-1.1250591	0.059017222	0.03473581
Bt.9637.1.S1_at	CK849182	Accession CK8491	1.1492101	-1.040818	1.1961186	0.024013	0.00182185
Bt.24497.1.S1_at	CK847032	Accession CK8470	1.1062574	-1.2855375	1.4221355	0.024013	0.00132034
Bt.24552.1.S1_at	CK845991	Accession CK8459	1.0716072	-1.6538173	1.7722427	0.022891732	9.48E-04
Bt.1404.2.S1_at	CK834854	Accession CK8348	1.1149298	-1.182129	1.3179908	0.04773802	0.02449315
Bt.17154.1.S1_at	CK816668	Accession CK8166	1.165725	-1.2262236	1.4294394	0.03635977	0.01431264
Bt.20253.2.S1_at	CK774004	Accession CK7740	1.1047343	-1.607455	1.7758108	0.040293388	0.01737789
Bt.13232.1.S1_a_at	CK773833	Accession CK7738	-1.0295459	1.1525774	-1.1866314	0.061472975	0.03740511
Bt.25807.1.A1_at	CK773598	Accession CK7735	1.221672	1.3660944	-1.118217	0.02901493	0.00740381
Bt.9191.1.S1_at	CK773562	Accession CK7735	1.052923	-1.2332492	1.2985165	0.060308963	0.03597382
Bt.17957.1.A1_at	CK773270	Accession CK7732	1.116241	-1.1447406	1.2778063	0.029807545	0.00822989
Bt.612.2.S1_at	CK770939	Accession CK7709	-1.053636	-1.3986102	1.3274132	0.027768422	0.00537406
Bt.28541.1.S1_at	CK770697	Accession CK7706	-1.0821354	-1.2694408	1.1730887	0.090761736	0.06664413
Bt.26530.3.S1_a_at	CK770537	Accession CK7705	-1.090421	1.1413953	-1.2446015	0.09959929	0.07468187
Bt.27398.1.A1_at	CK769290	Accession CK7692	-1.2835603	-1.3755001	1.0716287	0.06652952	0.04278577
Bt.28085.1.S1_at	CK730252	Accession CK7302	-1.0960273	1.1580786	-1.2692856	0.08424872	0.06001605
Bt.24451.1.S1_at	CF930166	Accession CF9301	1.0655762	-1.2570454	1.3394775	0.024570785	0.00343163
Bt.6964.3.S1_at	CB535112	Accession CB5351	1.0134351	-1.2950008	1.3123994	0.053965136	0.02982384
Bt.18862.1.S1_at	CB534665	Accession CB5346	1.1235484	-1.0923344	1.2272905	0.050002106	0.02653822
Bt.26255.1.S1_at	CB534578	Accession CB5345	1.0086743	1.2990705	-1.2878989	0.03316394	0.01150149
Bt.13620.1.A1_at	CB530676	Accession CB5306	-1.248611	-1.4839886	1.1885116	0.045694474	0.022434
Bt.15600.1.A1_a_at	CB530546	Accession CB5305	1.0658964	-1.2720698	1.3558947	0.024142498	0.0027186
Bt.17989.2.S1_at	CB468085	Accession CB4680	1.1810759	-1.1752741	1.388088	0.03864421	0.01604407
Bt.16483.1.S1_at	CB464689	Accession CB4646	1.1054233	1.4247525	-1.288875	0.08307558	0.0589455
Bt.21504.1.A1_at	CB460424	Accession CB4604	-1.1807244	1.2116805	-1.4306608	0.024766458	0.00372148
Bt.25957.1.S1_at	CB458376	Accession CB4583	1.1777967	-1.111983	1.3096899	0.049685627	0.02591378
Bt.29029.2.S1_at	CB456543	Accession CB4565	1.0717185	1.4152157	-1.3205107	0.03079631	0.00932291
Bt.8612.2.S1_at	CB456533	Accession CB4565	-1.0271962	-1.3689979	1.3327521	0.054761108	0.03061204
Bt.16911.1.A1_at	CB455970	Accession CB4559	-1.0221335	-1.4558349	1.42431	0.028367294	0.00624619
Bt.20606.2.S1_at	CB455885	Accession CB4558	-1.1126757	-1.7068572	1.5340115	0.024142498	0.00278899
Bt.24882.1.S1_at	CB452234	Accession CB4522	1.0856524	1.5805953	-1.4558945	0.025753139	0.00415884
Bt.17520.1.S1_at	CB447630	Accession CB4476	-1.0813516	1.2719313	-1.375405	0.0498451	0.02628245
Bt.5741.1.S1_at	CB446557	Accession CB4465	1.1175376	-1.0342137	1.1557726	0.034804247	0.01286747
Bt.22090.2.S1_at	CB443368	Accession CB4433	1.2299114	-1.2885183	1.5847634	0.036972128	0.01491352
Bt.6386.3.S1_a_at	CB442854	Accession CB4428	1.0247202	-1.2210625	1.2512474	0.091045685	0.06698132
Bt.19720.1.A1_at	CB440336	Accession CB4403	-1.1456856	-1.3755344	1.2006212	0.04321782	0.02029226
Bt.8902.2.S1_at	CB440332	Accession CB4403	-1.0292298	1.2409575	-1.2772303	0.02901493	0.00687643
Bt.27590.2.S1_at	CB436518	Accession CB4365	1.1785082	1.5276285	-1.2962391	0.086529866	0.06206913
Bt.13257.2.A1_at	CB433115	Accession CB4331	-1.0718855	-1.6785511	1.56598	0.032195967	0.0105803
Bt.7811.1.A1_at	CB432950	Accession CB4329	-1.0325835	1.2134582	-1.2529969	0.053369384	0.029111743
Bt.18715.1.A1_at	CB431783	Accession CB4317	1.0033402	-1.3774793	1.3820803	0.033150923	0.01142794
Bt.28377.1.S1_at	CB430996	Accession CB4309	-1.090972	-1.4202454	1.3018166	0.036995005	0.01497723
Bt.1950.1.S1_at	CB430170	Accession CB4301	1.0487839	-1.1694884	1.2265406	0.024373978	0.00285942
Bt.1214.1.S1_at	CB428771	Accession CB4287	-1.0709152	-1.1977304	1.1184176	0.04219014	0.01948201
Bt.1616.1.A1_at	CB428579	Accession CB4285	1.0841199	1.2940397	-1.1936315	0.09696177	0.0724301
Bt.20738.2.S1_at	CB427981	Accession CB4279	1.0757306	-1.174545	1.263494	0.04792172	0.02472287
Bt.25075.1.A1_at	CB423629	Accession CB4236	-1.0539672	-1.3779753	1.3074176	0.061540138	0.03753781
Bt.17121.1.S1_at	CB423296	Accession CB4232	1.3531402	1.018576	1.3284627	0.07724839	0.05316475
Bt.13216.2.A1_at	CB420640	Accession CB4206	-1.0646007	-1.308743	1.2293276	0.027768422	0.00545404
Bt.12066.1.S1_at	CB420418	Accession CB4204	1.156818	-1.1973381	1.3851023	0.024570785	0.003032

Bt.27322.1.S1_at	CB420367	Accession CB420367	1.1513529	-1.2633661	1.4545802	0.02901493	0.00702405
Bt.2066.1.S1_at	CB419220	Accession CB419220	1.0157629	-1.3011621	1.3216722	0.024766458	0.00379447
Bt.4578.3.S1_at	CB418472	Accession CB418472	1.073784	-1.2416189	1.1563022	0.07020697	0.0464408
Bt.21949.1.A1_at	CB222784	Accession CB222784	1.1597828	-1.3695229	1.5883491	0.022891732	4.47E-04
Bt.21079.1.A1_at	CB170964	Accession CB170964	1.0319276	-1.3710773	1.4148525	0.062433682	0.03856787
Bt.6361.1.S1_at	CB170566	Accession CB170566	1.0056586	-1.3460345	1.3536513	0.031530906	0.01014345
Bt.9412.2.S1_at	CB167904	Accession CB167904	-1.1127328	1.3015331	-1.4482585	0.022891732	8.36E-04
Bt.19820.1.A1_at	BP108657	Accession BP108657	1.0840926	-1.2188779	1.3213766	0.024013	0.00231389
Bt.22239.1.S1_at	BP105827	Accession BP105827	-1.050862	-1.4453369	1.3753822	0.02537716	0.00399937
Bt.3264.1.S1_at	BP105658	Accession BP105658	1.0603284	-1.0206892	1.0822659	0.055005025	0.03090388
Bt.27067.1.A1_at	BM446382	Accession BM446382	-1.116686	1.2231721	-1.3658991	0.024570785	0.0031857
Bt.16240.1.A1_at	BM446171	Accession BM446171	1.0763366	-1.4111551	1.518878	0.024570785	0.0031526
Bt.13428.2.S1_at	BM434841	Accession BM434841	1.6062145	1.1054013	1.45306	0.045480996	0.02216525
Bt.23544.1.S1_at	BM251341	Accession BM251341	-1.1751626	-1.6186237	1.3773615	0.041299004	0.01859185
Bt.26935.2.S1_at	BI774755	Accession BI774755	1.0430574	-1.7865868	1.8635126	0.046462327	0.02310311
Bt.24281.1.S1_at	BI537129	Accession BI537129	1.1544714	-1.2567036	1.4508283	0.03079631	0.00935143
Bt.20931.1.S1_at	BF655380	Accession BF655380	-1.0149467	-1.3428278	1.3230525	0.068167545	0.04446548
Bt.27115.1.A1_at	BF440568	Accession BF440568	1.1368027	-1.1783807	1.3395864	0.060939405	0.03695124
Bt.27259.2.S1_a_at	BF440269	Accession BF440269	-1.1572372	-1.4630315	1.2642452	0.024013	0.00215791
Bt.22650.1.A1_at	BF440195	Accession BF440195	-1.042262	-1.2643319	1.2130654	0.027768422	0.00577885
Bt.14340.1.A1_at	BF073200	Accession BF073200	-1.0225933	-1.2795898	1.2513183	0.024013	0.00208491
Bt.22400.1.A1_at	BF073015	Accession BF073015	-1.2252563	1.169295	-1.432686	0.043412656	0.02043309
Bt.21049.1.S1_at	BE809771	Accession BE809771	1.0781124	-1.2827798	1.3829808	0.02901493	0.00690085
Bt.28388.1.S1_at	BE755851	Accession BE755851	1.007857	-1.1450101	1.1540064	0.04417663	0.02107367
Bt.24412.1.S1_at	BE755394	Accession BE755394	1.08882	-1.2393428	1.3494213	0.04742311	0.0241335
Bt.19208.2.S1_at	BE753844	Accession BE753844	-1.1097449	-1.6714984	1.5062006	0.024570785	0.00320906
Bt.20501.1.S1_at	BE722116	Accession BE722116	1.0845809	-1.0922623	1.1846468	0.049312342	0.02561454
Bt.4582.1.A1_at	BE663363	Accession BE663363	1.1288611	1.5670753	-1.3881913	0.024013	0.00218613
Bt.26426.1.A1_at	BE481719	Accession BE481719	1.1875322	-1.0424864	1.2379863	0.039568648	0.0167223
Bt.2971.1.S1_at	AW656252	Accession AW656252	1.0549726	-1.1383929	1.2009734	0.04742311	0.02417096
Bt.27269.2.S1_at	AW464698	Accession AW464698	1.2299494	-1.0123998	1.2452004	0.03722907	0.01515473
Bt.26757.2.A1_a_at	AW430024	Accession AW430024	1.1344355	1.3315573	-1.1737621	0.0793643	0.0553587
Bt.15860.1.S1_at	AW416990	Accession AW416990	1.0323871	-1.3273457	1.3703346	0.03079631	0.00932849
Bt.7318.1.S1_at	AW315506	Accession AW315506	1.062955	-1.334105	1.4180937	0.022891732	8.10E-04
Bt.20298.2.S1_a_at	AV615989	Accession AV615989	1.2101585	-1.2210523	1.4776669	0.031530906	0.01016093
Bt.20581.2.S1_at	AV602975	Accession AV602975	1.2349423	-1.3451777	1.6612167	0.03534756	0.01361443
Bt.26496.1.A1_a_at	AV596992	Accession AV596992	1.0631074	1.3896918	-1.3071979	0.031317282	0.00973824
Bt.17637.2.S1_at	AF451188	Accession AF451188	1.0806298	1.3429487	-1.2427462	0.030777313	0.00900481
Bt.772.1.S1_at	AF451174	Accession AF451174	1.2483004	-1.2432652	1.5519685	0.02901493	0.00745738
Bt.793.1.S1_at	AF451171	Accession AF451171	1.1012937	1.4899583	-1.3529165	0.027768422	0.00563718
Bt.2962.1.S1_at	CK969618	Accession No CK969618	1.1882517	-1.1160761	1.3261794	0.046462327	0.02321212
Bt.372.1.S1_at	AKAP5	A kinase (PRKA) family class member 5	1.295214	-1.1208094	1.4516882	0.033150923	0.01135405
Bt.3730.1.S1_at	OPLAH	5-oxoprolinase (ATP-dependent)	1.1397064	1.0116717	1.1265575	0.060308963	0.03604655
Bt.7219.1.S1_at	ABAT	4-aminobutyrate aminotransferase	1.0962749	1.2723377	-1.160601	0.06538909	0.04137571
Bt.24730.1.S1_at	DHCR24	24-dehydrocholesterol reductase	-1.2328459	1.2442054	-1.5339134	0.09624607	0.07175944
Bt.22590.1.S1_at	AGPAT2	1-acylglycerol-3-phosphate acyltransferase 2	1.262184	1.4383298	-1.1395563	0.022891732	2.46E-04
BtAffx.1.11.S1_at	growth hormone release-inhibiting hormone	GHRH	1.0023762	-1.3930221	1.396332	0.036382046	0.01434713
BtAffx.1.10.S1_at	transition protein 2 (drosophila)	LOC781496 /// TNFRSF10B	1.0676252	-1.1151098	1.1905193	0.036972128	0.01484997
BtAffx.1.1.S1_at	fibroblast growth factor receptor 3	FGFR3	-1.0939668	1.2290751	-1.3445673	0.024414862	0.00290912
Bt.9999.2.A1_at	transcription factor B1	TFB1M	-1.0939668	1.2290751	-1.3445674	0.024414849	0.00290913
Bt.9999.1.A1_at	transcription factor B1	TFB1M	-1.0537273	-1.604711	1.5228902	0.024013035	0.00190966
Bt.9997.1.S1_at	non-SMC condensin II complex subunit 3	NCAPD3	1.0740823	-1.2244649	1.315176	0.042790364	0.01994608
Bt.9996.1.S1_at	24-dehydrocholesterol reductase	DHCR24	-1.203878	1.0850946	-1.3063216	0.024013	0.00242524
Bt.9995.2.S1_at	LYR motif containing 5	LYRM5	-1.203878	1.0850946	-1.3063216	0.024013035	0.00242524
Bt.9995.1.A1_at	LYR motif containing 5	LYRM5	-1.0730367	-1.2915621	1.2036514	0.02901493	0.00684149
Bt.9994.2.S1_at	CXXC finger protein 1	CXXC1	-1.1286045	-1.3746997	1.2180526	0.032539126	0.01093622
Bt.9994.1.S1_at	CXXC finger protein 1	CXXC1	-1.0325761	-1.2425196	1.2033203	0.025878632	0.00463116
Bt.9993.1.S1_at	aquaporin 7	AQP7	1.1077448	-1.4168901	1.5695527	0.034999527	0.01320982
Bt.9992.1.S1_at	troponin C type 2 (fast-twitch skeletal muscle)	TNNC2	-1.5390229	-1.2718848	-1.2100334	0.0498451	0.02636991
Bt.9991.1.S1_at	Pallidin homolog (mouse)	PLDN	-1.1182022	-1.4535872	1.2999324	0.031363796	0.00977487
Bt.9988.1.S1_at	Transducin (beta)-like 1	TBL1X	1.0420696	-1.1120833	1.1588681	0.033475503	0.01175783
Bt.9987.1.S1_at	solute carrier family 4 member 4	SLC45A1	1.0110695	1.4441868	-1.4283754	0.022891732	8.69E-04
Bt.9986.3.S1_a_at	exocyst complex component 2	EXOC2	1.0110694	1.4441867	-1.4283754	0.022891732	8.69E-04
Bt.9986.2.S1_at	exocyst complex component 2	EXOC2	-1.1068623	1.1750224	-1.300588	0.08693378	0.06260461
Bt.9986.1.S1_at	exocyst complex component 2	EXOC2	1.0101241	1.2169621	-1.2047651	0.04786793	0.02466129
Bt.9985.1.S1_at	secreted seminal vesicle protein 1	SSLP1	1.0101241	1.2169621	-1.204765	0.047867995	0.02466132
Bt.9983.1.S1_at	N(alpha)-acetyltransferase 10	NAA10	1.0533456	-1.1838343	1.2469866	0.032539126	0.01094602
Bt.9982.1.S1_at	proline rich 3	PRR3	1.051494	1.2994581	-1.2358207	0.029807545	0.0082342
Bt.9981.1.S1_at	tripartite motif-containing 5	TRIM54	1.0149978	-1.377382	1.3980397	0.022891732	9.97E-04
Bt.9980.1.S1_at	peptidoglycan recognition protein 1	PGLYRP1	1.0149978	-1.3773819	1.3980397	0.022891732	9.97E-04
Bt.9979.1.S1_at	cholinergic receptor, nicotinic 5	CHRNA5	-1.0580052	1.2575337	-1.3304772	0.039895266	0.01700131
Bt.9978.1.S1_at	cholinergic receptor, nicotinic 4	CHRN4	1.0795856	1.3515073	-1.251876	0.0498451	0.02634021
Bt.9975.1.S1_at	killer cell lectin-like receptor 1	KLRA1	-1.23471	-1.8594192	1.5059562	0.08823464	0.06414863
Bt.9974.2.S1_at	chemokine (C-C motif) subfamily 3	CCL3	1.0686746	-1.2366123	1.3215361	0.04569423	0.02247575
Bt.9974.1.S1_at	chemokine (C-C motif) subfamily 3	CCL3	-1.0460241	-1.5564499	1.4879675	0.03607441	0.01404735

Bt.9974.1.S1_a_at	chemokine (C-C motif)	CCL3	-1.0460242	-1.55645	1.4879676	0.036074318	0.01404731
Bt.9973.1.S2_at	integrin, beta 1 (fibronectin)	ITGB1	-1.0586838	1.3745424	-1.4552057	0.024013033	0.00122094
Bt.9972.1.S1_at	integrin, beta 6	ITGB6	-1.1377195	-1.8495759	1.6256871	0.02901493	0.00686156
Bt.997.2.S1_a_at	cytochrome b5 reductase	CYB5R1	1.1233817	-1.1403911	1.2810946	0.031530906	0.00995098
Bt.997.1.S1_at	cytochrome b5 reductase	CYB5R1	1.1875325	-1.2868338	1.528157	0.02414251	0.00261059
Bt.9969.1.S1_at	phosphatidylinositol 3-kinase	PITPNB	1.0417228	1.3207716	-1.2678725	0.024013	0.00157583
Bt.9968.1.A1_at	zinc finger protein 532	ZNF532	1.0417228	1.3207717	-1.2678726	0.024013035	0.00157583
Bt.9965.1.S1_at	dihydrolipoamide dehydrogenase	DLD	-1.0315311	1.2405194	-1.2796344	0.040293388	0.01755132
Bt.9958.1.S1_at	insulin-like growth factor 1	IGFBP6	-1.0856816	-1.2982574	1.1957994	0.045476165	0.02201496
Bt.9957.2.S1_at	stratifin	SFN	1.1275886	1.3066676	-1.1588159	0.024013035	0.00193076
Bt.9957.1.S1_at	stratifin	SFN	1.2143073	1.2337791	-1.0160352	0.029707072	0.00810384
Bt.9957.1.S1_a_at	stratifin	SFN	-1.0650724	-1.3407714	1.2588547	0.03626377	0.01417234
Bt.9956.1.S1_at	thioredoxin domain containing	TXNDC17	1.0760818	-1.1088841	1.1932501	0.0472649	0.02398318
Bt.9954.1.S1_at	protein phosphatase 1	PPP1CB	1.0853295	-1.3317124	1.4453468	0.022891732	6.94E-04
Bt.9953.1.S1_at	phosphatidylinositol 3-kinase	PIKC	1.2152978	-1.2293506	1.4940271	0.043822575	0.02081029
Bt.9949.3.S1_a_at	PDZ and LIM domain 7	PDLIM7	1.1870778	1.0853789	1.093699	0.055109352	0.03124942
Bt.9949.2.S1_at	PDZ and LIM domain 7	PDLIM7	1.1368499	1.3029972	-1.1461471	0.037121274	0.01508462
Bt.9949.1.S1_at	PDZ and LIM domain 7	PDLIM7	1.156818	-1.1973381	1.3851023	0.024570853	0.003032
Bt.9948.1.S1_at	Notch homolog 1, transmembrane	NOTCH1	-1.0709153	-1.1977305	1.1184175	0.042190105	0.01948201
Bt.9947.1.S1_at	Stannin	SNN	-1.030583	-1.3411018	1.301304	0.041864064	0.01919741
Bt.9945.1.S1_at	amino-terminal enhancer of	AES	1.1308227	-1.4746408	1.6675574	0.024766458	0.00375536
Bt.9944.1.S1_at	dihydropyrimidinase-like	DPYSL5	1.0729976	-1.4882534	1.5968922	0.024570853	0.00307612
Bt.9943.1.S1_at	haloacid dehalogenase	HDHD1	1.1008149	-1.0867684	1.1963309	0.040293388	0.01736935
Bt.9942.1.S1_at	oculocerebrorenal syndrome	OCRL	1.0537966	-1.3265488	1.3979129	0.022891732	5.57E-04
Bt.9940.1.S1_at	malignant T cell amplification	MCTS1	1.0561851	-1.0686837	1.1287278	0.031530906	0.00999404
Bt.9939.2.S1_at	ribosomal RNA processing	RRP9	1.0456483	2.121339	-2.0287309	0.03624472	0.01413928
Bt.9939.1.S1_at	ribosomal RNA processing	RRP9	-1.9695933	-1.1895244	-1.6557821	0.02901493	0.00751888
Bt.9933.1.S1_at	protein tyrosine phosphatase	PTPRS	1.031587	1.3143536	-1.2741083	0.024766458	0.00367927
Bt.9931.1.S1_at	ATG4 autophagy related	ATG4B	1.109802	-1.0960193	1.2163644	0.03507604	0.01331368
Bt.9926.1.S1_at	heat shock 27kDa protein	HSPB2	1.0853877	-1.2530657	1.360062	0.030303387	0.00856566
Bt.9923.2.A1_at	inositol polyphosphate 5-phosphatase	INPP5B	1.1474856	-1.1776825	1.3513738	0.04567429	0.02235228
Bt.9923.1.S1_at	inositol polyphosphate 5-phosphatase	INPP5B	1.0788621	-1.1678702	1.2599708	0.034999527	0.01323308
Bt.9921.1.A1_at	RAS protein activator	RASAL2	1.0485462	-1.1587833	1.2150378	0.038785268	0.01617621
Bt.9919.1.S1_at	chromosome 14 open reading	C10H14orf37	1.22375	1.3599807	-1.1113224	0.037026286	0.01501985
Bt.9918.1.S1_at	regulatory factor X, 2	RFX2	-1.4686967	1.0478112	1.5389167	0.04162844	0.01882055
Bt.9915.1.S1_at	dynamitin 1-like	DNM1L	1.0912977	1.4729056	-1.3496826	0.024570853	0.0030947
Bt.9914.1.S1_at	dolichyl-phosphate methyltransferase	DPM3	1.1083628	-1.1247672	1.2466502	0.031449206	0.00984594
Bt.9909.2.A1_at	Forkhead box P3	FOXP3	1.0394444	1.2198509	-1.1735605	0.03864426	0.01604747
Bt.9909.1.S1_at	coiled-coil domain containing	CCDC22	1.2146456	1.1701431	1.0380316	0.053735763	0.0296591
Bt.9905.1.S1_at	bromodomain containing	BRD4	-1.1186472	-1.8613433	1.6639234	0.02901493	0.00760711
Bt.9900.1.S1_at	amyloid beta precursor protein	APPBP2	-1.2190293	1.0898942	-1.3286128	0.02414251	0.00277166
Bt.99.1.S1_at	NADH dehydrogenase	NDUFB4	1.0804638	1.3624756	-1.2610099	0.02901493	0.00753378
Bt.9893.1.S1_at	G protein-coupled receptor	GPR88	1.1069392	1.3216166	-1.1939379	0.040254425	0.01726815
Bt.9892.1.S1_at	intermediate filament protein	IFFO1	1.0268463	1.3556072	-1.3201658	0.024570853	0.00328434
Bt.989.2.S1_at	craniofacial development	CFDP2	1.1011122	1.4403418	-1.308079	0.022891732	9.92E-04
Bt.989.2.A1_at	craniofacial development	CFDP2	1.0151155	1.3456911	-1.3256531	0.022891732	5.60E-04
Bt.989.1.S1_s_at	craniofacial development	CFDP2	-1.0869802	-1.2828515	1.1801975	0.034736946	0.01276552
Bt.9889.1.S1_at	zinc finger protein 148	ZNF148	1.0625775	-1.2978864	1.379105	0.030698093	0.00891655
Bt.9882.1.S1_at	fatty acid binding protein	FABP2	-1.0646007	-1.308743	1.2293277	0.027768528	0.00545404
Bt.9878.1.A1_at	SWI/SNF-related, matrix	SMARCAD1	-1.3308029	-1.5875714	1.1929425	0.0411942	0.01834291
Bt.9877.1.S1_at	heterogeneous nuclear	HNRNPU	1.1596566	1.5359298	-1.3244694	0.024013035	0.00161715
Bt.9874.1.S1_at	Mediator complex subunit	MED25	1.0768753	-1.1448689	1.232881	0.045480996	0.01251498
Bt.9869.1.A1_at	hypothetical LOC7862	MLH3	1.0768753	-1.1448689	1.232881	0.04548109	0.02215498
Bt.9868.3.S1_a_at	aarF domain containing	ADCK5	-1.0718853	-1.6785511	1.5659801	0.032195967	0.0105803
Bt.9868.2.S1_a_at	aarF domain containing	ADCK5	-1.1691178	1.1407262	-1.3336434	0.030796394	0.00916829
Bt.9868.1.S1_at	aarF domain containing	ADCK5	-1.058015	-1.3336484	1.2605193	0.030352615	0.00865916
Bt.9868.1.S1_a_at	aarF domain containing	ADCK5	1.0637405	-1.0831394	1.1521792	0.028761035	0.00654356
Bt.9867.1.A1_at	Usher syndrome 1C (autosomal	USH1C	-1.013435	-1.3623583	1.3442976	0.02901493	0.00730013
Bt.9866.1.S1_at	COX16 cytochrome c oxidase	COX16	1.0801699	-1.1131903	1.2024348	0.027084686	0.00491927
Bt.9863.1.S1_at	SHC SH2-domain binding	SHCBP1	1.053767	-1.0859132	1.1442995	0.036298547	0.01421159
Bt.9860.1.S1_at	eukaryotic translation initiation	EIF5	1.6062145	1.1054013	1.45306	0.04548109	0.02216525
Bt.986.1.A1_at	F-box protein 5	FBX05	1.0034766	1.1105162	-1.1066687	0.08696503	0.06268857
Bt.9859.1.S1_at	alpha-2-fucosyltransferase	SEC1	1.1004374	-1.3048927	1.4359525	0.027768528	0.0052927
Bt.9858.1.S1_at	mitogen-activated protein	MAP2K7	1.0394579	-1.2363486	1.2851323	0.025827987	0.00448637
Bt.9857.1.S1_at	coiled-coil-helix-coiled-coil	CHCHD3	-1.0990214	-1.4260451	1.2975589	0.032539126	0.01092446
Bt.9856.1.S1_at	autophagy/beclin-1 regulator	AMBRA1	-1.0521315	1.3235024	-1.3924987	0.03499949	0.01325044
Bt.9855.1.S1_at	solute carrier family 2, high	SLC25A34	-1.0521315	1.3235025	-1.3924987	0.034999527	0.01325043
Bt.9854.1.S1_at	N-acetylated alpha-linkage	NAALADL1	1.0549586	-1.183428	1.2484676	0.030352615	0.00865916
Bt.9853.1.S1_at	solute carrier family 2, high	SLC25A14	1.0793353	-1.303531	1.4069471	0.027862377	0.00588753
Bt.9852.1.S1_at	DNA-damage-inducible	DDIT3	-1.248611	-1.4839886	1.1885116	0.04569423	0.022434
Bt.9850.2.A1_at	transmembrane protein	TMEM171	1.287954	1.2796248	1.0065091	0.027768528	0.00537303
Bt.9850.1.A1_at	transmembrane protein	TMEM171	1.1552722	1.4012692	-1.2129341	0.08026992	0.05627403
Bt.9849.1.A1_at	hypothetical LOC5084	LOC508470	1.024874	-1.2116368	1.2417749	0.041296616	0.01855972
Bt.9848.1.A1_at	hypothetical protein LOC100335608	LOC100335608	1.0620278	-1.338788	1.42183	0.024570853	0.0030521
Bt.9848.1.A1_a_at	hypothetical protein LOC100335608	LOC100335608	1.2505199	-1.3410302	1.676985	0.04752833	0.02431838

Bt.9847.2.S1_at	chromosome 3 open r	C22H3ORF63	-1.0152949	-1.2185657	1.2002087	0.04035124	0.01770892
Bt.9847.1.S1_at	chromosome 3 open r	C22H3ORF63	1.1796391	-1.3261985	1.5644356	0.028171103	0.00603716
Bt.9845.1.S1_at	transmembrane anter	TAPT1	-1.0524583	1.2158012	-1.7595801	0.024766458	0.00374244
Bt.9838.1.S1_at	fatty acid binding prot	FABP6	1.1149298	-1.182129	1.3179909	0.047738083	0.02449318
Bt.9833.1.S1_a_at	coiled-coil-helix-coiled	CHCHD7	1.1574202	-1.3044078	1.509748	0.038198154	0.01576518
Bt.9832.2.S1_at	musculoskeletal, emb	MUSTN1	1.1776708	-1.1142632	1.3122352	0.02901493	0.00730252
Bt.9832.1.S1_at	musculoskeletal, emb	MUSTN1	1.2940911	-1.1373276	1.4718055	0.024766458	0.00368129
Bt.9832.1.S1_a_at	musculoskeletal, emb	MUSTN1	-1.1056798	-1.7639033	1.5953112	0.028761035	0.00652046
Bt.983.1.S1_at	hypoxanthine phospho	HPRT1	1.2122176	1.0993392	1.1026783	0.030098865	0.00842343
Bt.9828.1.S2_at	histidine triad nucleot	HINT3	1.1545354	-1.0523896	1.2150211	0.024570853	0.00345724
Bt.9828.1.S1_at	histidine triad nucleot	HINT3	1.181377	-1.3146108	1.5530512	0.03316548	0.0116255
Bt.9826.1.S1_at	COX5A protein	COX5A	-1.4019381	-1.0214703	-1.3724706	0.0411942	0.01833952
Bt.9825.1.S1_at	mitochondrial ribosom	MRPL35	-1.081653	1.2828892	-1.387641	0.040686555	0.01791359
Bt.9821.1.S1_at	aminoadipate-semiald	AASDHPPT	1.0458788	-1.3393998	1.4008497	0.02901493	0.00684165
Bt.982.1.S1_at	serpin peptidase inhib	SERPINA1	1.1217914	-1.1479417	1.2877511	0.024142498	0.00281454
Bt.982.1.S1_a_at	serpin peptidase inhib	SERPINA1	1.1217914	-1.1479417	1.2877511	0.02414251	0.00281454
Bt.9814.1.S1_at	ribosomal protein L36	RPL36A /// RPL36A	-1.017286	-1.1654503	1.1456467	0.047423076	0.02412178
Bt.9811.1.S1_at	proteasome (prosome)	PSMG2	1.0952418	1.4316639	-1.3071669	0.0472649	0.02382776
Bt.9810.1.S1_at	polymerase (DNA-dire	POLE4	1.1147062	-1.1040523	1.2306939	0.03410501	0.01221996
Bt.981.3.S1_at	Chloride intracellular	CLIC4	1.066376	-1.3864734	1.4785018	0.030480286	0.0088056
Bt.981.2.S1_at	Chloride intracellular	CLIC4	1.0843875	-1.4305513	1.5512719	0.028171103	0.00608922
Bt.981.1.S1_at	Chloride intracellular	CLIC4	-1.0027908	-1.3479642	1.3442129	0.036639847	0.01447468
Bt.9809.1.S1_at	PEST proteolytic signa	PCNP	1.1173598	-1.1906593	1.3303949	0.022891732	8.45E-04
Bt.9807.3.S1_at	glycoprotein (transme	GPNMB	-1.0225933	-1.2795898	1.2513185	0.024013035	0.00208491
Bt.9807.2.S1_at	glycoprotein (transme	GPNMB	-1.1072059	-1.515477	1.36874	0.02454042	0.00294832
Bt.9807.1.S1_at	glycoprotein (transme	GPNMB	-1.1072059	-1.5154768	1.3687398	0.02454049	0.00294833
Bt.9805.1.A1_at	serine hydroxymethyl	SHMT1	1.1342682	-1.2024986	1.3639557	0.022891732	4.14E-04
Bt.9804.1.S1_at	churchill domain conta	CHURC1	1.1858504	1.4988378	-1.263935	0.043956198	0.02090638
Bt.9801.1.S1_at	Myotubularin related	MTMR10	1.0580634	-1.3598078	1.4387628	0.022891732	7.40E-04
Bt.9800.1.A1_a_at	large subunit GTPase	LSG1	1.0580634	-1.3598078	1.4387629	0.022891732	7.40E-04
Bt.980.1.A1_at	HLA-B associated trans	BAT2	-1.2346349	1.2133138	-1.4979994	0.024013035	0.00180336
Bt.98.1.S1_at	arginine vasopressin r	AVPR2	-1.2346349	1.2133138	-1.4979994	0.024013035	0.00180336
Bt.9799.1.S1_at	cleavage stimulation f	CSTF3	1.0251177	-1.2455198	1.2768782	0.04569423	0.02245131
Bt.9797.1.S1_at	peptidase (mitochond	PMPCB /// PMPCB	1.0550643	1.365195	-1.2939448	0.024414862	0.00291598
Bt.9795.1.S1_at	cell cycle associated p	CAPRIN1	1.0550644	1.365195	-1.2939447	0.024414849	0.00291598
Bt.9793.1.A1_at	acyl-CoA thioesterase	ACOT2 /// ACOT4	1.0658965	-1.2720698	1.3558948	0.02414251	0.0027186
Bt.9792.1.S1_at	Arrestin domain conta	ARRDC4	-1.0974087	-1.7086674	1.557002	0.033487722	0.01189881
Bt.9791.1.S1_at	peptidylprolyl isomera	PPIF	1.0100516	-1.2120187	1.2242016	0.022891732	7.93E-04
Bt.979.1.A1_at	myosin IB	MYO1B	1.1259791	-1.1969175	1.347704	0.024013035	0.00159369
Bt.9789.1.S1_at	achaete-scute comple	ASCL2	1.197831	-1.1087571	1.3281037	0.022891732	4.72E-04
Bt.9786.1.S1_at	ST6 (alpha-N-acetyl-ne	ST6GALNAC2	1.1607224	-1.1020843	1.2792139	0.033626564	0.01197724
Bt.9785.1.S1_at	ATG14 autophagy rela	ATG14	1.0372767	-1.1489868	1.1918174	0.029446304	0.00797027
Bt.9784.1.S1_at	hypothetical LOC5402	LOC540231	1.1833484	-1.2324361	1.4584012	0.027768528	0.00544106
Bt.9783.1.S1_at	DEAD (Asp-Glu-Ala-As	DDX3X	-1.0303613	-1.6728368	1.6235439	0.028171103	0.00606955
Bt.978.1.S1_at	similar to polycystic ki	LOC784489	1.0323873	-1.3273455	1.3703345	0.030796394	0.00932853
Bt.9779.1.S1_at	similar to TLH29 prote	ISG12(B)	1.0106859	-1.5090175	1.5251426	0.025827987	0.00431897
Bt.9778.2.S1_a_at	Actin binding LIM prot	ABLIM1	1.1606089	1.3050976	-1.1244938	0.08867458	0.06459529
Bt.9778.1.S1_at	Actin binding LIM prot	ABLIM1	1.0583775	1.2502593	-1.181298	0.02901493	0.00737876
Bt.9777.1.S1_at	3-hydroxybutyrate def	BDH1	1.0583775	1.2502593	-1.181298	0.02901493	0.00737876
Bt.9774.1.S1_a_at	microRNA mir-147	MIR147	1.0687746	-1.3273298	1.4186163	0.022891732	7.18E-04
Bt.9768.1.S1_at	family with sequence	FAM3C	1.1024485	-1.0129539	1.1167295	0.049209397	0.02552629
Bt.9767.1.S1_a_at	squalene epoxidase	SQLE	1.1010344	-1.0603572	1.1674898	0.027768528	0.00534778
Bt.9764.1.A1_at	M-phase phosphoprot	MPHOSPH6	1.1591034	-1.1283126	1.307831	0.024013035	0.00133668
Bt.9760.1.S1_at	gap junction protein, b	GJB2	1.0572273	-1.427152	1.508824	0.028367294	0.00625484
Bt.976.1.A1_at	Interleukin enhancer b	ILF3	1.110157	-1.2402916	1.3769184	0.04162844	0.01882841
Bt.9759.2.S1_at	neuroguidin, EIF4E bin	NGDN	1.152268	-1.2169257	1.4022245	0.024570853	0.00310294
Bt.9759.1.S1_at	neuroguidin, EIF4E bin	NGDN	-1.0235975	-1.4461731	1.4128339	0.03730007	0.01523635
Bt.9759.1.S1_a_at	neuroguidin, EIF4E bin	NGDN	1.1191678	-1.2618895	1.412266	0.030786525	0.00902926
Bt.9756.1.S1_at	lipoic acid synthetase	LIAS	-1.014873	-1.2421731	1.223969	0.031530906	0.00925551
Bt.9755.1.S1_at	testis expressed 2	TEX2	-1.3461982	-1.8956906	1.4081808	0.034339253	0.01247079
Bt.9754.1.S1_at	NAD(P)H dehydrogena	NQO1	-1.3461982	-1.8956906	1.4081808	0.034339253	0.01247078
Bt.9753.1.S1_at	family with sequence	FAM53C	1.1948087	1.1513063	1.0377853	0.061540138	0.03757645
Bt.9750.2.S1_a_at	small nuclear ribonucl	SNRPG	-1.0361248	-1.4470338	1.3965825	0.019877227	8.43E-05
Bt.9750.1.S1_a_at	small nuclear ribonucl	SNRPG	1.0763366	-1.411155	1.5188779	0.024570853	0.0031526
Bt.9749.1.S1_at	signal peptidase comp	SPCS1	-1.1164397	-1.4101774	1.2631023	0.024013035	0.00238265
Bt.9745.1.A1_at	similar to keratin 13	LOC100296555	1.0585728	1.2501222	-1.1809506	0.02901493	0.00735802
Bt.9742.1.S1_at	programmed cell deat	PDCD6IP	1.0585728	1.2501222	-1.1809506	0.02901493	0.00735802
Bt.9741.1.S1_at	myotubularin related	MTMR4	1.1253303	1.3298831	-1.1817712	0.032178592	0.01050161
Bt.974.1.S1_at	Rho GTPase activating	ARHGAP22	-1.0769739	-1.4220604	1.3204223	0.031530906	0.01013534
Bt.9739.1.S1_at	suppression of tumori	ST13	-1.0575237	1.245409	-1.3170496	0.024048876	0.00251536
Bt.9737.1.S1_at	lymphocyte antigen 6	LY6G6C	-1.0575237	1.245409	-1.3170496	0.024048876	0.00251536
Bt.9736.1.S1_at	secretory leukocyte pe	SLPI	-1.0925106	1.2188836	-1.3316433	0.028171103	0.00603568
Bt.9735.2.A1_at	apolipoprotein M	APOM	-1.0925106	1.2188836	-1.3316433	0.028171103	0.00603568
Bt.9735.1.S1_at	apolipoprotein M	APOM	1.2893543	1.1763787	1.0960367	0.045396104	0.02191204
Bt.9734.1.S1_at	nucleoporin 62kDa	NUP62	1.2893543	1.1763787	1.0960367	0.045396075	0.02191203

Bt.9732.2.S1_at	GTP-binding protein 1	GTPBP10	-1.0673926	-1.2988139	1.21681	0.025827987	0.00454777
Bt.9732.1.A1_at	GTP-binding protein 1	GTPBP10	1.1526319	1.0008091	1.1517001	0.04920927	0.0254792
Bt.9731.1.S1_at	glutaredoxin 2	GLRX2	1.1526319	1.0008091	1.1517001	0.049209397	0.0254792
Bt.9730.1.S1_at	COP9 constitutive pho	COP55	1.1145139	1.2816441	-1.1499579	0.05916067	0.03499468
Bt.9729.1.A1_at	Kinesin family membe	KIF18A	-1.020123	1.2088846	-1.233211	0.027768528	0.00567124
Bt.9728.2.A1_at	ATPase, Na+/K+ transp	ATP1B3	-1.0116707	1.3601203	-1.3759938	0.030698093	0.00889741
Bt.9728.1.S1_at	ATPase, Na+/K+ transp	ATP1B3	-1.0116708	1.3601202	-1.3759937	0.030698093	0.00889742
Bt.9725.1.A1_at	immediate early resp	IER3IP1	1.0003809	-1.5563601	1.5569528	0.029030783	0.0077347
Bt.9724.1.S1_at	UHRF1 binding protei	UHRF1BP1L	1.000381	-1.5563601	1.5569531	0.029030748	0.00773469
Bt.9720.1.S1_at	SH3 domain containi	SH3RF1	-1.0221335	-1.455835	1.42431	0.028367294	0.00624618
Bt.972.1.S1_at	ubiquitin-conjugating	UBE2E2	-1.0451317	1.1835748	-1.2369916	0.040293388	0.01756963
Bt.9716.2.S1_at	thioredoxin-like 1	TXNL1	-1.0451317	1.1835748	-1.2369916	0.040293388	0.01756963
Bt.9716.1.A1_at	Thioredoxin-like 1	TXNL1	1.1038442	1.4366544	-1.3015012	0.055109352	0.03127803
Bt.9715.1.S1_at	AE binding protein 2	AEBP2	1.0798424	1.3795072	-1.2775078	0.032790437	0.01116961
Bt.9714.1.S1_at	actin, gamma 2, smoo	ACTG2	1.2081473	-1.2657804	1.5292491	0.032781206	0.01112013
Bt.9713.1.S1_at	UDP-N-acetyl-alpha-D	GALNT11	1.3014107	-1.2371126	1.6099916	0.0411942	0.01835786
Bt.9712.1.S1_at	TBC1 domain family, n	TBC1D12	1.0993832	-1.1834124	1.3010238	0.024013035	0.00125494
Bt.9711.1.S1_at	acyl-CoA oxidase 3, pr	ACOX3	1.0496427	-1.2400967	1.3016584	0.024013	0.00203933
Bt.9710.1.S1_at	PRP4 pre-mRNA proce	PRPF4B	1.0496427	-1.2400967	1.3016584	0.024013035	0.00203933
Bt.9708.2.S1_at	cutC copper transport	CUTC	-1.0294639	-1.3160557	1.2783893	0.03316394	0.01157648
Bt.9708.1.S1_at	cutC copper transport	CUTC	-1.0294639	-1.3160557	1.2783893	0.03316394	0.01157648
Bt.9706.2.S1_at	RAB5-interacting prot	RIP5	-1.2893727	-1.3605317	1.0551889	0.029509954	0.00800836
Bt.9706.1.A1_at	Src-like adaptor 2	SLA2	-1.2893727	-1.3605318	1.0551889	0.029509977	0.00800836
Bt.9704.1.S1_at	COX19 cytochrome c	COX19	-1.1070051	-1.2276651	1.1089967	0.045817506	0.02256876
Bt.9702.1.S1_at	crooked neck pre-mRN	CRNKL1	1.165725	-1.2262235	1.4294393	0.03635977	0.01431264
Bt.97.1.S1_at	fatty acid binding prot	FABP4	1.3977317	-1.1504475	1.6080167	0.058141094	0.03369307
Bt.9699.1.S1_at	cytochrome P450, fam	CYP26A1	1.0454493	1.3742455	-1.3145024	0.04004019	0.01711966
Bt.9698.1.S1_at	mitogen-activated pro	MAPK14	1.0454494	1.3742456	-1.3145024	0.04004019	0.01711966
Bt.9697.1.A1_at	alcohol dehydrogenas	ADH6	1.1023638	1.3400093	-1.2155781	0.024737129	0.00353138
Bt.9695.1.S1_at	synovial sarcoma tran	SS18	1.1445183	-1.2612182	1.4434873	0.07439305	0.05041973
Bt.9693.1.S1_at	serpin peptidase inhib	LOC786922	-1.0043452	-1.3074502	1.3017936	0.022891732	7.67E-04
Bt.9692.1.S1_at	common salivary prote	BSP30C	-1.1998101	-1.497932	1.2484741	0.054460157	0.03031283
Bt.9689.1.A1_at	3-hydroxy-3-methylgl	HMGCS2	1.10519	-1.2334272	1.3631713	0.029707072	0.00809944
Bt.9683.1.A1_at	lymphocyte antigen 6	LY6G6E	1.0599154	-1.156956	1.2262754	0.022891732	2.37E-04
Bt.9682.1.S1_at	lysozyme 1	LYZ1	1.0599154	-1.156956	1.2262754	0.022891732	2.37E-04
Bt.968.1.S1_at	histidine ammonia-lya	HAL	-1.0813516	1.2719313	-1.3754051	0.0498451	0.02628243
Bt.9679.1.S1_at	similar to extracellular	LOC100296618	-1.1274972	1.0482517	-1.1819009	0.024142498	0.00277099
Bt.9676.1.S1_a_at	hypothetical protein L	MYEOV2	-1.1274972	1.0482516	-1.1819009	0.024142511	0.002771
Bt.9673.1.S1_at	OCIA domain containi	OCIAD2	1.0142373	-1.3422356	1.3613454	0.024570785	0.00317037
Bt.9672.1.S1_at	shroom family membe	SHROOM3	1.0142373	-1.3422356	1.3613454	0.024570853	0.00317037
Bt.9667.2.S1_at	Apoptosis inhibitor 5	API5	1.0717942	-1.463989	1.5690949	0.024013035	0.00184819
Bt.9667.1.A1_at	Apoptosis inhibitor 5	API5	1.0215284	-1.3104088	1.3386198	0.027157558	0.00496134
Bt.9665.1.S1_at	general transcription f	GTF2E1	1.0632898	1.4436424	-1.357713	0.027768422	0.00549853
Bt.9664.2.S1_at	ubiquitin specific pept	USP8	1.0632898	1.4436424	-1.357713	0.027768528	0.00549853
Bt.9664.1.A1_at	ubiquitin specific pept	USP8	1.0806298	1.3429488	-1.2427464	0.030777326	0.00900482
Bt.9662.1.S1_at	prostaglandin E recept	PTGER4	1.2052895	-1.3025514	1.5699515	0.029807545	0.00821934
Bt.9661.1.S1_at	signal-induced prolifer	LOC534839 /// SIP	1.2052895	-1.3025513	1.5699514	0.029807545	0.00821935
Bt.9660.1.A1_s_at	tripartite motif-contai	TRIM8	-1.0988828	-1.4146253	1.2873304	0.028761035	0.00654491
Bt.9659.1.S1_a_at	ectonucleotide pyroph	ENPP3	-1.1462835	1.3637004	-1.5631872	0.040293388	0.01747863
Bt.9658.1.S1_at	ring finger protein 146	RNF146	-1.1462835	1.3637005	-1.5631872	0.040293388	0.01747862
Bt.9657.1.S1_at	acireductone dioxyger	ADI1	1.1302357	1.4266878	-1.2622923	0.039713833	0.01687529
Bt.9656.1.S1_at	MAP/microtubule affil	MARK4	1.1302357	1.4266877	-1.2622923	0.03971386	0.01687531
Bt.9655.2.S1_at	similar to enterocytin	LOC790332	-1.2666448	1.0621344	-1.345347	0.041864008	0.01916093
Bt.9654.1.S1_at	similar to Apolipoprot	LOC510193	-1.2666448	1.0621344	-1.3453472	0.041864064	0.01916093
Bt.9652.1.S1_at	RAB22A, member RAS	RAB22A	1.0073204	-1.2705609	1.2798619	0.041296616	0.01852618
Bt.965.2.S1_at	matrilin 1, cartilage m	MATN1	1.0073204	-1.2705609	1.2798618	0.041296616	0.01852621
Bt.965.1.S1_at	matrilin 1, cartilage m	MATN1	1.0363665	1.3304788	-1.2837918	0.029807545	0.00829725
Bt.9649.2.S1_at	transformation/transc	TRRAP	1.0363665	1.3304789	-1.2837919	0.029807545	0.00829723
Bt.9649.1.A1_at	transformation/transc	TRRAP	-1.0572577	1.2164235	-1.2860731	0.058492515	0.0339794
Bt.9648.1.S1_at	MCF.2 cell line deriv	MCF2L	-1.090249	1.1167852	-1.2175739	0.08912577	0.06500197
Bt.9643.1.S1_at	calcium binding protei	CHP	-1.1270628	-1.2003603	1.0650342	0.03480827	0.01298853
Bt.9640.1.A1_at	Spondin 1, extracellul	SPON1	-1.1270628	-1.2003603	1.0650342	0.03480827	0.01298853
Bt.964.1.S1_at	thymidine kinase 1, so	TK1	1.0470262	-1.1576048	1.2120426	0.030210141	0.00847592
Bt.9639.1.S1_at	copine I	CPNE1	1.042147	-1.3496815	1.4065666	0.019877227	6.64E-05
Bt.9637.1.S1_at	sorting nexin 5	SNX5	-1.0883094	-1.3710103	1.2597616	0.027768422	0.00573786
Bt.9636.1.S1_at	serine peptidase inhib	SPINK1	-1.0883094	-1.3710105	1.2597618	0.027768528	0.00573786
Bt.9634.1.S1_at	pseudouridylylate synth	PUS7L	-1.3085676	-2.1135204	1.6151403	0.033978608	0.01215065
Bt.9633.2.S1_at	mesenchyme homeob	MEOX2	-1.3085676	-2.1135204	1.6151403	0.033978593	0.01215065
Bt.9633.1.S1_at	PERP, TP53 apoptosis	PERP	1.1162409	-1.1447406	1.2778063	0.029807545	0.0082299
Bt.9632.2.S1_at	deleted in malignant b	DMBT1	-1.0243152	-1.4487815	1.4143901	0.02901493	0.0073375
Bt.9632.1.S1_a_at	deleted in malignant b	DMBT1	1.1810758	-1.1752741	1.3880879	0.03864426	0.01604409
Bt.9632.1.A1_at	deleted in malignant b	DMBT1	1.1644698	-1.2827843	1.4937637	0.0472649	0.02395861
Bt.9631.1.S1_at	mitofusin 1	MFN1	1.0716712	-1.1179947	1.1981227	0.064078934	0.0402135
Bt.9630.1.S1_at	transmembrane prote	TMPRSS2	-1.049884	1.3112653	-1.3766763	0.022891732	0.00100375
Bt.9629.3.S1_at	zinc finger protein 36	ZFP36L1	-1.1563681	-1.3389382	1.1578823	0.06590075	0.04209834

Bt.9629.2.S1_at	zinc finger protein 36,	ZFP36L1	-1.1005092	-1.4175434	1.2880796	0.047423076	0.0241975
Bt.9629.1.S1_at	zinc finger protein 36,	ZFP36L1	-1.0748788	1.1930909	-1.2824281	0.030480286	0.0088102
Bt.9628.1.S1_a_at	CWF19-like 1, cell cycl	CWF19L1	-1.0748788	1.1930909	-1.2824281	0.030480286	0.0088102
Bt.9625.1.S1_at	serine peptidase inhib	SPINK4	1.1213249	1.2623744	-1.1257882	0.059017222	0.03479385
Bt.9623.1.A1_at	glutamic-pyruvate tra	GPT	-1.1034386	1.0339093	-1.1408556	0.033487722	0.01180956
Bt.9622.2.S1_at	KTI12 homolog, chrom	KTI12	1.2116141	1.3079423	-1.079504	0.03348662	0.0117854
Bt.9622.1.A1_at	KTI12 homolog, chrom	KTI12	-1.0949398	-1.4389217	1.3141559	0.032178592	0.01053779
Bt.962.1.S1_at	golgin A7	GOLGA7	1.1386696	-1.0751495	1.2242401	0.041147	0.01823263
Bt.9611.1.A1_at	mesoderm induction e	MIER1	1.169093	1.485564	-1.2706977	0.04033661	0.0176181
Bt.961.1.S1_at	GATA zinc finger doma	GATAD1	1.169093	1.485564	-1.2706977	0.04033658	0.0176181
Bt.9609.1.S1_a_at	thiosulfate sulfurtrans	TSTD1	-1.1889054	-1.509374	1.2695494	0.04920927	0.02550475
Bt.9605.1.S1_at	membrane-spanning 4	MS4A8B	-1.1889054	-1.509374	1.2695494	0.049209397	0.02550473
Bt.9603.2.S1_at	integrator complex su	INTS8	-1.111116	-1.3964363	1.2567871	0.02901493	0.00710216
Bt.9603.1.A1_at	integrator complex su	INTS8	-1.1111159	-1.3964363	1.2567872	0.02901493	0.00710216
Bt.9603.1.A1_a_at	integrator complex su	INTS8	-1.1912564	1.0659629	-1.2698351	0.025753174	0.00419728
Bt.9602.1.S1_at	death associated prote	DAPL1	1.0050452	1.3671339	-1.360271	0.024013035	0.00190876
Bt.960.2.S1_at	SWI/SNF related, matr	SMARCA5	1.1739204	-1.384206	1.6249478	0.027768528	0.00551604
Bt.9599.3.S1_at	Inositol hexakisphosph	IP6K2	1.0497313	-1.3540539	1.4213927	0.037457496	0.01532713
Bt.9599.2.S1_at	inositol hexakisphosph	IP6K2	1.0497313	-1.354054	1.4213928	0.03745755	0.01532715
Bt.9599.1.A1_at	Inositol hexakisphosph	IP6K2	1.0231808	-1.6070856	1.6443392	0.024013	0.00164223
Bt.9598.1.S1_at	solute carrier family 3	SLC37A2	1.0231808	-1.6070857	1.6443392	0.024013035	0.00164223
Bt.9596.1.S1_at	trefoil factor 3 (intesti	TFF3	1.0841807	1.3801173	-1.2729588	0.025828011	0.00459976
Bt.9595.1.S1_at	gastrokine 3-like	LOC509961	1.0841807	1.3801173	-1.2729588	0.025827987	0.00459975
Bt.9593.1.S1_at	ATP-binding cassette,	ABCC3	1.0049785	-1.4225665	1.4296489	0.024570785	0.00311792
Bt.9590.1.S1_at	URB1 ribosome biogen	URB1	1.0049784	-1.4225667	1.4296489	0.024570853	0.00311791
Bt.959.2.S1_at	filamin A, alpha	FLNA	1.0033401	-1.3774792	1.3820803	0.033150923	0.01142793
Bt.959.1.S1_at	filamin A, alpha	FLNA	1.1202213	-1.1866646	1.329327	0.024013035	0.00185161
Bt.9589.1.S1_at	tropomyosin 4	TPM4	1.0337119	1.2433575	-1.2028086	0.07139212	0.04756137
Bt.9588.1.S1_at	ribosomal protein L7a	RPL7A	1.1069858	-1.1261102	1.246588	0.02901493	0.00671976
Bt.9586.1.A1_at	exportin 1 (CRM1 hom	XPO1	1.1069862	-1.1261104	1.2465886	0.02901493	0.0067197
Bt.9585.1.S1_at	aminolevulinat dehyd	ALAD	1.0334253	1.2063068	-1.1672899	0.09605997	0.07148491
Bt.9582.1.A1_at	phosphatidylinositol	PIGP /// PIGP	1.2130499	-1.3500501	1.6376781	0.030303387	0.00858774
Bt.9581.1.S1_at	bifunctional apoptosis	BFAR	1.0455353	-1.4303123	1.495442	0.024414862	0.00288948
Bt.958.2.S1_at	tumor necrosis factor,	TNFAIP6	1.0455352	-1.4303123	1.4954419	0.024414849	0.00288948
Bt.958.1.A1_at	tumor necrosis factor,	TNFAIP6	1.0655125	1.5683347	-1.4719064	0.030796394	0.00924533
Bt.9579.2.S1_at	basic transcription fac	BTF3L4	1.0655125	1.5683347	-1.4719064	0.030796394	0.00924533
Bt.9579.2.S1_a_at	basic transcription fac	BTF3L4	1.0150319	-1.6460307	1.6707737	0.030796394	0.00929581
Bt.9579.1.S1_at	basic transcription fac	BTF3L4	1.0314678	-1.3446863	1.3870007	0.027768528	0.00576064
Bt.9578.1.S2_at	protein phosphatase 1	PPP1CC	1.0682435	-1.2995116	1.3881948	0.030796394	0.00922207
Bt.9578.1.S1_at	protein phosphatase 1	PPP1CC	1.1731533	1.5135516	-1.2901566	0.02901493	0.0076572
Bt.9577.1.S1_a_at	chemokine (C-C motif	CCL25	1.1731533	1.5135515	-1.2901566	0.02901493	0.00765719
Bt.9576.3.S1_at	COMM domain contai	COMMMD4	1.2039729	-1.0732602	1.2921764	0.022891732	1.64E-04
Bt.9576.3.S1_a_at	COMM domain contai	COMMMD4	-1.0418502	1.4078219	-1.4667395	0.022891732	2.66E-04
Bt.9576.2.S1_a_at	COMM domain contai	COMMMD4	-1.0418502	1.4078219	-1.4667395	0.022891732	2.66E-04
Bt.9576.1.S1_a_at	COMM domain contai	COMMMD4	1.1541451	1.3229733	-1.1462798	0.024142498	0.0028152
Bt.9575.1.S1_at	PQ loop repeat contai	PQLC1	1.1541451	1.3229731	-1.1462798	0.02414251	0.0028152
Bt.9573.1.S1_a_at	FXRD domain containi	FXRD	1.0334864	1.274223	-1.2329364	0.046462327	0.02315915
Bt.9571.2.S1_at	RNA binding motif (RN	RBM3	1.0334864	1.274223	-1.2329364	0.046462454	0.02315915
Bt.9571.2.S1_a_at	RNA binding motif (RN	RBM3	-1.1097449	-1.6714984	1.5062006	0.024570853	0.00320906
Bt.9571.1.S1_at	RNA binding motif (RN	RBM3	1.0062634	1.223744	-1.216127	0.024013035	0.00140664
Bt.9570.1.S1_at	TNFAIP2 protein-like	LOC100337435 ///	-1.0650212	-1.3857479	1.301146	0.045079704	0.02166374
Bt.9569.1.S1_at	epithelial cell adhesio	EPCAM	-1.0650212	-1.385748	1.301146	0.04507961	0.0216637
Bt.9567.1.S1_at	transmembrane 7 sup	TM7SF2	-1.2606951	-1.065336	-1.183378	0.0912346	0.06718478
Bt.9566.1.S1_at	cadherin-related famil	CDHR1	-2.072471	-2.2158368	1.0691763	0.024013035	0.00241072
Bt.9565.1.S1_at	histone H2B variant P	LOC404073	1.0710297	1.3812948	-1.2896887	0.042781204	0.01983355
Bt.9564.1.S1_at	phospholipase A2, gro	PLA2G15	1.0710297	1.3812948	-1.2896886	0.042781204	0.01983355
Bt.9563.1.S1_at	ankyrin repeat, SAM	ASZ1	1.0483544	1.3820788	-1.3183317	0.025753139	0.00420488
Bt.9562.1.S1_at	sodium channel, volta	SCN5A	1.0483543	1.3820788	-1.3183318	0.025753174	0.00420488
Bt.9561.1.S1_at	mucin 1, cell surface	MUC1	1.0487839	-1.1694884	1.2265406	0.024373978	0.00285942
Bt.9560.1.S1_at	chemokine (C-C motif	CCL20	-1.0204736	-1.3541213	1.3269538	0.02901493	0.00717933
Bt.9559.2.S1_at	amyloid beta (A4) pre	APP	-1.0204736	-1.3541213	1.326954	0.02901493	0.00717931
Bt.9559.1.S1_at	solute carrier family 2	SLC25A5	1.1139874	-1.1283884	1.2570105	0.04033658	0.01765243
Bt.9558.1.S1_at	hypothetical protein L	LOC530205	1.1946303	-1.1941663	1.4265872	0.024570853	0.00324505
Bt.9556.1.S1_at	mesoderm specific tra	MEST	1.010032	-1.3731548	1.3869303	0.027768528	0.0056797
Bt.9554.1.A1_at	Similar to Mhc class I	LOC509006	1.1571729	1.3914495	-1.202456	0.02901493	0.00726064
Bt.9553.1.S1_at	zinc finger protein 33	ZNF335	-1.1456854	-1.3755343	1.2006211	0.043217786	0.02029223
Bt.9551.1.S1_at	similar to cDNA seque	LOC618886	1.0840926	-1.2188779	1.3213766	0.024013035	0.00231389
Bt.955.3.S1_a_at	golgi brefeldin A resist	GBF1	-1.0232611	1.2506151	-1.2797058	0.035463966	0.01370623
Bt.955.1.S1_at	golgi brefeldin A resist	GBF1	-1.0232611	1.2506151	-1.2797056	0.03546394	0.0137062
Bt.9549.1.S1_at	HOP homeobox	HOPX	1.3710206	-1.081643	1.4829549	0.02901493	0.00758342
Bt.9548.1.S1_at	ribosomal protein L39	RPL39	-1.0813643	-1.4750764	1.3640884	0.02901493	0.00744288
Bt.9547.1.S2_at	family with sequence	FAM32A	1.0889289	1.5221874	-1.3978758	0.028265802	0.00615256
Bt.9547.1.S1_at	family with sequence	FAM32A	1.1292583	-1.3233972	1.4944572	0.04567429	0.02235755
Bt.9546.2.S1_a_at	RNA binding motif pro	LOC534630 /// LO	1.1581928	-1.2926445	1.4971315	0.03276182	0.01105584
Bt.9546.1.S1_at	RNA binding motif pro	LOC613705	1.1557359	1.1217399	1.0303065	0.08010229	0.05606503

Bt.9545.1.S1_at	CDC5 cell division cycl	CDC5L	1.0286514	-1.3637518	1.4028251	0.02414251	0.00261578
Bt.9542.1.S1_at	protein tyrosine phosph	PTPN1	1.1791781	-1.1811514	1.3927878	0.02901493	0.00685556
Bt.9541.1.S1_at	CCHC-type zinc finger,	CNPB	1.2574667	-1.0821596	1.3607796	0.022891732	4.64E-04
Bt.9540.1.S1_at	translocase of outer m	TOMM7	1.0222288	1.2961648	-1.2679789	0.041676875	0.01892901
Bt.9537.2.S1_at	spire homolog 2 (Dros	SPIRE2	-1.0140338	-1.244245	1.2270253	0.025827987	0.00457608
Bt.9537.1.A1_a_at	spire homolog 2 (Dros	SPIRE2	1.1047342	-1.6074553	1.7758108	0.040293388	0.01737788
Bt.9535.1.S1_at	T-cell receptor gamma	TRGC6	1.1549913	1.2576965	-1.0889229	0.028367294	0.00619756
Bt.9532.1.S1_at	CD209 molecule	CD209	1.2101585	-1.2210523	1.4776669	0.031530906	0.01016093
Bt.9531.1.S1_at	histone H4-like	LOC617875	1.1393503	-1.6320784	1.859509	0.032178592	0.01054496
Bt.20352.1.S1_at	septin 2	septin 2	1.068914	1.3174765	-1.2325374	0.024766458	0.00381427
Bt.9530.1.S1_at	Guanine nucleotide bi	GNA12	-1.0306299	-1.6562512	1.6070281	0.024570853	0.00344339
Bt.9527.2.S1_at	Kruppel-like factor 10	KLF10	-1.0494815	-1.2807868	1.2203995	0.036972128	0.01486929
Bt.9525.1.A1_at	ring finger protein 113	RNF113A	1.0528502	-1.3009046	1.3696578	0.036972128	0.0149195
Bt.9522.1.S1_at	MYST histone acetyltr	MYST4	1.0803668	-1.3457812	1.4539374	0.022891732	9.76E-04
Bt.9521.1.S1_at	ras homolog gene fam	RHOD	1.0263438	-1.2847638	1.3186095	0.031530906	0.01011793
Bt.9520.1.S1_at	N(alpha)-acetyltransfe	NAA38	1.0845809	-1.0922623	1.1846468	0.049312342	0.02561454
Bt.9519.3.S1_at	sestrin 2	SESN2	-1.0001081	1.5199977	-1.5201062	0.024013035	0.00193756
Bt.9517.1.S1_a_at	SPC24, NDC80 kinetoc	SPC24	1.0056981	-1.393389	1.4013287	0.025377173	0.00396988
Bt.9516.2.A1_at	cell division cycle 37 h	CDC37L1	1.1192713	1.2633225	-1.1287009	0.040293388	0.01745135
Bt.9515.1.S1_at	prdX-deacetylase domai	PRDXDD1	-1.2696373	-1.5265878	1.2023809	0.022891732	7.69E-04
Bt.9514.1.S1_at	ankyrin repeat domai	ANKRD13A	-1.0690656	-1.175396	1.0994611	0.024766458	0.00359163
Bt.9510.2.A1_a_at	T-cell immunoglobulin	TIMD4	1.0456156	-1.4985199	1.5668758	0.024013035	0.00234382
Bt.951.1.S1_at	myeloid cell leukemia	MCL1	1.2349423	-1.3451777	1.6612167	0.03534756	0.01361443
Bt.9507.1.S1_at	haloacid dehalogenase	HDHD3	1.1140356	-1.1768264	1.3110263	0.02901493	0.00732951
Bt.9506.1.S1_at	M-phase phosphoprot	MPHOSPH8	-1.1126757	-1.7068576	1.5340117	0.02414251	0.00278898
Bt.9505.1.A1_at	kelch-like 26 (Drosoph	KLHL26	1.243487	-1.3052802	1.623099	0.033978593	0.01214077
Bt.9504.1.A1_at	chemokine (C-C motif)	CCL4	1.1128354	-1.5903302	1.7697759	0.02901493	0.00682799
Bt.9500.1.S1_a_at	epithelial stromal inte	EPST11	1.015763	-1.3011619	1.3216722	0.024766458	0.00379449
Bt.950.1.S1_at	ankyrin repeat and zin	ANKZF1	-1.4710537	-2.1555927	1.4653392	0.081801556	0.05757905
Bt.95.1.S1_at	parathyroid hormone	PTH	1.0757302	-1.1745452	1.2634938	0.047921848	0.02472293
Bt.9496.1.S1_at	zinc finger protein 609	ZNF609	-1.0670712	1.2898949	-1.3764098	0.03499949	0.01321179
Bt.9492.1.S1_at	hypothetical protein L	LOC506277	-1.0670713	1.2898949	-1.3764098	0.034999527	0.01321178
Bt.9491.1.S1_at	Ras homolog enriched	RHEB	-1.0284467	1.2089845	-1.2433761	0.06331019	0.03928364
Bt.9490.1.S1_at	ARP1 actin-related pro	ACTR1A	1.0242695	-1.5140306	1.5507753	0.031873036	0.01029398
Bt.9487.1.S1_at	190 kDa guanine nucle	RGNEF	1.2343838	1.5146172	-1.2270229	0.04507961	0.0216327
Bt.9486.1.S1_at	SET domain containin	SETD5	1.0383841	1.2472553	-1.2011502	0.03480421	0.01286712
Bt.9483.1.S1_at	integrin, alpha D	ITGAD	1.0479288	1.1949579	-1.1403043	0.034805436	0.01295973
Bt.948.1.S1_at	ubiquitin specific pept	USP11	-1.0009761	-1.3736207	1.3722813	0.025827987	0.00450288
Bt.9479.2.S1_at	PHD finger protein 11	PHF11	-1.0166714	1.2649733	-1.2860621	0.08093755	0.05685648
Bt.9470.2.S1_a_at	lysine (K)-specific dem	KDM4A	1.1301985	-1.2772939	1.4435956	0.02901493	0.0069894
Bt.9468.1.S1_at	spleen tyrosine kinase	SYK	-1.0950037	-1.4181833	1.2951403	0.029203497	0.007822
Bt.9460.1.S1_at	E74-like factor 1 (ets d	ELF1	-1.0950036	-1.4181833	1.2951404	0.02920351	0.007822
Bt.946.2.A1_a_at	adenylate kinase 2	AK2	1.0781124	-1.2827798	1.3829808	0.02901493	0.00690085
Bt.9459.1.S1_at	3-phosphoinositide de	PDPK1	-1.1228873	1.1369689	-1.2766879	0.02901493	0.00759469
Bt.9457.1.S1_at	similar to COX17 hom	MGC128036	1.0277398	-1.2836921	1.3193014	0.024013035	0.0023626
Bt.9455.1.A1_at	CD5 molecule-like	CD5L	1.2203884	1.4383147	-1.1785712	0.025827987	0.00441276
Bt.9454.1.S1_at	solute carrier family 4	SLC46A3	-1.0457803	-1.2860566	1.2297579	0.046260826	0.02290455
Bt.9449.1.S1_at	protein interacting wit	PROCA1	1.2109054	1.0024686	1.2079235	0.024013035	0.00183524
Bt.9448.1.S2_at	tropomyosin 3	TPM3	-1.005265	-1.534314	1.5262781	0.02901493	0.00674862
Bt.9445.1.S1_at	HMG box domain cont	HMGXB3	1.0504478	1.2984302	-1.236073	0.022891732	6.56E-04
Bt.9444.1.S1_at	serine/threonine kinas	STK17A	1.1985532	-1.0788484	1.2930572	0.034339253	0.01238057
Bt.9442.2.S1_a_at	Rho GTPase activating	ARHGAP9	1.0227491	-1.2338603	1.2619295	0.02901493	0.00729999
Bt.9438.1.S1_at	synaptotagmin binding	SYNCRIP	1.0227491	-1.2338603	1.2619295	0.02901493	0.0073
Bt.9434.1.S1_at	UBA domain containin	UBAC1	1.1990746	-1.4078856	1.6881597	0.027768528	0.00544899
Bt.9433.1.S1_at	DEAD (Asp-Glu-Ala-As	DDX24	-1.3386834	-1.4244753	1.0640868	0.049705237	0.02598922
Bt.9432.1.S1_at	cystatin F (leukocystat	CST7	1.0686474	-1.0627562	1.1357116	0.0498451	0.02641966
Bt.9431.2.S1_at	mKIAA1138 protein-lik	LOC788506 /// RE	1.0678717	1.287038	-1.2052366	0.03256693	0.01062305
Bt.9431.1.S1_at	REX1, RNA exonucleas	REXO1	1.0661306	1.2866001	-1.206794	0.02901493	0.0076205
Bt.9430.1.S1_at	mitochondrial ribosom	MRPL52	1.3002291	1.9919863	-1.5320272	0.032178592	0.01055185
Bt.9429.1.S1_at	general transcription f	GTF2H4	1.1135045	-1.3416017	1.4938796	0.031097788	0.00958904
Bt.9428.1.S1_at	mitochondrial ribosom	MRPS6	1.3054217	-1.2246907	1.5987377	0.030796394	0.00919414
Bt.9426.2.S1_at	transmembrane prote	TMEM42	-1.0266603	1.2045794	-1.2366939	0.024013035	0.00236465
Bt.9425.3.A1_at	Similar to signal peptid	LOC535156	-1.1807244	1.2116805	-1.4306608	0.024766458	0.00372148
Bt.9425.1.S1_at	signal peptide peptida	SPPL3	1.0835648	-1.1305946	1.2250725	0.024013035	0.00180757
Bt.9423.1.S1_at	platelet-derived growth	PDGFRA	-1.0648292	1.1803619	-1.2568837	0.047509477	0.02427516
Bt.9422.1.S1_at	G protein-coupled rec	GRK7	-1.0478778	-1.7223849	1.6436887	0.031050848	0.00954442
Bt.9421.1.S1_at	vitrin	VIT	-1.0478778	-1.7223849	1.6436887	0.031050848	0.00954419
Bt.9420.1.S1_at	rCG59523-like	LOC786966	1.0308121	-1.4606116	1.5056162	0.022891732	7.77E-04
Bt.942.2.S1_at	SAM domain and HD d	SAMHD1	1.0308121	-1.4606117	1.5056163	0.022891732	7.77E-04
Bt.9418.2.S1_at	integrin-linked kinase	ILKAP	1.1121392	-1.259389	1.4006159	0.027862377	0.00587344
Bt.9416.1.S1_at	microtubule associate	MICAL1	1.0799704	-1.3051481	1.4095213	0.024570853	0.00329583
Bt.9415.1.S1_at	XPA binding protein 2	XAB2	1.243765	-1.0994927	1.3675106	0.034590755	0.01263846
Bt.9414.1.S1_at	carbamoyl-phosphate	CAD	1.0498669	1.3195314	-1.256856	0.026534205	0.00478178
Bt.9412.3.S1_at	collagen, type XIV, alp	LOC781493	-1.0615395	-1.389507	1.3089546	0.041232325	0.01841614
Bt.9411.1.S1_at	breast carcinoma amp	BCAS4	1.1597826	-1.3695229	1.588349	0.022891732	4.47E-04

Bt.9410.1.S1_at	carbonic anhydrase 1	LOC786777	-1.3554853	1.0335332	-1.400939	0.030777326	0.00896322
Bt.941.1.S1_at	proteasome (prosome)	PSMD9	1.0297568	-1.3190126	1.3582622	0.024766458	0.00380486
Bt.9409.1.S1_a_at	SET binding factor 1	SBF1	1.0332506	1.4191887	-1.3735186	0.031308822	0.00971348
Bt.9408.1.S1_at	GTP binding protein 4	GTPBP4	-1.2223458	-1.3961669	1.1422029	0.04973036	0.02608757
Bt.9406.1.S1_at	RAB26, member RAS G	RAB26	1.1678299	-1.2008336	1.4023693	0.022891732	1.95E-04
Bt.9405.1.S1_at	TAF10 RNA polymeras	TAF10	1.2007128	1.2332088	-1.0270638	0.031449206	0.0098273
Bt.9402.2.S1_a_at	GH3 domain containin	GHDC	1.134933	-1.2793763	1.4520062	0.028583806	0.00633061
Bt.9401.1.S1_at	KDEL (Lys-Asp-Glu-Leu	KDEL1	1.2299113	-1.2885182	1.584763	0.036972128	0.01491358
Bt.9394.1.S1_at	vacuolar protein sortin	VPS53	-1.051051	-1.2854378	1.2230024	0.032914232	0.01123504
Bt.9391.2.S1_at	baculoviral IAP repeat	BIRC3	1.1094266	-1.2837551	1.424232	0.027768528	0.00558429
Bt.9390.1.S1_at	plexin domain contain	PLXDC1	-1.0508618	-1.4453368	1.3753823	0.025377173	0.00399937
Bt.9385.1.S1_at	tubulin folding cofacto	TBCC	-1.1763147	-1.4989592	1.2742841	0.077641584	0.05363542
Bt.9383.1.S1_at	retinoblastoma bindin	RBBP4	1.0991548	-1.2870604	1.4146787	0.024570853	0.00339047
Bt.9382.1.S1_at	GNDF family receptor	GFRA2	-1.2252564	1.1692948	-1.432686	0.043412596	0.02043307
Bt.9379.1.S1_at	monoamine oxidase A	MAOA	1.0055794	-1.5906556	1.5995305	0.03316394	0.01154606
Bt.9372.1.A1_at	CCR4-NOT transcriptic	CNOT7	1.0722094	-1.1672945	1.251584	0.0472649	0.02385523
Bt.9363.2.S1_at	cathepsin W	CTSW	1.0775682	-1.3529124	1.4578555	0.03507604	0.01333633
Bt.9362.1.S1_at	mitochondrial ribosom	MRPL2	1.1862917	-1.2484691	1.4810486	0.031097788	0.00960405
Bt.9360.1.S1_at	S100 calcium binding	S100A8	1.092124	-1.2474897	1.3624134	0.040756725	0.01797328
Bt.9354.1.S1_at	transmembrane prote	TMEM189	1.1108335	-1.2619023	1.4017633	0.046462454	0.02321481
Bt.9353.1.S1_at	elastin microfibril inte	EMILIN2	1.1090106	-1.0275147	1.1395247	0.027768528	0.0055453
Bt.9352.1.S1_at	rhomboïd domain con	RHBDD3	1.2621841	1.4383297	-1.1395562	0.022891732	2.46E-04
Bt.9351.3.S1_a_at	transmembrane chanr	TMC6	1.0163069	-1.281146	1.3020375	0.029822515	0.00832501
Bt.9351.1.S1_at	NFAT activating protei	NFAM1	1.0163069	-1.281146	1.3020375	0.029822515	0.00832501
Bt.9350.1.A1_at	ganglioside-induced d	GDAP1	-1.0386491	-1.3401258	1.2902585	0.029080378	0.00776847
Bt.935.2.S1_at	solute carrier family 3	SLC35A4	1.2610117	-1.8089963	2.2811654	0.024048876	0.00248832
Bt.9349.1.S1_at	coagulation factor VIII	LOC617475	-1.042262	-1.2643319	1.2130654	0.027768528	0.00577885
Bt.9348.1.S1_at	WDYHV motif contain	WDYHV1	1.1465914	-1.4917815	1.7104639	0.024013035	0.00227805
Bt.934.2.A1_at	PHD finger protein 20	PHF20	1.2575512	1.1656053	1.0788826	0.024013	0.00184648
Bt.9337.1.S1_at	ring finger protein 14	RNF145	1.2575513	1.1656053	1.0788826	0.024013035	0.00184647
Bt.9334.1.S1_at	RAB, member of RAS G	RABL4	-1.0237324	-1.3201023	1.2894994	0.041864008	0.01923082
Bt.9329.1.S1_at	small nuclear ribonuc	SNRPA1	-1.0237324	-1.3201023	1.2894993	0.041864064	0.01923084
Bt.9326.1.S1_at	DCN1, defective in cul	DCUN1D1	1.078188	-1.1948091	1.2882288	0.02901493	0.00746712
Bt.9324.1.S1_at	mitochondrial ribosom	MRPS11	-1.0571729	-1.37726	1.3027766	0.024013035	0.00224988
Bt.9323.1.S1_at	Hypothetical protein L	LOC100302389	-1.0591213	-1.167187	1.1020333	0.02901493	0.0066636
Bt.9322.1.S1_at	coiled-coil domain cor	CCDC76	1.0391374	1.3761125	-1.3242836	0.024570853	0.00340664
Bt.9321.1.S1_at	poly (ADP-ribose) poly	PARP4	1.0484463	-1.1390667	1.1942503	0.034999527	0.01320591
Bt.9320.1.S1_a_at	protein fucU homolog	MGC152007	1.128013	-1.1888837	1.3410763	0.02901493	0.00751319
Bt.9313.1.S1_at	hypothetical protein L	LOC509263	-1.1363246	-1.4579834	1.2830694	0.02901493	0.00768947
Bt.9312.2.S1_at	peptidylprolyl isomera	PP1L4	-1.1598	-1.3751498	1.1856784	0.04548109	0.02217806
Bt.9310.1.S1_at	chromosome 16 open	C16orf5	1.0355575	-1.5540665	1.6093254	0.032117034	0.01043592
Bt.931.2.S1_at	1-phosphatidylinositol	LOC100337091 ///	1.137162	-1.4621888	1.6627456	0.022891732	5.13E-04
Bt.9309.1.A1_at	nuclear factor of kappa	NFKB1	1.0695782	-1.1184766	1.1962981	0.02901493	0.00755854
Bt.9308.1.S1_at	protein tyrosine phosph	PTPRCAP	-1.3127462	1.1813084	-1.5507581	0.024013035	0.00219411
Bt.9306.3.S1_at	methionyl-tRNA synth	MARS	1.0896386	-1.4957159	1.6297897	0.024570853	0.00332137
Bt.9305.2.S1_at	midnolin	MIDN	1.0203115	1.2379055	-1.2132623	0.0498451	0.02641738
Bt.9304.1.S1_at	zinc finger protein 36	ZFP36L2	1.0355576	1.4058002	-1.3575296	0.027768528	0.00528173
Bt.9303.1.S1_at	tousled-like kinase 2	TLK2	1.1639779	-1.1155645	1.2984923	0.046260826	0.02285886
Bt.9300.1.A1_at	Opioid growth factor r	OGFRL1	-1.1751627	-1.6186239	1.3773615	0.041298978	0.01859184
Bt.9299.2.S1_at	trimethylguanosine sy	TGS1	-1.3203074	1.3238494	-1.7478883	0.059017222	0.03466093
Bt.9298.1.S1_at	alanyl-tRNA synthetas	AARSD1	-1.6297635	-1.1177777	-1.4580389	0.034805436	0.01291421
Bt.9297.1.A1_at	zinc finger, DHHC-type	ZDHHC19	1.0152879	-1.7038659	1.7299143	0.029807545	0.00829372
Bt.9296.1.A1_at	interferon-induced gu	LOC512486	1.2193459	-1.0250974	1.2499484	0.03480421	0.01283331
Bt.9292.1.A1_at	mitochondrial E3 ubiq	MUL1	1.0101653	-1.15915	1.1709331	0.034339253	0.01242065
Bt.9291.1.A1_at	transmembrane prote	TPRA1	1.0993797	-1.1022699	1.2118132	0.024013035	0.00159137
Bt.9289.2.S1_at	Carnitine palmitoyltra	CPT1A	1.1349736	-1.6054366	1.8221282	0.024013035	0.00238453
Bt.9288.3.A1_at	Actin filament associat	AFAP1L1	1.0691895	-1.1868819	1.2690018	0.029807545	0.00829977
Bt.9287.1.S1_at	hypothetical protein L	LOC100124511	-1.0041426	1.295883	-1.3012515	0.022891732	2.40E-04
Bt.9286.2.S1_at	Lipopolysaccharide-in	LITAF	-1.0041426	1.2958832	-1.3012515	0.022891732	2.40E-04
Bt.9283.1.A1_at	cellular repressor of E	CREG1	1.064982	-1.3390949	1.426112	0.022891732	9.18E-04
Bt.9282.1.S1_at	nucleoporin 62kDa	NUP62	1.2104703	-1.0172547	1.2313566	0.08424872	0.05997589
Bt.9281.1.A1_at	hypothetical LOC5176	MGC139228	-1.1142709	1.1704049	-1.3041481	0.030879559	0.00942754
Bt.9280.1.S1_at	mitochondrial ribosom	MRPL53	1.0805336	-1.2401798	1.340056	0.025828011	0.00438409
Bt.9278.1.S1_at	lysine (K)-specific dem	KDM2A	1.0805337	-1.2401794	1.3400557	0.025827987	0.00438408
Bt.9277.1.S1_at	protein tyrosine phosph	LOC100336920 ///	1.1561513	1.2960685	-1.1210198	0.03864421	0.01605851
Bt.9275.1.S1_at	WD repeat domain, ph	WIPI2	1.1561512	1.2960685	-1.1210198	0.03864426	0.01605853
Bt.9272.2.S1_at	N-acetyltransferase 10	NAT10	1.0426066	-1.2386988	1.2914757	0.03470898	0.01273071
Bt.9270.1.S1_at	UDP-Gal:betaGlcNAc t	B4GALT2	1.1867634	-1.1320763	1.3435067	0.025498856	0.00403657
Bt.927.1.S1_at	ADP-ribosylation facto	ARF1	1.2674911	-1.6501017	2.0914888	0.033150923	0.01140711
Bt.9269.2.S1_at	stress-associated endo	SERP1	-1.0102025	-1.1623526	1.1506133	0.022891732	5.88E-04
Bt.9268.1.S1_at	MOCO sulphurase C-ter	MOSC1	1.1544713	-1.2567036	1.4508283	0.030796394	0.00935144
Bt.9267.1.A1_at	apolipoprotein B mRNA	APOBEC3B	1.0781054	-1.178153	1.2701732	0.046462454	0.0231527
Bt.9265.2.S1_at	basic leucine zipper tra	BATF	-1.0941272	-1.3097118	1.1970379	0.02901493	0.00766478
Bt.9262.1.A1_at	Spi-B transcription fac	SPIB	-1.3037093	-1.6781938	1.2872455	0.030352592	0.00866604
Bt.926.1.S1_at	Calmodulin 3 (phosph	CALM3	-1.3037093	-1.6781938	1.2872455	0.030352615	0.00866605

Bt.9256.2.S1_a_at	chromosome 1 open r	C3H1ORF212	-1.0345825	-1.5198792	1.4690748	0.04004019	0.01709903
Bt.9255.1.A1_at	HD domain containing	HDCC2	-1.366513	-1.3254805	-1.0309567	0.024766458	0.00384788
Bt.9254.1.S1_at	rabaptin, RAB GTPase	RABEP2	-1.366513	-1.3254803	-1.0309567	0.024766458	0.00384788
Bt.9252.1.A1_at	jumonji domain conta	JMJD1C	-1.0460643	1.5676169	-1.6398281	0.022891732	8.80E-04
Bt.9251.2.S1_a_at	trafficking protein par	TRAPPC6A	1.08882	-1.2393428	1.3494213	0.047423076	0.02413335
Bt.9250.2.S1_at	interleukin-1 receptor	IRAK4	1.0122256	1.2056255	-1.1910641	0.024570853	0.00327114
Bt.9248.1.A1_at	RELT tumor necrosis fa	RELT	1.0655763	-1.257045	1.3394775	0.024570853	0.00343165
Bt.9245.1.S1_at	cancer susceptibility c	CASC3	1.2132665	1.6933894	-1.3957275	0.08744006	0.06326319
Bt.9244.1.A1_at	ring finger and SPRY d	RSPRY1	-1.0283304	1.2357925	-1.270803	0.033487722	0.01188512
Bt.9242.1.S1_at	mitochondrial ribosom	MRPL41	1.1062574	-1.2855375	1.4221355	0.024013035	0.00132034
Bt.9241.1.A1_at	TBC1 domain family, n	TBC1D20	1.0634353	-1.5790925	1.6792626	0.028583806	0.00636294
Bt.9240.1.A1_at	protein phosphatase G	PPP6C	1.2161409	-1.6273513	1.9790884	0.028753716	0.00646197
Bt.9239.1.S1_at	adenosine A2b recept	ADORA2B	1.0511357	1.350453	-1.2847562	0.024013	0.00144392
Bt.9238.1.S1_at	solute carrier family 3	SLC38A2	1.0511357	1.350453	-1.2847562	0.024013035	0.00144392
Bt.9237.1.S1_at	cyclin D-type binding-	CCNDBP1	1.1617261	-1.191174	1.383818	0.046648752	0.02334086
Bt.9236.1.S1_at	HECT, UBA and WWE d	HUWE1	-1.0516573	1.5164632	-1.5947996	0.03128365	0.00968356
Bt.9235.1.A1_at	tRNA splicing endonuc	TSEN15	1.1318666	-1.0144757	1.1482512	0.042790364	0.01995876
Bt.9233.3.S1_at	adhesion regulating m	ADRM1	-1.0748706	1.1179811	-1.201685	0.03442894	0.01253067
Bt.9233.2.S1_at	laminin, alpha 5	LAMA5	1.0716072	-1.6538175	1.7722427	0.022891732	9.48E-04
Bt.9230.1.S1_at	neuron derived neuro	NENF	1.1061405	-1.3052202	1.443757	0.027768528	0.00561838
Bt.923.2.S1_at	zinc finger, CCHC dom	ZCCHC3	-2.445851	-1.206919	-2.0265245	0.019877227	7.59E-05
Bt.9228.1.A1_at	Vacuolar protein sorti	VPS37C	-1.0688032	1.2305429	-1.3152082	0.024766458	0.00384253
Bt.9227.1.A1_at	tumor suppressing sub	TSSC4	-1.0610774	1.3101282	-1.3901474	0.024013035	0.00163304
Bt.9226.1.S1_at	hippocalcin-like 1	HPCAL1	-1.0550668	-1.3872312	1.3148278	0.032790437	0.01116758
Bt.9225.1.A1_at	hexokinase 3 (white ce	HK3	1.0634362	-1.5769081	1.676941	0.029030748	0.00772431
Bt.9224.1.S1_at	Similar to LOC152217	LOC783161	1.0580846	1.2362851	-1.1684179	0.030475453	0.00874419
Bt.9223.1.A1_at	FERM domain contain	FRMD8	-1.3926576	-1.9550242	1.4038082	0.04548109	0.02217533
Bt.9221.1.A1_at	EH domain binding pr	EHPBP11	1.0856524	1.5805953	-1.4558945	0.025753174	0.00415884
Bt.9220.1.S1_at	Nuclear prelamin A re	NARF	1.0506016	-1.3241786	1.3911842	0.041799407	0.01905344
Bt.9219.1.A1_at	mitogen-activated pro	MAP2K7	-1.0599014	-1.3447151	1.2687172	0.024570853	0.00345075
Bt.9218.1.A1_at	Similar to Krueppel-lik	LOC520939	-1.2849394	-1.705225	1.3270859	0.046462454	0.02316682
Bt.9217.1.A1_at	Major histocompatibil	LOC512672	-1.0816988	1.3152229	-1.4226749	0.024013035	0.00182874
Bt.9216.2.S1_at	tumor necrosis factor	TNFRSF25	1.1799045	1.3400418	-1.1357206	0.08299024	0.05876764
Bt.9215.2.S1_at	WW domain containin	WWOX	1.1196728	-1.3218287	1.4800156	0.027768528	0.00543722
Bt.9214.1.A1_at	solute carrier family 4	SLC45A4	1.0795164	-1.5581473	1.6820455	0.024013035	0.00161472
Bt.9213.2.S1_at	Fanconi anemia-associ	FAAP24	1.0006343	-1.2619462	1.2627466	0.024013	0.00179112
Bt.9212.1.A1_at	CBP/p300 homolog fa	LOC784935	1.0006343	-1.2619461	1.2627465	0.024013035	0.00179111
Bt.9211.1.S1_at	amyloid beta (A4) pre	APBB1IP	-1.2240465	1.1701527	-1.4323213	0.025713671	0.00410692
Bt.9210.1.S1_at	growth and transform	LOC617104	-1.142038	1.1602901	-1.3250954	0.02901493	0.00681056
Bt.9208.1.S1_at	triggering receptor exp	TREM1	1.1487205	-1.0923786	1.2548379	0.07343031	0.0496302
Bt.9207.1.S1_at	moesin	MSN	1.0957671	1.3754581	-1.2552466	0.024013	0.00236099
Bt.9206.1.S1_at	synaptotagmin-like 1	SYTL1	1.0957673	1.3754581	-1.2552466	0.024013035	0.00236099
Bt.9205.1.A1_at	hypothetical LOC5092	MGC152190	1.1205611	-1.2873085	1.4425077	0.022891732	8.41E-04
Bt.9203.1.S1_at	hypothetical protein L	LOC100140540	-1.0128213	-1.2612104	1.2452447	0.04625934	0.02281909
Bt.9202.1.S1_at	fibrinogen-like 2	FGL2	1.101106	1.4262034	-1.2952461	0.032487657	0.010783
Bt.9201.1.A1_at	tetraspanin 14	TSPAN14	1.03242	-1.3531519	1.3970212	0.024013035	0.00190538
Bt.9200.1.A1_at	WD repeat domain 70	LOC100335343	1.0798738	1.4804033	-1.370904	0.035804786	0.01386645
Bt.920.1.S1_at	ring finger protein 181	RNF181	1.0798738	1.4804032	-1.370904	0.035804786	0.01386645
Bt.9198.1.A1_at	HIV-1 Tat specific fact	HTATSF1	-1.0608218	1.2340561	-1.3091136	0.04367994	0.02062064
Bt.9197.1.S1_at	coiled-coil domain cor	CCDC28A	-1.0008149	1.3805625	-1.3816875	0.03499949	0.01314405
Bt.9196.1.A1_at	antigen identified by n	MKI67	-1.0008149	1.3805625	-1.3816875	0.034999527	0.01314405
Bt.9195.1.A1_at	SIVA1, apoptosis-induc	SIVA1	1.0619445	1.2388449	-1.1665815	0.022891732	9.85E-04
Bt.9194.1.S1_at	microtubule associate	MAST3	1.0619445	1.2388449	-1.1665815	0.022891732	9.85E-04
Bt.9192.1.A1_at	mannosyl (alpha-1,3-)	MGAT4B	1.1042337	1.3749547	-1.2451664	0.06371558	0.03989541
Bt.9191.1.S1_at	copine III-like	LOC100336172	-1.290796	1.1697388	-1.5098941	0.054460157	0.03023605
Bt.9190.1.S1_at	Sulfotransferase famil	SULT1C2	1.038285	-1.0753024	1.1164703	0.033487722	0.01190412
Bt.919.2.S1_at	SURP and G patch don	SUGP1	-1.0933597	-1.3267419	1.2134541	0.063427314	0.03958044
Bt.9189.2.S1_a_at	zinc finger CCHC-type	ZC3H14	1.221672	1.3660944	-1.118217	0.02901493	0.00740381
Bt.9186.1.A1_at	F-box and leucine-rich	FBXL3	1.0503149	-1.2897316	1.3546244	0.04567429	0.02236911
Bt.9185.1.A1_at	GRAM domain contain	GRAMD1C	-1.2622877	-1.3803511	1.0935313	0.042190105	0.01949988
Bt.9184.1.S1_at	mediator complex sub	MED19	-1.0421475	-1.2679418	1.2166625	0.035166986	0.01344512
Bt.9182.1.S1_at	ADP-ribosylation facto	ARF3	-1.1779641	1.2643025	-1.4893029	0.024013035	0.00180433
Bt.9180.3.S1_a_at	asparagine-linked glyco	ALG14	1.0811719	-1.2512686	1.3528365	0.03276182	0.01106724
Bt.9179.2.S1_at	ring finger protein 213	RNF213	1.1516763	1.1809623	-1.025429	0.060258247	0.03585685
Bt.9176.2.S1_at	cullin 4B	CUL4B	-1.0331991	1.2202004	-1.2607099	0.023475172	0.00107926
Bt.9175.1.A1_at	interleukin 1 receptor	IL1R1	-1.0331991	1.2202003	-1.2607099	0.023475185	0.00107927
Bt.9173.1.A1_at	neurobeachin-like 2	NBEAL2	1.2105801	1.4194734	-1.1725564	0.025828011	0.0045311
Bt.9172.1.A1_at	acidic repeat containi	ACRC	1.2105802	1.4194735	-1.1725564	0.025827987	0.00453109
Bt.9171.1.A1_at	transmembrane prote	TMEM160	-1.4609846	1.0700648	-1.5633482	0.032178592	0.01050252
Bt.9169.1.A1_at	notch 2	NOTCH2	1.1777966	-1.1119827	1.3096894	0.049686056	0.025914
Bt.9168.1.A1_at	MYST histone acetyltr	MYST2	-1.0055368	1.3941296	-1.4018487	0.02901493	0.00708938
Bt.9167.2.A1_at	nucleoporin 210kDa	NUP210	-1.1532809	-1.126965	-1.0233511	0.042278375	0.01957056
Bt.9166.1.A1_at	ubiquitin specific pept	USP3	1.0399055	-1.1959963	1.2437233	0.08305163	0.05886981
Bt.9164.1.A1_at	STAM binding protein	STAMPB	1.0785257	-1.4292041	1.5414335	0.04321782	0.02031085
Bt.9163.2.S1_at	purinergic receptor P2	P2RY10	1.0785257	-1.4292041	1.5414333	0.043217786	0.02031083

Bt.9162.1.A1_at	cysteine and histidine	CHORDC1	-1.0370419	1.2094508	-1.2542512	0.0495242	0.02579458
Bt.9159.1.S1_at	MOB1, Mps One Bind	MOBK2LA	-1.0370419	1.2094507	-1.2542511	0.04952423	0.0257946
Bt.9156.2.S1_at	cyclin-dependent kina	CDK13	-1.0457293	1.3945141	-1.4582841	0.024142448	0.0026443
Bt.9155.2.A1_at	SCY1-like 3 (S. cerevisi)	SCYL3	-1.0457293	1.3945141	-1.4582841	0.02414251	0.0026443
Bt.9155.1.A1_at	similar to Uncharacter	LOC784034	-1.0442593	1.1351019	-1.1853406	0.03079631	0.00913103
Bt.9154.1.S1_at	numb homolog (Drosophila)	NUMB	-1.0442593	1.1351019	-1.1853406	0.030796394	0.00913103
Bt.9153.1.S1_at	jun proto-oncogene	JUN	1.1834812	1.2900643	-1.090059	0.044219714	0.02112546
Bt.9151.1.S1_at	small ArfGAP 1	SMAP1	-1.2630208	1.0293574	-1.3000997	0.039596103	0.01676188
Bt.9150.1.A1_at	G-2 and S-phase expre	GTSE1	-1.2630208	1.0293574	-1.3000997	0.039596073	0.01676187
Bt.9149.1.S1_at	chromosome 1 open r	C16H1orf86	1.0086743	1.2990705	-1.2878989	0.03316394	0.01150149
Bt.9148.1.S1_at	abhydrolase domain c	ABHD8	-1.231213	1.1241479	-1.3840655	0.06612193	0.04229
Bt.9147.1.A1_at	WD repeat domain 77	WDR77	-1.16895	-1.0978955	-1.0647187	0.034472454	0.01257087
Bt.9145.1.A1_at	Poly (ADP-ribose) poly	PARP10	1.0546983	-1.3693292	1.4442292	0.04058248	0.01783908
Bt.9144.1.A1_at	ER lipid raft associat	ERLIN1	-1.1435218	1.3815196	-1.5797977	0.024013	0.00191492
Bt.9142.1.A1_at	hypothetical protein L	LOC532995	-1.1435218	1.3815196	-1.5797977	0.024013035	0.00191492
Bt.9141.3.S1_at	CCR4-NOT transcriptic	CNOT3	1.0970562	-1.1539377	1.2659345	0.02901493	0.00764441
Bt.9140.1.S1_at	geminin, DNA replicat	GMNN	1.0680715	1.1499543	-1.0766642	0.053372838	0.02616987
Bt.9139.1.A1_at	hypothetical LOC6163	LOC616332	1.0451106	-1.4154034	1.4792529	0.029807545	0.00821484
Bt.9138.1.A1_at	topoisomerase (DNA)	TOP3B	1.067383	-1.331158	1.4208554	0.02901493	0.00749876
Bt.9136.1.S1_at	mannosyl (alpha-1,6-)	LOC790576	1.067383	-1.331158	1.4208554	0.02901493	0.00749876
Bt.9135.1.A1_at	chromatin modifying p	CHMP4B	1.0177637	-1.2392967	1.2613113	0.09997659	0.07517675
Bt.9134.1.S1_at	slingshot homolog 3 (D	SSH3	-1.1120737	-1.3848493	1.2452855	0.03079631	0.00911986
Bt.9131.1.S1_at	V-set and transmembr	VSTM1	-1.1120738	-1.3848493	1.2452855	0.030796394	0.00911989
Bt.9130.2.A1_at	similar to Uncharacter	LOC100139027	1.1875324	-1.0424865	1.2379866	0.039568253	0.01672213
Bt.9130.1.S1_a at	nucleotide binding pro	NUBP1	-1.0987345	1.0883505	-1.1958083	0.031530906	0.00989737
Bt.9129.1.S1_at	lysine (K)-specific dem	LOC100140276	-1.0987346	1.0883505	-1.1958083	0.031530906	0.00989741
Bt.9128.1.A1_at	tetratricopeptide repe	TRANK1	-1.0180087	1.8924204	-1.9265003	0.024570785	0.00338239
Bt.9127.1.S1_at	nitric oxide synthase II	NOSIP	-1.0180086	1.8924204	-1.9265003	0.024570785	0.00338234
Bt.9126.1.S1_at	sterol-C5-desaturase (C	SC5DL	-1.1681902	-1.5397748	1.3180857	0.049795434	0.02618219
Bt.9124.1.A1_at	WAS/WASL interacting	WIPF1	1.0631074	1.3896918	-1.3071979	0.031317282	0.00973824
Bt.9119.1.A1_at	zinc finger, AN1-type	ZFAND3	-1.024381	1.3247136	-1.3570114	0.03752764	0.01538235
Bt.9118.1.S1_at	GDP-mannose 4,6-deh	GMDS	-1.0354542	1.1493065	-1.1900543	0.028583806	0.00637458
Bt.9115.1.S1_at	Janus kinase 1	JAK1	1.191751	-1.1566774	1.3784715	0.025753174	0.00415038
Bt.9114.1.A1_at	RAD23 homolog A (S. cerevisiae)	RAD23A	-2.384517	-1.9539434	-1.2203614	0.025827987	0.00441953
Bt.9111.2.S1_at	potassium channel tet	KCTD20	-1.293061	-1.0702038	-1.2082381	0.047587253	0.02438216
Bt.9111.1.S1_at	Required for meiotic r	RMND5A	-1.1596197	-1.4972849	1.2911861	0.07326541	0.04934413
Bt.9107.1.S1_a at	phosphatidylinositol b	PICALM	-1.0204909	1.1751803	-1.1992607	0.030796394	0.00917701
Bt.9106.1.A1_at	Gigaxonin	GAN	-1.0667297	1.1457406	-1.2221954	0.047867995	0.02465576
Bt.9103.1.A1_at	phosphatidylinositol t	PITPNM1	1.0454651	-1.1316235	1.1830729	0.02901493	0.00722889
Bt.9102.2.A1_at	RAS guanyl releasing p	RASGRP1	1.129907	-1.2458806	1.4077293	0.024013035	0.00220221
Bt.910.3.S1_at	ubiquitin-fold modifie	UFM1	1.0679692	-1.2016339	1.2833081	0.03316394	0.01160152
Bt.91.1.S1_at	agouti related protein	AGRP	1.1048585	1.3968009	-1.2642351	0.027768528	0.00574152
Bt.9099.1.A1_at	Small nuclear RNA act	SNAPC5	1.0126122	-1.6643014	1.6852919	0.024737129	0.00352124
Bt.9097.2.S1_at	GRAM domain contain	GRAMD1A	1.0430574	-1.7865868	1.8635126	0.046462544	0.02310311
Bt.9095.1.S1_at	hydroxysteroid (17-be	HSD17B4	1.1041878	1.3014477	-1.178647	0.024013035	0.00182855
Bt.9094.1.S1_at	unkempt homolog (Drosophila)	UNK	1.0192322	-1.157311	1.1795685	0.08744006	0.06333997
Bt.9093.1.A1_at	DCN1, defective in cul	DCUN1D5	-1.0006204	1.2996526	-1.3004588	0.024013035	0.00237235
Bt.9092.1.S1_at	polymerase (RNA) II (D	POLR2G	1.2305111	-1.2058955	1.4838678	0.023475185	0.00108019
Bt.9091.1.S1_at	NTF2-like export facto	NXT1	-1.0528262	-1.2691712	1.2054899	0.039568253	0.01671545
Bt.9086.1.S1_at	adaptor-related prote	AP152	-1.116686	1.2231721	-1.3658991	0.024570785	0.0031857
Bt.9084.1.S1_at	kringle containing tran	KREMEN2	-1.1140451	1.1690209	-1.3023419	0.049019262	0.02532373
Bt.9083.1.S1_at	TNF receptor-associat	TRAF1	1.0660459	-1.3751374	1.4659595	0.024013035	0.00236202
Bt.9082.1.S1_at	lectin, galactoside-bin	LGALS4	1.0659683	-1.4407976	1.5358444	0.041391153	0.01866258
Bt.9081.1.S1_at	selenocysteine lyase	SCLY	1.0604684	1.1914145	-1.1234794	0.07439305	0.05047161
Bt.9080.1.S1_at	COX19 cytochrome c	COX19	1.2187331	1.2204316	-1.0013937	0.02901493	0.00728374
Bt.9078.2.S1_a at	spermidine synthase	SRM	1.0495689	-1.2398605	1.3013191	0.039045706	0.01639092
Bt.9076.1.S1_at	lactamase, beta	LACTB	1.0812137	1.2300613	-1.1376671	0.032487586	0.01073526
Bt.9072.1.S1_at	aminoacyl tRNA synth	AIMP1	1.0812137	1.2300613	-1.1376672	0.032487657	0.01073525
Bt.9071.2.S1_a at	N-acetyltransferase 15	NAT15	1.0350761	-1.5314621	1.5851798	0.03091214	0.00945933
Bt.9070.1.S1_at	golgi to ER traffic prot	GET4	-1.1572372	-1.4630315	1.2642452	0.024013035	0.00215791
Bt.9069.1.S1_at	ankyrin repeat domain	ANKRD10	1.2299494	-1.0123998	1.2452005	0.037228912	0.01515467
Bt.9066.1.S1_at	ATG13 autophagy rela	ATG13	1.0996157	-1.1564193	1.2716168	0.040293388	0.0174061
Bt.9064.1.S1_at	signal transducer and	STAT1	1.0484376	-1.1910573	1.2487491	0.036972128	0.01472891
Bt.9062.1.S1_at	SPARC related modula	SMOC1	1.148033	-1.2542267	1.4398936	0.024013035	0.00158196
Bt.9060.1.S1_at	TAO kinase 2	TAOK2	1.1513529	-1.263366	1.4545802	0.02901493	0.00702405
Bt.9057.1.A1_at	TRK-fused gene	TFG	-1.3992357	-1.1794636	-1.1863322	0.0672912	0.0436085
Bt.9056.1.S1_at	glutathione synthetas	GSS	1.0734847	-1.3966444	1.4992763	0.034339253	0.01247376
Bt.9055.2.S1_a at	tRNA 5-methylaminon	TRMU	1.1019936	-1.2479275	1.3752081	0.024013035	0.00126796
Bt.9053.2.S1_a at	MACRO domain conta	MACROD1	-1.2120328	1.4017907	-1.6990165	0.090254225	0.06614391
Bt.9052.3.S1_at	TAF6 RNA polymerase	TAF6	1.1825947	-1.0385326	1.228163	0.037910566	0.0155929
Bt.9051.1.S1_at	signal recognition part	SRP19	1.1825947	-1.0385326	1.2281631	0.037910473	0.01559286
Bt.9050.1.S1_a at	F-box and WD repeat	FBXW5	1.1209329	1.2695606	-1.1325929	0.041676875	0.01893868
Bt.9049.1.S1_at	erbB-2-like	LOC505709	1.0007647	1.2142303	-1.2133025	0.028265815	0.00613345
Bt.9048.2.S1_a at	presenilin enhancer 2	PSENEN	1.0007647	1.2142302	-1.2133024	0.028265802	0.00613345
Bt.9047.1.S1_at	D-dopachrome tauton	DDT	1.0201867	1.2973211	-1.2716507	0.027768422	0.00560013

Bt.9045.1.S1_at	ribonucleoprotein, P	RAVER1	1.0201867	1.2973211	-1.2716507	0.027768528	0.00560013
Bt.9044.1.S1_at	inverted formin 2	INF2	1.0207835	-1.6810889	1.716028	0.024013	0.00124063
Bt.9042.1.A1_at	eukaryotic translation	EIF5	1.0207835	-1.6810892	1.7160282	0.024013035	0.00124063
Bt.9041.1.S1_at	serine/arginine-rich sp	SRSF11	1.1059321	-1.4539667	1.6079886	0.024013035	0.00157516
Bt.9040.1.A1_at	WAS protein homolog	WHAMM	1.075442	-1.2514858	1.3459378	0.038198154	0.01575939
Bt.9039.1.S1_at	splicing factor, arginin	SFRS15	1.0105337	-1.2018967	1.214557	0.030796394	0.00933782
Bt.9036.1.A1_at	zinc finger CCCH-type	ZC3H7A	1.1366192	1.2561381	-1.105153	0.024142498	0.00265712
Bt.9035.1.S1_at	GATS protein-like 3	GATSL3	1.1366192	1.2561381	-1.105153	0.02414251	0.00265712
Bt.9034.1.S1_at	proline rich 15	PRR15	1.1195332	-1.4781119	1.6547953	0.07503731	0.05111
Bt.9033.2.S1_at	translocation associat	TRAM1	1.0027432	1.3620533	-1.358327	0.027768422	0.00520567
Bt.9031.1.S1_at	polypyrimidine tract b	PTBP1	1.0027432	1.3620533	-1.358327	0.027768528	0.00520567
Bt.9030.1.S1_at	toll-like receptor 4	TLR4	-1.4115078	-1.8981717	1.344783	0.031530906	0.01002294
Bt.903.1.S1_at	Solute carrier family 4	SLC44A1	1.0230254	1.1649014	-1.1386827	0.0595265	0.03529522
Bt.9029.1.S1_at	dopamine receptor D1	DRD1	-1.0281217	1.2073231	-1.2412751	0.028367294	0.00622661
Bt.9028.1.S1_at	tyrosinase	TYR	1.0487094	-1.1470975	1.2029718	0.036972128	0.01490995
Bt.9027.1.S1_at	nuclear factor of kappa	NFKBIA	1.0784311	1.3261743	-1.2297254	0.024570853	0.00299615
Bt.9026.1.S1_at	inositol 1,4,5-triphosp	ITPR2	1.1215283	-1.235396	1.3855314	0.030879559	0.00941027
Bt.9025.1.S1_at	inositol 1,4,5-triphosp	ITPR3 /// LOC1003	-1.0888188	1.2158225	-1.3238103	0.024013035	0.00122647
Bt.9023.1.S1_at	inhibitor of kappa ligh	IKKBK	-1.1319175	-1.4243389	1.2583417	0.043638524	0.02057025
Bt.9022.3.S1_at	glutamine-rich 1	QRICH1	1.0301236	1.2857567	-1.2481577	0.026862508	0.00485993
Bt.9021.1.S1_at	solute carrier family 2	SLC25A24	-1.017504	1.2873646	-1.3098986	0.033158624	0.01158624
Bt.9020.1.S2_at	bladder cancer associa	BLCAP	-1.1579325	1.2197202	-1.4123539	0.036972128	0.01486834
Bt.9019.1.S1_at	hypothetical protein L	MGC127733	1.0481946	-1.8837982	1.9745872	0.022891732	6.43E-04
Bt.9014.1.A1_at	acid phosphatase 6, ly	ACP6	-1.0217242	-1.4503204	1.4194833	0.024144251	0.00256239
Bt.9013.1.S1_at	similar to glutamine ar	LOC537018	1.0736157	1.3205279	-1.2299819	0.024570853	0.00334123
Bt.9012.1.S1_at	obscurin, cytoskeletal	OBSCN	1.1340678	-1.1385593	1.2912035	0.03950563	0.01663983
Bt.901.2.S1_a_at	non-metastatic cells 6	NME6	1.0071676	-1.2120543	1.2207417	0.0402274	0.01722813
Bt.9004.1.S1_at	branched chain amino	BCAT2	-1.0000669	-1.2264798	1.2263978	0.042987745	0.0201285
Bt.9003.1.S1_at	hypothetical protein L	KIAA1797	1.1555737	1.3419647	-1.1612973	0.032539126	0.01093356
Bt.900.1.S1_at	GRB10 interacting GYP	GIGYF1	1.2746375	1.3182013	-1.0341774	0.04033658	0.01767398
Bt.9.2.S1_a_at	protein kinase, cGMP-	PRKG1	1.0980603	1.2949594	-1.1793154	0.022891732	4.49E-04
Bt.8998.3.S1_a_at	G protein pathway sug	GPS2	-1.0153093	-1.4342345	1.4126084	0.025827987	0.00447655
Bt.8995.1.A1_at	cryptochrome 1 (phot	CRY1	-1.0001178	-1.3844209	1.3842579	0.027768528	0.00525247
Bt.8994.1.S1_at	phospholipase C, delta	PLCD3	-1.0623932	-1.4630021	1.3770816	0.02901493	0.00694204
Bt.8991.1.S1_at	FtsJ homolog 1	LOC518818	1.306883	1.2827182	1.0188388	0.027768528	0.00574634
Bt.8987.1.S1_at	dual specificity phosph	DUSP27	1.0189142	-1.4753747	1.5032803	0.030796394	0.00929817
Bt.8984.1.S1_at	poly (ADP-ribose) poly	PARP1	1.0572915	-1.2060046	1.2750984	0.031530906	0.01013338
Bt.8982.1.S1_at	myosin binding protei	MYBPC3	1.0572915	-1.2060046	1.2750984	0.031530906	0.01013338
Bt.8979.1.A1_at	cytoplasmic polyaden	CPEB2	1.0745915	-1.1521139	1.2380519	0.02414251	0.00256179
Bt.8976.1.S1_at	transcription factor 7-	TCF7L2	1.1801373	-1.2111262	1.4292951	0.024142498	0.00269917
Bt.8972.1.S1_at	deoxynucleotidyltrans	DNTTIP1	1.1801373	-1.2111262	1.4292951	0.02414251	0.00269917
Bt.8971.1.A1_a_at	Wiskott-Aldrich syndr	LOC100336560	1.2090834	1.3143978	-1.0871028	0.061783127	0.03794314
Bt.8970.1.S1_at	oxidoreductase NAD-b	OXNAD1	-1.090972	-1.4202454	1.3018166	0.03699499	0.01497723
Bt.8969.1.S1_at	synaptosomal-associ	SNAP29	1.0078571	-1.1450101	1.1540065	0.04417656	0.02107362
Bt.8967.1.S1_at	myostatin	MSTN	-1.034345	1.1928769	-1.2338463	0.022891732	3.57E-04
Bt.8966.1.S2_at	thiamine triphosphata	THTPA	1.0885085	-1.2678869	1.3801055	0.028583806	0.00638338
Bt.8964.2.S1_a_at	protein phosphatase 1	PPP1R1A	-1.0601543	1.3118488	-1.3907621	0.024013	0.00214866
Bt.8963.1.S1_at	lysyl oxidase-like 1	LOXL1	-1.0601543	1.3118488	-1.3907621	0.024013035	0.00214866
Bt.8962.3.S1_s_at	ubiquitin specific pept	USP18	1.144701	-1.1750468	1.3450772	0.024013035	0.00200466
Bt.8960.1.S1_at	GATA binding protein	GATA4	-1.0023706	-1.2842442	1.281207	0.027768528	0.00580415
Bt.8959.1.S1_at	inhibitor of kappa ligh	IKBKG	1.0619788	-1.3835286	1.469278	0.024013035	0.0013589
Bt.8957.1.S1_at	chemokine (C-X-C mot	CXCR4	1.0363947	1.3286347	-1.2819774	0.050076544	0.0266839
Bt.8954.1.S1_at	liver expressed antimi	LEAP2	1.1893405	-1.4340607	1.7055864	0.04973036	0.02608098
Bt.8953.1.S1_at	prostaglandin E syntha	PTGES	1.1650678	1.2439378	-1.0676956	0.024013035	0.00215255
Bt.8950.1.S1_at	NADH dehydrogenase	NDUFA13	1.0329522	-1.130436	1.1676863	0.024766458	0.00385062
Bt.8949.1.S1_at	conserved helix-loop-h	CHUK	1.0061405	-1.3920796	1.4006276	0.024570785	0.00336007
Bt.8948.1.S1_at	lysyl oxidase	LOX	1.0061405	-1.3920796	1.4006276	0.024570853	0.00336006
Bt.8947.1.S1_at	legumain	LGMN	1.3570862	-1.37577	1.8670384	0.035166968	0.01348656
Bt.8946.2.S1_a_at	solute carrier organic	SLCO1A2	1.0680649	-1.2135962	1.2961996	0.03635977	0.0143109
Bt.8945.1.S1_at	toll-like receptor 2	TLR2	1.2417666	-1.3240348	1.6441423	0.022891732	3.98E-04
Bt.8942.1.S1_at	chymotrypsin-like elas	CELA3B	-1.1919639	-1.7272593	1.4490869	0.030303387	0.00857244
Bt.8941.1.S1_at	chitinase, acidic	CHIA	1.0491294	1.4416066	-1.3740981	0.022891732	7.69E-04
Bt.894.1.S1_at	ubiquitin-conjugating	UBE2Q1	-1.0613974	-1.317498	1.2412862	0.024766458	0.00361423
Bt.8939.1.S1_at	TYRO protein tyrosine	TYROBP	1.0730076	-1.1760646	1.2619262	0.032487657	0.01075422
Bt.8938.1.S1_at	lymphocyte antigen 9	LY96	1.0838768	-1.2995358	1.4085368	0.025610184	0.00407229
Bt.8933.2.S1_at	adaptor-related prote	AP3S2	1.1995692	1.5360873	-1.2805325	0.022891732	7.16E-04
Bt.893.1.S1_at	NADH dehydrogenase	NDUFB6	1.1995692	1.5360873	-1.2805324	0.022891732	7.16E-04
Bt.8928.1.S1_at	N-acetyltransferase 14	NAT14	1.003756	-1.2773796	1.2821776	0.033487722	0.01187042
Bt.8925.2.S1_at	dolichol kinase	DOLK	1.003756	-1.2773796	1.2821776	0.033487722	0.01187042
Bt.892.1.S1_at	cytochrome c oxidase	COX7A2L	1.1780818	-1.1373404	1.3398799	0.031930793	0.0103352
Bt.8919.1.S1_at	RAB33B, member RAS	RAB33B	1.0133009	1.3040439	-1.2869266	0.034708954	0.0127211
Bt.8917.1.S1_at	arachidonate lipoxyme	ALOX12E	1.0133009	1.3040439	-1.2869266	0.03470898	0.0127211
Bt.8915.1.A1_at	dehydrogenase E1 and	DHTKD1	-1.0494062	-1.3548005	1.2910163	0.028761035	0.00649347
Bt.8912.1.A1_at	CUGBP, Elav-like famil	CELF1	-1.0128751	-1.2656802	1.2495916	0.022891732	2.04E-04
Bt.8911.1.A1_at	hypothetical LOC5080	LOC508041	1.0717185	1.4152157	-1.3205107	0.030796394	0.00932291

Bt.891.1.S1_at	interleukin 34	IL34	1.0198394	1.2163651	-1.1927027	0.024013	0.00180767
Bt.8906.1.S1_at	lectin, galactoside-binding	LGALS9	1.0198394	1.2163651	-1.1927027	0.024013042	0.00180767
Bt.8905.1.S1_at	itchy E3 ubiquitin protein	ITCH	-1.2375281	-1.0158799	-1.2181836	0.0411942	0.01836999
Bt.8904.1.S1_at	mitogen-activated protein kinase	MAP2K5	-1.2375281	-1.0158799	-1.2181836	0.0411942	0.01836999
Bt.8903.1.S1_at	chromosome 8 open reading frame	C14H8ORF70	1.103878	1.1098922	-1.0054482	0.059792753	0.03549535
Bt.8902.3.S1_a_at	islet cell autoantigen 1	ICA1	-1.1337734	-1.4544358	1.2828275	0.060308963	0.03605751
Bt.89.1.S1_at	cholinergic receptor, nicotinic	CHRNA7	-1.173096	-1.0482763	-1.1190712	0.06973509	0.0457791
Bt.8897.1.S1_at	von Ebner minor salivary gland	LPLUNC1	1.1573282	1.511452	-1.3059839	0.065527715	0.04158579
Bt.8893.1.S1_at	opioid growth factor receptor	OGFR	-1.0469544	1.44191	-1.509614	0.024570853	0.00337381
Bt.889.2.S1_a_at	ATPase type 13A2	ATP13A2	-1.0086129	1.2627488	-1.2736248	0.025828011	0.00440885
Bt.8889.1.S1_at	ret proto-oncogene	RET	-1.008613	1.2627487	-1.2736248	0.025827987	0.00440884
Bt.8888.2.S1_at	importin 8	IPO8	1.1825522	-1.2794013	1.5129589	0.031530906	0.01007281
Bt.8887.1.S1_at	transmembrane protein	TMEM62	1.0963542	-1.1172168	1.2248656	0.05786057	0.03324427
Bt.8885.1.S1_at	basic leucine zipper nuclear	BLZF1	1.0597993	-1.1705011	1.2404963	0.0472649	0.02398248
Bt.8883.1.S1_at	butyrophilin, subfamily 1	BTN3A2	1.0094513	1.178889	-1.1678512	0.03635977	0.01428776
Bt.8881.1.A1_at	EPH receptor A1	EPHA1	-1.0200468	-1.742673	1.7084247	0.029312633	0.00791257
Bt.888.1.S1_at	BCL2/adenovirus E1B	BNIP3L	-1.0200468	-1.7426732	1.7084247	0.029312653	0.00791256
Bt.8874.1.S1_at	rCG42310-like	LOC514296	1.1007205	-1.271666	1.3997489	0.040293388	0.01752431
Bt.8872.1.S2_at	ATPase, Ca++ transporter	ATP2B1	1.1007205	-1.271666	1.399749	0.040293388	0.0175243
Bt.8870.3.S1_at	transmembrane protein	TMBIM4	-1.1707098	1.0590917	-1.239889	0.073257364	0.04918339
Bt.8870.2.S1_at	LLP homolog, long-terminal	LLPH	-1.1023483	1.2084674	-1.332152	0.02901493	0.00710652
Bt.887.1.S1_at	dynein, cytoplasmic 1, heavy	LOC519789	-1.1023483	1.2084674	-1.332152	0.02901493	0.00710652
Bt.8869.2.S1_at	Zinc finger, DHHC-type 2	ZDHHC17	1.3511496	1.8750143	-1.3877178	0.082490444	0.05818054
Bt.8869.1.S1_at	similar to serine/arginine	LOC534002	1.1068938	-1.3649596	1.5108652	0.030303387	0.00854715
Bt.8868.1.S1_at	xylosylprotein beta 1,4-galactosyl	B4GALT7	1.1068938	-1.3649596	1.5108652	0.030303387	0.00854715
Bt.8867.1.S1_at	choline kinase beta	CHKB	1.3047107	-1.0176957	1.3277985	0.07770535	0.05380453
Bt.8861.1.S1_at	aryl hydrocarbon receptor	AH1	1.188252	-1.1160761	1.3261796	0.046462544	0.02321203
Bt.886.1.S1_at	proteasome (prosome) subunit	PSMA5	-1.0987704	1.168219	-1.2836044	0.024570785	0.0030576
Bt.8857.1.S2_at	ubiquitin 1 /// ubiquitin	LOC783466 /// UB	-1.0987704	1.168219	-1.2836044	0.024570853	0.0030576
Bt.8857.1.S1_at	ubiquitin 1	UBQLN1	1.0107224	-1.550396	1.5670199	0.06538909	0.04139526
Bt.8856.1.S1_at	Rh family, B glycoprotein	RHBG	-1.1695383	1.2518934	-1.4641373	0.025828011	0.00437725
Bt.8850.1.S1_at	seryl-tRNA synthetase	SARS2	-1.1695385	1.2518934	-1.4641374	0.025827987	0.00437725
Bt.8848.1.S1_at	transmembrane protein	TMEM106C	1.0549726	-1.138393	1.2009734	0.047423076	0.02417098
Bt.8845.3.A1_a_at	acyl-CoA dehydrogenase	ACAD9	1.2390326	-1.7642905	2.1860132	0.053039756	0.02878766
Bt.8841.1.A1_at	small acidic protein	SMAP	1.2139413	1.2689196	-1.045289	0.038569864	0.01594584
Bt.884.1.S1_at	myoferlin	MYOF	1.3917089	1.5017774	-1.0790888	0.045216974	0.02179362
Bt.8835.1.S1_at	eukaryotic translation initiation	EIF2B5	-1.1503882	1.1257899	-1.2950956	0.043822575	0.02081185
Bt.8834.2.S1_a_at	nurim (nuclear envelope)	NRM	1.0567768	1.3879268	-1.3133584	0.024013035	0.00146745
Bt.8831.1.S1_at	LSM14B, SCD6 homolog	LSM14B	1.0194685	1.6381755	-1.6068918	0.027285445	0.00501358
Bt.8829.1.S1_at	intraflagellar transporter	IFT122	1.248184	1.3844647	-1.1091832	0.04454344	0.02134308
Bt.8826.1.S1_at	dynamitin 2	DNM2	1.1362562	1.6483597	-1.4506936	0.041676875	0.01888248
Bt.8825.1.S1_at	dynamitin 1	DNM1	1.1441466	1.4796431	-1.2932287	0.03429115	0.01233512
Bt.8823.3.S1_a_at	chromosome 9 open reading	C8H9ORF46	-1.1370134	-1.6327944	1.4360379	0.0472649	0.0238082
Bt.8822.1.A1_at	potassium inwardly-rectifying	KCNJ10	1.1704397	-1.2935766	1.5140533	0.025753174	0.00422243
Bt.8821.1.S1_at	La ribonucleoprotein c	LARP1	-1.0651704	1.1894324	-1.2669481	0.024766458	0.00382144
Bt.8820.2.S1_at	hematopoietic cell-specific	HCLS1	1.1021641	1.2763126	-1.1580058	0.027363783	0.00504731
Bt.8815.1.S1_at	growth factor receptor	GRB2	1.0060785	1.2634571	-1.2558235	0.02901493	0.00767882
Bt.8809.1.S1_at	sodium channel, voltage	SCN4B	1.045511	-1.47485	1.541972	0.02414251	0.00264171
Bt.8807.1.S1_at	golgin A5	GOLGA5	1.0622133	-1.3642709	1.4491466	0.024766458	0.00384917
Bt.8806.1.S1_at	neurochondrin	NCDN	-1.0401373	1.1348562	-1.1804063	0.037895717	0.01556001
Bt.8805.1.S1_at	calcineurin binding protein	CABIN1 /// LOC50	-1.3698974	-1.8681772	1.3637352	0.036972128	0.01480507
Bt.8804.1.S1_at	NEL-like 2 (chicken)	NELL2	-1.3698971	-1.8681772	1.3637353	0.036972128	0.01480508
Bt.8803.1.A1_at	complement component	C1R	1.0574112	-1.2764385	1.3497204	0.038785268	0.01616919
Bt.8802.1.S1_at	family with sequence	FAM57A	-1.0025126	1.2009709	-1.2039884	0.039706968	0.01683688
Bt.8800.1.S1_at	ST3 beta-galactosidase	ST3GAL3	1.0879834	-1.124538	1.2234786	0.07651567	0.05239836
Bt.88.1.S1_at	cholinergic receptor, nicotinic	CHRNA7	1.0367572	-1.1528006	1.1951743	0.04096433	0.0181024
Bt.8798.2.S1_at	aldehyde dehydrogenase	ALDH1A3 /// LOC5	-1.1223044	-1.2750235	1.1360763	0.022891732	9.75E-04
Bt.8797.1.S1_at	RAP1 GTPase activator	RAP1GAP	-1.1075544	-1.7106817	1.5445576	0.035166968	0.01350281
Bt.8795.1.S1_at	dysferlin, limb girdle muscle	DYSF	-1.0395547	-1.4955553	1.4386499	0.034804247	0.01288864
Bt.8794.2.S1_at	tyrosylprotein sulfotransferase	TPST1	-1.0395547	-1.4955554	1.43865	0.03480421	0.01288863
Bt.8792.1.S1_at	ORAI calcium release-activated	ORAI3	-1.0465828	-1.3263049	1.2672718	0.024570853	0.00313946
Bt.8790.1.S1_at	solute carrier family 4, member	SLC43A2	1.0001261	1.1934357	-1.1932851	0.05762643	0.03306902
Bt.879.1.S1_at	similar to keratin 6A	LOC100301161	-1.0191073	-1.4331981	1.4063269	0.032487586	0.01079093
Bt.8789.1.S1_at	HIV-1 Tat interactive protein	HTATIP2	-1.0191072	-1.433198	1.4063269	0.032487657	0.01079095
Bt.8788.2.S1_a_at	WD repeat domain 33	WDR33	-1.1237462	1.3684198	-1.5377566	0.028171103	0.00609213
Bt.8787.1.S1_at	adiponectin receptor	ADIPOR1	1.1171721	-1.1035496	1.2328548	0.02901493	0.00750713
Bt.8781.1.S1_at	glutamine-fructose-6-phosphate	GFPT2	1.1282922	1.2369848	-1.0963337	0.024142498	0.00278941
Bt.8777.1.S1_at	Similar to FLJ00089 protein	LOC527187	1.1282922	1.2369848	-1.0963337	0.02414251	0.00278941
Bt.8775.2.S1_a_at	adaptor-related protein	AP1B1	1.1247054	-1.1350449	1.2765913	0.024013035	0.00207048
Bt.8772.1.S1_at	Phosphatidylinositol transfer	PITPNA	1.295214	-1.1208094	1.4516882	0.033150923	0.01135405
Bt.8766.1.S1_at	N-acylsphingosine amidase	ASAH1	1.055992	-1.2756804	1.3471082	0.036685135	0.0145185
Bt.876.2.S1_at	olfactomedin 1	OLFM1	1.055992	-1.2756804	1.3471082	0.036685134	0.0145185
Bt.8759.1.S1_at	chromosome X open reading	CXHXORF23	1.0168006	-1.4545373	1.4789745	0.022891732	9.89E-04
Bt.8753.1.S1_at	actin-like 6B	ACTL6B	1.0600715	-1.0365474	1.0988144	0.046260826	0.02291791
Bt.8752.1.S1_at	190 kDa guanine nucleotide	RGNEF	1.0439396	-1.280022	1.3362656	0.022891732	3.10E-04

Bt.8751.1.S1_a_at	polycomb group ring f	PCGF2	1.0169463	1.3189331	-1.2969545	0.024048876	0.00245932
Bt.8748.1.S1_at	transmembrane prote	TMEM135	1.1049331	-1.1609647	1.2827884	0.03251003	0.01082136
Bt.8745.1.S1_at	zinc finger CCH-type	ZC3H12A	1.0751575	-1.2412801	1.3345716	0.022891732	7.14E-04
Bt.8743.1.S1_at	transforming, acidic co	TACC3	1.0605772	-1.1121409	1.1795112	0.04379717	0.02070693
Bt.8739.1.S1_at	aldehyde dehydrogen	ALDH9A1	1.0986882	-1.154257	1.2681687	0.035166968	0.01352002
Bt.8738.1.S1_at	heat shock 105kDa/11	HSPH1	-1.0649009	1.2740427	-1.3567291	0.02901493	0.00698757
Bt.8736.2.S1_at	chromosome 1 open r	LOC520588	1.0735271	-1.0942911	1.174751	0.027768528	0.00516485
Bt.8735.2.S1_a_at	translocase of inner m	TIMM22	1.221755	-1.0403076	1.2710011	0.04711232	0.0236394
Bt.8731.1.S1_at	mCG141481-like	LOC100335204	1.3417035	1.0275526	1.3057274	0.022891732	7.43E-04
Bt.8730.1.S1_at	Rap guanine nucleotid	RAPGEF2	1.0644401	1.5546314	-1.4605156	0.030777326	0.00899155
Bt.8722.1.S1_at	acid phosphatase 2, ly	ACP2	-1.0336477	-1.173356	1.1351606	0.036972128	0.01482489
Bt.8721.1.A1_at	sperm flagellar 1	SPEF1	1.0356876	-1.2524713	1.297169	0.022891732	7.87E-04
Bt.872.2.S1_at	docking protein 4	DOK4	-1.9022766	-1.9234401	1.0111253	0.04200343	0.01932455
Bt.872.1.S1_at	polymerase (RNA) II (C	POLR2C	1.0531571	-1.1342177	1.1945094	0.029312653	0.00788332
Bt.8719.1.S1_a_at	phosphoseryl-tRNA kin	PSTK	1.324352	1.3194101	1.0037456	0.033150923	0.0114564
Bt.8715.1.S1_at	DEAH (Asp-Glu-Ala-His	DHX15	-1.0197666	1.3515779	-1.378294	0.021954797	1.09E-04
Bt.8713.1.S1_at	BMS1 homolog, ribosc	BMS1	-1.0495894	-1.2983159	1.2369751	0.03699499	0.01498101
Bt.8712.1.S1_at	stromal interaction mo	STIM1	1.1865766	1.7316489	-1.4593654	0.024013035	0.00178367
Bt.8706.1.S1_at	mitogen-activated pro	MAPKAPK3	1.1288611	1.5670753	-1.3881915	0.024013035	0.00218613
Bt.870.1.S1_at	ankyrin repeat and SO	ASB5	1.106551	1.2288328	-1.1105071	0.028171103	0.00604664
Bt.87.1.S1_at	transient receptor pot	TRPC2	-1.558073	-2.5029626	1.6064476	0.02901493	0.00731525
Bt.8699.1.S1_at	zinc finger protein 385	ZNF385A	-1.0049043	1.3831263	-1.3899095	0.036972128	0.01469308
Bt.8694.2.S1_at	CASK interacting prote	CASKIN2	-1.0272077	1.1330868	-1.1639155	0.022891732	0.00101921
Bt.8694.1.S1_at	similar to Uncharacter	LOC512110	1.0124432	1.2052094	-1.190397	0.027768528	0.0053903
Bt.8690.2.S1_at	pleckstrin homology d	PLEKHB2	1.0557437	-1.1764368	1.2420156	0.024013035	0.00242676
Bt.869.2.S1_at	ubiquitin-like with PH	UHRF2	1.0792915	-1.0967627	1.1837265	0.040293388	0.01731522
Bt.869.1.S1_at	dolichyl-phosphate ma	DPM1	-1.0864727	1.2973231	-1.4095063	0.02414251	0.00281169
Bt.8686.1.S1_at	tumor rejection antigen	HSP90B1	-1.0215111	1.161703	-1.1866925	0.028062016	0.00594954
Bt.8684.1.S1_at	Ctr9, Paf1/RNA polym	CTR9	1.0605532	-1.1542583	1.2241522	0.04416338	0.02103613
Bt.8683.1.S1_at	hypothetical protein L	LOC512391 /// LO	-1.0587666	1.4075989	-1.4903187	0.019877227	5.08E-05
Bt.868.2.S1_at	roadblock domain con	ROBLD3	-1.0956552	-1.2988238	1.1854312	0.08744006	0.06328137
Bt.8679.3.S1_at	dihydrolipoamide S-ac	DLAT	1.0250689	1.5476866	-1.5098366	0.030796394	0.00928571
Bt.8676.1.S1_at	TNF receptor-associat	LOC783305 /// TR	1.0946128	-1.1744809	1.2856019	0.027768528	0.00566403
Bt.8673.3.A1_at	Helicase with zinc fing	HELZ	-1.2985655	-1.0384938	-1.2504318	0.02901493	0.00711409
Bt.8671.1.S1_at	metallo-beta-lactamas	MBLAC2	1.1311983	1.2598	-1.1136863	0.04540309	0.0219475
Bt.8667.1.S1_at	chromosome 3 open r	C22H3ORF23	1.0854769	-1.2103968	1.3138576	0.027157558	0.00497089
Bt.8654.1.S1_at	PHD finger protein 21	PHF21A	-1.1206006	-1.4839227	1.3242209	0.024048876	0.00250346
Bt.8650.1.A1_at	stromal interaction mo	STIM2	-3.3287203	-1.8958752	-1.7557697	0.042987745	0.02014196
Bt.865.1.S1_at	Rho GTPase activating	ARHGAP30	1.0547787	-1.1480185	1.2109054	0.019877227	4.14E-05
Bt.8647.1.S1_at	ankyrin repeat domain	ANKRD46	1.1678171	1.3810555	-1.1825956	0.032781206	0.01111942
Bt.8646.1.S1_at	lymphotoxin beta rece	LTBR	1.0944674	1.691189	-1.5452166	0.022891732	5.69E-04
Bt.8644.1.S1_at	potassium voltage-gat	KCND1	1.1357101	1.9932283	-1.7550502	0.025827987	0.00448404
Bt.8643.2.S1_at	reticulocalbin 2, EF-ha	RCN2	1.0174661	1.245652	-1.2242689	0.035166968	0.01348217
Bt.8642.1.S1_at	COBL-like 1	COBL1	1.0597208	1.3226498	-1.2481117	0.04973036	0.02611283
Bt.8641.1.A1_at	G1 to S phase transitio	GSPT2	1.2254229	1.0947824	1.1193302	0.024013035	0.00163593
Bt.8640.1.S1_at	diphosphoinositol pen	PIIP5K2	1.3087343	-1.2056749	1.577908	0.030796394	0.00935862
Bt.864.2.S1_at	serine/arginine-rich sp	SRSF1	1.2510275	-1.0637723	1.3308084	0.024013035	0.00190907
Bt.8637.1.S1_at	similar to F47B8.14	LOC525174	1.1788638	-1.11224	1.3111794	0.024013035	0.00136479
Bt.8635.2.S1_at	hypothetical LOC5120	MGC139698	1.1021872	-1.1511436	1.2687757	0.041864064	0.01921837
Bt.8630.1.S1_at	neuroplastin	NPTN	1.1033839	-1.26531	1.3961227	0.041864064	0.01916574
Bt.8624.2.S1_at	arginase, type II	ARG2	1.1175376	-1.0342137	1.1557726	0.03480421	0.01286747
Bt.8620.1.S1_at	solute carrier family 2	SLC26A11	1.113101	-1.1539565	1.2844702	0.025753174	0.00418939
Bt.8619.1.S1_at	SH3-domain binding p	SH3BP5	-1.2228901	-1.3254796	1.083891	0.024013035	0.00242205
Bt.8617.1.S1_at	cannabinoid receptor	CNRIP1	-1.0280795	1.3370095	-1.3745522	0.03044046	0.00871264
Bt.8609.1.S1_s_at	centromere protein C	CENPC1	-1.0280795	1.3370095	-1.3745521	0.030440537	0.00871266
Bt.8608.1.S1_at	Zinc finger protein 605	ZNF605	-1.0385884	1.2723771	-1.3214761	0.022891732	5.77E-04
Bt.8601.1.S1_at	Rho guanine nucleotid	ARHGEF19	-1.7445194	-1.2206246	-1.4292022	0.0472649	0.02395663
Bt.860.1.S1_at	glyoxylate reductase	GLYR1	-1.0516521	-1.231741	1.1712437	0.023475185	0.00109496
Bt.86.1.S1_at	serpin peptidase inhib	SERPINF2	1.129887	-1.2273359	1.3867509	0.046888255	0.02349383
Bt.8597.1.S1_at	Topoisomerase (DNA)	TOP3B	1.0780343	-1.1262318	1.2141166	0.024013035	0.00240957
Bt.8593.3.S1_at	odd-skipped related 2	OSR2	-1.5542371	-1.4856762	-1.046148	0.04548109	0.0221387
Bt.8592.2.S1_at	poly(A) binding protein	PABPC1L	-1.053636	-1.3986102	1.3274132	0.027768528	0.00537406
Bt.8591.1.S1_at	hepatoma-derived gro	HDGFRP2	1.1473744	1.3488374	-1.1755861	0.027674964	0.00512427
Bt.8587.1.S1_at	5'-3' exoribonuclease	XRN2	1.1473745	1.3488375	-1.1755861	0.027674954	0.00512427
Bt.8586.1.S1_at	similar to Myeloid-ass	LOC512150	1.1027807	-1.2497863	1.3782402	0.024570853	0.00347291
Bt.8583.2.S1_at	mannosyl (alpha-1,3-)	MGAT1	1.0684133	-1.242043	1.3270153	0.025827987	0.00457918
Bt.8582.1.S1_at	ubiquitin 1	UBN1	1.0943766	1.6592603	-1.5161693	0.022891732	7.46E-04
Bt.858.2.S1_at	CTF18, chromosome t	CHTF18	1.0943764	1.65926	-1.5161693	0.022891732	7.46E-04
Bt.8578.1.S1_at	catechol-O-methyltran	COMT	-1.0165839	-1.3418827	1.3199921	0.027768528	0.00582845
Bt.8570.1.A1_at	synaptosomal-associa	SNAP23	-1.1633977	1.0012197	-1.1648167	0.037231553	0.01518206
Bt.8568.1.S1_at	phospholipid transfer	PLTP	1.0626501	-1.2279412	1.3048718	0.034999527	0.01322555
Bt.8566.1.S1_at	acidic (leucine-rich) nu	ANP32A	1.0056587	-1.3460344	1.3536513	0.031530906	0.01014345
Bt.8563.1.S2_at	Cytochrome b5 type B	CYB5B	-1.0074487	-1.3931468	1.3828464	0.036074318	0.01402778
Bt.8562.1.S1_at	small nuclear RNA acti	SNAPC3	1.0282829	-1.2430471	1.2782041	0.02901493	0.00756033
Bt.8560.1.S1_at	solute carrier family 3	SLC39A5	1.0928215	-1.1338996	1.2391498	0.049362168	0.0256753

Bt.856.1.S1_at	Deoxyribonuclease I-like	DNASE1L3	-1.2573988	-1.2337345	-1.019181	0.039046455	0.01641883
Bt.855.2.S1_at	ribosome binding protein	LOC505941	-1.2573988	-1.2337345	-1.019181	0.039046455	0.01641883
Bt.852.1.S1_at	major histocompatibility complex class II	BOLA-DRA	1.081614	-1.3684967	1.4801852	0.031050848	0.00954567
Bt.8549.2.S1_at	endothelial cell-specific protein	ECSCR	1.1768854	-1.0933434	1.2867398	0.029807545	0.00823792
Bt.8549.1.S2_at	collagen, type I, alpha 1	COL1A1	1.0034226	-1.2474345	1.251704	0.024013035	0.00160084
Bt.8548.1.S1_at	adiponectin, C1Q and collagen domain containing	ADIPOQ	1.1546444	-1.199108	1.3845433	0.044360068	0.02122386
Bt.8547.1.S1_at	signaling lymphocytic kinase	SLAMF1	1.0140523	1.1356802	-1.1199425	0.02873816	0.00643816
Bt.8545.1.S1_at	mitochondrial ribosomal protein S19	MRPL43	1.0140523	1.1356802	-1.1199425	0.028738162	0.00643816
Bt.8544.1.S1_at	CD69 molecule	CD69	1.0301336	1.4406365	-1.3984948	0.022891732	5.83E-04
Bt.8543.1.S1_at	protein phosphatase 1	PPP1R16B	1.0301337	1.4406364	-1.3984946	0.022891732	5.83E-04
Bt.854.1.S1_at	low density lipoprotein receptor	LOC533894	-1.0630242	-1.4327228	1.3477801	0.041296616	0.01856159
Bt.8533.3.A1_a_at	NAD synthetase 1	NADSYN1	1.081724	-1.0904589	1.1795756	0.032539126	0.01090955
Bt.8531.2.S1_at	CDKN2A interacting protein	CDKN2AIPNL	1.1530381	1.2287064	-1.0656251	0.04517718	0.02174252
Bt.853.1.S1_at	mitochondrial ribosomal protein S18	MRPL45	1.095069	-1.1989347	1.3129163	0.0472649	0.02394446
Bt.8518.2.A1_at	Phosphodiesterase 8B	PDE8B	1.0597293	1.2496239	-1.1791916	0.031530906	0.0101612
Bt.8515.1.S1_at	ubiquitin protein ligase	UBR5	1.0629549	-1.334105	1.11480936	0.022891732	8.10E-04
Bt.8513.1.A1_at	N-acetylglucosaminidase	GNPTAB	-1.0358881	-1.2549751	1.2114968	0.030480286	0.00877303
Bt.8508.1.A1_at	cAMP responsive element binding protein	CREB3L2	-1.0358881	-1.2549752	1.211497	0.030480286	0.00877301
Bt.8504.1.A1_at	fragile X mental retardation protein	FMR1	1.2325062	-1.2230947	1.5074718	0.024766458	0.00372371
Bt.8503.1.S1_at	minichromosome maintenance complex component 3	MCM3	1.1511836	-1.0426477	1.2002789	0.036972128	0.01472881
Bt.850.1.S1_at	inositol polyphosphate 5-phosphatase	INPP1	-1.3675432	-1.4097161	1.0308385	0.038785268	0.01622677
Bt.8496.1.S1_at	adhesion molecule with extracellular domain	AMIGO3	1.1396945	1.4167725	-1.243116	0.027768528	0.00563681
Bt.8494.1.S1_at	similar to tubby like protein 1	LOC100294795	1.0431889	1.2075557	-1.1575619	0.049799785	0.02621968
Bt.8492.1.A1_at	junctional adhesion molecule	JAM3	-1.0262587	1.2146035	-1.2464975	0.04096433	0.01812274
Bt.8491.1.S1_at	SPARC related modulator	SMOC2	1.025448	-1.276219	1.308696	0.042790364	0.0199087
Bt.8487.1.A1_at	cut-like homeobox 1	CUX1	1.0625803	-1.31516	1.3974631	0.069664516	0.04554041
Bt.8486.2.S1_at	TRAF2 and NCK interacting protein	TNIK	-1.062143	-1.2512933	1.1780837	0.006459689	4.57E-06
Bt.8485.1.A1_at	par-3 partitioning defective	PARD3	1.2483006	-1.2432652	1.5519685	0.02901493	0.00745738
Bt.8484.1.S1_at	tight junction protein	TJP3	1.1373911	1.27681	-1.1225779	0.06455664	0.04060453
Bt.8482.1.A1_at	mitogen activated protein kinase	LOC100335371	1.0781014	-1.1192806	1.206698	0.022891732	1.73E-04
Bt.848.1.S1_at	NADH dehydrogenase	NDUFV2	1.1445262	-1.200224	1.3736879	0.03885797	0.01628465
Bt.8479.1.A1_at	nitric oxide synthase 2	NOS2	1.1012937	1.4899583	-1.3529165	0.027768528	0.00563718
Bt.8476.1.A1_at	distal-less homeobox 5	DLX5	-1.0298457	-1.335578	1.2968718	0.024013035	0.00183352
Bt.8473.2.S1_at	peroxisomal biogenesis factor 11B	PEX11B	-1.1748245	1.249132	-1.4675108	0.024013035	0.00138695
Bt.8451.2.S1_at	methylmalonic aciduria	MMAB	-1.0191929	1.2123705	-1.2356395	0.09520125	0.07064404
Bt.8448.1.S1_at	zinc finger protein 532	ZNF532	-1.1089511	-1.4666047	1.3225154	0.038785268	0.01621033
Bt.8441.3.S1_at	starch binding domain	STBD1	1.1147609	1.258515	-1.1289551	0.049705237	0.02599426
Bt.8439.1.S1_at	suppressor of Ty 6 homolog	SUPT6H	1.1328714	-1.2110656	1.3719816	0.034805436	0.01296287
Bt.8437.1.A1_at	Zinc finger homeobox	ZFHX4	1.1249348	1.4510857	-1.2899287	0.024013035	0.00239321
Bt.8436.1.S1_at	interferon, alpha-inducible protein	IFI6	1.1205993	-1.0231735	1.1465673	0.024570853	0.00300976
Bt.8435.1.S1_at	actin, alpha 1, skeletal	ACTA1	1.0207837	1.281608	-1.2555139	0.024766458	0.00384669
Bt.8433.1.S1_at	surfeit 4	SURF4	-1.0539612	1.2061185	-1.2712021	0.02901493	0.00738462
Bt.8431.1.S1_at	lipin 2	LPIN2	-1.0257518	-1.2584585	1.2268645	0.031530906	0.00998615
Bt.8427.1.S1_at	phosphatase and actin-binding protein	PHACTR1	1.1224935	1.3535997	-1.2058865	0.041799407	0.01904033
Bt.8424.1.A1_at	Cytochrome P450, family 29C	CYP2J2	1.1224935	1.3535997	-1.2058865	0.041799407	0.01904033
Bt.8410.1.S1_at	coiled-coil domain containing protein	CCDC18	-1.2514197	-1.833427	1.4650776	0.024013035	0.00177983
Bt.8400.1.A1_at	thymocyte selection-a	TOX	1.1090703	-1.439048	1.5960054	0.027768528	0.00582597
Bt.840.1.S1_at	craniofacial development	CFDP1	1.1326925	-1.2076938	1.3679457	0.025377173	0.0039922
Bt.84.1.S1_at	solute carrier family 3	SLC34A2	-1.0071371	-1.2951047	1.2859269	0.047813945	0.02456589
Bt.8396.1.A1_at	Protein FAM149B1	FAM149B1	-1.0172421	-1.3102947	1.2880855	0.042190105	0.01949066
Bt.8392.2.S1_at	Cleavage and polyadenylation specificity factor	CPSF7	-1.0292298	1.2409575	-1.2772303	0.02901493	0.00687643
Bt.8382.2.S1_at	ras homolog gene family B	RHOB	1.0754279	-1.3277335	1.4278818	0.024048876	0.00250975
Bt.8374.1.S1_at	ryanodine receptor 2	RYR2	1.1262633	-1.1881107	1.3381255	0.024013035	0.00235989
Bt.8371.1.S1_at	low-density lipoprotein receptor	LOC100337021 ///	1.0461316	1.3256387	-1.2671815	0.029312653	0.00791338
Bt.837.1.S1_at	up-regulated during viral infection	LOC493778	1.0431056	1.5434558	-1.4796736	0.025827987	0.00444373
Bt.8363.2.S1_at	potassium channel, subunit	KCNK1	1.0630096	-1.2550033	1.3340807	0.033150923	0.01144549
Bt.836.1.S1_at	fumarylacetoacetate hydrolase	FAHD1	1.5847368	-1.089927	1.7272475	0.027768528	0.0053102
Bt.8356.1.S1_at	transmembrane emp24 domain containing protein	TMED10	1.1091107	-1.0427276	1.1565002	0.042790364	0.01988735
Bt.8355.1.S1_at	heterogeneous nuclear ribonucleoprotein	HNRNPH2	1.0313398	1.3450407	-1.3041685	0.025827987	0.0045198
Bt.8353.3.S1_at	HEAT repeat containing protein	HEATR1	1.2041078	-1.1474967	1.3817097	0.034999527	0.01325777
Bt.8353.2.S1_at	Lectin, galactoside-binding	LGALS8	1.0710549	-1.558061	1.6687689	0.024013	0.00222035
Bt.8352.2.S1_a_at	zinc finger, MYND-type	ZMYND15	1.0710549	-1.558061	1.6687689	0.024013035	0.00222035
Bt.8351.1.S1_at	chromosome 11 open reading frame 73	C29H11orf73	1.2594651	-1.430691	1.8019053	0.025827987	0.00458524
Bt.8350.2.S1_at	adaptor-related protein with multiple domains	AP3B1	1.0419354	1.382948	-1.3272876	0.034124497	0.01225106
Bt.8348.1.S1_at	similar to UPF0378 family	LOC517133	1.0419353	1.3829479	-1.3272876	0.03412455	0.01225107
Bt.8345.1.S1_at	leptin receptor overexpression	LEPROT	1.0829397	-1.1104821	1.2025852	0.040293388	0.01748761
Bt.8344.1.S1_at	ladinin 1	LAD1	1.1180041	-1.4368411	1.6063942	0.027768528	0.00534761
Bt.8343.1.S1_at	G protein-coupled receptor	GPR171	1.0315468	1.2550457	-1.2166637	0.035463966	0.01370939
Bt.8338.1.S1_at	Cbp/p300-interacting protein	CITED4	1.0315468	1.2550457	-1.2166637	0.035463966	0.01370938
Bt.8333.1.S1_at	DnaJ (Hsp40) homolog	DNAJC2	1.0380901	-1.349373	1.4007707	0.03316394	0.01152517
Bt.8331.1.S1_at	UPF0598 protein	LOC618766	-1.0207636	-1.405035	1.3764548	0.024766458	0.00375512
Bt.833.2.S1_at	anaphase promoting complex	ANAPC5	-1.1127328	1.3015331	-1.4482585	0.022891732	8.36E-04
Bt.8329.1.S1_at	Cytoglobin	CYGB	1.0465326	1.2456932	-1.1903052	0.025827987	0.00453515
Bt.8328.1.S1_at	solute carrier family 11	SLC11A2	-1.0332865	-1.2046769	1.1658691	0.042984426	0.02007965
Bt.8327.1.S1_at	furry homolog (Drosophila)	FRY	1.0362997	1.633925	-1.5766915	0.02414251	0.00268544

Bt.8326.1.A1_at	transcription factor 3	TCF3	-1.1052902	1.0945483	-1.2097934	0.03971386	0.01689593
Bt.8324.1.S1_at	NOP16 nucleolar prote	NOP16	-1.033376	-1.310302	1.267982	0.025827987	0.0043813
Bt.8321.2.S1_at	similar to Genetic sup	LOC538506	1.0094534	-1.2348853	1.2465593	0.034339253	0.01246444
Bt.832.1.S1_at	hydroxyacyl-CoA dehy	HADHB	1.0764062	-1.3485868	1.4516273	0.027768528	0.00546249
Bt.8319.3.S1_at	microtubule associate	MTUS1	1.1492105	-1.0408177	1.1961186	0.024013035	0.00182184
Bt.8318.1.S1_at	CD276 molecule	CD276	1.2523599	-1.1611632	1.4541942	0.025878632	0.00464535
Bt.8316.1.S1_at	Uncharacterized prote	LOC782502	-1.2235892	-1.7621564	1.4401536	0.022891732	8.62E-04
Bt.8309.1.S1_at	checkpoint with forkh	CHFR	-1.2235892	-1.7621564	1.4401536	0.022891732	8.62E-04
Bt.8308.2.S1_at	neuropilin 2	NRP2	1.0795568	-1.7294121	1.8669986	0.024013035	0.00143151
Bt.8307.1.S1_at	glycolipid transfer pro	GLTPD1	-1.0143466	-1.2666969	1.2487812	0.024013035	0.00211974
Bt.8306.1.S1_at	retinoic acid receptor	RARA	1.0979004	-1.1822107	1.2979496	0.035166968	0.0134233
Bt.8305.1.A1_at	fragile X mental retard	FXR1	1.0225606	-1.4087312	1.4405131	0.022891732	3.37E-04
Bt.8300.1.S1_at	importin 9	IPO9	1.0528021	-1.1258849	1.185334	0.043822575	0.02080738
Bt.83.2.A1_at	DnaJ (Hsp40) homolog	DNAJC5	1.1144981	-1.0966572	1.2222223	0.04127428	0.01846404
Bt.8292.3.S1_at	Mediator complex sub	MED13L	1.025448	-1.276219	1.308696	0.042790364	0.0199087
Bt.2345.1.S1_at	PLD4	phospholipase D f	1.0716072	-1.6538175	1.7722427	0.022891732	9.48E-04