

Probesets differentially expressed in 303 infected vs. control (cut-off: p.adj <= 0.05)

probeset ID	Gene symbol	Gene Entrez ID	Gene name	logFC	FC	P.Value	adj.P.Val
Bt.28345.1.S1_at	ANKRD17	508405	ankyrin repeat domain 17	1,456	2,743	6,628E-03	0,032783
Bt.234.1.S1_at	IL18	281249	interleukin 18 (interferon-gamma-inducing factor)	1,440	2,714	7,235E-03	0,033570
Bt.23611.3.S1_at	TIPARP	540975	TCDD-inducible poly(ADP-ribose) polymerase	1,340	2,531	1,245E-02	0,042252
Bt.24217.1.S1_at	NFE2	514006	nuclear factor (erythroid-derived 2), 45kDa	-1,364	-2,575	1,095E-02	0,039242
Bt.12504.1.S1_at	CLU	280750	clusterin	-1,670	-3,182	1,852E-03	0,016635

Probesets differentially expressed in 303-infected vs. control and 534-infected vs. control (cut-off: p.adj <= 0.05)

probeset ID	Gene symbol	Gene Entrez ID	Gene name	logFC	FC	P.Value	adj.P.Val
Bt.19496.1.A1_at				2,753	6,743	3,035E-07	0,000141
Bt.23911.1.A1_at	XIST	338325	X (inactive)-specific transcript	2,603	6,078	1,270E-06	0,000295
Bt.28320.1.A1_at				2,528	5,769	2,532E-06	0,000392
Bt.6566.2.S1_a_at				2,279	4,854	2,194E-05	0,002512
Bt.647.1.S1_at	MTPN	541099	myotrophin	2,194	4,575	4,399E-05	0,002707
Bt.11778.1.A1_at				2,178	4,526	4,974E-05	0,002707
Bt.18321.1.A1_at	GNB4	525962	guanine nucleotide binding protein (G protein), beta polypeptide 4	2,158	4,464	5,823E-05	0,002707
Bt.23678.1.A1_at	RQCD1	536537	RCD1 required for cell differentiation1 homolog (S. pombe)	2,158	4,463	5,834E-05	0,002707
Bt.12745.3.S1_at	ANTXR2	510080	anthrax toxin receptor 2	2,093	4,266	9,681E-05	0,004084
Bt.2096.2.S1_at	EHD4	505206	EH-domain containing 4	2,070	4,200	1,150E-04	0,004446
Bt.17932.2.S1_a_at	CCNL1	514613	cyclin L1	2,017	4,048	1,712E-04	0,005775
Bt.20947.2.S1_at	LOC100140708	100140708	similar to IQ motif containing GTPase activating protein 2	2,015	4,041	1,742E-04	0,005775
Bt.22594.1.S1_at	LOC789894	789894	similar to PAP-associated domain-containing protein 5 (Topoisomerase-related function protein 4-2) (TRF4-2)	1,959	3,887	2,630E-04	0,007072
Bt.27386.1.A1_at	ANKRD50	527956	ankyrin repeat domain 50	1,941	3,840	2,983E-04	0,007284
Bt.18060.1.A1_at				1,922	3,789	3,424E-04	0,007943
Bt.1699.2.S1_a_at	RBPJ	767928	similar to Recombining binding protein suppressor of hairless (J kappa-recombination signal-binding protein) (RBP-J kappa) (RBP-J) (RBP-JK) (CBF-1) (Renal carcinoma antigen NY-REN-30); recombination signal binding protein for immunoglobulin kappa J region	1,884	3,691	4,465E-04	0,008711
Bt.11954.1.S1_at	SLTM	515193	similar to SAFB-like transcription modulator (Modulator of estrogen-induced transcription)	1,883	3,688	4,505E-04	0,008711
Bt.13284.1.A1_at				1,882	3,687	4,516E-04	0,008711
Bt.2663.2.S1_at	KRAS	541140	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1,880	3,681	4,594E-04	0,008711
Bt.7131.2.S1_at	PLDN	614408	pallidin homolog (mouse)	1,874	3,666	4,785E-04	0,008711
Bt.15806.1.A1_at	IREB2	539404	similar to iron-responsive element binding protein 2	1,868	3,649	5,010E-04	0,008711

probesets

Bt.24258.2.S1_at	MAN1A1	530027	mannosidase, alpha, class 1A, member 1	1,866	3,645	5,069E-04	0,008711
Bt.9710.1.S1_at	PRPF4B	512236	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1,840	3,580	6,057E-04	0,009319
Bt.20931.1.S1_at	PPP1CB	538829	protein phosphatase 1, catalytic subunit, beta isoform	1,836	3,570	6,226E-04	0,009319
Bt.22109.1.S1_at	GOPC	541186	golgi-associated PDZ and coiled-coil motif containing	1,824	3,541	6,747E-04	0,009693
Bt.9438.1.S1_at	SYNCRIP	511763	synaptotagmin binding, cytoplasmic RNA interacting protein	1,813	3,513	7,291E-04	0,009693
Bt.3311.3.S1_at				1,812	3,512	7,312E-04	0,009693
Bt.24221.2.S1_at				1,780	3,434	9,091E-04	0,011558
Bt.25292.1.A1_at				1,776	3,426	9,295E-04	0,011558
Bt.7672.1.A1_at				1,774	3,419	9,466E-04	0,011558
Bt.15677.1.A1_at	LOC100299693	100299693	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1,763	3,393	1,018E-03	0,011968
Bt.17514.1.S1_at				1,761	3,389	1,032E-03	0,011968
Bt.25051.1.A1_at	TTC14	512635	tetratricopeptide repeat domain 14	1,738	3,336	1,196E-03	0,013538
Bt.16124.2.S1_at				1,733	3,325	1,234E-03	0,013630
Bt.6276.2.S1_at	RAB6A	616537	RAB6A, member RAS oncogene family; RAB6B, member RAS oncogene family	1,724	3,304	1,308E-03	0,014119
Bt.6180.2.S1_at	FRG1	512533	FSHD region gene 1; hypothetical LOC780996	1,717	3,287	1,372E-03	0,014425
Bt.21071.1.S1_at				1,714	3,281	1,399E-03	0,014425
Bt.9847.1.S1_at	C22H3orf63	510095	chromosome 3 open reading frame 63 ortholog	1,708	3,266	1,458E-03	0,014551
Bt.26872.1.S1_at	NIPSNAP3A	534363	nipsnap homolog 3A (C. elegans)	1,705	3,260	1,481E-03	0,014551
Bt.24590.2.S1_at	LSM14A	538838	LSM14A, SCD6 homolog A (S. cerevisiae)	1,703	3,255	1,505E-03	0,014551
Bt.24537.1.A1_at	ZRANB2	508905	zinc finger, RAN-binding domain containing 2	1,690	3,226	1,635E-03	0,015483
Bt.24691.1.A1_at	MLL5	539121	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	1,675	3,193	1,793E-03	0,016635
Bt.9845.1.S1_at	TAPT1	615598	transmembrane anterior posterior transformation 1	1,669	3,180	1,864E-03	0,016635
Bt.22626.2.S1_at	ANKRD12	534739	ankyrin repeat domain 12	1,657	3,154	2,005E-03	0,017432
Bt.2478.2.S1_at	VPS26A	510574	vacuolar protein sorting 26 homolog A (S. pombe)	1,655	3,150	2,029E-03	0,017432
Bt.13706.2.S1_at	COMMD10	538706	COMM domain containing 10	1,651	3,140	2,087E-03	0,017610
Bt.29874.1.S1_at	EIF2C3	406231	eukaryotic translation initiation factor 2C, 3	1,637	3,110	2,275E-03	0,018852
Bt.25965.1.A1_at	NCOR1	507663	nuclear receptor co-repressor 1	1,632	3,100	2,340E-03	0,018864
Bt.1615.1.A1_at	DENND4A	514906	DENN/MADD domain containing 4A	1,631	3,098	2,358E-03	0,018864
Bt.28621.1.S1_at				1,620	3,075	2,519E-03	0,019808
Bt.23342.1.S1_at				1,612	3,056	2,658E-03	0,020221
Bt.19645.1.A1_at	CHD1	505123	chromodomain helicase DNA binding protein 1	1,603	3,037	2,810E-03	0,021029
Bt.17148.2.S1_at	FEM1C	541180	fem-1 homolog c (C. elegans)	1,596	3,022	2,930E-03	0,021320
Bt.20770.1.A1_at				1,591	3,012	3,020E-03	0,021560
Bt.16661.1.A1_at	BAZ1A	540621	bromodomain adjacent to zinc finger domain, 1A	1,582	2,993	3,191E-03	0,022431
Bt.9176.2.S1_at	CUL4B	539668	cullin 4B	1,574	2,976	3,349E-03	0,023195
Bt.6943.1.S1_at				1,564	2,957	3,542E-03	0,024167

probesets

Bt.9603.2.S1_at	INTS8	100124522	integrator complex subunit 8	1,561	2,951	3,605E-03	0,024243
Bt.20080.1.S1_at	WSB1	614851	WD repeat and SOCS box-containing 1	1,540	2,908	4,085E-03	0,026693
Bt.7150.2.S1_at	BIRC6	534211	baculoviral IAP repeat-containing 6	1,536	2,900	4,186E-03	0,026933
Bt.18474.2.A1_at	SHOC2	511417	soc-2 suppressor of clear homolog (C. elegans)	1,532	2,892	4,278E-03	0,026933
Bt.2177.2.S1_at	FAM114A1	511583	similar to Family with sequence similarity 114, member A1	1,530	2,887	4,344E-03	0,026933
Bt.6824.1.A1_at	TET2	538481	similar to CXXC finger 6	1,529	2,886	4,353E-03	0,026933
Bt.13614.1.A1_at	ARMC1	514000	armadillo repeat containing 1	1,523	2,874	4,510E-03	0,027186
Bt.22620.1.S1_at	ZBTB1	526903	zinc finger and BTB domain containing 1	1,523	2,874	4,511E-03	0,027186
Bt.24678.1.A1_at	TBC1D9	537817	TBC1 domain family, member 9 (with GRAM domain)	1,520	2,869	4,581E-03	0,027252
Bt.120.1.S1_at	ROCK2	282041	E2F transcription factor 6; Rho-associated, coiled-coil containing protein kinase 2	1,516	2,861	4,694E-03	0,027298
Bt.29953.2.S1_at	CCNYL1	538167	cyclin Y-like 1	1,511	2,851	4,835E-03	0,027694
Bt.22564.2.S1_at	GGTA1	281780	alpha-galactosyltransferase 1 (glycoprotein)	1,496	2,820	5,283E-03	0,029893
Bt.23265.1.S1_at	SPRED1	519882	sprouty-related, EVH1 domain containing 1	1,489	2,807	5,494E-03	0,030409
Bt.9631.1.S1_at	MFN1	515180	similar to mitofusin 1	1,487	2,803	5,560E-03	0,030409
Bt.21982.1.S1_a_at	IQGAP1	532715	IQ motif containing GTPase activating protein 1	1,483	2,796	5,680E-03	0,030409
Bt.17311.2.S1_at	RP2	534054	retinitis pigmentosa 2 (X-linked recessive)	1,481	2,791	5,767E-03	0,030409
Bt.4095.2.S1_at	TOR1B	533928	torsin family 1, member B (torsin B)	1,481	2,791	5,767E-03	0,030409
Bt.17129.2.A1_at				1,472	2,774	6,051E-03	0,031547
Bt.2105.2.A1_at	LATS1	535935	LATS, large tumor suppressor, homolog 1 (Drosophila)	1,460	2,751	6,489E-03	0,032760
Bt.11073.1.S1_at	C8H9orf21	616897	chromosome 9 open reading frame 21 ortholog	1,460	2,750	6,496E-03	0,032760
Bt.16920.1.A1_s_at				1,451	2,733	6,827E-03	0,033345
Bt.13818.1.S1_at	SIRT1	613629	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	1,442	2,718	7,153E-03	0,033570
Bt.5542.2.S1_at	LOC540136	540136	similar to Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP); similar to rCG48740; hypothetical protein LOC790872	1,442	2,717	7,173E-03	0,033570
Bt.28750.1.S1_at	IL13RA1	407110	interleukin 13 receptor, alpha 1	1,442	2,716	7,181E-03	0,033570
Bt.28702.1.S1_at				1,440	2,714	7,235E-03	0,033570
Bt.8264.1.A1_at				1,436	2,705	7,423E-03	0,034101
Bt.864.2.S1_at	SRSF1	615796	splicing factor, arginine/serine-rich 1	1,431	2,697	7,601E-03	0,034232
Bt.28189.2.S1_at				1,431	2,696	7,627E-03	0,034232
Bt.24692.1.S1_at	ADRBK2	282136	adrenergic, beta, receptor kinase 2	1,430	2,694	7,673E-03	0,034232
Bt.633.3.S1_at	SFXN1	511375	sideroflexin 1	1,426	2,687	7,841E-03	0,034254
Bt.8353.3.S1_at	HEATR1	506978	HEAT repeat containing 1	1,424	2,683	7,920E-03	0,034254
Bt.26700.1.S1_at	HNMT	613413	histamine N-methyltransferase	1,423	2,681	7,962E-03	0,034254
Bt.9162.1.A1_at	CHORDC1	505144	cysteine and histidine-rich domain (CHORD)-containing 1	1,420	2,676	8,094E-03	0,034254
Bt.18167.1.A1_at				1,420	2,675	8,111E-03	0,034254
Bt.17444.1.S1_at				1,419	2,675	8,120E-03	0,034254

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Bt.3964.1.S1_at	SLC2A3	282358	solute carrier family 2 (facilitated glucose transporter), member 3	1,412	2,660	8,481E-03	0,035306
Bt.24447.2.S1_at	F2RL2	512581	coagulation factor II (thrombin) receptor-like 2	1,411	2,659	8,522E-03	0,035306
Bt.11034.1.S1_at	MID1IP1	615572	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	1,406	2,651	8,725E-03	0,035603
Bt.2098.2.S1_at	ARHGEF12	503575	Rho guanine nucleotide exchange factor (GEF) 12	1,406	2,650	8,747E-03	0,035603
Bt.1455.1.S1_at				1,400	2,639	9,029E-03	0,036098
Bt.4787.1.S1_at	EEF2K	521730	eukaryotic elongation factor-2 kinase	1,398	2,635	9,152E-03	0,036098
Bt.28133.1.S1_at	MLL3	789336	similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lysine N-methyltransferase, H3 lysine-4 specific MLL3) (Homologous to ALR protein) (Lysine N-methyltransferase 2C)	1,396	2,631	9,239E-03	0,036098
Bt.25055.1.A1_at	IPMK	615135	inositol polyphosphate multikinase	1,395	2,631	9,262E-03	0,036098
Bt.10153.1.S1_at	EIF2C4	528046	eukaryotic translation initiation factor 2C, 4	1,395	2,629	9,305E-03	0,036098
Bt.21987.2.S1_a_at	PPIG	783720	peptidylprolyl isomerase G (cyclophilin G)	1,394	2,627	9,349E-03	0,036098
Bt.23618.1.A1_at				1,392	2,625	9,413E-03	0,036098
Bt.8169.1.S1_at	SLC39A6	524456	solute carrier family 39 (zinc transporter), member 6	1,380	2,603	1,006E-02	0,037836
Bt.24376.1.S1_at	MTSS1	523498	metastasis suppressor 1	1,379	2,601	1,011E-02	0,037836
Bt.24546.1.S1_at	SMEK1	407220	SMEK homolog 1, suppressor of mek1	1,375	2,595	1,031E-02	0,038279
Bt.19243.2.S1_at	SNX6	532685	similar to sorting nexin 6; sorting nexin 6	1,368	2,581	1,074E-02	0,039242
Bt.27529.1.S1_at	NUP155	506738	nucleoporin 155kDa	1,364	2,574	1,095E-02	0,039242
Bt.27177.1.A1_at	MAP7D3	506950	MAP7 domain containing 3	1,361	2,569	1,112E-02	0,039382
Bt.648.2.S1_at	LRRFIP1	616994	leucine rich repeat (in FLII) interacting protein 1	1,350	2,549	1,182E-02	0,041433
Bt.1711.1.A1_at	LOC615263	615263	hypothetical protein LOC615263	1,349	2,547	1,188E-02	0,041433
Bt.13990.2.S1_at	ZCCHC8	539598	zinc finger, CCHC domain containing 8	1,341	2,533	1,238E-02	0,042252
Bt.3197.1.A1_at	CCAR1	767587	cell division cycle and apoptosis regulator 1	1,341	2,533	1,241E-02	0,042252
Bt.6800.1.A1_at				1,339	2,530	1,249E-02	0,042252
Bt.12606.1.S1_a_at				1,337	2,526	1,265E-02	0,042252
Bt.21348.1.A1_a_at	SNRNP48	513601	small nuclear ribonucleoprotein 48kDa (U11/U12)	1,337	2,526	1,266E-02	0,042252
Bt.13324.1.S1_a_at	IDH1	281235	isocitrate dehydrogenase 1 (NADP+), soluble; similar to Isocitrate dehydrogenase 1 (NADP+), soluble	1,334	2,522	1,282E-02	0,042485
Bt.29945.1.S1_at	PCMTD1	521261	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1,333	2,519	1,293E-02	0,042548
Bt.22090.2.S1_at				1,330	2,514	1,311E-02	0,042849
Bt.22822.2.S1_at				1,327	2,509	1,332E-02	0,043230
Bt.24697.1.A1_at	KIF3A	541246	kinesin family member 3A	1,312	2,482	1,443E-02	0,045863
Bt.19799.1.S1_at	SPAG9	540689	sperm associated antigen 9	1,301	2,464	1,522E-02	0,047738
Bt.6017.2.S1_at				1,301	2,463	1,527E-02	0,047738
Bt.12220.1.S1_a_at				1,300	2,462	1,533E-02	0,047738
Bt.2318.2.S1_at				1,294	2,452	1,580E-02	0,048890

probesets

Bt.22126.1.S1_at	TSPAN5	538668	tetraspanin 5	-1,380	-2,603	1,005E-02	0,037836
Bt.18202.1.A1_at				-1,456	-2,743	6,641E-03	0,032783
Bt.8319.1.S1_at	MTUS1	515016	mitochondrial tumor suppressor 1	-1,482	-2,794	5,714E-03	0,030409
Bt.1927.1.S1_at	CRISPLD2	505329	cysteine-rich secretory protein LCCL domain containing 2	-1,550	-2,928	3,855E-03	0,025555
Bt.2047.1.S1_at	ADM	280713	adrenomedullin	-1,816	-3,522	7,108E-04	0,009693
Bt.24314.1.A1_at				-1,953	-3,871	2,744E-04	0,007072
Bt.4209.2.S1_a_at	C3	280677	complement component 3	-1,983	-3,954	2,198E-04	0,006374
Bt.15290.1.A1_at				-2,209	-4,625	3,879E-05	0,002707

Probesets differentially expressed in 534 infected vs. control (cut-off: p.adj <= 0.05)

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Bt.24940.1.A1_at				2,762	6,784	2,698E-06	1,043E-04
Bt.5395.1.S1_a_at	VCAN	282662	versican	2,116	4,336	3,182E-04	2,636E-03
Bt.24975.1.S1_at	YTHDC2	541024	YTH domain containing 2	2,037	4,104	5,290E-04	3,880E-03
Bt.20867.1.A1_at	RPUSD3	534606	RNA pseudouridylate synthase domain containing 3	1,988	3,966	7,210E-04	4,646E-03
Bt.7839.1.A1_at	SON	516462	SON DNA binding protein	1,978	3,939	7,658E-04	4,716E-03
Bt.6973.2.A1_at				1,976	3,935	7,725E-04	4,716E-03
Bt.21695.1.S1_at				1,962	3,897	8,410E-04	4,902E-03
Bt.25081.1.S1_at				1,957	3,881	8,718E-04	4,994E-03
Bt.20407.2.A1_at	CPEB4	538794	cytoplasmic polyadenylation element binding protein 4	1,933	3,818	1,007E-03	5,498E-03
Bt.12164.1.S1_at				1,909	3,754	1,164E-03	6,210E-03
Bt.8521.1.A1_at				1,890	3,707	1,298E-03	6,766E-03
Bt.27023.1.S1_at				1,868	3,649	1,483E-03	7,237E-03
Bt.2451.2.A1_at	CREBZF	538594	CREB/ATF bZIP transcription factor	1,861	3,632	1,543E-03	7,237E-03
Bt.8872.1.S1_at	ATP2B1	282641	ATPase, Ca ⁺⁺ transporting, plasma membrane 1	1,850	3,606	1,639E-03	7,237E-03
Bt.19425.1.S1_at	LARP4	539286	La ribonucleoprotein domain family, member 4	1,849	3,601	1,657E-03	7,237E-03
Bt.22714.1.A1_at	TMOD3	533257	tropomodulin 3 (ubiquitous)	1,848	3,601	1,658E-03	7,237E-03
Bt.3105.1.S1_at	CLINT1	538540	clathrin interactor 1	1,848	3,599	1,664E-03	7,237E-03
Bt.10920.1.S1_at	TTC3	506569	tetratricopeptide repeat domain 3	1,847	3,598	1,669E-03	7,237E-03
Bt.28265.2.S1_at				1,833	3,564	1,809E-03	7,609E-03
Bt.27865.2.S1_at	VPRBP		Vpr (HIV-1) binding protein	1,832	3,561	1,820E-03	7,609E-03
Bt.3741.1.S1_at	TSC1	533440	tuberous sclerosis 1	1,828	3,551	1,863E-03	7,718E-03
Bt.27429.2.A1_at	SF3B1	510177	splicing factor 3b, subunit 1, 155kDa	1,824	3,541	1,905E-03	7,823E-03
Bt.20759.1.A1_at				1,811	3,510	2,051E-03	8,130E-03
Bt.11220.2.S1_a_at	RALB	505238	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	1,810	3,507	2,068E-03	8,130E-03
Bt.4773.3.S1_a_at	ATP6V1A	282147	ATPase, H ⁺ transporting, lysosomal 70kDa, V1 subunit A	1,797	3,476	2,223E-03	8,667E-03
Bt.12001.3.A1_at	ARFGEF2	539295	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	1,760	3,386	2,745E-03	1,043E-02

probesets

Bt.18234.1.S1_at	IGSF6	100140740	similar to DORA protein	1,758	3,383	2,766E-03	1,043E-02
Bt.10884.2.S1_at				1,753	3,370	2,853E-03	1,063E-02
Bt.22543.1.S1_at				1,750	3,364	2,893E-03	1,063E-02
Bt.16683.1.S1_at	C1D	506667	C1D nuclear receptor co-repressor	1,750	3,364	2,897E-03	1,063E-02
Bt.864.2.S1_a_at	SRSF1	615796	splicing factor, arginine/serine-rich 1	1,746	3,355	2,958E-03	1,072E-02
Bt.27936.1.S1_at				1,728	3,313	3,268E-03	1,149E-02
Bt.6497.1.S1_at	SMEK2	516489	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	1,723	3,302	3,355E-03	1,170E-02
Bt.25965.2.S1_at	NCOR1	507663	nuclear receptor co-repressor 1	1,711	3,273	3,596E-03	1,218E-02
Bt.27024.1.A1_at	CCAR1	767587	cell division cycle and apoptosis regulator 1	1,708	3,267	3,652E-03	1,221E-02
Bt.24391.1.A1_at				1,698	3,245	3,850E-03	1,249E-02
Bt.27436.1.A1_at	INO80	505992	INO80 homolog (S. cerevisiae)	1,693	3,234	3,946E-03	1,272E-02
Bt.7236.1.S1_at	PIK3R1	282307	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	1,682	3,209	4,190E-03	1,341E-02
Bt.2415.2.S1_at	ID2	505025	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	1,679	3,201	4,275E-03	1,349E-02
Bt.8824.1.S1_at				1,674	3,192	4,371E-03	1,364E-02
Bt.28626.1.S1_at	LOC521363	521363	similar to GC-rich sequence DNA-binding factor (GCF) (Transcription factor 9) (TCF-9)	1,672	3,186	4,438E-03	1,364E-02
Bt.26597.1.S1_at				1,665	3,170	4,606E-03	1,397E-02
Bt.23673.1.A1_at				1,656	3,152	4,810E-03	1,440E-02
Bt.8690.1.S1_at	PLEKHB2	783000	pleckstrin homology domain containing, family B (evectins) member 2; similar to pleckstrin homology domain containing, family B (evectins) member 2	1,653	3,145	4,901E-03	1,448E-02
Bt.3311.1.S1_at				1,652	3,142	4,930E-03	1,448E-02
Bt.28780.2.A1_at	FGD4	505234	FYVE, RhoGEF and PH domain containing 4	1,649	3,137	4,993E-03	1,457E-02
Bt.17193.1.A1_at				1,646	3,129	5,087E-03	1,466E-02
Bt.11240.1.A1_at	TET2	538481	similar to CXXC finger 6	1,641	3,119	5,219E-03	1,486E-02
Bt.6392.1.S1_at	TRPM6	527597	transient receptor potential cation channel, subfamily M, member 6	1,632	3,099	5,473E-03	1,539E-02
Bt.10692.1.S1_at	LOC100299693	100299693	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1,628	3,092	5,576E-03	1,549E-02
Bt.2943.1.A1_at	CTR9	534265	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	1,624	3,082	5,713E-03	1,574E-02
Bt.24759.2.S1_at				1,623	3,080	5,732E-03	1,574E-02
Bt.4781.1.S1_at	ADAM10	282132	ADAM metallopeptidase domain 10	1,619	3,072	5,841E-03	1,594E-02
Bt.656.2.S1_at	CORO1C	515798	coronin, actin binding protein, 1C	1,604	3,041	6,314E-03	1,675E-02
Bt.19295.2.S1_at	APOLD1	538827	apolipoprotein L domain containing 1	1,604	3,040	6,317E-03	1,675E-02
Bt.21987.1.S1_at	PPIG	783720	peptidylprolyl isomerase G (cyclophilin G)	1,600	3,032	6,445E-03	1,697E-02
Bt.910.3.S1_at	UFM1	530547	ubiquitin-fold modifier 1	1,599	3,029	6,501E-03	1,697E-02
Bt.11772.1.A1_at	C18H16orf87	614339	chromosome 18 open reading frame, human C16orf87	1,596	3,023	6,587E-03	1,698E-02
Bt.25082.1.A1_at	MCOLN3	514345	mucolipin 3	1,592	3,015	6,723E-03	1,718E-02

probesets

Bt.9445.1.S1_at	HMGXB3	509419	HMG box domain containing 3	1,591	3,013	6,756E-03	1,718E-02
Bt.18794.1.S1_at				1,589	3,008	6,840E-03	1,718E-02
Bt.20506.1.S1_at				1,588	3,007	6,856E-03	1,718E-02
Bt.28222.1.S1_at	STRN3	516375	striatin, calmodulin binding protein 3	1,587	3,005	6,888E-03	1,718E-02
Bt.20852.1.A1_at	GNAS	281793	GNAS complex locus	1,580	2,990	7,149E-03	1,760E-02
Bt.18519.1.A1_at	RSBN1	508231	round spermatid basic protein 1	1,579	2,988	7,180E-03	1,760E-02
Bt.8263.1.A1_at				1,577	2,983	7,266E-03	1,760E-02
Bt.21412.1.A1_at	TXLNG	515927	taxilin gamma	1,576	2,981	7,310E-03	1,760E-02
Bt.179.1.S1_at	SLC25A16	282524	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	1,575	2,980	7,319E-03	1,760E-02
Bt.18551.1.S1_at	PHF20L1	511990	PHD finger protein 20-like 1	1,570	2,970	7,516E-03	1,798E-02
Bt.11538.1.A1_at				1,546	2,919	8,510E-03	2,015E-02
Bt.10260.1.S1_at				1,537	2,902	8,884E-03	2,073E-02
Bt.27421.1.S1_at	ARHGEF2	505940	rho/rac guanine nucleotide exchange factor (GEF) 2	1,537	2,902	8,888E-03	2,073E-02
Bt.16140.1.A1_at	AGPAT5	530414	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1,537	2,901	8,892E-03	2,073E-02
Bt.27858.1.A1_at	TMED5	534351	transmembrane emp24 protein transport domain containing 5	1,528	2,884	9,276E-03	2,141E-02
Bt.21444.1.S1_at	CDK2	519217	cyclin-dependent kinase 2	1,518	2,864	9,758E-03	2,230E-02
Bt.5928.1.S1_at	HMBOX1	539099	homeobox containing 1	1,515	2,859	9,890E-03	2,249E-02
Bt.18474.1.A1_at	SHOC2	511417	soc-2 suppressor of clear homolog (C. elegans)	1,513	2,854	1,000E-02	2,264E-02
Bt.829.2.S1_at	GOLPH3	531359	golgi phosphoprotein 3 (coat-protein)	1,502	2,833	1,055E-02	2,348E-02
Bt.3072.2.S1_at				1,500	2,829	1,065E-02	2,354E-02
Bt.4874.2.S1_a_at	LUC7L3	539955	cisplatin resistance-associated overexpressed protein	1,490	2,809	1,120E-02	2,460E-02
Bt.28462.1.S1_at	LTV1	507702	LTV1 homolog (S. cerevisiae)	1,489	2,807	1,124E-02	2,460E-02
Bt.8292.3.S1_at	MED13L	517336	mediator complex subunit 13-like	1,484	2,797	1,152E-02	2,510E-02
Bt.24703.1.S1_at	NBN	522943	nibrin	1,480	2,790	1,172E-02	2,541E-02
Bt.16148.2.A1_a_at	LOC532848	532848	centrosomal protein KIAA1731-like	1,477	2,783	1,193E-02	2,561E-02
Bt.6863.1.A1_at				1,472	2,775	1,218E-02	2,592E-02
Bt.13419.2.A1_at	SEC63	541040	SEC63 homolog (S. cerevisiae)	1,471	2,772	1,228E-02	2,601E-02
Bt.22440.1.S1_at	DCAF12	525161	WD repeat domain 40A	1,466	2,762	1,257E-02	2,652E-02
Bt.20414.3.S1_at	ROCK1	785911	E2F transcription factor 6; Rho-associated, coiled-coil containing protein kinase 2	1,464	2,760	1,266E-02	2,657E-02
Bt.21855.1.S1_at	TMED7	100125926	transmembrane emp24 protein transport domain containing 7	1,456	2,744	1,317E-02	2,728E-02
Bt.27028.1.S1_at				1,456	2,744	1,317E-02	2,728E-02
Bt.21170.1.A1_at	RASA2	533491	RAS p21 protein activator 2	1,444	2,721	1,395E-02	2,841E-02
Bt.22020.2.S1_at	LIN7C	510125	lin-7 homolog C (C. elegans)	1,444	2,720	1,397E-02	2,841E-02
Bt.22840.1.S1_a_at	CD46	280851	CD46 molecule, complement regulatory protein	1,437	2,707	1,443E-02	2,911E-02
Bt.15629.1.S1_at	NSRP1	539841	nuclear speckle splicing regulatory protein 1	1,434	2,702	1,464E-02	2,940E-02

probesets

Bt.18165.1.A1_at	MAPK6	538094	mitogen-activated protein kinase 6	1,432	2,698	1,476E-02	2,953E-02
Bt.4079.2.S1_a_at	TARDBP	540632	TAR DNA binding protein	1,431	2,696	1,484E-02	2,955E-02
Bt.2808.1.S1_at	RBM18	508615	RNA binding motif protein 18	1,422	2,679	1,548E-02	3,043E-02
Bt.13222.1.S1_at	TMX3	615687	thioredoxin-related transmembrane protein 3	1,419	2,674	1,570E-02	3,048E-02
Bt.16061.2.S1_at	COG6	509305	component of oligomeric golgi complex 6	1,417	2,670	1,587E-02	3,067E-02
Bt.20258.2.S1_at				1,409	2,655	1,646E-02	3,147E-02
Bt.633.2.S1_at	SFXN1	511375	sideroflexin 1	1,406	2,649	1,670E-02	3,164E-02
Bt.4823.1.S1_at	ARPP19	282658	cAMP-regulated phosphoprotein, 19 kD	1,405	2,649	1,673E-02	3,164E-02
Bt.28408.1.S1_at	MED1	520734	mediator complex subunit 1	1,404	2,646	1,684E-02	3,164E-02
Bt.20271.1.S1_at				1,404	2,646	1,684E-02	3,164E-02
Bt.29959.1.S1_at	CNOT6	534707	CCR4-NOT transcription complex, subunit 6	1,401	2,641	1,703E-02	3,187E-02
Bt.2891.1.S1_at	YWHAZ	287022	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	1,396	2,632	1,743E-02	3,248E-02
Bt.3689.3.S1_a_at	C28H10orf35	510161	chromosome 10 open reading frame 35 ortholog	1,391	2,623	1,783E-02	3,310E-02
Bt.20939.1.A1_at				1,388	2,617	1,814E-02	3,352E-02
Bt.16142.3.A1_at	YWHAH	286862	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	1,386	2,613	1,829E-02	3,367E-02
Bt.23985.1.A1_at	ATRX	514473	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i>)	1,378	2,598	1,899E-02	3,482E-02
Bt.4554.1.S1_at	COMMD8	507292	COMM domain containing 8	1,377	2,597	1,907E-02	3,483E-02
Bt.4824.1.A1_at	EXOC5	531907	exocyst complex component 5	1,375	2,594	1,918E-02	3,490E-02
Bt.23224.2.S1_at				1,365	2,576	2,008E-02	3,580E-02
Bt.7092.1.S1_at				1,365	2,575	2,013E-02	3,580E-02
Bt.17473.1.S1_at	RPE	533764	ribulose-5-phosphate-3-epimerase	1,360	2,567	2,055E-02	3,639E-02
Bt.15742.1.S1_at	CD47	282661	CD47 molecule	1,354	2,556	2,113E-02	3,714E-02
Bt.19472.1.A1_at	FAM175B	510233	similar to LOC510233 protein; hypothetical protein LOC510233	1,352	2,552	2,134E-02	3,736E-02
Bt.7389.3.S1_a_at	TCERG1	540964	transcription elongation regulator 1	1,348	2,545	2,175E-02	3,794E-02
Bt.21372.1.S1_at	WHSC1L1	513054	Wolf-Hirschhorn syndrome candidate 1-like 1	1,345	2,541	2,199E-02	3,821E-02
Bt.24286.1.S1_at	GPR137B	613826	G protein-coupled receptor 137B	1,342	2,536	2,227E-02	3,854E-02
Bt.27072.1.A1_at	PB1	506557	polybromo 1	1,342	2,534	2,234E-02	3,854E-02
Bt.16374.1.A1_at	FUBP3	541080	far upstream element (FUSE) binding protein 3	1,341	2,533	2,244E-02	3,856E-02
Bt.4557.1.S1_at	IFNAR1	282257	interferon, alpha; receptor	1,339	2,530	2,262E-02	3,861E-02
Bt.807.1.S1_at				1,339	2,529	2,263E-02	3,861E-02
Bt.9300.1.A1_at	OGFRL1	519626	opioid growth factor receptor-like 1	1,337	2,527	2,277E-02	3,870E-02
Bt.9591.2.S1_at				1,336	2,525	2,291E-02	3,879E-02
Bt.7805.2.S1_a_at	NUCKS1	505585	nuclear casein kinase and cyclin-dependent kinase substrate 1; similar to Nuclear casein kinase and cyclin-dependent kinase substrate 1	1,335	2,523	2,300E-02	3,880E-02
Bt.12957.1.A1_a_at	TNRC6B	528167	trinucleotide repeat containing 6B	1,330	2,513	2,356E-02	3,937E-02

probesets

Bt.25022.1.S1_at				1,329	2,512	2,367E-02	3,937E-02
Bt.17161.1.S1_at				1,329	2,512	2,367E-02	3,937E-02
Bt.5602.1.A1_at	ZNF331	516156	hypothetical protein LOC516156	1,323	2,502	2,425E-02	4,004E-02
Bt.2763.1.S1_at	PARG	281377	poly (ADP-ribose) glycohydrolase	1,321	2,498	2,448E-02	4,028E-02
Bt.10033.1.S1_at	TNRC6A	541118	trinucleotide repeat containing 6A	1,317	2,492	2,487E-02	4,069E-02
Bt.16241.1.A1_at				1,315	2,489	2,510E-02	4,075E-02
Bt.22716.1.A1_at	RUFY1	528153	RUN and FYVE domain containing 1	1,315	2,488	2,512E-02	4,075E-02
Bt.23129.2.S1_at	LAMC1	532572	laminin, gamma 1 (formerly LAMB2)	1,312	2,483	2,548E-02	4,120E-02
Bt.26316.1.A1_at				1,309	2,478	2,581E-02	4,151E-02
Bt.3414.3.A1_a_at	AGFG1	536149	ArfGAP with FG repeats 1	1,307	2,474	2,604E-02	4,167E-02
Bt.6455.1.S1_at	CUL4A	617935	cullin 4A	1,305	2,470	2,629E-02	4,192E-02
Bt.9326.1.S1_at	DCUN1D1	539869	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	1,302	2,465	2,664E-02	4,216E-02
Bt.18224.1.S1_at				1,301	2,465	2,670E-02	4,216E-02
Bt.28468.1.A1_at	SMAD5	768050	SMAD family member 5	1,301	2,464	2,675E-02	4,216E-02
Bt.26811.1.S1_at	SLC30A5	508169	solute carrier family 30 (zinc transporter), member 5	1,300	2,462	2,689E-02	4,216E-02
Bt.21173.1.S1_at	HUWE1	511826	HECT, UBA and WWE domain containing 1	1,296	2,455	2,738E-02	4,267E-02
Bt.13455.2.A1_at	SACM1L	530577	SAC1 suppressor of actin mutations 1-like (yeast)	1,295	2,453	2,748E-02	4,267E-02
Bt.17129.1.A1_at				1,290	2,445	2,803E-02	4,321E-02
Bt.25433.1.S1_at	C1GALT1C1	531644	C1GALT1-specific chaperone 1	1,280	2,429	2,926E-02	4,480E-02
Bt.1781.1.A1_at				1,278	2,425	2,951E-02	4,504E-02
Bt.7610.1.A1_at				1,277	2,423	2,968E-02	4,515E-02
Bt.28376.1.S1_at				1,269	2,409	3,075E-02	4,663E-02
Bt.10397.2.S1_at	RNF20	513326	ring finger protein 20	1,263	2,400	3,150E-02	4,745E-02
Bt.4976.1.S1_at				1,260	2,396	3,183E-02	4,780E-02
Bt.13285.1.A1_at	LARP1	505690	La ribonucleoprotein domain family, member 1	1,260	2,394	3,195E-02	4,783E-02
Bt.22341.1.A1_at	VPS13C	783566	vacuolar protein sorting 13 homolog C (S. cerevisiae)	1,256	2,388	3,246E-02	4,842E-02
Bt.28267.2.S1_a_at				1,249	2,376	3,348E-02	4,925E-02
Bt.269.1.S1_at	ATP2C1	327663	ATPase, Ca++ transporting, type 2C, member 1	1,247	2,374	3,365E-02	4,925E-02
Bt.24333.1.S1_at	TLK1	537517	tousled-like kinase 1	1,247	2,374	3,369E-02	4,925E-02
Bt.23143.2.S1_at	CSDE1	513993	cold shock domain containing E1, RNA-binding	1,246	2,372	3,381E-02	4,925E-02
Bt.20762.2.S1_at	SPRYD7	615298	SPRY domain containing 7	1,246	2,372	3,386E-02	4,925E-02
Bt.2294.1.S1_a_at	UBA7	497204	ubiquitin-like modifier activating enzyme 7	-1,249	-2,376	3,345E-02	4,925E-02
Bt.100.1.S1_at	ADRB2	281605	adrenergic, beta-2-, receptor, surface	-1,288	-2,441	2,833E-02	4,353E-02
Bt.24231.1.A1_at	CEP78	537926	centrosomal protein 78kDa	-1,290	-2,446	2,798E-02	4,321E-02
Bt.8436.1.S1_at	IFI6	512913	interferon, alpha-inducible protein 6	-1,358	-2,563	2,078E-02	3,666E-02
Bt.9792.1.S1_at	ARRDC4	538517	arrestin domain containing 4	-1,411	-2,658	1,632E-02	3,143E-02
Bt.16725.2.A1_at	UBE2L6	509471	ubiquitin-conjugating enzyme E2L 6	-1,424	-2,683	1,535E-02	3,043E-02
Bt.26735.1.S1_at	SLC46A2	511556	solute carrier family 46, member 2	-1,476	-2,782	1,198E-02	2,561E-02
Bt.12327.1.S1_at	TXNIP	506790	thioredoxin interacting protein	-1,502	-2,831	1,058E-02	2,348E-02

probesets

Bt.22980.1.S1_at	TRIM21	359715	tripartite motif-containing 21	-1,811	-3,510	2,052E-03	8,130E-03
Bt.8962.3.S1_s_at	USP18	515202	ubiquitin specific peptidase 18	-1,854	-3,615	1,605E-03	7,237E-03
Bt.8238.1.A1_at	TRIB3	538465	tribbles homolog 3 (Drosophila)	-1,859	-3,627	1,561E-03	7,237E-03
Bt.16326.1.S1_at	TMEM140	515475	transmembrane protein 140	-2,082	-4,233	3,981E-04	3,078E-03
Bt.9519.1.S1_at	SESN2	509863	sestrin 2	-2,304	-4,939	8,914E-05	9,618E-04

Gene Functional Classification

s303-control, 1 cluster

Gene Group 1		Enrichment Score: 0.5675	
AFFYMETRIX_ID	Gene Name	Gene Symbol	Up/Down
Bt.24697.1.A1_at	kinesin family member 3A	KIF3A	1
Bt.28345.1.S1_at	ankyrin repeat domain 17	ANKRD17	1
Bt.19645.1.A1_at	chromodomain helicase DNA binding protein 1	CHD1	1
Bt.4095.2.S1_at	torsin family 1, member B (torsin B)	TOR1B	1
Category	Term	Count	PValue
GOTERM_MF_FAT	GO:0005524~ATP binding	4	0,0013
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	4	0,0014
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	4	0,0016
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	4	0,0016
GOTERM_MF_FAT	GO:0001882~nucleoside binding	4	0,0017
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	4	0,0028
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	4	0,0028
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	4	0,0032
GOTERM_MF_FAT	GO:0000166~nucleotide binding	4	0,0053

s534-control, 7 clusters

Gene Group 1		Enrichment Score: 2.0353	
AFFYMETRIX_ID	Gene Name	Gene Symbol	Up/Down
Bt.2808.1.S1_at	RNA binding motif protein 18	RBM18	1
Bt.27023.1.S1_at	RNA-binding region (RNP1, RRM) containing 3	NA	1
Bt.4079.2.S1_a_at	TAR DNA binding protein	TARDBP	1
Bt.18224.1.S1_at	CUG triplet repeat, RNA binding protein 1		1
Bt.20407.2.A1_at	cytoplasmic polyadenylation element binding protein 4	CPEB4	1
Category	Term	Count	PValue
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	5	2,982E-08
INTERPRO	IPR000504:RNA recognition motif, RNP-1	5	3,185E-08
SMART	SM00360:RRM	5	6,216E-07
GOTERM_MF_FAT	GO:0000166~nucleotide binding	5	9,268E-04

GFC

SP_PIR_KEYWORDS rna-binding 2 0,0241

Gene Group 2 Enrichment Score: 1.76603

AFFYMETRIX_ID	Gene Name	Gene Symbol	Up/Down
Bt.2294.1.S1_a_at	ubiquitin-like modifier activating enzyme 7	UBA7	-1
Bt.16725.2.A1_at	ubiquitin-conjugating enzyme E2L 6	UBE2L6	-1
Bt.17148.2.S1_at	fem-1 homolog c (C. elegans)	FEM1C	1
Bt.8962.3.S1_s_at	ubiquitin specific peptidase 18	USP18	-1
Bt.8263.1.A1_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1		1
Bt.910.3.S1_at	ubiquitin-fold modifier 1	UFM1	1
Bt.6455.1.S1_at	cullin 4A	CUL4A	1

Category	Term	Count	PValue
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	7	2,716E-10
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	7	2,716E-10
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	7	4,655E-10
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	7	4,770E-10
GOTERM_BP_FAT	GO:0030163~protein catabolic process	7	7,632E-10
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	7	1,230E-09
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	7	2,544E-09
GOTERM_BP_FAT	GO:0006508~proteolysis	7	1,151E-07
GOTERM_BP_FAT	GO:0032020~ISG15-protein conjugation	3	2,331E-06
KEGG_PATHWAY	bta04120:Ubiquitin mediated proteolysis	4	1,953E-05
SP_PIR_KEYWORDS	ubl conjugation pathway	4	5,129E-05

Gene Group 3 Enrichment Score: 1.6820

AFFYMETRIX_ID	Gene Name	Gene Symbol	Up/Down
Bt.21170.1.A1_at	RAS p21 protein activator 2	RASA2	1
Bt.21982.1.S1_a_at	IQ motif containing GTPase activating protein 1	IQGAP1	1
Bt.24678.1.A1_at	TBC1 domain family, member 9 (with GRAM domain) similar to IQ motif containing GTPase activating protein	TBC1D9	1
Bt.20947.2.S1_at	2	LOC100140708	1

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Bt.28780.2.A1_at	FYVE, RhoGEF and PH domain containing 4	FGD4	1
Category	Term	Count	PValue
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transduction	5	1,143E-07
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	5	2,584E-07
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	5	2,949E-07
GOTERM_MF_FAT	GO:0005096~GTPase activator activity	4	4,037E-06
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	4	1,099E-05
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	4	1,524E-05
GOTERM_MF_FAT	GO:0005099~Ras GTPase activator activity	3	1,319E-04
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	2	0,0562
KEGG_PATHWAY	bta04810:Regulation of actin cytoskeleton	2	0,0755

Gene Group 4	Enrichment Score: 1.3822		
AFFYMETRIX_ID	Gene Name	Gene Symbol	Up/Down
Bt.18165.1.A1_at	mitogen-activated protein kinase 6	MAPK6	1
Bt.9710.1.S1_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	PRPF4B	1
Bt.27436.1.A1_at	INO80 homolog (S. cerevisiae)	INO80	1
Bt.8238.1.A1_at	tribbles homolog 3 (Drosophila)	TRIB3	-1
Bt.21444.1.S1_at	cyclin-dependent kinase 2	CDK2	1
Bt.24975.1.S1_at	YTH domain containing 2	YTHDC2	1
Bt.4095.2.S1_at	torsin family 1, member B (torsin B)	TOR1B	1
Bt.6392.1.S1_at	transient receptor potential cation channel, subfamily M, member 6	TRPM6	1
Bt.16725.2.A1_at	ubiquitin-conjugating enzyme E2L 6	UBE2L6	-1
Bt.24697.1.A1_at	kinesin family member 3A	KIF3A	1
Bt.19645.1.A1_at	chromodomain helicase DNA binding protein 1	CHD1	1
Bt.2294.1.S1_a_at	ubiquitin-like modifier activating enzyme 7	UBA7	-1
Bt.23985.1.A1_at	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	ATRX	1
Bt.24333.1.S1_at	tousled-like kinase 1	TLK1	1
Bt.120.1.S1_at, Bt.20414.3.S1_at	E2F transcription factor 6; Rho-associated, coiled-coil containing protein kinase 2	ROCK2, ROCK1	1
Bt.24692.1.S1_at	adrenergic, beta, receptor kinase 2	ADRBK2	1

Category	Term	Count	PValue
GOTERM_MF_FAT	GO:0005524~ATP binding	16	3,843E-15
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	16	4,390E-15
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	16	9,787E-15
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	16	1,124E-14
GOTERM_MF_FAT	GO:0001882~nucleoside binding	16	1,221E-14
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	16	1,613E-13
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	16	1,613E-13
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	16	3,143E-13
GOTERM_MF_FAT	GO:0000166~nucleotide binding	16	4,053E-12
INTERPRO	IPR017442:Serine/threonine protein kinase-related	6	1,353E-07
UP_SEQ_FEATURE	domain:Protein kinase	5	2,745E-07
INTERPRO	IPR000719:Protein kinase, core	6	4,010E-07
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	8	5,427E-07
SP_PIR_KEYWORDS	atp-binding	7	9,739E-07
INTERPRO	IPR002290:Serine/threonine protein kinase	5	1,421E-06
GOTERM_BP_FAT	GO:0016310~phosphorylation	8	1,513E-06
GOTERM_MF_FAT	GO:0004672~protein kinase activity	8	1,863E-06
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	7	2,902E-06
INTERPRO	IPR008271:Serine/threonine protein kinase, active site	5	5,348E-06
SP_PIR_KEYWORDS	serine/threonine-protein kinase	5	5,565E-06
SMART	SM00220:S_TKc	5	5,931E-06
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	8	6,433E-06
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	8	6,433E-06
SP_PIR_KEYWORDS	nucleotide-binding	7	7,320E-06
INTERPRO	IPR017441:Protein kinase, ATP binding site	5	1,009E-05
UP_SEQ_FEATURE	binding site:ATP	4	7,036E-05
UP_SEQ_FEATURE	active site:Proton acceptor	4	3,703E-04
GOTERM_MF_FAT	GO:0004386~helicase activity	4	4,234E-04
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	4	5,392E-04
SP_PIR_KEYWORDS	kinase	4	0,0015
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded	5	0,0032
GOTERM_CC_FAT	organelle	5	0,0032
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	5	0,0032
GOTERM_BP_FAT	GO:0032020~ISG15-protein conjugation	2	0,0055
SP_PIR_KEYWORDS	serine/threonine-specific protein kinase	2	0,0114
GOTERM_CC_FAT	GO:0005694~chromosome	3	0,0120

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SP_PIR_KEYWORDS	transferase	4	0,0126
UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	2	0,0132
INTERPRO	IPR000961:AGC-kinase, C-terminal	2	0,0199
SP_PIR_KEYWORDS	ATP	2	0,0254
SMART	SM00133:S_TK_X	2	0,0312
UP_SEQ_FEATURE	domain:PH	2	0,0324
SP_PIR_KEYWORDS	phosphotransferase	2	0,0329

Gene Group 5 Enrichment Score: 0.77695

AFFYMETRIX_ID	Gene Name	Gene Symbol	Up/Down
Bt.269.1.S1_at	ATPase, Ca++ transporting, type 2C, member 1	ATP2C1	1
Bt.4773.3.S1_a_at	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A	1
Bt.8872.1.S1_at	ATPase, Ca++ transporting, plasma membrane 1	ATP2B1	1
Bt.17311.2.S1_at	retinitis pigmentosa 2 (X-linked recessive)	RP2	1

Category	Term	Count	PValue
GOTERM_BP_FAT	GO:0009145~purine nucleoside triphosphate biosynthetic process	4	1,005E-06
GOTERM_BP_FAT	GO:0009206~purine ribonucleoside triphosphate biosynthetic process	4	1,005E-06
GOTERM_BP_FAT	GO:0009201~ribonucleoside triphosphate biosynthetic process	4	1,005E-06
GOTERM_BP_FAT	GO:0009142~nucleoside triphosphate biosynthetic process	4	1,040E-06
GOTERM_BP_FAT	GO:0009205~purine ribonucleoside triphosphate metabolic process	4	1,305E-06
GOTERM_BP_FAT	GO:0009199~ribonucleoside triphosphate metabolic process	4	1,305E-06
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	4	1,346E-06
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	4	1,520E-06
GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	4	1,757E-06
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	4	1,757E-06
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	4	2,073E-06

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GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	4	2,303E-06
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	4	2,363E-06
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	4	3,393E-06
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	4	4,880E-06
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	4	5,601E-06
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process	4	5,601E-06
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	4	2,091E-05
GOTERM_MF_FAT	GO:0019829~cation-transporting ATPase activity	3	2,458E-05
GOTERM_MF_FAT	GO:0042625~ATPase activity, coupled to transmembrane movement of ions	3	1,236E-04
GOTERM_BP_FAT	GO:0006754~ATP biosynthetic process	3	2,504E-04
GOTERM_MF_FAT	GO:0042626~ATPase activity, coupled to transmembrane movement of substances	3	2,917E-04
GOTERM_BP_FAT	GO:0046034~ATP metabolic process	3	2,957E-04
GOTERM_MF_FAT	GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	3	2,981E-04
GOTERM_MF_FAT	GO:0043492~ATPase activity, coupled to movement of substances	3	2,981E-04
GOTERM_MF_FAT	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity	3	3,517E-04
GOTERM_MF_FAT	GO:0015399~primary active transmembrane transporter activity	3	3,517E-04
GOTERM_MF_FAT	GO:0022890~inorganic cation transmembrane transporter activity	3	3,874E-04
GOTERM_MF_FAT	GO:0042623~ATPase activity, coupled	3	0,0011
GOTERM_MF_FAT	GO:0005524~ATP binding	4	0,0013
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	4	0,0014
GOTERM_MF_FAT	GO:0016887~ATPase activity	3	0,0016
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	4	0,0016
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	4	0,0016
GOTERM_MF_FAT	GO:0001882~nucleoside binding	4	0,0017
INTERPRO	IPR004014:ATPase, P-type cation-transporter, N-terminal	2	0,0020

INTERPRO	IPR006068:ATPase, P-type cation-transporter, C-terminal	2	0,0023
GOTERM_MF_FAT	GO:0015085~calcium ion transmembrane transporter activity	2	0,0026
GOTERM_MF_FAT	GO:0005388~calcium-transporting ATPase activity	2	0,0026
INTERPRO	IPR018303:ATPase, P-type phosphorylation site	2	0,0026
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	4	0,0028
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	4	0,0028
INTERPRO	IPR008250:ATPase, P-type, ATPase-associated region	2	0,0029
PIR_SUPERFAMILY	PIRSF001297:Na(+)/K(+)-transporting ATPase alpha chain	2	0,0031
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	4	0,0032
INTERPRO	IPR001757:ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	2	0,0042
GOTERM_BP_FAT	GO:0006812~cation transport	3	0,0048
GOTERM_MF_FAT	GO:0000166~nucleotide binding	4	0,0053
SP_PIR_KEYWORDS	atp-binding	3	0,0053
GOTERM_MF_FAT	GO:0015082~di-, tri-valent inorganic cation transmembrane transporter activity	2	0,0062
INTERPRO	IPR005834:Haloacid dehalogenase-like hydrolase	2	0,0069
SP_PIR_KEYWORDS	hydrolase	3	0,0088
GOTERM_BP_FAT	GO:0006811~ion transport	3	0,0097
SP_PIR_KEYWORDS	nucleotide-binding	3	0,0105
GOTERM_MF_FAT	GO:0015662~ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	2	0,0142
GOTERM_BP_FAT	GO:0006816~calcium ion transport	2	0,0254
GOTERM_BP_FAT	GO:0015674~di-, tri-valent inorganic cation transport	2	0,0351

Gene Group 6**AFFYMETRIX_ID**

	Enrichment Score: 0.3898	Gene Name	Gene Symbol	Up/Down
Bt.21855.1.S1_at		transmembrane emp24 protein transport domain containing 7	TMED7	1
Bt.27858.1.A1_at		transmembrane emp24 protein transport domain containing 5	TMED5	1
Bt.22126.1.S1_at		tetraspanin 5	TSPAN5	-1
Bt.25433.1.S1_at		C1GALT1-specific chaperone 1	C1GALT1C1	1

Category	Term	Count	PValue
INTERPRO	IPR000348:emp24/gp25L/p24	2	0,0015
INTERPRO	IPR009038:GOLD	2	0,0020
SP_PIR_KEYWORDS	transmembrane	4	0,0111
UP_SEQ_FEATURE	topological domain:Cytoplasmic	3	0,0172
SP_PIR_KEYWORDS	membrane	4	0,0190
UP_SEQ_FEATURE	transmembrane region	3	0,0480

Gene Group 7**AFFYMETRIX_ID**

Bt.13990.2.S1_at

Bt.23985.1.A1_at

Bt.24537.1.A1_at

Bt.28780.2.A1_at

Category

GOTERM_MF_FAT

GOTERM_MF_FAT

GOTERM_MF_FAT

GOTERM_MF_FAT

GOTERM_MF_FAT

Enrichment Score: 0.0171

Gene Name

zinc finger, CCHC domain containing 8

alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, *S. cerevisiae*)

zinc finger, RAN-binding domain containing 2

FYVE, RhoGEF and PH domain containing 4

Gene Symbol

ZCCHC8

ATRX

ZRANB2

FGD4

Up/Down

1

1

1

1

Count

4

4

4

4

4

PValue

0,0032

0,0062

0,0172

0,0178

0,0183