Supplemental table 3. Differentially expressed genes in heifers of the PI and control groups, day 160 of gestation.

Gene Identification	Gene Name	LogFold	Ratio
AFFX-BioC-3_at	BIOTIN SYNTHESIS PROTEIN BIOC	-0.23054404	0.832974367
AFFX-BioC-5_at	BIOTIN SYNTHESIS PROTEIN BIOC	-0.24708439	0.846912371
AFFX-BioDn-3_at	DETHIOBIOTIN SYNTHETASE	-0.2432203	0.844889208
AFFX-BioDn-5_at	DETHIOBIOTIN SYNTHETASE	-0.237819	0.849775264
AFFX-Bt_Cyph_5_at	PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B)	0.092022026	1.063581924
AFFX-Bt_Cyph_M_at	PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B)	0.060799322	1.020669361
AFFX-Bt_eIF-4E_3_at	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E	-0.12648477	0.874231656
AFFX-Bt-ef1a-5_at	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-0.03471622	0.984016881
AFFX-Bt-ef1a-M_at	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-0.05014881	0.947494618
AFFX-Bt-gapd-3_at	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	0.078488264	1.066509628
AFFX-Bt-gapd-5_at	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	0.10458921	1.094165675
AFFX-Bt-gapd-M_at	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	0.055625129	1.059421891
AFFX-Bt-X03453-2_s_at	,CONTROL X03453 /FEA=CDS_2 /DB_XREF=CAA27178.1 GI:15137 GOA:P06956	-0.08128581	0.944531075
AFFX-CreX-3_at	CYCLIZATION RECOMBINASE	-0.17514571	0.883954679
AFFX-CreX-5_at	CYCLIZATION RECOMBINASE	-0.2035355	0.87160749
AFFX-r2-Ec-bioC-3_at	BIOTIN SYNTHESIS PROTEIN BIOC	-0.19097208	0.842656599
AFFX-r2-Ec-bioC-5_at	BIOTIN SYNTHESIS PROTEIN BIOC	-0.17980747	0.848569463
AFFX-r2-Ec-bioD-3_at	DETHIOBIOTIN SYNTHETASE	-0.17517629	0.878158238
AFFX-r2-Ec-bioD-5_at	DETHIOBIOTIN SYNTHETASE	-0.19559074	0.864322551
AFFX-r2-P1-cre-3_at	CYCLIZATION RECOMBINASE	-0.09416552	0.935447092
AFFX-r2-P1-cre-5_at	CYCLIZATION RECOMBINASE	-0.159339	0.893959605
Bt.10006.1.A1_at	,GB:CK848153 /DB_XREF=GI:45210276 /DB_XREF=970871 /TID=BT.10006.1 /CNT=6	-0.16259742	0.871113449
Bt.10043.1.S1_at	,GB:CK981092 /DB_XREF=GI:45499072 /DB_XREF=4112739 /CLONE=9BOV42_C02 /TID=BT.10043.1 /CNT=13 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.10043	-0.23325659	0.805910948
Bt.1007.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DM BETA-CHAIN, EXPRESSED	0.148730472	1.05226645
Bt.10076.1.S1_at	RCSD DOMAIN CONTAINING 1	-0.12702545	0.887973097
Bt.10077.1.S2_at	INTERFERON RESPONSIVE FACTOR 1	0.289086767	1.107181151
Bt.10116.1.A1_at	,GB:CK769666 /DB_XREF=GI:42723760 /DB_XREF=957731 /TID=BT.10116.1 /CNT=14 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.10116 /UG_TITLE=TRANSCRIBED	0.352099378	1.223423884
Bt.1020.1.S1_at	SIMILAR TO DUAL SPECIFICITY PROTEIN KINASE CLK1 (CDC-LIKE KINASE 1)	-0.2437699	0.799779164
Bt.10236.1.S1_at	SIMILAR TO ARMET PROTEIN PRECURSOR (ARGININE-RICH PROTEIN)	0.352479645	1.317160148
Bt.10245.1.S1_at	FUSED TOES HOMOLOG	-0.15023051	0.851097727

Bt.10271.1.A1_at	,GB:CB171569 /DB_XREF=GI:28157697 /DB_XREF=PKO602601340.R1 /TID=BT.10271.1 /CNT=24 /FEA=EST /TIER=STACK /STK=9 /UG=BT.10271	0.10263419	1.062855246
Bt.10277.2.S1_a_at	SIMILAR TO NUCLEOLAR PROTEIN 5A (56KDA WITH KKE/D REPEAT)	0.330342362	1.280430141
Bt.10278.1.S1_at	,GB:CB172509 /DB_XREF=GI:28158637 /DB_XREF=UMJ603014336.R1 /TID=BT.10278.1 /CNT=82 /FEA=EST /TIER=STACK /STK=28 /UG=BT.10278	0.108854122	1.057758756
Bt.1031.1.S1_at	CATHEPSIN H	0.125257901	1.102196862
Bt.10398.1.S1_at	,GB:CK846010 /DB_XREF=GI:45206097 /DB_XREF=968461 /TID=BT.10398.1 /CNT=9 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.10398 /UG_TITLE=TRANSCRIBED	-1.15148399	0.383755633
Bt.10579.1.S1_at	,GB:CK957651 /DB_XREF=GI:45472031 /DB_XREF=4098130 /CLONE=10BOV4_B09 /TID=BT.10579.1 /CNT=26 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.10579	0.205503309	1.166991423
Bt.10608.2.S1_a_at	HYPOTHETICAL LOC505736	0.354976618	1.245245164
Bt.1085.1.S1_at	SFT2 DOMAIN CONTAINING 2	0.141051601	1.070670174
Bt.10855.1.S1_at	SIMILAR TO REGULATOR OF G-PROTEIN SIGNALLING 2, 24KDA	-0.38168707	0.914814258
Bt.1087.1.S1_at	,GB:CB455930 /DB_XREF=GI:29262312 /DB_XREF=713115 /TID=BT.1087.1 /CNT=36 /FEA=EST /TIER=STACK /STK=6 /UG=BT.1087 /UG_TITLE=TRANSCRIBED	0.270673024	1.242471667
Bt.1088.1.S1_a_at	,GB:CK948232 /DB_XREF=GI:45462612 /DB_XREF=4073036 /CLONE=10BOV24_E21 /TID=BT.1088.1 /CNT=14 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.1088	-0.09812032	0.89980966
Bt.1088.2.S1_at	,GB:CK778198 /DB_XREF=GI:42730511 /DB_XREF=965353 /TID=BT.1088.2 /CNT=6 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.1088 /UG_TITLE=TRANSCRIBED	-0.0663563	0.935172599
Bt.10903.2.S1_at	,GB:CK961569 /DB_XREF=GI:45475949 /DB_XREF=4076141 /CLONE=9BOV10_N06 /TID=BT.10903.2 /CNT=35 /FEA=EST /TIER=STACK /STK=9 /UG=BT.10903	0.288127428	1.173924533
Bt.10935.1.S1_at	TOLL INTERACTING PROTEIN	-0.09777569	0.947395098
Bt.1094.1.S1_at	,GB:CB419744 /DB_XREF=GI:29185111 /DB_XREF=592623 /TID=BT.1094.1 /CNT=17	-0.85902004	0.906958655
Bt.10949.1.S1_at	,GB:BF653247 /DB_XREF=GI:11918379 /DB_XREF=277028 /TID=BT.10949.1 /CNT=7	-0.25459947	0.919663687
Bt.10956.1.S1_at	,GB:CB454068 /DB_XREF=GI:29260450 /DB_XREF=710759 /TID=BT.10956.1 /CNT=11 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.10956 /UG_TITLE=TRANSCRIBED	-0.18878115	0.877925375
Bt.10969.1.S1_at	RIBOSOMAL PROTEIN S15A	-0.10029449	0.913929378
Bt.10994.1.S1_at	,GB:BM087882 /DB_XREF=GI:16998510 /DB_XREF=500731 /TID=BT.10994.1 /CNT=9	0.149176917	1.154639116
Bt.11088.1.S1_a_at	CD97 ANTIGEN	-0.13411444	0.92692037
Bt.11105.1.S1_at	NUCLEASE SENSITIVE ELEMENT BINDING PROTEIN 1	-0.14367477	0.974015219
Bt.11156.1.S1_at	SIMILAR TO HYPOTHETICAL UPF0184 PROTEIN C9ORF16 HOMOLOG	0.42021972	1.319715559
Bt.11167.1.S1_at	SIMILAR TO CG14407-PA	0.630262698	1.604606023
Bt.11208.1.S1_at	SIMILAR TO CALMODULIN 1	0.162332162	1.113454319
Bt.11259.1.S1_at	SIMILAR TO PUTATIVE ISG12(A) PROTEIN	1.415595861	4.273349609
Bt.1131.1.S1_at	PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B)	0.087069092	1.080108333
Bt.1137.1.S1_at	,GB:CK848303 /DB_XREF=GI:45210555 /DB_XREF=971046 /TID=BT.1137.1 /CNT=29 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.1137 /UG_TITLE=TRANSCRIBED	-0.14423611	0.968401389

Bt.11389.1.S1_a_at	SIMILAR TO CYCLIN I	0.087727888	1.047396714
Bt.11389.1.S1_at	SIMILAR TO CYCLIN I	0.053975111	1.045484413
Bt.11433.1.A1_at	RIBOSOMAL PROTEIN, LARGE, P1	0.153204307	1.136526397
Bt.11581.1.S1_at	SIMILAR TO PLATELET FACTOR 4 PRECURSOR (PF-4) (CXCL4) (ONCOSTATIN A)	0.197827108	1.187266505
Bt.1165.1.S1_at	ADENYLATE CYCLASE 7	-0.11297866	0.913529836
Bt.1167.1.S1_at	SIMILAR TO DEK ONCOGENE (DNA BINDING)	-0.08827048	0.942680899
Bt.1169.1.S1_at	SIMILAR TO GAMMA ADDUCIN (ADDUCIN-LIKE PROTEIN 70)	-0.09753694	0.91047216
Bt.1178.1.S1_at	TROPOMYOSIN 2	0.642697893	1.506847084
Bt.11826.1.S1_at	,GB:CK960760 /DB_XREF=GI:45475140 /DB_XREF=4101654 /CLONE=10BOV8_E05	-0.16380091	0.890247889
Bt.11847.1.A1_at	X (INACTIVE)-SPECIFIC TRANSCRIPT	-0.41913931	0.693094531
Bt.11857.1.A1_at	,GB:AU278571 /DB_XREF=GI:21681881 /DB_XREF=AU278571 /CLONE=PLACENTA0784 /TID=BT.11857.1 /CNT=1 /FEA=EST /TIER=CONSEND	-0.150176	0.937727181
Bt.1193.1.S1_at	PHOSPHOARGININE PHOSPHATASE	0.060013064	1.026427019
Bt.11990.1.S1_at	,GB:BE809771 /DB_XREF=GI:10240883 /DB_XREF=215525 /TID=BT.11990.1 /CNT=12	-0.22806061	0.847712758
Bt.1200.2.A1_a_at	,GB:AV607578 /DB_XREF=GI:9737951 /DB_XREF=AV607578 /CLONE=E1KI041G03 /TID=BT.1200.2 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.1200	0.470405888	1.465218118
Bt.12176.1.A1_at	T CELL RECEPTOR GAMMA CHAIN VARIABLE REGION BVG7	-0.14959821	0.812770719
Bt.12196.1.S1_at	,GB:CK956156 /DB_XREF=GI:45470536 /DB_XREF=4096229 /CLONE=10BOV35_C04 /TID=BT.12196.1 /CNT=14 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.12196 /UG_TITLE=TRANSCRIBED SEQUENCE WITH MODERATE SIMILARITY TO PROTEIN REF:NP_002829.2 (H.SAPIENS) PROTEIN TYROSINE PHOSPHATASE, RECEPTOR	-0.11283503	0.93778975
Bt.12206.1.S1_x_at	NEUTROPHIL BETA-DEFENSIN-9 LIKE PEPTIDE	0.447030402	1.347706841
Bt.12241.1.S1_at	CHEMOKINE RECEPTOR 7	-0.20790439	0.984851453
Bt.1226.1.S1_a_at	SIMILAR TO RIBOSOMAL PROTEIN L28	0.047647034	1.023282432
Bt.12290.1.S1_at	PC4 AND SFRS1 INTERACTING PROTEIN 1	-0.13448604	0.825398975
Bt.12309.1.S1_at	HEAT SHOCK 70 KDA PROTEIN 8	-0.05199656	0.999087914
Bt.12314.1.S1_at	6-PHOSPHOFRUCTO-2-KINASE	-0.36834791	0.801194499
Bt.12322.1.S1_at	S-ADENOSYLHOMOCYSTEINE HYDROLASE	0.159601605	1.152506126
Bt.12327.1.S1_at	SIMILAR TO THIOREDOXIN INTERACTING PROTEIN ISOFORM 2	-0.18989343	0.877815856
Bt.12348.1.A1_at	,GB:CK975040 /DB_XREF=GI:45493014 /DB_XREF=4106148 /CLONE=9BOV32_P11 /TID=BT.12348.1 /CNT=10 /FEA=EST /TIER=STACK /STK=7 /UG=BT.12348	-0.11198635	0.941194056
Bt.12360.1.S1_at	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 17 ISOFORM B	0.400532816	1.224879179
Bt.12366.1.S1_at	SIMILAR TO CYCLIN L2 ISOFORM 1	-0.27559172	0.806252097
Bt.12404.1.S1_at	,GB:BI536672 /DB_XREF=GI:15377782 /DB_XREF=393857 /TID=BT.12404.1 /CNT=18 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.12404 /UG_TITLE=TRANSCRIBED	-0.16189873	0.886592351
Bt.12423.1.S1_at	,GB:CB166723 /DB_XREF=GI:28152848 /DB_XREF=CTD602999955.R1 /TID=BT.12423.1 /CNT=25 /FEA=EST /TIER=STACK /STK=6 /UG=BT.12423	-0.0922783	0.978341073

Bt.12429.1.S1_at	ENDOTHELIAL DIFFERENTIATION-RELATED FACTOR 1	0.148800183	1.116563766
Bt.1244.1.S1_at	SIMILAR TO 6-PHOSPHOGLUCONATE DEHYDROGENASE (DECARBOXYLATING)	-0.09486993	0.931759084
Bt.12461.1.S1_at	ENHANCER OF RUDIMENTARY HOMOLOG (DROSOPHILA)	0.095545935	1.028143808
Bt.12469.1.S1_at	TU TRANSLATION ELONGATION FACTOR, MITOCHONDRIAL	0.070528926	1.051511366
Bt.12490.2.A1_x_at	IGG1 HEAVY CHAIN CONSTANT REGION	0.293604768	1.291004018
Bt.12500.2.S1_a_at	LYMPHOCYTE CYTOSOLIC PROTEIN 1 (L-PLASTIN)	-0.07083106	0.942502053
Bt.12504.1.S1_at	CLUSTERIN	0.780145064	1.639443941
Bt.12553.1.S1_at	HAPTOGLOBIN	-0.26454891	1.050601127
Bt.12613.1.S1_at	SIMILAR TO KRUPPEL-LIKE FACTOR 6	-0.41785043	0.74697657
Bt.1269.1.S1_a_at	RIBOSOMAL PROTEIN S12	0.019982395	1.015185391
Bt.12722.1.A1_at	SIMILAR TO PDZ DOMAIN CONTAINING 6	-0.32629762	0.884221041
Bt.12739.1.S1_at	SIMILAR TO MEMBRANE-ASSOCIATED RING FINGER (C3HC4) 2 ISOFORM 1	0.573124834	1.584067487
Bt.12739.2.S1_a_at	SIMILAR TO MEMBRANE-ASSOCIATED RING FINGER (C3HC4) 2 ISOFORM 1	0.457473372	1.438082477
Bt.12805.1.S1_at	SIMILAR TO HUMAN HYPOTHETICAL PROTEIN FLJ22662	0.316355307	1.238068258
Bt.1283.1.S1_at	BARRIER TO AUTOINTEGRATION FACTOR 1	0.140427461	1.099417229
Bt.12859.1.S1_at	SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H1	-0.13731616	0.898506472
Bt.12870.1.S1_at	SIMILAR TO 55 KDA ERYTHROCYTE MEMBRANE PROTEIN (P55) (MEMBRANE	0.252554923	1.212114916
Bt.12875.1.S1_at	EPITHELIAL MEMBRANE PROTEIN 3	0.196296153	1.146196287
Bt.12896.1.S1_at	CALMODULIN 2	-0.07678902	0.927059829
Bt.1290.1.A1_a_at	SIMILAR TO PROTEASOME BETA 2 SUBUNIT	0.155985276	1.117587518
Bt.12906.2.S1_at	SIMILAR TO GELSOLIN PRECURSOR (ACTIN-DEPOLYMERIZING FACTOR) (ADF)	0.785175302	1.921138989
Bt.12911.1.S1_at	RIBOSOMAL PROTEIN L26	0.046168763	1.007796132
Bt.12957.1.A1_at	,GB:CB170194 /DB_XREF=GI:28156322 /DB_XREF=YIR603162978.R1 /TID=BT.12957.1	-0.14481754	0.873592673
Bt.12986.1.S1_at	MAD2 MITOTIC ARREST DEFICIENT-LIKE 1 (YEAST)	0.357974908	1.228678525
Bt.1302.1.S1_at	APEX NUCLEASE (MULTIFUNCTIONAL DNA REPAIR ENZYME) 1	0.229540979	1.101364882
Bt.1309.1.A1_at	,GB:AW425689 /DB_XREF=GI:6953636 /DB_XREF=58040 /TID=BT.1309.1 /CNT=2	0.088752363	1.05853786
Bt.13128.1.S1_at	SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT B, IRON SULFUR (IP)	0.149537184	1.145437154
Bt.13170.1.S1_at	SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT C, INTEGRAL MEMBRANE	0.118238425	1.081095861
Bt.13261.1.A1_at	,GB:CB464510 /DB_XREF=GI:29270895 /DB_XREF=725723 /TID=BT.13261.1 /CNT=9 /FEA=EST /TIER=STACK /STK=7 /UG=BT.13261 /UG_TITLE=TRANSCRIBED	-0.07710792	0.959290645
Bt.13293.1.S1_at	SIMILAR TO B-LYMPHOCYTE ACTIVATION MARKER BLAST-1 PRECURSOR (BCM1	0.050207096	0.987003167
Bt.13296.2.A1_at	SIMILAR TO CG15270-PA, ISOFORM A	0.625426288	1.428967816
Bt.1330.1.S1_at	ALDOSE REDUCTASE	-1.13250738	0.459382218
Bt.13311.1.S1_at	SIMILAR TO TRANSLATION FACTOR SUI1 HOMOLOG	-0.08179312	0.959659757
Bt.1334.1.S1_at	,GB:BI538156 /DB_XREF=GI:15379257 /DB_XREF=428556 /TID=BT.1334.1 /CNT=18 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.1334 /UG_TITLE=TRANSCRIBED	0.074428899	1.054038751

Bt.13401.1.S1_at	,GB:CK848852 /DB_XREF=GI:45211573 /DB_XREF=971669 /TID=BT.13401.1 /CNT=18 /FEA=EST /TIER=STACK /STK=6 /UG=BT.13401 /UG_TITLE=TRANSCRIBED	0.181290886	1.140069053
Bt.13491.1.S1_at	,GB:BM106294 /DB_XREF=GI:17037364 /DB_XREF=509991 /TID=BT.13491.1 /CNT=5	0.450867321	1.353805002
Bt.13496.2.S1_a_at	CD63 PROTEIN	0.176947873	1.127919028
Bt.13510.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DO BETA	-0.20875814	0.859284062
Bt.13553.2.S1_a_at	HYPOTHETICAL PROTEIN	0.296207028	1.2272545
Bt.13574.1.S1_at	ADP-RIBOSYLATION-LIKE FACTOR 6 INTERACTING PROTEIN 5	0.110964598	1.0655362
Bt.1358.1.S1_at	PDZ AND LIM DOMAIN 1 (ELFIN)	0.255350174	1.368319944
Bt.13589.1.A1_at	DUAL SPECIFICITY PHOSPHATASE 11	0.204218018	1.101896241
Bt.13628.1.S1_at	SIMILAR TO TRANSGLUTAMINASE 3 PRECURSOR	0.12553391	1.111895943
Bt.1370.1.S1_at	ARGININOSUCCINATE SYNTHETASE	-0.57202016	0.673800318
Bt.13702.1.S1_at	,GB:CK849544 /DB_XREF=GI:45212880 /DB_XREF=972550 /TID=BT.13702.1 /CNT=20	-0.15976346	0.861450419
Bt.13705.1.S1_at	SIGNAL SEQUENCE RECEPTOR, BETA (TRANSLOCON-ASSOCIATED PROTEIN	0.064549232	0.963740136
Bt.1372.2.S1_at	,GB:AW464378 /DB_XREF=GI:7034546 /DB_XREF=BP230015B10F5 /CLONE=BP230015B10F5 /TID=BT.1372.2 /CNT=22 /FEA=EST /TIER=CONSEND	0.202750973	1.130775996
Bt.13739.1.S1_at	,GB:CB171573 /DB_XREF=GI:28157701 /DB_XREF=PKO602601345.R1	0.230241062	1.081414679
Bt.13769.1.S1_at	,GB:BE751908 /DB_XREF=GI:10165900 /DB_XREF=204161 /TID=BT.13769.1 /CNT=6	0.378701264	1.335628663
Bt.1377.1.S1_at	CHEMOKINE C-C MOTIF RECEPTOR 1	0.218317301	1.066675899
Bt.13798.1.S1_at	,GB:CF931206 /DB_XREF=GI:38281241 /DB_XREF=CF--06-R-J06 /TID=BT.13798.1	0.461995035	1.15653032
Bt.13829.1.S1_at	,GB:CK982442 /DB_XREF=GI:45500422 /DB_XREF=4114846 /CLONE=9BOV44_J21	-0.08757626	0.981348989
Bt.13851.1.S1_at	INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR	0.175410828	1.112833361
Bt.13873.1.S1_at	,GB:CB538791 /DB_XREF=GI:29407735 /DB_XREF=776818 /TID=BT.13873.1 /CNT=9	-0.30060505	0.7853576
Bt.13887.1.S1_at	,GB:CK941653 /DB_XREF=GI:45456033 /DB_XREF=4064986 /CLONE=10BOV11_E11 /TID=BT.13887.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.13887 /UG_TITLE=TRANSCRIBED SEQUENCE WITH STRONG SIMILARITY TO PROTEIN	0.199007344	1.103102383
Bt.13898.1.S1_at	RIBOSOMAL PROTEIN S27-LIKE	0.119704371	1.089176223
Bt.13902.1.S1_at	,GB:CK847334 /DB_XREF=GI:45208728 /DB_XREF=969966 /TID=BT.13902.1 /CNT=12 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.13902 /UG_TITLE=TRANSCRIBED	0.452767895	1.335602074
Bt.13920.1.S1_at	,GB:BI535453 /DB_XREF=GI:15376561 /DB_XREF=398992 /TID=BT.13920.1 /CNT=4	0.33167394	1.220860291
Bt.13987.1.A1_at	,GB:CB170166 /DB_XREF=GI:28156294 /DB_XREF=YIR603162946.R1 /TID=BT.13987.1	-0.26597735	0.858268938
Bt.1399.1.S1_at	ATPASE, VACUOLAR, 14 KD	0.177823216	1.151718601
Bt.13991.1.A1_at	PROLINE-RICH NUCLEAR RECEPTOR COACTIVATOR 1	-0.10874573	0.931564481
Bt.14005.1.S1_at	CD53 ANTIGEN	-0.07928819	0.959523095
Bt.14047.1.A1_at	TRIPARTITE MOTIF-CONTAINING 6	0.217010949	1.12727455
Bt.14098.1.S1_at	SIMILAR TO MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 2 (APC-	0.186815081	1.0756136
Bt.14136.1.A1_at	,GB:CB421505 /DB_XREF=GI:29188625 /DB_XREF=594527 /TID=BT.14136.1 /CNT=6	0.351384685	1.237554621
Bt.14186.1.S1_at	ACTIN, BETA	-0.02657193	0.9892742

Bt.14228.1.S1_at	SIMILAR TO RIBOSOMAL PROTEIN L36	0.040573001	1.029409113
Bt.1430.1.S1_at	PREFOLDIN 5	0.070967036	1.012557872
Bt.1432.2.S1_at	SIMILAR TO PAROXISOME PROLIFERATIVE ACTIVATED RECEPTOR, GAMMA,	0.056244823	1.008002507
Bt.14326.1.S1_at	SIMILAR TO SPERMINE SYNTHASE	0.178123095	1.132924079
Bt.1457.1.A1_at	,GB:CK978412 /DB_XREF=GI:45496386 /DB_XREF=4109621 /CLONE=9BOV38_A04	0.246577932	1.106782634
Bt.14590.1.A1_at	SIMILAR TO TYROSINE-PROTEIN KINASE BLK (B LYMPHOCYTE KINASE) (P55-BLK)	-0.25107767	0.7833729
Bt.1476.1.S1_at	,GB:BM252021 /DB_XREF=GI:17887649 /DB_XREF=BOTL0100018_E10	-0.18990672	0.771518108
Bt.15384.1.S1_at	RIBOSOMAL PROTEIN L35A	0.078363698	1.083454637
Bt.15436.2.S1_a_at	RIBOSOMAL PROTEIN L10	0.055122043	1.039866099
Bt.1548.1.S1_at	,GB:CK771078 /DB_XREF=GI:42725172 /DB_XREF=959314 /TID=BT.1548.1 /CNT=33 /FEA=EST /TIER=STACK /STK=9 /UG=BT.1548 /UG_TITLE=TRANSCRIBED	0.15084391	1.071637635
Bt.1552.1.S1_at	SERYL-TRNA SYNTHETASE	0.176292704	1.071453301
Bt.15530.1.S1_at	RIBOSOMAL PROTEIN L12	0.032805191	1.019700869
Bt.15534.1.S1_a_at	SIMILAR TO TUBULIN, ALPHA 1	0.17217578	1.149029885
Bt.15545.1.S1_at	EUKARYOTIC TRANSLATION INITIATION FACTOR 4A, ISOFORM 1	0.149909852	1.109554716
Bt.15548.1.A1_at	,GB:BP108827 /DB_XREF=GI:28311115 /DB_XREF=BP108827 /CLONE=ORCS12492	0.214454813	1.147552102
Bt.1556.1.S1_at	SIMILAR TO RIBONUCLEASE UK114 (14.5 KDA TRANSLATIONAL INHIBITOR	0.299797527	1.262472873
Bt.15561.1.S1_at	,GB:CB464457 /DB_XREF=GI:29270842 /DB_XREF=725668 /TID=BT.15561.1 /CNT=26 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.15561 /UG_TITLE=TRANSCRIBED	0.058180601	1.004512456
Bt.15615.1.S1_at	,GB:CK848560 /DB_XREF=GI:45211041 /DB_XREF=971340 /TID=BT.15615.1 /CNT=7 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.15615 /UG_TITLE=TRANSCRIBED	0.241767766	1.207217256
Bt.15616.1.S1_at	,GB:CK770544 /DB_XREF=GI:42724638 /DB_XREF=958731 /TID=BT.15616.1 /CNT=4	0.273560608	1.166754862
Bt.15684.1.S1_at	,GB:CB531064 /DB_XREF=GI:29393386 /DB_XREF=742313 /TID=BT.15684.1 /CNT=49 /FEA=EST /TIER=STACK /STK=7 /UG=BT.15684 /UG_TITLE=TRANSCRIBED	0.082946892	1.025411216
Bt.15705.1.S1_at	DESTRIN (ACTIN DEPOLYMERIZING FACTOR)	0.624063476	1.437119495
Bt.15705.1.S2_at	DESTRIN (ACTIN DEPOLYMERIZING FACTOR)	0.579218551	1.38182057
Bt.15711.2.S1_a_at	SIMILAR TO POLY(RC) BINDING PROTEIN 2	0.081443043	1.063936491
Bt.15713.1.A1_at	,GB:CB439472 /DB_XREF=GI:29224517 /DB_XREF=689121 /TID=BT.15713.1 /CNT=7 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.15713 /UG_TITLE=TRANSCRIBED	0.190883235	1.207482353
Bt.15716.1.S1_at	,GB:CB168620 /DB_XREF=GI:28154746 /DB_XREF=VQT602700424.R1	0.211669495	1.091814485
Bt.15724.1.S1_at	SIMILAR TO CG17680-PA	0.143636814	1.059112151
Bt.15725.1.A1_at	,GB:CK953752 /DB_XREF=GI:45468132 /DB_XREF=4093549 /CLONE=10BOV32_C12 /TID=BT.15725.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.15725	0.262837616	1.205891494
Bt.15729.1.S1_at	PROTEASOME ACTIVATOR SUBUNIT 2	0.228047022	1.175080121
Bt.15736.1.S1_at	,GB:CB531703 /DB_XREF=GI:29394667 /DB_XREF=754568 /TID=BT.15736.1 /CNT=24 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.15736 /UG_TITLE=TRANSCRIBED	-0.0918883	0.924106893
Bt.15742.1.S2_at	CD47 ANTIGEN	-0.08961207	0.966556206

Bt.1577.1.S1_at	COMPLEMENT COMPONENT 1, Q SUBCOMPONENT, ALPHA POLYPEPTIDE	0.455861823	1.316084046
Bt.15782.1.S1_at	SIMILAR TO CD59 ANTIGEN P18-20	0.28321651	1.460850435
Bt.15794.1.S1_at	SIMILAR TO METHYL-CPG BINDING DOMAIN PROTEIN 2 ISOFORM 1	0.086095802	1.06984492
Bt.1582.1.S1_at	HYPOTHETICAL PROTEIN	0.100421004	1.036624095
Bt.15837.1.S1_at	SIMILAR TO PROTEASOME SUBUNIT ALPHA TYPE 6 (PROTEASOME IOTA CHAIN)	0.111859865	1.050428718
Bt.15844.1.S1_at	CYTOSKELETON ASSOCIATED PROTEIN 1	0.157515456	1.07183078
Bt.15851.1.S1_at	EUKARYOTIC TRANSLATION INITIATION FACTOR 4A, ISOFORM 2	-0.04763541	0.939854573
Bt.15865.1.S1_at	PROTEASOME SUBUNIT, BETA TYPE 8 [PROSOME, MACROPAIN] [LARGE	0.104704364	1.060915104
Bt.15882.2.S1_a_at	SIMILAR TO SORCIN (22 KDA PROTEIN) (CP-22) (V19)	0.101299656	1.014696196
Bt.15886.1.S1_at	,GB:CK849044 /DB_XREF=GI:45211929 /DB_XREF=971891 /TID=BT.15886.1 /CNT=27 /FEA=EST /TIER=STACK /STK=7 /UG=BT.15886 /UG_TITLE=TRANSCRIBED	0.15513752	1.052600761
Bt.15903.1.S1_at	SIMILAR TO THIOPURINE S-METHYLTRANSFERASE (THIOPURINE	0.205956141	1.130149151
Bt.15912.1.S1_at	HYPOTHETICAL PROTEIN	0.088184122	1.084044725
Bt.15931.1.S1_at	SIMILAR TO RIBOSOMAL PROTEIN L14	0.037570548	1.014455147
Bt.15968.1.S1_at	,GB:CK975868 /DB_XREF=GI:45493842 /DB_XREF=4107148 /CLONE=9BOV33_J03	-0.54707624	0.694126553
Bt.15975.1.A1_at	SUPEROXIDE DISMUTASE 1, SOLUBLE	0.14480662	1.064252513
Bt.16018.1.S1_a_at	CASPASE 4, APOPTOSIS-RELATED CYSTEINE PROTEASE	0.114308117	1.05856876
Bt.16025.1.S1_at	CYTOCHROME C OXYDASE SUBUNIT 4	0.082472108	1.019188303
Bt.16032.1.S1_at	ANNEXIN I	-0.01651514	0.998545899
Bt.16039.1.S1_at	SIMILAR TO 30 KDA PROTEIN	0.140474482	1.085201647
Bt.16040.1.S1_at	SH3 DOMAIN BINDING GLUTAMIC ACID-RICH PROTEIN LIKE 3	0.049986543	1.044133302
Bt.16048.1.S1_at	PROTEOGLYCAN 1 PRECURSOR-LIKE	-0.03972847	0.994938908
Bt.16070.1.S1_at	,GB:AV604129 /DB_XREF=GI:9734502 /DB_XREF=AV604129 /CLONE=E1KI020H09 /TID=BT.16070.1 /CNT=4 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.16070	0.071219412	1.008356575
Bt.16070.3.A1_at	,GB:AV594085 /DB_XREF=GI:9710482 /DB_XREF=AV594085 /CLONE=E1CA011E07 /TID=BT.16070.3 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.16070	1.021301036	1.091849534
Bt.16072.1.S1_at	SERINE INCORPORATOR 2	-0.12010112	0.92403544
Bt.16101.1.S1_at	GRANULYSIN	-0.33473666	0.72031426
Bt.16101.1.S1_s_at	GRANULYSIN	-0.37124488	0.674933003
Bt.16118.1.S1_at	SIMILAR TO C-TYPE LECTIN DOMAIN FAMILY 2, MEMBER E	-0.02308489	0.973968816
Bt.16126.1.S1_at	,GB:CK973853 /DB_XREF=GI:45491827 /DB_XREF=4104739 /CLONE=9BOV28_E18	-0.19085677	0.862149077
Bt.16127.1.S1_at	,GB:CK961787 /DB_XREF=GI:45476167 /DB_XREF=4076107 /CLONE=9BOV10_L20	-0.08072415	0.946183569
Bt.16132.2.S1_a_at	SIMILAR TO TRANSCRIPTION ELONGATION FACTOR B (SIII), POLYPEPTIDE 1	0.15855103	1.088554864
Bt.1617.2.S1_a_at	CLATHRIN, LIGHT POLYPEPTIDE (LCA)	0.122860348	1.034087063
Bt.16201.1.S1_at	SIMILAR TO CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100	0.25218323	1.197046471

Bt.16201.2.A1_at	SIMILAR TO CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100	0.372569123	1.359733731
Bt.16370.1.S1_at	HYPOTHETICAL LOC535023	-0.40721429	0.719999143
Bt.16425.1.A1_at	,GB:CB420023 /DB_XREF=GI:29185672 /DB_XREF=592935 /TID=BT.16425.1 /CNT=1	0.209738581	1.229001175
Bt.1658.1.S1_at	SIMILAR TO DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (MAP KINASE PHOSPHATASE-1) (MKP-1) (PROTEIN-TYROSINE PHOSPHATASE CL100) (DUAL	-0.73467968	0.622721047
Bt.16673.1.S1_at	,GB:CB431657 /DB_XREF=GI:29208917 /DB_XREF=607653 /TID=BT.16673.1 /CNT=8 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.16673 /UG_TITLE=TRANSCRIBED	0.339598244	1.265249402
Bt.1678.1.S1_at	,GB:CK775904 /DB_XREF=GI:42732154 /DB_XREF=967044 /TID=BT.1678.1 /CNT=42 /FEA=EST /TIER=STACK /STK=7 /UG=BT.1678 /UG_TITLE=TRANSCRIBED	0.271722278	1.156937801
Bt.1679.1.S1_at	SIMILAR TO 5-AMINOIMIDAZOLE-4-CARBOXAMIDE RIBONUCLEOTIDE	0.193274965	1.144832172
Bt.16790.1.S1_at	RIBOSOMAL PROTEIN L5	0.191105933	1.193606262
Bt.16875.1.A1_at	,GB:CB424375 /DB_XREF=GI:29194356 /DB_XREF=598623 /TID=BT.16875.1 /CNT=1	-0.15838695	0.904093813
Bt.16887.1.A1_at	,GB:CK961353 /DB_XREF=GI:45475733 /DB_XREF=4102439 /CLONE=10BOV9_E22	0.231736578	1.108333661
Bt.16916.1.S1_at	,GB:CB448382 /DB_XREF=GI:29254764 /DB_XREF=702517 /TID=BT.16916.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.16916 /UG_TITLE=TRANSCRIBED	-0.40485151	0.852850884
Bt.16916.3.S1_at	,GB:CK955508 /DB_XREF=GI:45469888 /DB_XREF=4095428 /CLONE=10BOV34_A19 /TID=BT.16916.3 /CNT=5 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.16916	-0.59220401	0.822923431
Bt.17036.1.A1_s_at	TRYPTOPHANYL-TRNA SYNTHETASE	0.137193685	0.997096084
Bt.17090.1.S1_at	,GB:CK975625 /DB_XREF=GI:45493599 /DB_XREF=4106617 /CLONE=9BOV33_C24 /TID=BT.17090.1 /CNT=15 /FEA=EST /TIER=CONSEND /STK=5 /UG=BT.17090	0.17133919	1.015079939
Bt.1718.3.S1_at	,GB:CK973898 /DB_XREF=GI:45491872 /DB_XREF=4104682 /CLONE=9BOV28_C09 /TID=BT.1718.3 /CNT=6 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.1718	0.208364914	1.164690159
Bt.17195.1.A1_at	,GB:CB427688 /DB_XREF=GI:29200989 /DB_XREF=603281 /TID=BT.17195.1 /CNT=1	-0.14361816	0.868122521
Bt.1729.1.A1_at	FERRITIN, LIGHT POLYPEPTIDE	0.116107277	1.0381379
Bt.17318.1.S1_at	CKLF-LIKE MARVEL TRANSMEMBRANE DOMAIN CONTAINING 6	-0.09269404	0.909762655
Bt.17353.1.A1_at	,GB:CB428945 /DB_XREF=GI:29203502 /DB_XREF=604718 /TID=BT.17353.1 /CNT=1	0.636571983	1.788938219
Bt.1758.1.S1_at	SIMILAR TO NONHISTONE CHROMOSOMAL PROTEIN HMG-17 (HIGH-MOBILITY	0.152775681	1.051536769
Bt.17595.2.S1_a_at	CHROMOSOME 1 OPEN READING FRAME 37	-0.61839101	0.908098473
Bt.1760.1.S1_at	SIMILAR TO OLIGORIBONUCLEASE, MITOCHONDRIAL PRECURSOR (SMALL	0.42315382	1.211798639
Bt.1768.1.A1_at	SIMILAR TO THO COMPLEX SUBUNIT 4 (THO4) (ALLY OF AML-1 AND LEF-1)	0.157566252	1.1195827
Bt.17848.1.S1_at	SIMILAR TO PROTEIN KINASE C BINDING PROTEIN 1 ISOFORM A	-0.17453227	0.832479949
Bt.17942.1.S1_at	,GB:CK773433 /DB_XREF=GI:42727576 /DB_XREF=962073 /TID=BT.17942.1 /CNT=12	-0.30035595	0.751348978
Bt.17968.1.S1_at	SIMILAR TO 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 8 (26S	0.145976624	1.096553932
Bt.17999.3.A1_a_at	,GB:CK952670 /DB_XREF=GI:45467050 /DB_XREF=4092122 /CLONE=10BOV30_H01 /TID=BT.17999.3 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.17999	0.700237282	1.587644615
Bt.1819.1.S1_at	SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2KDA PROTEIN	0.113584186	1.107683409

Bt.1823.1.S1_at	PEROXIREDOXIN 1	0.220834654	1.157400238
Bt.18234.1.S1_at	SIMILAR TO IMMUNOGLOBULIN SUPERFAMILY, MEMBER 6	0.253747032	1.115444161
Bt.18375.1.S1_at	,GB:CB443472 /DB_XREF=GI:29232531 /DB_XREF=694376 /TID=BT.18375.1 /CNT=2	0.364740348	1.271312996
Bt.1844.1.S1_at	,GB:BM104814 /DB_XREF=GI:17035884 /DB_XREF=506074 /TID=BT.1844.1 /CNT=4	0.175269543	1.137958221
Bt.18469.2.A1_at	,GB:CB444924 /DB_XREF=GI:29235438 /DB_XREF=696139 /TID=BT.18469.2 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.18469 /UG_TITLE=TRANSCRIBED	-0.22861873	0.933962879
Bt.1847.1.S1_at	,GB:CB441122 /DB_XREF=GI:29227826 /DB_XREF=691449 /TID=BT.1847.1 /CNT=3	0.329778957	1.315934822
Bt.1855.1.S1_at	CYSTATIN C (AMYLOID ANGIOPATHY AND CEREBRAL HEMORRHAGE)	0.156924018	1.158371019
Bt.18570.2.A1_s_at	SIMILAR TO PROTEASOME BETA 2 SUBUNIT	0.149115627	1.061497565
Bt.18623.1.A1_at	SIMILAR TO MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 2 (APC-	0.330555517	1.292072812
Bt.18689.2.A1_at	,GB:CB448793 /DB_XREF=GI:29255175 /DB_XREF=702954 /TID=BT.18689.2 /CNT=1	0.326351874	1.2234504
Bt.18751.1.S1_at	SIMILAR TO PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II ALPHA (PIP5KII-ALPHA) (1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE)	0.133777822	1.062653177
Bt.18751.2.A1_s_at	SIMILAR TO PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II ALPHA (PIP5KII-ALPHA) (1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE)	0.204772707	1.075176542
Bt.18756.1.S1_at	,GB:BE757079 /DB_XREF=GI:10171071 /DB_XREF=211422 /TID=BT.18756.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.18756 /UG_TITLE=TRANSCRIBED	0.332460703	1.192155307
Bt.18969.1.S1_at	,GB:CB452339 /DB_XREF=GI:29258721 /DB_XREF=707195 /TID=BT.18969.1 /CNT=3	-0.61673237	0.645973303
Bt.19161.1.S1_at	SIMILAR TO ACTIVATING TRANSCRIPTION FACTOR 4	0.075473881	1.059726181
Bt.19195.1.A1_at	,GB:CK777838 /DB_XREF=GI:42730151 /DB_XREF=964983 /TID=BT.19195.1 /CNT=5 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.19195 /UG_TITLE=TRANSCRIBED	0.176545546	1.022495818
Bt.19204.1.S1_at	,GB:CB458416 /DB_XREF=GI:29264800 /DB_XREF=717065 /TID=BT.19204.1 /CNT=4	0.354988083	1.31908001
Bt.1927.1.S1_at	,GB:CK981861 /DB_XREF=GI:45499841 /DB_XREF=4114518 /CLONE=9BOV44_M05	-0.31880868	0.868934105
Bt.19295.1.S1_at	,GB:CK847570 /DB_XREF=GI:45209199 /DB_XREF=970220 /TID=BT.19295.1 /CNT=6	1.307247275	2.528548963
Bt.19365.1.S1_at	SIMILAR TO GRANZYME B PRECURSOR (T-CELL SERINE PROTEASE 1-3E) (CYTOTOXIC T-LYMPHOCYTE PROTEINASE 2) (LYMPHOCYTE PROTEASE) (SECT)	-1.06139314	0.468325604
Bt.1937.1.S1_at	,GB:CK771765 /DB_XREF=GI:42725893 /DB_XREF=960153 /TID=BT.1937.1 /CNT=25 /FEA=EST /TIER=CONSEND /STK=5 /UG=BT.1937 /UG_TITLE=TRANSCRIBED	-0.19821565	0.823088369
Bt.19429.2.S1_a_at	,GB:CK978709 /DB_XREF=GI:45496683 /DB_XREF=4110280 /CLONE=9BOV38_L15 /TID=BT.19429.2 /CNT=3 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.19429	-0.14452379	0.951914648
Bt.19706.1.S1_at	,GB:CK972254 /DB_XREF=GI:45490228 /DB_XREF=4102828 /CLONE=9BOV24_F03	-0.21976623	0.790390431
Bt.19718.1.A1_at	,GB:CB531616 /DB_XREF=GI:29394491 /DB_XREF=754476 /TID=BT.19718.1 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.19718 /UG_TITLE=TRANSCRIBED	4.565947709	0.899529144
Bt.1973.1.S1_at	SIMILAR TO SMALL NUCLEAR RIBONUCLEOPROTEIN D2	0.131835206	1.05550699
Bt.1978.1.S1_a_at	T CELL RECEPTOR, BETA CLUSTER	0.077372382	1.041418945
Bt.1978.1.S1_at	SIMILAR TO T-CELL RECEPTOR BETA CHAIN C REGION	0.150066199	1.023678588
Bt.19807.1.S1_at	T CELL RECEPTOR, BETA CLUSTER	0.180774472	1.128075236

Bt.19845.1.S1_at	SIMILAR TO SKAP55 HOMOLOGUE	0.201493534	1.067776112
Bt.19845.2.A1_at	,GB:CF764403 /DB_XREF=GI:37713622 /DB_XREF=CES003973 /CLONE=CCL003973 /TID=BT.19845.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.19845	0.11729673	1.03133133
Bt.1986.1.S1_at	,GB:CB535381 /DB_XREF=GI:29402041 /DB_XREF=768798 /TID=BT.19845.2 /CNT=1	0.238879912	1.121711074
Bt.19997.1.S1_at	SIMILAR TO CYSTATIN B (LIVER THIOL PROTEINASE INHIBITOR) (CPI-B) (STEFIN B)	-1.38867548	0.056730333
Bt.20.1.S1_at	,GB:CK964923 /DB_XREF=GI:45482897 /DB_XREF=4079807 /CLONE=9BOV18_F24 /TID=BT.19997.1 /CNT=19 /FEA=EST /TIER=STACK /STK=8 /UG=BT.19997	0.140230218	1.076633416
Bt.2000.1.S1_s_at	NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 7, 14.5KDA	0.119376617	1.088759201
Bt.20096.2.S1_a_at	SIMILAR TO HUNTINGTIN INTERACTING PROTEIN K	0.169241099	1.134332966
Bt.20113.1.S1_at	SIMILAR TO CASPASE 6 ISOFORM ALPHA PREPROPROTEIN	0.204572747	1.151878959
Bt.20116.1.S1_at	,GB:CK770029 /DB_XREF=GI:42724123 /DB_XREF=958147 /TID=BT.20116.1 /CNT=22 /FEA=EST /TIER=STACK /STK=6 /UG=BT.20116 /UG_TITLE=TRANSCRIBED	-0.86418132	0.838169293
Bt.20132.2.S1_at	,GB:AW485306 /DB_XREF=GI:7055412 /DB_XREF=64948 /TID=BT.20132.2 /CNT=2	0.158297931	1.073389988
Bt.20145.1.S1_at	SIMILAR TO PRELI	0.156402431	1.125782253
Bt.20151.1.S1_at	SIMILAR TO DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 7 PRECURSOR	0.783142028	2.035495208
Bt.20164.1.S1_at	,GB:CB435760 /DB_XREF=GI:29217112 /DB_XREF=616036 /TID=BT.20164.1 /CNT=75 /FEA=EST /TIER=STACK /STK=6 /UG=BT.20164 /UG_TITLE=TRANSCRIBED	0.512917648	1.365673587
Bt.20171.1.S1_at	,GB:CK770804 /DB_XREF=GI:42724898 /DB_XREF=959020 /TID=BT.20171.1 /CNT=22 /FEA=EST /TIER=STACK /STK=6 /UG=BT.20171 /UG_TITLE=TRANSCRIBED	-0.37549071	0.703910078
Bt.20205.1.S1_at	SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE G (C1 INHIBITOR),	0.280101838	1.100368598
Bt.20210.1.S1_at	,GB:CB461072 /DB_XREF=GI:29267456 /DB_XREF=720998 /TID=BT.20210.1 /CNT=15	-0.14376799	0.957206956
Bt.20226.1.A1_at	SIMILAR TO CYSTEINE-RICH MOTOR NEURON 1 PROTEIN PRECURSOR (CRIM-1)	0.456139955	1.346754907
Bt.20245.1.S1_at	,GB:BE665547 /DB_XREF=GI:10026138 /DB_XREF=154628 /TID=BT.20245.1 /CNT=24 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.20245 /UG_TITLE=TRANSCRIBED	0.226730256	1.1856954
Bt.20308.1.S1_at	,GB:CB437738 /DB_XREF=GI:29221046 /DB_XREF=685615 /TID=BT.20308.1 /CNT=2	-0.13927406	0.862558811
Bt.20356.1.S1_at	HYPOTHETICAL LOC510480	0.602098852	1.712952014
Bt.20367.1.S1_at	,GB:CB430615 /DB_XREF=GI:29206839 /DB_XREF=606517 /TID=BT.20367.1 /CNT=19 /FEA=EST /TIER=STACK /STK=7 /UG=BT.20367 /UG_TITLE=TRANSCRIBED	-0.13288662	0.905553135
Bt.20371.1.S1_at	,GB:CK848774 /DB_XREF=GI:45211432 /DB_XREF=971584 /TID=BT.20371.1 /CNT=27 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.20371 /UG_TITLE=TRANSCRIBED	0.144022577	1.114416978
Bt.20383.1.S1_at	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1	0.38921215	1.342492148
Bt.20416.1.S1_at	SIMILAR TO PROTEASOME SUBUNIT BETA TYPE 9 PRECURSOR (PROTEASOME CHAIN 7) (MACROPAIN CHAIN 7) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX	0.12417047	1.034902355
Bt.20421.2.S1_a_at	SIMILAR TO DOLICHYL-PHOSPHATE MANNOSYLTRANSFERASE POLYPEPTIDE 2,	-0.76058681	0.665368799
Bt.20472.1.S1_at	,GB:CB534856 /DB_XREF=GI:29400989 /DB_XREF=768220 /TID=BT.20472.1 /CNT=14 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.20472 /UG_TITLE=TRANSCRIBED	0.289622435	1.124360035
Bt.20484.1.S1_at	SIMILAR TO IRON-SULFUR CLUSTER ASSEMBLY ENZYME ISOFORM ISCU2	0.217436637	1.111726011

Bt.20532.1.S1_at	SIMILAR TO PROTEASOME SUBUNIT BETA TYPE 9 PRECURSOR (PROTEASOME CHAIN 7) (MACROPAIN CHAIN 7) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX	0.120973478	1.089812017
Bt.20549.1.S1_at	,GB:CB464749 /DB_XREF=GI:29271134 /DB_XREF=725980 /TID=BT.20549.1 /CNT=11 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.20549 /UG_TITLE=TRANSCRIBED	0.093450773	1.092431413
Bt.2055.1.S1_at	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN),BETA POLYPEPTIDE 2	0.146251506	1.144495089
Bt.20562.1.S1_at	,GB:CK975718 /DB_XREF=GI:45493692 /DB_XREF=4106728 /CLONE=9BOV33_H15 /TID=BT.20562.1 /CNT=54 /FEA=EST /TIER=STACK /STK=17 /UG=BT.20562	0.19352763	1.12870498
Bt.20573.1.S1_at	,GB:CB456419 /DB_XREF=GI:29262801 /DB_XREF=713678 /TID=BT.20573.1 /CNT=6	-0.18052798	0.86089416
Bt.20604.1.S1_at	SIMILAR TO THREONYL-TRNA SYNTHETASE	0.061237493	0.996574414
Bt.20778.2.S1_at	SIMILAR TO TG-INTERACTING FACTOR ISOFORM A	-1.34654617	0.839640776
Bt.20888.1.S1_at	,GB:CB464973 /DB_XREF=GI:29271358 /DB_XREF=726225 /TID=BT.20888.1 /CNT=3	0.954998343	1.894653626
Bt.20895.1.S1_at	HYPOTHETICAL PROTEIN	0.154842944	1.072508107
Bt.209.3.S1_at	LYSOZYME, MACROPHAGE	0.058924453	1.014995028
Bt.20905.1.S1_at	,GB:CB451376 /DB_XREF=GI:29257758 /DB_XREF=706140 /TID=BT.20905.1 /CNT=25 /FEA=EST /TIER=STACK /STK=6 /UG=BT.20905 /UG_TITLE=TRANSCRIBED	-0.19591274	0.857819212
Bt.2091.1.S1_at	,GB:CK846550 /DB_XREF=GI:45207173 /DB_XREF=969056 /TID=BT.2091.1 /CNT=50 /FEA=EST /TIER=STACK /STK=8 /UG=BT.2091 /UG_TITLE=TRANSCRIBED	-0.85302265	0.590270253
Bt.20925.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ BETA	-1.58792813	0.054172484
Bt.20971.1.S1_at	CALPAIN, LARGE POLYPEPTIDE L2	0.169448144	1.126690408
Bt.20986.1.S1_at	TUMOR SUPPRESSOR DELETED IN ORAL CANCER-RELATED 1	0.146016336	1.063728282
Bt.21012.3.S1_a_at	SIMILAR TO F32D8.4	-0.92426559	0.758103549
Bt.2109.1.S1_at	,GB:CK849902 /DB_XREF=GI:45213570 /DB_XREF=973072 /TID=BT.2109.1 /CNT=15 /FEA=EST /TIER=STACK /STK=9 /UG=BT.2109 /UG_TITLE=TRANSCRIBED SEQUENCE WITH STRONG SIMILARITY TO PROTEIN REF:NP_037415.1 (H.SAPIENS)	0.084750947	1.039028937
Bt.2116.1.S1_at	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE, 6	0.221367262	1.117134714
Bt.21173.1.S1_at	,GB:AV594776 /DB_XREF=GI:9711175 /DB_XREF=AV594776 /CLONE=E1CA015G05 /TID=BT.21173.1 /CNT=3 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.21173	-0.61285397	0.933741742
Bt.21220.1.S1_at	,GB:CK778786 /DB_XREF=GI:42731099 /DB_XREF=965957 /TID=BT.21220.1 /CNT=5 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.21220 /UG_TITLE=TRANSCRIBED	0.313752229	1.10783279
Bt.21224.1.S1_at	,GB:CB452167 /DB_XREF=GI:29258549 /DB_XREF=707014 /TID=BT.21224.1 /CNT=8 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.21224 /UG_TITLE=TRANSCRIBED	-0.14708522	0.863433811
Bt.21368.1.S1_s_at	SIMILAR TO IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 1 PRECURSOR (IMMUNOGLOBULIN-RELATED 14.1 PROTEIN) (IMMUNOGLOBULIN OMEGA	0.197985587	1.150444984
Bt.21374.2.S1_a_at	SIMILAR TO APG3P	0.182602226	1.132360251
Bt.21379.2.S1_at	,GB:BE755355 /DB_XREF=GI:10169347 /DB_XREF=209172 /TID=BT.21379.2 /CNT=2	0.582105551	1.330798001
Bt.21387.1.S1_at	,GB:CB429918 /DB_XREF=GI:29205444 /DB_XREF=605767 /TID=BT.21387.1 /CNT=10	0.320728513	1.17326006

Bt.21431.1.S1_at	,GB:CK948133 /DB_XREF=GI:45462513 /DB_XREF=4073174 /CLONE=10BOV24_M15 /TID=BT.21431.1 /CNT=16 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.21431	0.092165157	1.080561076
Bt.21459.1.S1_at	HYPOTHETICAL PROTEIN	-0.85405226	0.858943657
Bt.21476.1.S1_at	SIMILAR TO CG6878-PA	0.267498596	1.190337642
Bt.21480.1.A1_s_at	,GB:AV618700 /DB_XREF=GI:9754370 /DB_XREF=AV618700 /CLONE=E0RU006E01	0.108224547	1.107853774
Bt.21482.1.A1_at	,GB:CK834840 /DB_XREF=GI:45065674 /DB_XREF=4059343 /CLONE=8BOV_7F15 /TID=BT.21482.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.21482 /UG_TITLE=TRANSCRIBED SEQUENCE WITH MODERATE SIMILARITY TO PROTEIN	-0.61170882	0.53699431
Bt.215.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ ALPHA	-1.73135442	0.055613745
Bt.21503.1.S1_at	PROTEIN PHOSPHATASE 1, CATALYTIC SUBUNIT, ALPHA ISOFORM	0.073438054	0.996579059
Bt.21576.1.S1_at	SIMILAR TO COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	0.512206881	1.30170631
Bt.2158.1.S1_at	,GB:BI681359 /DB_XREF=GI:15634276 /DB_XREF=460730 /TID=BT.2158.1 /CNT=11	-0.19623177	0.866209549
Bt.2158.2.S1_at	,GB:BF773657 /DB_XREF=GI:12121494 /DB_XREF=283035 /TID=BT.2158.2 /CNT=2	-0.22398159	0.856624407
Bt.21602.1.S1_at	SIMILAR TO AXIN 1	0.224905862	1.097008861
Bt.21607.1.S1_at	,GB:CK944409 /DB_XREF=GI:45458789 /DB_XREF=4068586 /CLONE=10BOV16_K11 /TID=BT.21607.1 /CNT=18 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.21607	-0.26366723	0.792722235
Bt.21635.2.A1_a_at	26S PROTEASOME P40.5 SUBUNIT	0.227341154	1.170272884
Bt.21685.1.A1_at	,GB:CK946273 /DB_XREF=GI:45460653 /DB_XREF=4070778 /CLONE=10BOV19_F19	-0.30232761	0.831435477
Bt.2169.1.S1_at	SIMILAR TO TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (ALPHA-L-FUCOSIDASE I)	0.217634028	0.923868944
Bt.21724.2.S1_a_at	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE 1	0.424262217	1.411322992
Bt.21732.1.S1_at	SIMILAR TO RIBONUCLEASE T2 PRECURSOR (RIBONUCLEASE 6)	0.117157144	1.031865699
Bt.21740.1.S1_at	,GB:CK962844 /DB_XREF=GI:45480818 /DB_XREF=4077439 /CLONE=9BOV12_D08 /TID=BT.21740.1 /CNT=19 /FEA=EST /TIER=STACK /STK=6 /UG=BT.21740	-0.08512932	0.981089688
Bt.21775.1.S1_at	,GB:CB461304 /DB_XREF=GI:29267688 /DB_XREF=721258 /TID=BT.21775.1 /CNT=40 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.21775 /UG_TITLE=TRANSCRIBED	-0.14951973	0.971328346
Bt.21803.1.A1_at	SIMILAR TO 5-NUCLEOTIDASE, CYTOSOLIC III ISOFORM 1	0.167757587	1.168227627
Bt.21805.1.S1_at	SIMILAR TO ZINC FINGER, FYVE DOMAIN CONTAINING 21	0.428710571	1.320452123
Bt.21820.2.S1_at	HYPOTHETICAL PROTEIN	0.369797085	1.249439107
Bt.21836.1.S1_at	SIMILAR TO SEC61 ALPHA SUBUNIT HOMOLOG	0.250933019	1.164907872
Bt.21866.1.S1_at	,GB:CB537825 /DB_XREF=GI:29406769 /DB_XREF=775483 /TID=BT.21866.1 /CNT=6	0.706027096	1.855400507
Bt.21883.1.S1_at	PLACENTA-SPECIFIC 8	-0.18768851	1.626159952
Bt.21931.1.S1_at	,GB:BE667577 /DB_XREF=GI:10028168 /DB_XREF=155303 /TID=BT.21931.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.21931 /UG_TITLE=TRANSCRIBED	0.146495431	1.145695622
Bt.21950.1.S1_at	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 1	0.342779263	1.599617298
Bt.21950.1.S1_s_at	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 1	0.359534999	1.510496146
Bt.21975.1.S1_at	PERFORIN 1 (PORE FORMING PROTEIN)	-0.35106639	0.772872657

Bt.21994.1.S1_at	,GB:CB536687 /DB_XREF=GI:29404644 /DB_XREF=771727 /TID=BT.21994.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.21994 /UG_TITLE=TRANSCRIBED	0.250721235	1.087574151
Bt.21996.1.S1_at	IMMUNOGLOBULIN HEAVY CONSTANT EPSILON	-0.25785157	1.422563127
Bt.22004.1.A1_at	,GB:CB458586 /DB_XREF=GI:29264970 /DB_XREF=717264 /TID=BT.22004.1 /CNT=3	-0.26420401	0.840737675
Bt.22009.1.S1_at	SIMILAR TO CHEMOKINE (C-X-C MOTIF) LIGAND 16	0.425072162	1.269519212
Bt.22010.1.S1_at	SIMILAR TO PRO-APOPTOTIC BCL-2 PROTEIN ISOFORM A	0.209442777	1.104381172
Bt.22016.1.S1_at	,GB:CB165724 /DB_XREF=GI:28151849 /DB_XREF=LHG603001167.R1 /TID=BT.22016.1 /CNT=26 /FEA=EST /TIER=STACK /STK=9 /UG=BT.22016	0.087839545	1.046015395
Bt.2203.1.S1_at	,GB:CK770899 /DB_XREF=GI:42724993 /DB_XREF=959126 /TID=BT.2203.1 /CNT=42 /FEA=EST /TIER=STACK /STK=6 /UG=BT.2203 /UG_TITLE=TRANSCRIBED	0.590797827	1.452376713
Bt.22050.1.S1_at	SIMILAR TO TYROSINE-PROTEIN KINASE HCK (P56-HCK/P59-HCK) (HEMOPOIETIC	0.156477017	0.961968108
Bt.22108.1.S1_at	,GB:CK979590 /DB_XREF=GI:45497570 /DB_XREF=4111482 /CLONE=9BOV40_N17 /TID=BT.22108.1 /CNT=15 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.22108	0.192885026	1.11017301
Bt.22198.1.S1_at	GLUTATHIONE S-TRANSFERASE A4	0.904511362	1.709170824
Bt.22204.1.A1_at	,GB:CB438670 /DB_XREF=GI:29222916 /DB_XREF=687548 /TID=BT.22204.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.22204 /UG_TITLE=TRANSCRIBED	0.238418949	1.145809912
Bt.22224.1.S1_at	,GB:BM251510 /DB_XREF=GI:17887102 /DB_XREF=BOTL0100006XH08R	-0.14632028	0.908211474
Bt.22243.1.S1_at	,GB:CK954419 /DB_XREF=GI:45468799 /DB_XREF=4094429 /CLONE=10BOV33_H04 /TID=BT.22243.1 /CNT=26 /FEA=EST /TIER=STACK /STK=7 /UG=BT.22243	0.122034606	1.079709699
Bt.22275.1.A1_at	SIMILAR TO INTERFERON-STIMULATED GENE 20 KDA PROTEIN (PROMYELOCYTIC	0.217250069	1.14499616
Bt.22303.1.S1_at	,GB:CB450627 /DB_XREF=GI:29257009 /DB_XREF=705304 /TID=BT.22303.1 /CNT=2 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.22303 /UG_TITLE=TRANSCRIBED	-0.08570673	0.930912653
Bt.22329.1.S1_at	FK506-BINDING PROTEIN 1A	0.192064765	1.13066161
Bt.22359.3.S1_at	SIMILAR TO SUDD SUPPRESSOR OF BIMD6 HOMOLOG ISOFORM 1	-0.38951155	0.939149866
Bt.22503.1.A1_at	SIMILAR TO PROTEIN C21ORF59	0.175706667	1.102741008
Bt.22533.1.S1_at	OXYGEN REGULATED PROTEIN, 150 KDA	0.110357874	1.083910245
Bt.22568.1.S1_at	RIBOSOMAL PROTEIN L29	0.018511671	0.99942261
Bt.22615.2.A1_a_at	,GB:AV591682 /DB_XREF=GI:9702675 /DB_XREF=AV591682 /CLONE=E1BR020A05 /TID=BT.22615.2 /CNT=4 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.22615	0.194238518	1.125758137
Bt.22633.1.S1_at	,GB:BE667924 /DB_XREF=GI:10028515 /DB_XREF=155865 /TID=BT.22633.1 /CNT=8	0.234109335	1.067898941
Bt.22636.1.S1_at	,GB:CK979099 /DB_XREF=GI:45497079 /DB_XREF=4110618 /CLONE=9BOV39_J17 /TID=BT.22636.1 /CNT=16 /FEA=EST /TIER=STACK /STK=6 /UG=BT.22636	0.152153646	1.142344576
Bt.22672.1.A1_at	HYDROXYPROSTAGLANDIN DEHYDROGENASE 15-(NAD)	-0.69255594	0.938831421
Bt.22759.1.S1_at	,GB:CK846142 /DB_XREF=GI:45206359 /DB_XREF=968611 /TID=BT.22759.1 /CNT=24	0.206637135	1.25889368
Bt.22763.2.S1_a_at	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A SYNTHASE 1	0.315382056	1.320813429
Bt.22767.1.S1_at	MHC CLASS I HEAVY CHAIN	-0.78669635	0.449206126
Bt.22772.1.S1_at	RIBOSOMAL PROTEIN S28	0.021168252	1.0125866

Bt.22783.1.S1_at	ENOLASE 1	0.071676973	1.041037773
Bt.22803.1.S1_at	SIMILAR TO TUBULIN, BETA 5	0.304485591	1.198031291
Bt.22803.1.S2_at	,GB:CK847941 /DB_XREF=GI:45209885 /DB_XREF=970638 /TID=BT.22803.1 /CNT=140 /FEA=EST /TIER=STACK /STK=10 /UG=BT.22803 /UG_TITLE=TRANSCRIBED	0.094115825	1.061159404
Bt.22843.1.S1_at	SIMILAR TO COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING	0.105925917	1.032624298
Bt.22865.1.S1_at	RHO FAMILY, SMALL GTP BINDING PROTEIN RAC1	0.157160501	1.149543611
Bt.22865.1.S2_at	RHO FAMILY, SMALL GTP BINDING PROTEIN RAC1	0.053014601	1.042030931
Bt.22867.1.S1_at	HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ ALPHA, TYPE 1	-0.99117969	0.018536448
Bt.22867.1.S1_x_at	HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ ALPHA, TYPE 1	-0.42032827	0.648631344
Bt.22867.2.A1_at	HYPOTHETICAL PROTEIN	1.378783869	276.2367281
Bt.22978.1.S1_a_at	INTERFERON INDUCED TRANSMEMBRANE PROTEIN 1 (9-27)	0.000943242	1.003551537
Bt.22978.2.S1_at	HYPOTHETICAL PROTEIN	-0.04140399	0.991519825
Bt.23001.1.S1_a_at	SIMILAR TO 40S RIBOSOMAL PROTEIN S20	0.039777769	1.013518887
Bt.23002.1.S1_s_at	CYTOCHROME C OXIDASE SUBUNIT VIA POLYPEPTIDE 1	0.111495851	1.086879165
Bt.2307.1.S1_s_at	SIMILAR TO CYTOPLASMIC DYNEIN LIGHT CHAIN 1	0.079889402	1.127952167
Bt.23097.3.S1_at	,GB:BE755225 /DB_XREF=GI:10169217 /DB_XREF=208988 /TID=BT.23097.3 /CNT=3	0.262959493	1.264286128
Bt.231.1.S1_at	THIOREDOXIN	0.224136319	1.14270295
Bt.23123.1.S1_at	DIFFERENTIATED EMBRYO CHONDROCYTE EXPRESSED GENE 1	0.232501419	1.125497099
Bt.23161.2.A1_at	HEAT SHOCK 70 KD PROTEIN 1	0.850354709	1.581668347
Bt.23170.1.S1_at	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F	-0.04001152	0.971142002
Bt.23172.2.S1_at	RIBOSOMAL PROTEIN S23	-0.02436825	0.972430015
Bt.23173.1.S1_at	HYPOTHETICAL PROTEIN	0.125310732	1.117561029
Bt.23174.1.S1_at	SIMILAR TO CD74 ANTIGEN ISOFORM B	0.015379018	1.000285538
Bt.23174.2.S1_at	CHLORIDE INTRACELLULAR CHANNEL 1	0.073669619	1.037998314
Bt.23179.1.S2_at	HEAT SHOCK 90KD PROTEIN 1, ALPHA	0.074215042	1.073696261
Bt.23180.1.S1_at	PROFILIN 1	0.097639591	1.06649027
Bt.23182.1.S1_at	FARNESYL DIPHOSPHATE SYNTHASE (FARNESYL PYROPHOSPHATE	0.342562339	1.308047409
Bt.23192.1.S1_at	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 1B, 41KDA	0.10959225	1.100249496
Bt.23212.1.S1_at	SIMILAR TO C-4 METHYLSTEROL OXIDASE (METHYLSTEROL MONOOXYGENASE)	0.246839187	1.18365728
Bt.23227.1.S1_at	,GB:CK960999 /DB_XREF=GI:45475379 /DB_XREF=4102171 /CLONE=10BOV9_J18	0.156055077	1.135794026
Bt.23236.1.A1_at	,GB:AW653573 /DB_XREF=GI:7419399 /DB_XREF=102328 /TID=BT.23236.1 /CNT=18 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.23236 /UG_TITLE=TRANSCRIBED	-0.05596482	0.944505582
Bt.23250.2.S1_at	L-ARGININE:GLYCINE AMIDINOTRANSFERASE	0.796421085	1.554964016
Bt.23256.1.S1_at	,GB:BP107597 /DB_XREF=GI:28309885 /DB_XREF=BP107597 /CLONE=ORCS10973 /TID=BT.23256.1 /CNT=79 /FEA=EST /TIER=STACK /STK=29 /UG=BT.23256	-0.01811168	0.997570942
Bt.23263.1.S1_s_at	,GB:CB170873 /DB_XREF=GI:28157001 /DB_XREF=IBC602600677.R1 /TID=BT.23263.1 /CNT=112 /FEA=EST /TIER=STACK /STK=40 /UG=BT.23263	0.098889794	1.073260313

Bt.23268.1.S1_at	NIEMANN-PICK DISEASE, TYPE C2	0.261051211	1.253475615
Bt.23277.1.A1_at	,GB:CK849163 /DB_XREF=GI:45212154 /DB_XREF=972026 /TID=BT.23277.1 /CNT=9 /FEA=EST /TIER=CONSEND /STK=5 /UG=BT.23277 /UG_TITLE=TRANSCRIBED	-0.24627436	0.770268193
Bt.23277.3.S1_a_at	,GB:CK953829 /DB_XREF=GI:45468209 /DB_XREF=4093653 /CLONE=10BOV32_G20 /TID=BT.23277.3 /CNT=17 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.23277	-0.13063035	0.875924466
Bt.23278.1.S1_at	ALLOGRAFT INFLAMMATORY FACTOR 1	0.508622485	1.355691393
Bt.23291.1.S1_at	,GB:CB530156 /DB_XREF=GI:29391563 /DB_XREF=736926 /TID=BT.23291.1 /CNT=53 /FEA=EST /TIER=STACK /STK=10 /UG=BT.23291 /UG_TITLE=TRANSCRIBED	0.064373423	1.013399727
Bt.23296.1.S1_at	HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ ALPHA, TYPE 1	-0.26242033	0.711723387
Bt.23310.1.S1_at	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE B/B' ISOFORM B'	0.120771167	1.064526533
Bt.23314.1.A1_s_at	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F	-0.1071007	0.937299918
Bt.23326.1.S1_at	SIMILAR TO ACTIN, CYTOPLASMIC 2 (GAMMA-ACTIN)	0.035774183	1.000401183
Bt.23326.2.A1_at	ACTIN, CYTOPLASMIC 2	0.585863747	1.236950287
Bt.23335.1.S1_at	,GB:CF614104 /DB_XREF=GI:37239530 /DB_XREF=CES013519 /CLONE=CCL011299 (NULL) /TID=BT.23335.1 /CNT=9 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.23335	-0.061966	0.947199996
Bt.23342.1.S1_at	SIMILAR TO ADAPTOR-RELATED PROTEIN COMPLEX 1, MU 2 SUBUNIT (MU-ADAPTIN 2) (ADAPTOR PROTEIN COMPLEX AP-1 MU-2 SUBUNIT) (GOLGI ADAPTOR	-0.20626346	0.873449869
Bt.23348.1.S1_a_at	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 1	0.344654034	1.460947199
Bt.23348.2.S1_a_at	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 1	0.402012774	1.514971843
Bt.23361.1.S1_at	SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE BINDING PROTEIN	0.125195185	1.138522851
Bt.23381.1.S1_at	RIBOSOMAL PROTEIN L10A	0.025684025	1.00968533
Bt.23399.1.S1_at	SIMILAR TO PYRUVATE KINASE, ISOZYMES M1/M2 (PYRUVATE KINASE MUSCLE	0.194293137	1.212280618
Bt.234.1.S1_at	INTERLEUKIN 18 (INTERFERON-GAMMA-INDUCING FACTOR)	0.472420174	1.453815373
Bt.2340.1.S1_at	SCOTIN	0.249607773	1.196535614
Bt.23401.1.S1_at	SIMILAR TO FOUR AND A HALF LIM DOMAINS PROTEIN 1 (FHL-1) (SKELETAL	0.10735182	1.087518651
Bt.23405.1.S1_at	C6ORF49-LIKE PROTEIN	0.200754646	1.126798477
Bt.2342.1.S1_at	,GB:CK946927 /DB_XREF=GI:45461307 /DB_XREF=4071584 /CLONE=10BOV1_H09	-0.12201649	0.912598486
Bt.23465.1.S1_at	,GB:CF763275 /DB_XREF=GI:37712493 /DB_XREF=CES006079 /CLONE=CCL006079 /TID=BT.23465.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.23465	-4.62835729	2.367967216
Bt.23488.1.S1_at	SIMILAR TO PROPERDIN P FACTOR, COMPLEMENT	0.281724387	1.265491518
Bt.23490.1.S1_at	SIMILAR TO RIBOSOMAL PROTEIN L30	0.024568557	1.005270664
Bt.23496.1.S1_at	HYPOTHETICAL PROTEIN	0.094989318	1.026097736
Bt.23512.1.S1_at	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 12	0.143513156	1.059990213
Bt.23522.1.S1_at	INTEGRAL MEMBRANE PROTEIN 2B	0.137752846	1.140435224
Bt.23527.1.S1_at	HYPOTHETICAL PROTEIN	0.327359872	1.155633502
Bt.23529.1.S1_at	,GB:CK728106 /DB_XREF=GI:42581620 /DB_XREF=BEND_0A02-006-D02 /TID=BT.23529.1 /CNT=9 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.23529	0.077661731	1.0447988

Bt.23542.1.S1_at	,GB:BI773839 /DB_XREF=GI:15774816 /DB_XREF=465552 /TID=BT.23542.1 /CNT=21 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.23542 /UG_TITLE=TRANSCRIBED	0.215623484	1.10957321
Bt.23548.1.S1_at	HYPOTHETICAL PROTEIN	0.02505141	1.006869748
Bt.23550.1.S1_at	PUTATIVE DIACYLGLYCEROL O-ACYLTRANSFERASE	-0.15790448	0.898839661
Bt.23580.1.S1_at	,GB:CF764503 /DB_XREF=GI:37713722 /DB_XREF=CES003771 /CLONE=CCL003771 /TID=BT.23580.1 /CNT=3 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.23580	-4.16185932	0.556459672
Bt.23589.2.S1_at	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR, TYPE 1	-0.14739251	0.816520623
Bt.23590.1.S1_at	SIMILAR TO DNA-DIRECTED RNA POLYMERASE I 16 KDA POLYPEPTIDE (RPA16)	0.176132391	1.107998332
Bt.23603.1.S1_a_at	F-BOX PROTEIN 9	0.090893336	1.085449043
Bt.23603.2.S1_a_at	F-BOX PROTEIN 9	0.248410027	1.166616808
Bt.23603.3.S1_at	F-BOX PROTEIN 9	0.149958198	1.062377051
Bt.23619.1.S1_a_at	,GB:CK948126 /DB_XREF=GI:45462506 /DB_XREF=4072946 /CLONE=10BOV24_A03 /TID=BT.23619.1 /CNT=4 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.23619	0.090300942	1.205763878
Bt.2366.1.S1_at	SIMILAR TO VESICLE-ASSOCIATED MEMBRANE PROTEIN 8	0.250869699	1.201742428
Bt.23669.1.A1_at	,GB:BF601395 /DB_XREF=GI:11698617 /DB_XREF=266363 /TID=BT.23669.1 /CNT=5	0.346638296	1.280338073
Bt.2404.1.S1_at	SIMILAR TO MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 INTERACTING	0.170097916	1.070055282
Bt.24074.1.A1_at	SIMILAR TO PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II ALPHA (PIP5KII-ALPHA) (1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE)	0.096979273	1.01560096
Bt.24112.1.A1_at	,GB:CK846762 /DB_XREF=GI:45207596 /DB_XREF=969305 /TID=BT.24112.1 /CNT=3	0.69539122	1.504043674
Bt.2416.1.S1_at	TESTIS ENHANCED GENE TRANSCRIPT (BAX INHIBITOR 1)	0.076705762	1.04217496
Bt.24217.1.S1_at	NUCLEAR FACTOR (ERYTHROID-DERIVED 2), 45KDA	0.169425632	1.149469476
Bt.24220.1.S1_at	MYOTROPHIN	-0.07197231	0.93304176
Bt.24238.1.A1_at	,GB:CK947002 /DB_XREF=GI:45461382 /DB_XREF=4071698 /CLONE=10BOV1_M03 /TID=BT.24238.1 /CNT=17 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.24238	0.240852245	1.055437794
Bt.2424.1.S1_at	DIHYDROPYRIMIDINE DEHYDROGENASE	0.396871594	1.184801318
Bt.24417.1.A1_at	,GB:BI849511 /DB_XREF=GI:15962030 /DB_XREF=476924 /TID=BT.24417.1 /CNT=5	0.081379494	1.054054124
Bt.24417.2.S1_at	,GB:CF930364 /DB_XREF=GI:38279532 /DB_XREF=CF-03-R-K24 /TID=BT.24417.2	0.117881547	1.022076975
Bt.24449.2.S1_at	,GB:BF651419 /DB_XREF=GI:11916549 /DB_XREF=274202 /TID=BT.24449.2 /CNT=2 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.24449 /UG_TITLE=TRANSCRIBED	-1.88826514	0.802450377
Bt.24480.1.S1_at	,GB:CK777500 /DB_XREF=GI:42729813 /DB_XREF=964625 /TID=BT.24480.1 /CNT=7	-0.29284435	0.829701565
Bt.2450.1.S1_at	ATPASE, H+ TRANSPORTING, LYSOSOMAL 9KDA, V0 SUBUNIT E	0.193788758	1.117605589
Bt.24522.2.S1_at	SIMILAR TO KRUPPEL-LIKE FACTOR 6	-0.36806723	0.803521844
Bt.24522.3.S1_a_at	SIMILAR TO KRUPPEL-LIKE FACTOR 6	-0.38343636	0.734010935
Bt.2466.1.S1_at	,GB:BM434219 /DB_XREF=GI:18455941 /DB_XREF=1RT05A08 /TID=BT.2466.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.2466 /UG_TITLE=TRANSCRIBED	0.293349169	1.246544304
Bt.24665.1.S1_at	,GB:BI681515 /DB_XREF=GI:15634436 /DB_XREF=460928 /TID=BT.24665.1 /CNT=6	-0.1479383	0.947137461
Bt.24674.1.A1_s_at	LYSOSOMAL-ASSOCIATED MEMBRANE PROTEIN 1	0.118046819	1.088393858

Bt.247.1.S1_at	ANNEXIN A5	0.196774277	1.166796214
Bt.2474.1.S1_at	FUSION, DERIVED FROM T(12;16) MALIGNANT LIPOSARCOMA	-0.10581389	0.956967032
Bt.24750.2.S1_a_at	ENDOTHELIN CONVERTING ENZYME 1	0.137197725	1.094349645
Bt.24760.1.S1_at	,GB:CK770702 /DB_XREF=GI:42724796 /DB_XREF=958908 /TID=BT.24760.1 /CNT=14 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.24760 /UG_TITLE=TRANSCRIBED	0.342788147	0.83811548
Bt.24795.1.A1_at	SIMILAR TO INTERFERON-INDUCED PROTEIN WITH TETRATRICOPEPTIDE	0.639579217	1.712741734
Bt.24884.2.S1_at	SIMILAR TO GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR	0.467110763	1.169375745
Bt.24986.1.A1_at	,GB:CK727311 /DB_XREF=GI:42580825 /DB_XREF=BEND_0A01-005-C06	-0.29022269	0.811175879
Bt.25072.1.S1_at	,GB:CK979098 /DB_XREF=GI:45497078 /DB_XREF=4110471 /CLONE=9BOV39_D14 /TID=BT.25072.1 /CNT=18 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.25072 /UG_TITLE=TRANSCRIBED SEQUENCE WITH STRONG SIMILARITY TO PROTEIN	0.380526161	1.38231033
Bt.25102.1.S1_a_at	,GB:CK772143 /DB_XREF=GI:42726286 /DB_XREF=960585 /TID=BT.25102.1 /CNT=13 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.25102 /UG_TITLE=TRANSCRIBED	-0.07719287	1.020755483
Bt.2515.1.S1_at	H2A HISTONE FAMILY, MEMBER Z	0.185904618	1.181636285
Bt.2520.1.S1_at	,GB:CB460448 /DB_XREF=GI:29266832 /DB_XREF=720334 /TID=BT.2520.1 /CNT=15	-0.1002324	0.914984784
Bt.2529.1.S1_at	METALLOTHIONEIN-2	-0.95145611	0.704126857
Bt.25420.1.A1_at	,GB:CK769833 /DB_XREF=GI:42723927 /DB_XREF=957937 /TID=BT.25420.1 /CNT=3	-0.22774235	0.897361031
Bt.2556.1.S1_at	HYDROXYPROSTAGLANDIN DEHYDROGENASE 15-(NAD)	-0.82458191	0.808959646
Bt.2562.1.S1_at	GLUCOSE REGULATED PROTEIN 58KD	0.046822624	0.974445154
Bt.2573.1.S1_at	CD9 ANTIGEN (P24)	0.163386027	1.140220554
Bt.2575.1.S1_at	PROTEASOME ACTIVATOR 28 ALPHA SUBUNIT	0.053131611	1.018134605
Bt.25887.1.A1_at	,GB:CB426311 /DB_XREF=GI:29198229 /DB_XREF=601486 /TID=BT.25887.1 /CNT=4 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.25887 /UG_TITLE=TRANSCRIBED	-0.21022752	0.810971386
Bt.2590.1.A1_at	,GB:CK970235 /DB_XREF=GI:45488209 /DB_XREF=4086019 /CLONE=9BOV31_I20 /TID=BT.2590.1 /CNT=12 /FEA=EST /TIER=STACK /STK=6 /UG=BT.2590	-0.0671036	0.955417257
Bt.2592.1.A1_x_at	MHC CLASS I ANTIGEN	0.183307564	1.101309057
Bt.25929.1.A1_at	MITOCHONDRIAL NADH:UBIQUINONE OXIDOREDUCTASE B14.7	-1.70518294	0.982344495
Bt.2600.1.A1_at	,GB:AW267109 /DB_XREF=GI:9257594 /DB_XREF=0601-3 /TID=BT.2600.1 /CNT=3	0.269493281	1.168326223
Bt.2612.1.S1_at	TCTEL1 PROTEIN	0.219169043	1.245129325
Bt.26122.2.S1_at	SIMILAR TO UBIQUITOUSLY-EXPRESSED TRANSCRIPT ISOFORM 1	0.183045833	1.119824584
Bt.26149.1.A1_at	,GB:CK778525 /DB_XREF=GI:42730838 /DB_XREF=965687 /TID=BT.26149.1 /CNT=2	0.544965731	1.185374249
Bt.26155.1.A1_at	,GB:CK775223 /DB_XREF=GI:42731473 /DB_XREF=966346 /TID=BT.26155.1 /CNT=2 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.26155 /UG_TITLE=TRANSCRIBED	0.699522396	1.533865697
Bt.2625.1.S1_at	HYPOTHETICAL LOC540543	-0.19861231	0.838823184
Bt.2641.2.S1_at	,GB:CK946480 /DB_XREF=GI:45460860 /DB_XREF=4071041 /CLONE=10BOV19_A18	0.084953598	1.073756029
Bt.265.1.S1_at	UBIQUINOL-CYTOCHROME C REDUCTASE, RIESKE IRON-SULFUR POLYPEPTIDE 1	0.138965243	1.096025257
Bt.26533.1.S1_at	,GB:BF654164 /DB_XREF=GI:11919296 /DB_XREF=278223 /TID=BT.26533.1 /CNT=6	0.619176876	1.445973241

Bt.26537.1.S1_at	LEUCINE RICH REPEAT CONTAINING 33	0.160248193	1.085494508
Bt.2657.1.S1_a_at	SIMILAR TO UNC-112 RELATED PROTEIN 2 SHORT FORM	0.307317486	1.260680467
Bt.2663.1.A1_at	,GB:CK977831 /DB_XREF=GI:45495805 /DB_XREF=4109160 /CLONE=9BOV37_M23 /TID=BT.2663.1 /CNT=4 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.2663	0.442373291	1.302167293
Bt.26636.2.S1_at	NATURAL KILLER CELL GROUP 7 SEQUENCE	-1.95300764	0.675499677
Bt.26700.1.S1_at	HISTAMINE N-METHYLTRANSFERASE	0.477157755	1.27382064
Bt.26796.1.S1_at	,GB:CK776010 /DB_XREF=GI:42732260 /DB_XREF=967152 /TID=BT.26796.1 /CNT=17 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.26796 /UG_TITLE=TRANSCRIBED	-0.47548437	0.660220215
Bt.26825.1.A1_at	SIMILAR TO 5-3 EXORIBONUCLEASE 2	0.504728534	1.45385885
Bt.2686.1.S1_at	SIMILAR TO 40S RIBOSOMAL PROTEIN S16	0.066248597	1.039550457
Bt.269.1.S1_at	ATPASE, CA++ TRANSPORTING, TYPE 2C, MEMBER 1	0.20163204	1.128530297
Bt.26983.1.S1_at	,GB:CK776788 /DB_XREF=GI:42733038 /DB_XREF=968151 /TID=BT.26983.1 /CNT=15 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.26983 /UG_TITLE=TRANSCRIBED	0.226654744	1.17255883
Bt.27061.1.S1_at	,GB:CK770721 /DB_XREF=GI:42724815 /DB_XREF=958929 /TID=BT.27061.1 /CNT=16 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.27061 /UG_TITLE=TRANSCRIBED	-0.1876999	0.843174323
Bt.27118.1.A1_at	SIMILAR TO TEMPORARILY ASSIGNED GENE NAME FAMILY MEMBER (TAG-58)	-0.07867493	0.950204954
Bt.27261.1.S1_at	,GB:CK775944 /DB_XREF=GI:42732194 /DB_XREF=967085 /TID=BT.27261.1 /CNT=10 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.27261 /UG_TITLE=TRANSCRIBED	1.19304645	2.233136708
Bt.27261.2.S1_at	,GB:BM256142 /DB_XREF=GI:17891741 /DB_XREF=518435 /TID=BT.27261.2 /CNT=2 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.27261 /UG_TITLE=TRANSCRIBED	1.298188983	2.355362887
Bt.2728.1.S1_at	,GB:AU098038 /DB_XREF=GI:9636226 /DB_XREF=AU098038 /CLONE=CLN330 /TID=BT.2728.1 /CNT=13 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.2728	-0.21966439	0.848768665
Bt.27283.1.S1_x_at	BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BL3-7 PRECURSOR	0.054086518	1.013378787
Bt.27285.1.S1_at	,GB:CF930747 /DB_XREF=GI:38280313 /DB_XREF=CF--05-R-A05 /TID=BT.27285.1	0.734247306	2.065508869
Bt.27288.1.S1_at	,GB:CK834383 /DB_XREF=GI:45064795 /DB_XREF=4058697 /CLONE=8BOV_2J23	0.343425554	1.293884535
Bt.2729.1.S1_at	SIMILAR TO ADAPTER-RELATED PROTEIN COMPLEX 3 SIGMA 1 SUBUNIT (SIGMA-	0.219371779	1.228963252
Bt.27358.1.S1_at	,GB:BM032243 /DB_XREF=GI:16745813 /DB_XREF=497875 /TID=BT.27358.1 /CNT=4 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.27358 /UG_TITLE=TRANSCRIBED	0.424231331	1.39757687
Bt.27358.2.S1_at	,GB:CK847463 /DB_XREF=GI:45208986 /DB_XREF=970102 /TID=BT.27358.2 /CNT=2 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.27358 /UG_TITLE=TRANSCRIBED	0.225693433	1.166580041
Bt.27364.1.S1_at	,GB:CK849718 /DB_XREF=GI:45213200 /DB_XREF=972817 /TID=BT.27364.1 /CNT=9	-0.51580042	0.676440778
Bt.27382.1.A1_at	,GB:CK847972 /DB_XREF=GI:45209945 /DB_XREF=970670 /TID=BT.27382.1 /CNT=2 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.27382 /UG_TITLE=TRANSCRIBED	-1.26216583	0.96815905
Bt.27410.1.S1_at	,GB:CK846729 /DB_XREF=GI:45207530 /DB_XREF=969265 /TID=BT.27410.1 /CNT=7 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.27410 /UG_TITLE=TRANSCRIBED	-0.21816696	0.875626495
Bt.275.1.S1_at	NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-	0.211486235	1.150042126
Bt.27675.1.A1_at	V-KIT HARDY-ZUCKERMAN 4 FELINE SARCOMA VIRAL ONCOGENE HOMOLOG	-1.37676604	0.720231764

Bt.27696.1.A1_at	SH3 DOMAIN BINDING GLUTAMIC ACID-RICH PROTEIN LIKE	-0.22032742	0.859020516
Bt.27723.2.A1_a_at	,GB:CK848566 /DB_XREF=GI:45211050 /DB_XREF=971348 /TID=BT.27723.2 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.27723 /UG_TITLE=TRANSCRIBED	-0.7594908	0.74285721
Bt.27760.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, A	0.648774	2.11982815
Bt.27822.1.A1_at	,GB:CK847894 /DB_XREF=GI:45209789 /DB_XREF=970583 /TID=BT.27822.1 /CNT=3 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.27822 /UG_TITLE=TRANSCRIBED	0.365569136	1.185880467
Bt.27822.2.S1_at	,GB:CB429221 /DB_XREF=GI:29204054 /DB_XREF=605022 /TID=BT.27822.2 /CNT=9 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.27822 /UG_TITLE=TRANSCRIBED	0.444752788	1.272799605
Bt.27886.1.S1_s_at	,GB:CK848230 /DB_XREF=GI:45210422 /DB_XREF=970960 /TID=BT.27886.1 /CNT=17 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.27886 /UG_TITLE=TRANSCRIBED	0.324144708	1.193553553
Bt.27920.1.A1_at	,GB:CK848117 /DB_XREF=GI:45210211 /DB_XREF=970831 /TID=BT.27920.1 /CNT=3	0.582755845	1.550775057
Bt.27926.1.S1_at	,GB:CB170237 /DB_XREF=GI:28156365 /DB_XREF=CEY603161530.R1 /TID=BT.27926.1 /CNT=11 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.27926	0.179200927	1.019860443
Bt.27975.1.S1_s_at	CALMODULIN 2	-0.07003481	0.931180897
Bt.28004.2.S1_a_at	SIMILAR TO T-CELL RECEPTOR ALPHA CHAIN V REGION HPB-MLT PRECURSOR	-0.45224017	0.585577719
Bt.28009.1.S1_at	KERATIN 8	-0.15208387	0.894941737
Bt.28011.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DRB3	0.041066819	0.947772274
Bt.28047.1.A1_at	,GB:CK976492 /DB_XREF=GI:45494466 /DB_XREF=4107484 /CLONE=9BOV34_H03 /TID=BT.28047.1 /CNT=2 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.28047	0.988014582	1.583687277
Bt.28123.1.S1_at	,GB:CK953446 /DB_XREF=GI:45467826 /DB_XREF=4093202 /CLONE=10BOV31_E01 /TID=BT.28123.1 /CNT=7 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.28123	-0.30082065	0.795014668
Bt.2814.1.S1_at	TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION	0.090398877	1.087770354
Bt.2816.1.S1_at	F1FO-ATP SYNTHASE COMPLEX FO MEMBRANE DOMAIN G SUBUNIT	0.10216723	1.054326886
Bt.28164.1.A1_at	,GB:CK957681 /DB_XREF=GI:45472061 /DB_XREF=4098223 /CLONE=10BOV4_F06	0.269396659	1.207484042
Bt.282.1.S1_at	VOLTAGE-DEPENDENT ANION CHANNEL 3	0.197753801	1.102751903
Bt.28207.1.S1_at	SIMILAR TO RING FINGER PROTEIN 19	0.167424705	1.129880922
Bt.2821.1.S1_at	SIMILAR TO PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE 7	0.203804068	1.123888023
Bt.2822.1.S1_at	SIMILAR TO 60S RIBOSOMAL PROTEIN L8	0.022443446	1.026227399
Bt.28225.1.A1_at	SIMILAR TO SAM-DOMAIN PROTEIN SAMSN-1 (SAM DOMAIN, SH3 DOMAIN AND NUCLEAR LOCALISATION SIGNALS PROTEIN 1) (SH3-SAM ADAPTOR PROTEIN)	-0.25478232	0.793565512
Bt.28225.2.S1_at	SIMILAR TO SAM-DOMAIN PROTEIN SAMSN-1 (SAM DOMAIN, SH3 DOMAIN AND NUCLEAR LOCALISATION SIGNALS PROTEIN 1) (SH3-SAM ADAPTOR PROTEIN)	-0.31630804	0.773051432
Bt.28226.2.S1_at	SIMILAR TO TRIAD3 PROTEIN ISOFORM A	-1.32411036	0.884133558
Bt.28226.3.A1_s_at	SIMILAR TO TRIAD3 PROTEIN ISOFORM A	0.187229693	1.110402522
Bt.28279.1.S1_at	,GB:CK952708 /DB_XREF=GI:45467088 /DB_XREF=4092065 /CLONE=10BOV30_E16 /TID=BT.28279.1 /CNT=21 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.28279	-0.11026955	0.879822563
Bt.28383.1.S1_at	GRANULYSIN	-0.18109385	0.775937768

Bt.28390.1.S1_at	MYOSIN, HEAVY POLYPEPTIDE 7, CARDIAC MUSCLE, BETA	-0.15513751	0.883915919
Bt.2841.1.S1_at	TRYPTOPHANYL-TRNA SYNTHETASE	0.107363196	0.958121216
Bt.2841.2.S1_a_at	TRYPTOPHANYL-TRNA SYNTHETASE	0.151693484	0.987866787
Bt.2844.1.S1_at	SIMILAR TO N-ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (CMP-N-	0.333062015	1.213382
Bt.28447.1.S1_x_at	IGM	0.236763187	1.128063602
Bt.28449.1.S1_s_at	SIMILAR TO IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM	0.237119023	1.144216559
Bt.2847.1.S1_a_at	MYOSIN, LIGHT PEPTIDE 6, ALKALI, SMOOTH MUSCLE AND NON-MUSCLE	0.142322842	1.103197145
Bt.28518.1.S1_at	PANCREATIC TRYPSIN INHIBITOR	0.4308993	1.523630959
Bt.28518.1.S1_s_at	SPLEEN TRYPSIN INHIBITOR	0.156886935	1.124346429
Bt.28561.1.S1_at	,GB:CK962924 /DB_XREF=GI:45480898 /DB_XREF=4077468 /CLONE=9BOV12_E13	-0.34157806	0.795893367
Bt.28624.1.S1_at	,GB:CK946867 /DB_XREF=GI:45461247 /DB_XREF=4071708 /CLONE=10BOV1_M13	0.154169617	1.142279987
Bt.28638.1.A1_at	,GB:CK977811 /DB_XREF=GI:45495785 /DB_XREF=4108932 /CLONE=9BOV37_D11	1.040506123	2.749424335
Bt.28662.1.A1_at	,GB:CK975790 /DB_XREF=GI:45493764 /DB_XREF=4106820 /CLONE=9BOV33_L11	0.682805488	1.749295079
Bt.287.1.S1_at	RIBONUCLEASE K6	0.106692895	1.063296624
Bt.2873.1.S1_at	SIMILAR TO TRANSMEMBRANE PROTEIN 14C	0.109210772	1.07833991
Bt.28732.1.S1_at	T-CELL RECEPTOR DELTA CHAIN	0.133576192	0.896836002
Bt.28732.1.S1_s_at	T-CELL RECEPTOR DELTA CHAIN	-0.12460637	0.933670362
Bt.28761.1.A1_s_at	SULFIDE DEHYDROGENASE LIKE	0.168245065	1.037449287
Bt.2877.1.S1_at	SIMILAR TO GLUTAREDOXIN-1 (THIOLTRANSFERASE-1) (TTASE-1)	0.193887737	1.135921836
Bt.2878.1.S1_at	POLYUBIQUITIN	-0.05751559	0.958720467
Bt.2878.1.S1_x_at	POLYUBIQUITIN	-0.02527385	0.984487179
Bt.2888.1.S1_at	OSTEOCLAST STIMULATING FACTOR 1	0.099515777	1.063465215
Bt.28911.1.S1_at	ART5 PROTEIN	0.981169684	1.542632206
Bt.28945.1.A1_at	,GB:CK947597 /DB_XREF=GI:45461977 /DB_XREF=4072558 /CLONE=10BOV23_P23	-0.44278379	0.617910995
Bt.29002.1.A1_at	,GB:CK950115 /DB_XREF=GI:45464495 /DB_XREF=4075162 /CLONE=10BOV2_E11	-0.38444287	0.680193314
Bt.29423.1.A1_at	,GB:CK971488 /DB_XREF=GI:45489462 /DB_XREF=4087550 /CLONE=9BOV4_I15 /TID=BT.29423.1 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.29423	0.736020145	1.776625422
Bt.2956.1.A1_at	SIMILAR TO COILED-COIL DOMAIN CONTAINING 23	0.293129299	1.245443093
Bt.29689.1.S1_s_at	T-CELL RECEPTOR DELTA CHAIN	-0.09189957	0.981530779
Bt.29777.1.S1_x_at	,GB:AJ012799.1 /DB_XREF=GI:3892093 /TID=BT.29777.1 /CNT=3 /FEA=MRNA /TIER=CONSEND /STK=0 /UG=BT.29777 /UG_TITLE=MRNA FOR GLUTATHIONE-S-TRANSFERASE (GST) SPECIFIC IMMUNOGLOBULIN LIGHT CHAIN VARIABLE	0.616597665	1.383594198
Bt.2981.1.S1_at	SIMILAR TO PROTEIN KINASE C RECEPTOR	-0.04201058	0.950866576
Bt.29815.1.S1_x_at	MHC CLASS I HEAVY CHAIN	0.572000911	1.577657356
Bt.29821.1.S1_at	MHC CLASS I HEAVY CHAIN	0.66408327	1.851636973
Bt.29823.1.S1_x_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, B	-0.07275	0.565575511
Bt.29824.1.S1_s_at	MHC CLASS I MOLECULE PRECURSOR	1.482538697	198.6183417

Bt.29851.1.S1_at	,GB:CK945876 /DB_XREF=GI:45460256 /DB_XREF=4070333 /CLONE=10BOV18_D06 /TID=BT.29851.1 /CNT=7 /FEA=MRNA /TIER=CONSEND /STK=0 /UG=BT.29851	-0.02802303	1.204886865
Bt.2988.1.S1_at	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), GAMMA 11	0.170273413	1.173544032
Bt.3001.1.S1_at	CHROMOSOME 14 OPEN READING FRAME 147	0.540991458	1.392633757
Bt.3005.1.S1_at	LACTATE DEHYDROGENASE B	0.090377015	1.007805312
Bt.3036.1.S1_at	HYPOTHETICAL PROTEIN	0.039835549	1.029544454
Bt.3046.2.S1_at	FICOLIN B	0.149600361	1.084700048
Bt.3079.1.S1_at	SIMILAR TO ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT ISOFORM B	0.114613198	1.046594992
Bt.3091.1.S1_at	RIBOSOMAL PROTEIN L23	0.024918403	1.011970133
Bt.3162.1.S1_at	PROCOLLAGEN-PROLINE, 2-OXOGLUTARATE 4-DIOXYGENASE	0.220050666	1.180656557
Bt.3193.1.A1_at	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 6	0.235273074	1.16252975
Bt.3230.1.A1_at	AMINOLEVULINATE, DELTA-, SYNTHASE 2 (SIDEROBLASTIC/HYPOCHROMIC	0.991653732	1.706147945
Bt.3240.1.S1_at	,GB:CK982493 /DB_XREF=GI:45500473 /DB_XREF=4115170 /CLONE=9BOV45_O09 /TID=BT.3240.1 /CNT=36 /FEA=EST /TIER=STACK /STK=9 /UG=BT.3240	0.204774784	1.125773786
Bt.3264.1.S1_at	SIMILAR TO SET PROTEIN (PHOSPHATASE 2A INHIBITOR I2PP2A) (I-2PP2A) (TEMPLATE ACTIVATING FACTOR I) (TAF-I) (HLA-DR ASSOCIATED PROTEIN II)	-0.14746586	1.023211537
Bt.3288.1.A1_at	HYPOTHETICAL LOC514374	0.158532286	1.085463632
Bt.3311.1.S1_at	TISSUE INHIBITOR OF METTALOPROTEINASE 2	-0.3018194	0.795009113
Bt.3312.1.S1_at	,GB:AF004361 /DB_XREF=GI:2653768 /DB_XREF=AF004361 /TID=BT.3312.1 /CNT=11 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.3312 /UG_TITLE=TRANSCRIBED	0.405214055	1.370603004
Bt.3352.1.S1_at	AGOUTI PROTEIN	0.58251702	1.585297895
Bt.3404.1.S1_at	RIBOSOMAL PROTEIN L36A	0.098117247	1.017893862
Bt.344.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DM ALPHA-CHAIN, EXPRESSED	0.12715348	1.098275724
Bt.3487.1.S1_at	TRIOSEPHOSPHATE ISOMERASE	0.255853079	1.170715086
Bt.350.1.S1_at	MHC CLASS II	-0.91597399	0.120277646
Bt.350.1.S1_s_at	MHC CLASS II ANTIGEN	-0.0718901	0.857884837
Bt.350.1.S1_x_at	MHC CLASS II	-0.87476384	0.132605481
Bt.351.1.S1_at	CORONIN, ACTIN BINDING PROTEIN, 1A	0.034750948	1.010476969
Bt.3537.1.S1_at	SULFOTRANSFERASE FAMILY, CYTOSOLIC, 1A, PHENOL-PREFERRING, MEMBER 1	0.209858345	1.108527962
Bt.3562.1.S1_at	LOW DENSITY LIPOPROTEIN RECEPTOR	0.468404968	1.278378004
Bt.3567.1.S1_at	UDP-GLUCOSE PYROPHOSPHORYLASE 2	0.125396475	1.039437136
Bt.357.1.S1_at	S100 CALCIUM BINDING PROTEIN A12 (CALGRANULIN C)	0.157831511	1.127069477
Bt.3573.1.S2_at	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-0.06477897	0.921757996
Bt.3624.1.S1_at	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE, 10	0.160316792	1.154590307
Bt.3626.1.S1_at	RIBOSOMAL PROTEIN S11	-0.03201443	0.997215233
Bt.367.1.S1_at	OXIDISED LOW DENSITY LIPOPROTEIN (LECTIN-LIKE) RECEPTOR 1	1.308169403	1.728751566
Bt.3694.1.S1_at	ORNITHINE DECARBOXYLASE ANTIZYME 1-LIKE	0.0458326	1.030068333

Bt.3729.1.S1_at	SIMILAR TO S-PHASE KINASE-ASSOCIATED PROTEIN 1A ISOFORM B	0.06637654	1.11713607
Bt.3734.1.A1_at	,GB:CB430832 /DB_XREF=GI:29207272 /DB_XREF=606752 /TID=BT.3734.1 /CNT=8 /FEA=EST /TIER=STACK /STK=6 /UG=BT.3734 /UG_TITLE=TRANSCRIBED	0.207297449	1.21197647
Bt.3742.1.S1_at	SIMILAR TO SELENOPROTEIN K	0.171927764	1.076333042
Bt.3750.1.S1_at	S100 CALCIUM BINDING PROTEIN A11 (CALGIZZARIN)	0.132340011	1.136729024
Bt.380.1.S1_at	ATPASE INHIBITORY FACTOR 1	0.215137488	1.142611165
Bt.3800.1.S1_at	PURINE NUCLEOSIDE PHOSPHORYLASE	0.477127504	1.35623224
Bt.3805.1.S1_at	MHC CLASS I JSP.1	-0.25254616	0.840381101
Bt.3809.1.S1_at	LACTATE DEHYDROGENASE A	0.187842464	1.09996454
Bt.3839.1.S1_at	RIBOSOMAL PROTEIN L10	0.031224018	1.025315503
Bt.3843.1.S1_at	IMMUNOGLOBULIN J CHAIN	0.184049718	1.187330173
Bt.3866.1.S1_at	DAZ ASSOCIATED PROTEIN 2	0.051710309	1.063246466
Bt.3867.1.S1_at	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT B,	0.087292434	1.040637861
Bt.3890.1.S1_at	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 1A	0.209129781	1.271879031
Bt.391.2.S1_at	PROTEIN KINASE, CAMP-DEPENDENT, CATALYTIC, BETA	-0.1612426	0.919977431
Bt.3921.1.S1_at	SIMILAR TO RIBOSOMAL PROTEIN S10	-0.05006385	0.96625805
Bt.393.1.S1_at	CATHEPSIN B	0.197223906	1.129967196
Bt.393.1.S2_at	CATHEPSIN B	0.111049372	1.056444467
Bt.3988.1.S1_at	BENZODIAZEPINE RECEPTOR (PERIPHERAL)	0.19151759	1.19837799
Bt.400.1.S1_at	CYTOCHROME C OXIDASE SUBUNIT VIIB	0.127615997	1.029609347
Bt.4012.1.S1_at	SIMILAR TO RIBOSOMAL PROTEIN L18A	0.016800066	1.004177072
Bt.4020.1.S1_at	RNF10 PROTEIN	0.171587795	1.119695161
Bt.4053.1.S1_at	THROMBOXANE A2 RECEPTOR	-0.54696247	0.699115055
Bt.409.1.S1_at	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), GAMMA 5	0.123349439	1.128351438
Bt.4093.1.S1_at	BILIVERDIN REDUCTASE B (FLAVIN REDUCTASE (NADPH))	0.393844577	1.195348384
Bt.4095.1.A1_at	,GB:CB466670 /DB_XREF=GI:29273055 /DB_XREF=732218 /TID=BT.4095.1 /CNT=6	-0.35478318	0.783297061
Bt.4141.1.S1_at	COATOMER PROTEIN COMPLEX, SUBUNIT EPSILON	0.149900719	1.098327601
Bt.4150.1.S1_at	CATENIN, BETA LIKE 1	0.19651139	1.117316019
Bt.4184.1.S2_at	HYPOXIA-INDUCIBLE FACTOR 1, ALPHA SUBUNIT (BASIC HELIX-LOOP-HELIX	-0.1400178	0.858967185
Bt.4205.1.S1_at	GLUTATHIONE PEROXIDASE 4 (PHOSPHOLIPID HYDROPEROXIDASE)	0.263374384	1.200109164
Bt.4208.1.S1_at	INTERLEUKIN 8 RECEPTOR, BETA	0.16870877	1.248068426
Bt.4209.2.S1_a_at	COMPLEMENT COMPONENT 3	0.468637966	1.29045095
Bt.4213.1.S1_at	BASIC TRANSCRIPTION FACTOR 3	0.066695467	1.014193415
Bt.4241.1.S1_at	RIBOSOMAL PROTEIN S14	0.019045234	1.010016695
Bt.4242.1.A1_at	SIMILAR TO N-TERMINAL ASN AMIDASE	0.148139175	1.114472518
Bt.4310.1.A1_at	SIMILAR TO REGULATOR OF G-PROTEIN SIGNALING 1 (RGS1) (EARLY RESPONSE	-1.20320515	0.441641803
Bt.4314.1.S1_at	ANNEXIN A2	0.274701785	1.235134569

Bt.4317.1.S1_at	GLUTATHIONE PEROXIDASE 1	0.113524741	1.059105747
Bt.4323.1.S1_at	ARCHAEMETZINCINS-2	0.212940887	1.149050645
Bt.4323.2.S1_a_at	ARCHAEMETZINCINS-2	0.25392294	1.136071003
Bt.4336.1.S1_at	D COMPONENT OF COMPLEMENT (ADIPSIN)	0.170742354	1.074939412
Bt.435.1.S1_at	TISSUE INHIBITOR OF METTALOPROTEINASE 2	0.208860013	1.231144788
Bt.4355.1.S1_at	PEROXIREDOXIN 5	0.264780235	1.182896905
Bt.4357.1.S1_at	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 2	0.783173798	1.899907115
Bt.4363.1.S1_at	,GB:AW652347 /DB_XREF=GI:7418173 /DB_XREF=100288 /TID=BT.4363.1 /CNT=9	-0.88986356	0.81959729
Bt.4388.1.S1_at	,GB:AW482029 /DB_XREF=GI:7052135 /DB_XREF=40100 /TID=BT.4388.1 /CNT=26 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.4388 /UG_TITLE=TRANSCRIBED	-0.10826785	0.863986973
Bt.4389.1.S1_at	SPLEEN TRYPSIN INHIBITOR	0.227268476	1.163034794
Bt.4404.1.A1_at	PANCREATIC ANIONIC TRYPSINOGEN	-0.09914459	1.256508468
Bt.4406.1.S1_at	SIMILAR TO 60S RIBOSOMAL PROTEIN L35	0.013213472	1.002065709
Bt.4410.1.S1_at	HYPOTHETICAL LOC506986	0.122517015	1.121706185
Bt.4415.1.S1_at	HEAT SHOCK 27KDA PROTEIN 1	0.160521146	1.127011034
Bt.4442.1.S1_at	ATP6IP1 PROTEIN	0.171104818	1.150268317
Bt.4476.1.S1_at	PEROXIREDOXIN 3	-0.11900085	0.900713137
Bt.4515.1.S1_at	SIMILAR TO CHROMOSOME 3 OPEN READING FRAME 10	0.233739008	1.1193104
Bt.4540.1.S1_at	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F1 COMPLEX, GAMMA	0.099687683	1.05595988
Bt.4574.1.S1_at	HYPOTHETICAL PROTEIN	0.156554498	1.123448362
Bt.4594.1.S1_at	MHC CLASS II (BOLA-DQB) PRECURSOR	-0.18236435	0.932570134
Bt.4606.1.S1_at	SIMILAR TO KRUPPEL-LIKE FACTOR 6	-0.51421471	0.680447873
Bt.4606.2.S1_at	SIMILAR TO KRUPPEL-LIKE FACTOR 6	-0.35284825	0.769182213
Bt.4618.1.S1_at	FINKEL-BISKIS-REILLY MURINE SARCOMA VIRUS (FBR-MUSV) UBIQUITOUSLY	0.031044282	1.018966549
Bt.4620.1.S1_at	POLY(RC) BINDING PROTEIN 1	0.044729752	1.055198609
Bt.4635.1.S1_at	CALPONIN 2	0.10600571	1.064940894
Bt.4637.1.A1_a_at	CYTOCHROME C OXIDASE SUBUNIT VIII, HEART	0.122742028	1.048181781
Bt.4659.1.S1_at	,GB:CK953255 /DB_XREF=GI:45467635 /DB_XREF=4092864 /CLONE=10BOV31_F23 /TID=BT.4659.1 /CNT=59 /FEA=EST /TIER=STACK /STK=21 /UG=BT.4659	0.10773232	0.999486268
Bt.4670.1.S1_at	,GB:CK774445 /DB_XREF=GI:42728588 /DB_XREF=963207 /TID=BT.4670.1 /CNT=30 /FEA=EST /TIER=CONSEND /STK=5 /UG=BT.4670 /UG_TITLE=TRANSCRIBED	0.20390307	1.146674504
Bt.4675.1.S1_a_at	MYXOVIRUS (INFLUENZA) RESISTANCE 1, (MURINE HOMOLOG)	-0.28809669	0.814256073
Bt.469.1.A1_at	TRANSFORMING GROWTH FACTOR, BETA 1 (CAMURATI-ENGELMANN DISEASE)	0.336994454	1.307414033
Bt.4694.1.S1_at	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 2 BETA, 36KDA	0.180793148	1.12618953
Bt.4711.1.S1_at	SIMILAR TO 40S RIBOSOMAL PROTEIN S9	0.031894418	1.005717786
Bt.4725.1.S1_at	B-CELL TRANSLOCATION GENE 1, ANTI-PROLIFERATIVE	-0.16200446	0.873880021
Bt.4730.1.S1_at	CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, BETA	0.120396304	1.04636838

Bt.4733.1.S1_at	PHOSPHOGLYCERATE DEHYDROGENASE	0.301074475	1.281473535
Bt.4741.1.S1_at	SIMILAR TO SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING	-0.07974047	0.929370734
Bt.4751.1.S1_a_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ ALPHA 1	-0.59797553	0.370046194
Bt.4751.2.S1_a_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DQ ALPHA 1	0.2186127	1.348121606
Bt.4757.1.S1_at	RHO GDP DISSOCIATION INHIBITOR (GDI) BETA	-0.04595668	0.951221209
Bt.4762.1.S1_at	MHC CLASS I HEAVY CHAIN	-0.38857674	0.747565362
Bt.4763.1.S1_at	ANTIGEN CD3Z, ZETA POLYPEPTIDE	-0.04895216	1.030744091
Bt.4768.1.S2_at	JUNCTIONAL ADHESION MOLECULE 1	0.561375482	1.195914224
Bt.4770.1.S1_at	SIMILAR TO PROGRAMMED CELL DEATH 4 ISOFORM 1	-0.09023709	0.944948992
Bt.4790.1.S1_at	INTEGRIN LINKED KINASE	0.573650996	1.414182682
Bt.4795.1.S1_at	SOLUTE CARRIER FAMILY 6 (NEUROTRANSMITTER TRANSPORTER, SEROTONIN),	0.69423547	1.378044187
Bt.4823.2.S1_a_at	CAMP-REGULATED PHOSPHOPROTEIN	0.17133793	1.130481854
Bt.4837.1.A1_at	ALDOLASE C, FRUCTOSE-BISPHOSPHATE	0.318084844	1.200945177
Bt.4839.1.S1_at	PHOSPHATIDYLETHANOLAMINE BINDING PROTEIN	0.064034411	1.008593288
Bt.4842.1.S1_at	RIBOSOMAL PROTEIN L18	-0.02308664	0.974864406
Bt.4843.1.S2_at	V-AKT MURINE THYMOMA VIRAL ONCOGENE HOMOLOG 1	0.144806978	1.071105091
Bt.4873.1.S1_at	CYTOCHROME B-5 REDUCTASE	0.149190575	1.11927345
Bt.4880.1.S1_at	NRAS-RELATED GENE	0.151680689	1.067432751
Bt.4884.1.S1_at	,GB:AW660357 /DB_XREF=GI:7426184 /DB_XREF=98353 /TID=BT.4884.1 /CNT=26 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.4884 /UG_TITLE=TRANSCRIBED	0.099252838	1.111268043
Bt.4898.1.S1_at	BRAIN ABUNDANT, MEMBRANE ATTACHED SIGNAL PROTEIN 1	0.041333237	0.991150039
Bt.4902.1.S1_at	CTSZ PROTEIN	0.291630756	1.144341076
Bt.4907.2.S1_a_at	,GB:CB426719 /DB_XREF=GI:29199047 /DB_XREF=601929 /TID=BT.4907.2 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.4907 /UG_TITLE=TRANSCRIBED	0.171079222	1.105806479
Bt.4915.1.S1_at	,GB:CK771290 /DB_XREF=GI:42725384 /DB_XREF=959545 /TID=BT.4915.1 /CNT=63	0.033312831	1.023735656
Bt.4917.1.S1_at	SIMILAR TO RAB1, MEMBER RAS ONCOGENE FAMILY	0.074585047	1.029670307
Bt.4942.1.S1_at	,GB:CB422054 /DB_XREF=GI:29189716 /DB_XREF=595122 /TID=BT.4942.1 /CNT=79 /FEA=EST /TIER=STACK /STK=32 /UG=BT.4942 /UG_TITLE=TRANSCRIBED	0.188186535	1.150738519
Bt.4967.1.S1_at	SIMILAR TO 40S RIBOSOMAL PROTEIN S3A (V-FOS TRANSFORMATION EFFECTOR	-0.03210655	0.969009139
Bt.4970.1.S1_at	CYTOCHROME C OXIDASE SUBUNIT VIIA POLYPEPTIDE 2 (LIVER)	0.138104659	1.10138734
Bt.50.1.S1_at	CD8 ANTIGEN, ALPHA POLYPEPTIDE (P32)	-0.27648685	0.789204659
Bt.5019.1.S1_at	PALMITOYL-PROTEIN THIOESTERASE 1 (CEROID-LIPOFUSCINOSIS, NEURONAL 1,	0.279143872	1.173975368
Bt.5021.1.S1_at	FIBRILLIN 1	-2.86919374	0.115816049
Bt.5029.1.S1_at	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT D	0.088027626	1.044766404
Bt.5037.1.S1_at	S100 CALCIUM-BINDING PROTEIN A10	0.172953721	1.137121245
Bt.5051.1.S1_a_at	RIBOSOMAL PROTEIN S27A	0.030163221	1.027343071
Bt.5052.1.S1_at	RAN, MEMBER RAS ONCOGENE FAMILY	0.105399629	1.076422704

Bt.5054.1.S1_a_at	RIBOSOMAL PROTEIN L24	0.04540006	1.014462828
Bt.5070.1.S1_at	POLYUBIQUITIN	-0.08526921	0.910723764
Bt.5070.1.S1_x_at	POLYUBIQUITIN	-0.06039643	0.943496235
Bt.5082.1.S1_at	MHC CLASS I JSP.1	0.100892462	1.054371631
Bt.5089.1.S1_at	H3 HISTONE, FAMILY 3A	0.093799784	1.062524073
Bt.5089.1.S2_at	H3 HISTONE, FAMILY 3A	0.09841842	1.102293398
Bt.5089.1.S3_at	H3 HISTONE, FAMILY 3A	0.179161463	1.108707421
Bt.5106.2.S1_at	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA STIMULATING	0.059446406	1.040649246
Bt.5112.1.A1_a_at	,GB:CK948858 /DB_XREF=GI:45463238 /DB_XREF=4073574 /CLONE=10BOV25_C07 /TID=BT.5112.1 /CNT=42 /FEA=EST /TIER=CONSEND /STK=5 /UG=BT.5112	0.359120872	1.365087911
Bt.5131.1.S1_at	HYPOTHETICAL PROTEIN MGC3234	0.223889386	1.156749668
Bt.5154.1.S1_at	HEAT SHOCK 70 KD PROTEIN 2	0.508573973	1.368874315
Bt.5154.1.S1_s_at	HEAT SHOCK 70 KD PROTEIN 2	0.563801624	1.361358243
Bt.5180.1.S1_at	UNCOUPLING PROTEIN 2 (MITOCHONDRIAL, PROTON CARRIER)	0.143242499	1.089687916
Bt.5183.1.S1_at	TUBULIN, ALPHA 1	0.348476973	1.332186753
Bt.5183.2.S1_at	TUBULIN, ALPHA 1	0.394359044	1.272663366
Bt.5230.1.S1_at	INHIBITOR OF DNA BINDING 3	0.169922245	1.192449925
Bt.5243.1.S1_at	,GB:CK950574 /DB_XREF=GI:45464954 /DB_XREF=4089907 /CLONE=10BOV27_K18 /TID=BT.5243.1 /CNT=108 /FEA=EST /TIER=STACK /STK=35 /UG=BT.5243	0.062503284	1.023581284
Bt.5252.1.S1_at	SIMILAR TO PHOSPHOGLYCERATE MUTASE	0.36853465	1.251613571
Bt.5266.1.S1_at	,GB:CK948189 /DB_XREF=GI:45462569 /DB_XREF=4072994 /CLONE=10BOV24_C15	0.039728322	0.986799855
Bt.5269.1.S1_at	BETA-2-MICROGLOBULIN	-0.03472716	0.977582206
Bt.5269.2.S1_a_at	BETA-2-MICROGLOBULIN	-0.02056004	0.981354043
Bt.5269.2.S1_at	BETA-2-MICROGLOBULIN	-0.0490169	0.989101583
Bt.5300.1.S1_at	,GB:BG467202 /DB_XREF=GI:13396177 /DB_XREF=1A08E04A /TID=BT.5300.1 /CNT=29 /FEA=EST /TIER=STACK /STK=7 /UG=BT.5300 /UG_TITLE=TRANSCRIBED	0.202935095	1.089921468
Bt.5305.1.A1_at	NUCLEAR FACTOR (ERYTHROID-DERIVED 2)-LIKE 2	0.23764313	1.089742579
Bt.5319.1.S1_at	ANTI-OXIDANT PROTEIN 2 (NON-SELENIUM GLUTATHIONE PEROXIDASE, ACIDIC	0.168881483	1.081733591
Bt.5319.2.S1_a_at	ANTI-OXIDANT PROTEIN 2 (NON-SELENIUM GLUTATHIONE PEROXIDASE, ACIDIC	0.201102787	1.106896444
Bt.5324.1.S1_s_at	MHC CLASS I JSP.1	-0.06480846	1.011742834
Bt.5334.1.S1_at	LAMININ RECEPTOR 1 (RIBOSOMAL PROTEIN SA, 67 KDA)	-0.03971097	0.952457204
Bt.5378.1.S1_at	NADH DEHYDROGENASE 1 BETA SUBCOMPLEX 8	0.123005904	1.071255853
Bt.5381.2.S1_x_at	CASEIN BETA	-1.36617121	0.799237178
Bt.5388.1.S1_at	H3 HISTONE, FAMILY 3A	0.070894076	1.072580975
Bt.5390.1.S1_at	MAJOR VAULT PROTEIN	0.328701821	1.230695209
Bt.5399.1.S2_at	SIMILAR TO NAD KINASE (POLY(P)/ATP NAD KINASE)	-0.0988346	0.941491196

Bt.5406.1.S1_at	,GB:CK944984 /DB_XREF=GI:45459364 /DB_XREF=4069444 /CLONE=10BOV17_O05 /TID=BT.5406.1 /CNT=23 /FEA=EST /TIER=STACK /STK=6 /UG=BT.5406	0.171673495	1.147203101
Bt.5434.1.S1_at	DEFENDER AGAINST CELL DEATH 1	0.130497042	1.121334993
Bt.5442.1.S1_at	SIMILAR TO TRANSMEMBRANE PROTEIN 50A (SMALL MEMBRANE PROTEIN 1)	0.094575392	1.059016982
Bt.5466.2.S1_a_at	RIBOSOMAL PROTEIN S4, X-LINKED	-0.03867026	0.972043587
Bt.5467.1.S1_at	PROSAPOSIN	0.164351152	1.078486115
Bt.5467.1.S2_a_at	PROSAPOSIN	0.142265621	1.083975922
Bt.5467.1.S2_at	PROSAPOSIN	0.12876107	1.084350305
Bt.5467.2.S1_a_at	PROSAPOSIN	0.164692963	1.107409436
Bt.5472.1.S1_at	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 1 (GALECTIN 1)	0.149761074	1.118922575
Bt.5475.1.S1_at	ADAPTOR-RELATED PROTEIN COMPLEX 3, DELTA 1 SUBUNIT	0.09596493	1.070913703
Bt.5483.1.S1_at	NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 8, 23KDA (NADH-	0.222592688	1.12107906
Bt.5491.1.S1_at	SIMILAR TO PRENYLATED RAB ACCEPTOR PROTEIN 1 (PRA1 FAMILY PROTEIN 1)	0.364207733	1.313092619
Bt.5493.1.S1_at	S100 CALCIUM-BINDING PROTEIN A4 (CALCIUM PROTEIN,CALVASCULIN,	0.126839901	1.091583354
Bt.5510.1.S1_at	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F1 COMPLEX, EPSILON	0.075683307	1.066122073
Bt.5519.1.S1_at	SIMILAR TO MELANOMA ANTIGEN FAMILY D, 1 ISOFORM B	-0.27519918	0.819450875
Bt.552.1.S1_at	CHEMOKINE (C-C MOTIF) LIGAND 5	-0.24944778	0.741487321
Bt.5520.1.S1_at	ISOCITRATE DEHYDROGENASE 2 (NADP+), MITOCHONDRIAL	0.103317399	1.065356088
Bt.5525.1.S1_at	,GB:CK848938 /DB_XREF=GI:45211730 /DB_XREF=971768 /TID=BT.5525.1 /CNT=47 /FEA=EST /TIER=STACK /STK=7 /UG=BT.5525 /UG_TITLE=TRANSCRIBED	0.369730712	1.108558315
Bt.5534.1.S1_at	THIOREDOXIN REDUCTASE 1	-0.15127536	0.833567811
Bt.5542.1.A1_at	SIMILAR TO NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED	-0.05482843	0.988621287
Bt.5542.2.S1_at	SIMILAR TO NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED	-0.05822876	0.978593632
Bt.5571.1.S1_at	HYPOTHETICAL PROTEIN	0.198591722	1.112717192
Bt.5573.1.S1_at	CE5 PROTEIN-LIKE	0.045656473	1.000184185
Bt.5599.1.S1_at	SIMILAR TO CHROMOSOME 9 OPEN READING FRAME 19	0.247312432	1.259056369
Bt.5699.1.S1_at	SIMILAR TO COATED VESICLE MEMBRANE PROTEIN	0.160545512	1.074558399
Bt.57.1.S1_at	NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 5, 15KDA (NADH-	0.095694164	0.98270903
Bt.5732.2.A1_at	,GB:CK848553 /DB_XREF=GI:45211027 /DB_XREF=971332 /TID=BT.5732.2 /CNT=1	-0.41630982	0.799765598
Bt.5754.1.S1_at	SERINE/THREONINE KINASE RECEPTOR ASSOCIATED PROTEIN	0.12056613	0.987816993
Bt.5878.1.A1_at	SIMILAR TO SERINE DEHYDRATASE	0.034768544	1.049398157
Bt.5878.2.S1_at	SIMILAR TO SERINE DEHYDRATASE	0.046158365	1.081214122
Bt.5892.1.S1_at	,GB:BF601967 /DB_XREF=GI:11699190 /DB_XREF=267082 /TID=BT.5892.1 /CNT=8	0.293853938	1.301219922
Bt.5897.1.S1_at	SIMILAR TO UBIQUITIN D	-0.0747072	0.960307644
Bt.5897.2.S1_at	SIMILAR TO UBIQUITIN-LIKE PROTEIN FAT10 (DIUBIQUITIN)	-0.20321588	0.844846123
Bt.6000.1.A1_at	,GB:BE683291 /DB_XREF=GI:10070012 /DB_XREF=182774 /TID=BT.6000.1 /CNT=8	0.064966838	0.914462594
Bt.6000.2.S1_at	,GB:CF930613 /DB_XREF=GI:38280041 /DB_XREF=CF--04-R-I19 /TID=BT.6000.2	0.20118562	1.090865395

Bt.6015.1.S1_at	,GB:BG690364 /DB_XREF=GI:13932165 /DB_XREF=338871 /TID=BT.6015.1 /CNT=15 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.6015 /UG_TITLE=TRANSCRIBED	-1.62274917	0.745516122
Bt.6082.1.S1_at	,GB:BF773728 /DB_XREF=GI:12121619 /DB_XREF=283190 /TID=BT.6082.1 /CNT=18	0.439798009	1.340984356
Bt.6091.1.S1_at	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	0.076853148	1.06978505
Bt.6111.1.S1_at	SIMILAR TO CG9324-PA	0.108868413	1.041211346
Bt.6126.1.S1_at	TRANSPORTER 2, ABC(ATP BINDING CASSETTE)	0.102839535	1.103082079
Bt.6130.1.S1_at	SIMILAR TO RIBOPHORIN II PRECURSOR	-0.1261142	0.977910455
Bt.615.1.S1_at	HYPOTHETICAL GENE SUPPORTED BY NM_012329	0.251937649	1.078809012
Bt.6151.1.S1_at	,GB:CB446844 /DB_XREF=GI:29253226 /DB_XREF=700581 /TID=BT.6151.1 /CNT=31 /FEA=EST /TIER=STACK /STK=7 /UG=BT.6151 /UG_TITLE=TRANSCRIBED	0.241300562	1.127032838
Bt.6176.1.S1_at	,GB:BE236381 /DB_XREF=GI:9021099 /DB_XREF=144153 /TID=BT.6176.1 /CNT=4	-0.0576753	0.958535986
Bt.6230.1.S1_at	,GB:CK831725 /DB_XREF=GI:45058042 /DB_XREF=4055451 /CLONE=8BOV_25H05 /TID=BT.6230.1 /CNT=8 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.6230	0.192171946	1.105614456
Bt.6239.1.S1_at	,GB:BE756758 /DB_XREF=GI:10170750 /DB_XREF=210995 /TID=BT.6239.1 /CNT=5 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.6239 /UG_TITLE=TRANSCRIBED	0.272711553	1.070820567
Bt.630.1.S1_at	CD81 ANTIGEN (TARGET OF ANTIPROLIFERATIVE ANTIBODY 1)	0.114550206	1.059091712
Bt.632.1.S1_at	TISSUE INHIBITOR OF METALLOPROTEINASE 1 (ERYTHROID POTENTIATING	0.253415193	1.225858297
Bt.6334.1.A1_at	SIMILAR TO DEGENERATIVE SPERMATOCYTE HOMOLOG 1, LIPID DESATURASE	0.124506043	1.053526364
Bt.6360.1.S1_at	,GB:CK951391 /DB_XREF=GI:45465771 /DB_XREF=4090520 /CLONE=10BOV28_E07 /TID=BT.6360.1 /CNT=17 /FEA=EST /TIER=CONSEND /STK=2 /UG=BT.6360	0.124783706	1.083966799
Bt.641.1.S1_at	SIMILAR TO PROTEASOME SUBUNIT ALPHA TYPE 2 (PROTEASOME COMPONENT	0.101484499	1.047104277
Bt.643.1.S1_at	,GB:CB465019 /DB_XREF=GI:29271404 /DB_XREF=726276 /TID=BT.643.1 /CNT=23 /FEA=EST /TIER=STACK /STK=10 /UG=BT.643 /UG_TITLE=TRANSCRIBED	-0.05900668	0.969532188
Bt.6434.2.S1_at	SIMILAR TO RING FINGER PROTEIN 149	-0.57232491	0.908260048
Bt.6442.1.S1_at	TROPOMYOSIN 1 (ALPHA)	0.413365596	1.572813296
Bt.6460.1.S1_at	CHEMOKINE RECEPTOR 7 ???	0.152483997	1.074073018
Bt.647.1.S1_at	MYOTROPHIN	-0.25037517	0.780916553
Bt.648.1.A1_at	,GB:CK944329 /DB_XREF=GI:45458709 /DB_XREF=4068628 /CLONE=10BOV16_M05 /TID=BT.648.1 /CNT=9 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.648	-0.09041977	0.947857005
Bt.6494.1.S1_at	MITOCHONDRIAL NADH:UBIQUINONE OXIDOREDUCTASE ESSS SUBUNIT	0.214118102	1.129979188
Bt.6496.1.S1_at	HEPATITIS B VIRUS X INTERACTING PROTEIN	0.238582282	1.18608845
Bt.65.1.S1_at	NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 2, 8KDA	0.157610301	1.083184851
Bt.662.1.S1_at	X-BOX BINDING PROTEIN 1	0.122160885	1.088125652
Bt.6665.1.S1_at	,GB:BE665432 /DB_XREF=GI:10026001 /DB_XREF=154465 /TID=BT.6665.1 /CNT=4	-0.19369986	0.895281965
Bt.6679.1.S1_at	SIMILAR TO NUCLEAR AUTOANTIGENIC SPERM PROTEIN (NASP)	-0.37793252	0.874204606
Bt.6680.1.S1_a_at	SIMILAR TO FK506-BINDING PROTEIN 2 PRECURSOR (PEPTIDYL-PROLYL CIS-	0.263983218	1.214858332
Bt.6700.1.A1_at	SIMILAR TO TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI)	0.961061114	1.875446724

Bt.6705.1.S1_at	,GB:CK957222 /DB_XREF=GI:45471602 /DB_XREF=4097633 /CLONE=10BOV3_M16 /TID=BT.6705.1 /CNT=16 /FEA=EST /TIER=CONSEND /STK=1 /UG=BT.6705	0.277636964	1.21370104
Bt.6714.1.S1_a_at	UBIQUITIN-LIKE 5	0.148170376	1.099973891
Bt.6714.3.S1_a_at	UBIQUITIN-LIKE 5	0.115248141	1.106092833
Bt.6718.1.S1_at	SIMILAR TO GLYCOGEN PHOSPHORYLASE, BRAIN FORM	0.316666907	1.235353114
Bt.676.1.S1_at	SIMILAR TO H2A HISTONE FAMILY, MEMBER V ISOFORM 1	0.066816628	1.037936814
Bt.6775.1.S1_at	SIMILAR TO ANNEXIN A3 (ANNEXIN III) (LIPOCORTIN III) (PLACENTAL	0.454286344	1.391754913
Bt.6784.1.A1_at	,GB:BF440184 /DB_XREF=GI:11500067 /DB_XREF=BS29000203303 /CLONE=BS29000203303 /TID=BT.6784.1 /CNT=1 /FEA=EST /TIER=CONSEND /STK=1	-0.10136895	0.921532757
Bt.6817.1.S1_at	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 1B	0.098551429	1.020390768
Bt.6827.1.S1_at	PROTEASOME ALPHA 3 SUBUNIT ISOFORM 1	0.144048006	1.122000899
Bt.6840.1.S1_a_at	SIMILAR TO FK506 BINDING PROTEIN 11 PRECURSOR (PEPTIDYL-PROLYL CIS-	0.157563261	1.089754115
Bt.685.1.A1_at	,GB:CK770170 /DB_XREF=GI:42724264 /DB_XREF=958308 /TID=BT.685.1 /CNT=13 /FEA=EST /TIER=STACK /STK=7 /UG=BT.685 /UG_TITLE=TRANSCRIBED SEQUENCE	0.287381455	1.208846875
Bt.6969.1.S1_at	,GB:BF707172 /DB_XREF=GI:11998833 /DB_XREF=282688 /TID=BT.6969.1 /CNT=5	-0.3716434	0.848071665
Bt.70.1.S1_at	NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 10, 22KDA	0.106955787	1.079505301
Bt.7011.1.S1_at	,GB:CK849489 /DB_XREF=GI:45212776 /DB_XREF=972468 /TID=BT.7011.1 /CNT=39 /FEA=EST /TIER=STACK /STK=8 /UG=BT.7011 /UG_TITLE=TRANSCRIBED	0.132265124	1.08624134
Bt.7013.1.S1_at	SIMILAR TO INTERLEUKIN-32 PRECURSOR (IL-32) (NATURAL KILLER CELLS	-0.18007123	0.919398906
Bt.7032.1.S1_at	SIMILAR TO THYROID HORMONE RECEPTOR INTERACTOR 3	0.440946098	1.135217463
Bt.7040.1.S1_at	SIMILAR TO PROTEASOME SUBUNIT BETA TYPE 1 (PROTEASOME COMPONENT C5) (MACROPAIN SUBUNIT C5) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX	0.164441786	1.113282881
Bt.7052.1.S1_at	RIBOSOMAL PROTEIN L5	-0.02454134	0.970048589
Bt.7056.1.S1_at	HEMOGLOBIN, BETA [BETA GLOBIN]	0.228041469	1.242924442
Bt.7056.2.A1_x_at	HEMOGLOBIN, GAMMA	0.345898917	1.31860136
Bt.7066.1.S1_at	,GB:BF651608 /DB_XREF=GI:11916738 /DB_XREF=274433 /TID=BT.7066.1 /CNT=4 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.7066 /UG_TITLE=TRANSCRIBED	0.203809223	1.178407511
Bt.7069.1.S1_at	CHROMOSOME 20 OPEN READING FRAME 36	-0.22278087	0.795968892
Bt.7074.1.A1_at	,GB:BE754146 /DB_XREF=GI:10168138 /DB_XREF=207570 /TID=BT.7074.1 /CNT=5	0.068520793	1.017340785
Bt.7078.1.S1_at	,GB:CK974977 /DB_XREF=GI:45492951 /DB_XREF=4106057 /CLONE=9BOV32_L16 /TID=BT.7078.1 /CNT=85 /FEA=EST /TIER=STACK /STK=7 /UG=BT.7078	0.419422887	1.489495876
Bt.7078.1.S2_at	,GB:CK848993 /DB_XREF=GI:45211833 /DB_XREF=971829 /TID=BT.7078.1 /CNT=85 /FEA=EST /TIER=STACK /STK=24 /UG=BT.7078 /UG_TITLE=TRANSCRIBED	0.340080846	1.382639333
Bt.7105.1.S1_at	SIMILAR TO DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1	-0.1361459	0.912603042
Bt.712.1.S2_at	SIMILAR TO MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM22 HOMOLOG	0.306477912	1.213976446
Bt.7133.1.S1_at	ORNITHINE DECARBOXYLASE	0.236408956	1.068979697

Bt.7170.1.S1_at	,GB:CK947788 /DB_XREF=GI:45462168 /DB_XREF=4072942 /CLONE=10BOV23_P23 /TID=BT.7170.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.7170	-0.365549	0.77494983
Bt.7181.1.S1_at	CALPAIN, SMALL SUBUNIT 1	0.295848018	1.202509802
Bt.7187.1.S1_at	SIMILAR TO 40S RIBOSOMAL PROTEIN S7 (S8)	0.043326469	1.032291111
Bt.7193.1.S1_at	CYTOCHROME C OXIDASE SUBUNIT VIA POLYPEPTIDE 1	0.201362085	1.110513221
Bt.7194.1.S1_at	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F1 COMPLEX, ALPHA	0.066336872	1.015342557
Bt.7204.1.S1_at	FC FRAGMENT OF IGG, LOW AFFINITY IIIA, RECEPTOR FOR (CD16)	0.367934914	1.15726408
Bt.7206.1.S1_at	GABA(A) RECEPTOR-ASSOCIATED PROTEIN-LIKE 2	0.234733427	1.173202328
Bt.7225.1.S1_at	TYROSINE 3-MONOOXYGENASE/TRYOTOPHAN 5-MONOOXYGENASE ACTIVATION	0.216924462	1.179478424
Bt.7236.1.S1_at	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT, POLYPEPTIDE 1 (P85	-0.24296719	0.817786707
Bt.7240.1.S1_at	,GB:NM_174098.2 /DB_XREF=GI:31342853 /GEN=LAP3 /TID=BT.7240.1 /CNT=35 /FEA=FLMRNA /TIER=FL+STACK /STK=10 /LL=281271 /UG=BT.7240 /DEF=BOS	0.281389586	1.220047241
Bt.7283.1.S1_at	TRANSALDOLASE 1	0.174852853	1.174352103
Bt.7288.1.S1_at	SIMILAR TO TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR	0.112833209	1.03934887
Bt.7358.1.S1_at	,GB:CB170173 /DB_XREF=GI:28156301 /DB_XREF=YIR603162953.R1 /TID=BT.7358.1	0.145167321	1.098975533
Bt.7403.1.S1_at	NUCLEOLIN	0.043172367	1.034384467
Bt.7416.1.S1_at	,GB:BF074071 /DB_XREF=GI:10867582 /DB_XREF=221398 /TID=BT.7416.1 /CNT=12 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.7416 /UG_TITLE=TRANSCRIBED	-0.09384893	0.955544673
Bt.7440.1.S1_at	SIMILAR TO PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG	-0.20648533	1.017014351
Bt.7452.1.S1_at	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 1 (EIF1) (PROTEIN	0.02413715	1.006082691
Bt.7459.1.S1_at	SIMILAR TO V-ETS ERYTHROBLASTOSIS VIRUS E26 ONCOGENE HOMOLOG 1	-0.09357571	0.951233099
Bt.746.1.S1_at	PROTEOLIPID PROTEIN 2 (COLONIC EPITHELIUM-ENRICHED)	0.11474191	1.114242164
Bt.7467.1.S1_at	,GB:BF601482 /DB_XREF=GI:11698704 /DB_XREF=266471 /TID=BT.7467.1 /CNT=5	-0.07785002	0.981639858
Bt.7468.1.S1_at	,GB:BE753844 /DB_XREF=GI:10167836 /DB_XREF=207024 /TID=BT.7468.1 /CNT=23	-0.14923618	0.978906404
Bt.7471.1.S1_at	SIMILAR TO H2A HISTONE FAMILY, MEMBER J ISOFORM 2	0.245370677	1.182171251
Bt.75.1.S1_at	CYTOCHROME C OXIDASE SUBUNIT VIB	0.096985611	1.042824515
Bt.7505.1.S1_at	,GB:BF775951 /DB_XREF=GI:12123851 /DB_XREF=286242 /TID=BT.7505.1 /CNT=21	-0.08396185	0.883876242
Bt.7542.1.S1_at	SIMILAR TO BCL-2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC-	0.194703375	1.109007412
Bt.7552.1.S1_at	SIMILAR TO ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT ISOFORM B	0.212901612	1.13484259
Bt.7588.1.A1_at	,GB:CK848334 /DB_XREF=GI:45210613 /DB_XREF=971083 /TID=BT.7588.1 /CNT=11	0.037434166	1.002504445
Bt.7594.1.S1_at	SIMILAR TO DIAMINE ACETYLTRANSFERASE 1 (SPERMIDINE/SPERMINE N(1)-ACETYLTRANSFERASE 1) (SSAT) (SSAT-1) (PUTRESCINE ACETYLTRANSFERASE)	0.066586823	1.036706947
Bt.7631.1.S1_at	,GB:CK846923 /DB_XREF=GI:45207914 /DB_XREF=969486 /TID=BT.7631.1 /CNT=33 /FEA=EST /TIER=STACK /STK=8 /UG=BT.7631 /UG_TITLE=TRANSCRIBED	-0.65740976	0.837211173
Bt.7655.1.S1_at	,GB:CB169061 /DB_XREF=GI:28155187 /DB_XREF=IMU602702714.R1 /TID=BT.7655.1 /CNT=56 /FEA=EST /TIER=STACK /STK=11 /UG=BT.7655 /UG_TITLE=TRANSCRIBED	-0.16124023	0.862151674
Bt.7670.1.A1_at	,GB:CK769300 /DB_XREF=GI:42723394 /DB_XREF=956861 /TID=BT.7670.1 /CNT=5	0.333293931	1.372952566

Bt.7676.2.S1_a_at	CALRETICULIN	0.129581287	1.098824238
Bt.77.1.S1_at	CYTOCHROME C OXIDASE SUBUNIT VIIC	0.117672207	1.066423073
Bt.7770.1.S1_at	CYCLIN G1	0.114303695	1.077398785
Bt.7776.1.S1_at	TUMOR PROTEIN, TRANSLATIONALLY-CONTROLLED 1	-0.04129236	0.985755102
Bt.7776.1.S1_s_at	TUMOR PROTEIN, TRANSLATIONALLY-CONTROLLED 1	-0.07249399	0.95062282
Bt.7776.2.S1_s_at	TUMOR PROTEIN, TRANSLATIONALLY-CONTROLLED 1	-0.04121307	0.960547471
Bt.7783.1.S1_a_at	IGM HEAVY CHAIN CONSTANT REGION	0.060437705	1.024979943
Bt.7798.1.S1_at	SIMILAR TO DYNEIN, CYTOPLASMIC, LIGHT CHAIN 2A	0.156998845	1.100237148
Bt.7804.1.S1_at	GLYCOGENIN	0.187566327	1.030671732
Bt.7814.1.S1_at	SIMILAR TO ADP-RIBOSYLATION FACTOR 4	0.140048916	1.113692056
Bt.7870.1.S1_at	PYROPHOSPHATASE (INORGANIC)	0.162780556	1.09702312
Bt.7910.1.S1_a_at	,GB:BE684349 /DB_XREF=GI:10071973 /DB_XREF=184725 /TID=BT.7910.1 /CNT=6	0.939971104	2.271710265
Bt.7912.1.A1_at	,GB:CB448807 /DB_XREF=GI:29255189 /DB_XREF=702968 /TID=BT.7912.1 /CNT=2	-0.14324337	0.881359013
Bt.7916.1.S1_at	SIMILAR TO DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN	0.095373558	0.983367258
Bt.7917.1.S1_at	,GB:CK948090 /DB_XREF=GI:45462470 /DB_XREF=4073080 /CLONE=10BOV24_H09	-0.19345265	0.861074001
Bt.7929.1.S1_at	HYPOTHETICAL PROTEIN	0.140862783	1.104403492
Bt.7931.1.S1_at	SIMILAR TO T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN)	0.102418733	1.123652832
Bt.7938.1.S1_at	CATHEPSIN S	0.084676805	1.035389327
Bt.7968.1.S1_at	SIMILAR TO PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 2	0.232727292	1.256246577
Bt.8015.1.S1_a_at	RIBOSOMAL PROTEIN S24	-0.03280522	0.976176108
Bt.8022.1.S1_at	CATHEPSIN C	0.210752476	1.133110792
Bt.8077.1.S1_at	PHOSPHOGLYCERATE KINASE 1	0.15796295	1.121448878
Bt.8081.1.S1_a_at	HYPOTHETICAL LOC514954	-0.04300839	0.966494271
Bt.8121.1.S1_x_at	MHC CLASS 1 PRECURSOR	0.056969389	1.021953866
Bt.8122.1.S1_at	THYMOSIN BETA 4, X CHROMOSOME	-0.0158351	0.998157683
Bt.8125.1.S1_a_at	RIBOSOMAL PROTEIN, LARGE, P1	-0.03421135	0.965068318
Bt.8125.2.S1_x_at	RIBOSOMAL PROTEIN, LARGE, P1	-0.01719965	0.981466634
Bt.8140.1.S1_at	FC FRAGMENT OF IGE, HIGH AFFINITY I, RECEPTOR FOR; GAMMA POLYPEPTIDE	0.374305384	1.322451532
Bt.8191.1.S1_at	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), ISOFORM 3	0.176398697	1.222749927
Bt.8212.1.S1_at	,GB:CK972315 /DB_XREF=GI:45490289 /DB_XREF=4102918 /CLONE=9BOV24_I21	0.116029522	1.07859039
Bt.8254.1.S1_at	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5, 16KDA	-0.06049473	0.95395773
Bt.8258.1.S1_at	,GB:CK949665 /DB_XREF=GI:45464045 /DB_XREF=4075040 /CLONE=10BOV26_P09	-0.16351261	0.886118936
Bt.8258.2.S1_at	,GB:BE236703 /DB_XREF=GI:9021421 /DB_XREF=145484 /TID=BT.8258.2 /CNT=8	-0.10633314	0.906554433
Bt.8265.1.A1_at	,GB:BM286733 /DB_XREF=GI:17995759 /DB_XREF=526920 /TID=BT.8265.1 /CNT=6	0.328139969	1.100248239
Bt.8331.1.S1_at	,GB:CK772747 /DB_XREF=GI:42726890 /DB_XREF=961320 /TID=BT.8331.1 /CNT=17	0.392468988	1.22100515
Bt.8343.1.S1_at	HYPOTHETICAL PROTEIN	0.208767035	1.130059032
Bt.837.1.S1_at	UP-REGULATED DURING VASCULAR CALCIFICATION	0.137038785	1.083654165

Bt.8382.2.S1_at	SIMILAR TO RHOB GENE	-0.28104804	0.761023167
Bt.8482.1.A1_at	MITOGEN-ACTIVATED PROTEIN KINASE 1	0.165010133	1.068813611
Bt.8504.1.A1_at	SIMILAR TO FRAGILE X MENTAL RETARDATION 1	-0.13064134	0.947904796
Bt.8505.1.A1_at	,GB:BF440420 /DB_XREF=GI:11500303 /DB_XREF=BS29000103503 /CLONE=BS29000103503 /TID=BT.8505.1 /CNT=2 /FEA=EST /TIER=CONSEND /STK=1	-0.37807759	0.791627986
Bt.8544.1.S1_at	CD69 ANTIGEN (P60, EARLY T-CELL ACTIVATION ANTIGEN)	-0.50762047	0.700818207
Bt.8552.1.S1_at	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR ALPHA	-0.05738642	0.91944629
Bt.8586.1.S1_at	SIMILAR TO MYELOID-ASSOCIATED DIFFERENTIATION MARKER	-0.835889	0.320341226
Bt.868.1.S1_a_at	SIMILAR TO LATE ENDOSOMAL/LYSOSOMAL MP1 INTERACTING PROTEIN (P14)	0.240011829	1.155147901
Bt.8686.1.S1_at	TUMOR REJECTION ANTIGEN (GP96) 1	0.248878547	1.16016099
Bt.8787.1.S1_at	ADIPONECTIN RECEPTOR-1	0.208024585	1.089559862
Bt.8820.1.S1_a_at	HEMATOPOIETIC CELL-SPECIFIC LYN SUBSTRATE 1	-0.11771051	0.951680198
Bt.8875.2.S1_at	,GB:CK775459 /DB_XREF=GI:42731709 /DB_XREF=966585 /TID=BT.8875.2 /CNT=215 /FEA=EST /TIER=STACK /STK=38 /UG=BT.8875 /UG_TITLE=IMMUNOGLOBULIN	0.500167223	1.58086334
Bt.888.1.S1_at	BCL2/ADENOVIRUS E1B 19KDA INTERACTING PROTEIN 3-LIKE	0.265396317	1.212216101
Bt.893.1.S1_at	NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 6, 17KDA	0.159325868	1.083758897
Bt.8939.1.S1_at	TYRO PROTEIN TYROSINE KINASE BINDING PROTEIN	0.210572668	1.146607745
Bt.8945.1.S1_at	TOLL-LIKE RECEPTOR 2	0.249722354	1.043201615
Bt.8947.1.S1_at	LEGUMAIN	0.297427393	1.18345019
Bt.8950.1.S1_at	CELL DEATH-REGULATORY PROTEIN GRIM19	0.127361864	1.088164971
Bt.8957.1.S1_at	CHEMOKINE (C-X-C MOTIF) RECEPTOR 4	-0.84845166	0.570273627
Bt.9020.1.S2_at	BLADDER CANCER ASSOCIATED PROTEIN	0.147026371	1.070723761
Bt.9027.1.S1_at	NUCLEAR FACTOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS	-0.39783732	0.813999566
Bt.9041.1.S1_at	,GB:CK770241 /DB_XREF=GI:42724335 /DB_XREF=958387 /TID=BT.9041.1 /CNT=22 /FEA=EST /TIER=CONSEND /STK=5 /UG=BT.9041 /UG_TITLE=TRANSCRIBED	-0.16939057	0.885730003
Bt.9042.1.A1_at	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)	0.125908175	1.080988264
Bt.9047.1.S1_at	TUBULIN, ALPHA 1	0.268090987	1.186443162
Bt.9064.1.S1_at	,GB:CK849770 /DB_XREF=GI:45213304 /DB_XREF=972897 /TID=BT.9064.1 /CNT=22 /FEA=EST /TIER=STACK /STK=6 /UG=BT.9064 /UG_TITLE=TRANSCRIBED	0.081242801	0.986898991
Bt.9136.1.S1_at	SIMILAR TO ALPHA-1,6-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGLUCOSAMINYLTRANSFERASE (MANNOSIDE	0.13051577	1.04270221
Bt.9164.1.A1_at	SIMILAR TO STAM BINDING PROTEIN	-0.56961958	0.842673116
Bt.9193.1.S1_at	,GB:BM251639 /DB_XREF=GI:17887231 /DB_XREF=BOTL0100011_E09	-0.10996763	0.915371891
Bt.9202.1.S1_at	SIMILAR TO FIBROLEUKIN PRECURSOR (FIBRINOGEN-LIKE PROTEIN 2) (PT49)	0.463541107	1.373774334
Bt.9208.1.S1_at	TRIGGERING RECEPTOR EXPRESSED ON MYELOID CELLS-1	0.475413209	1.52356409
Bt.9225.1.A1_at	SIMILAR TO HEXOKINASE TYPE III (HK III)	0.467514021	1.382369995

Bt.9267.1.A1_at	,GB:CB531127 /DB_XREF=GI:29393510 /DB_XREF=742377 /TID=BT.9267.1 /CNT=11 /FEA=EST /TIER=STACK /STK=10 /UG=BT.9267 /UG_TITLE=TRANSCRIBED	0.720380032	1.677132408
Bt.9269.1.S1_at	SIMILAR TO RIBOSOME ASSOCIATED MEMBRANE PROTEIN 4	0.168732049	1.060070277
Bt.927.1.S1_at	ADP-RIBOSYLATION FACTOR 1	0.105213393	1.077184993
Bt.9278.1.S1_at	,GB:CK977712 /DB_XREF=GI:45495686 /DB_XREF=4109060 /CLONE=9BOV37_I19	-0.20230553	0.845633259
Bt.9296.1.A1_at	SIMILAR TO INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GTP-	0.159056402	1.12561965
Bt.9360.1.S1_at	SIMILAR TO CALGRANULIN A (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8) (MRP-8) (CYSTIC FIBROSIS ANTIGEN) (CFAG) (P8) (LEUKOCYTE L1	0.155393325	1.112083737
Bt.9363.1.A1_at	,GB:BM251259 /DB_XREF=GI:17886851 /DB_XREF=BOTL0100004XB09R /TID=BT.9363.1 /CNT=6 /FEA=EST /TIER=CONSEND /STK=4 /UG=BT.9363	-0.3458248	0.615873485
Bt.9363.2.S1_at	,GB:CK945488 /DB_XREF=GI:45459868 /DB_XREF=4069677 /CLONE=10BOV17_H22 /TID=BT.9363.2 /CNT=23 /FEA=EST /TIER=CONSEND /STK=0 /UG=BT.9363	-0.44128087	0.60015939
Bt.9385.1.S1_at	SIMILAR TO BETA-TUBULIN COFACTOR C	0.353774075	1.436373619
Bt.9405.1.S1_at	SIMILAR TO TAF10 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-	0.115875848	1.095867626
Bt.9428.1.S1_at	HYPOTHETICAL PROTEIN	0.693664616	1.735573992
Bt.9541.1.S1_at	SIMILAR TO CELLULAR NUCLEIC ACID BINDING PROTEIN 1	0.066794684	1.026635365
Bt.9546.2.S1_a_at	,GB:BM363646 /DB_XREF=GI:18107015 /DB_XREF=BS320057B10E08 /CLONE=BS320057B10E08 /TID=BT.9546.2 /CNT=5 /FEA=EST /TIER=CONSEND	-0.12663351	0.955902247
Bt.9548.1.S1_at	HYPOTHETICAL PROTEIN	-0.02385796	0.97174665
Bt.9549.1.S1_at	HOMEODOMAIN ONLY PROTEIN	-0.1238346	0.951858855
Bt.9559.1.S1_at	SOLUTE CARRIER FAMILY 25 MEMBER 5	0.195052162	1.205933825
Bt.9570.1.S1_at	,GB:CK847032 /DB_XREF=GI:45208132 /DB_XREF=969613 /TID=BT.9570.1 /CNT=12	0.659853318	1.878326126
Bt.9578.1.S2_at	PROTEIN PHOSPHATASE 1, CATALYTIC SUBUNIT, GAMMA ISOFORM	-0.06236514	0.930633083
Bt.9588.1.S1_at	SIMILAR TO 60S RIBOSOMAL PROTEIN L7A	0.053033278	1.022212201
Bt.9589.1.S1_at	,GB:CK775656 /DB_XREF=GI:42731906 /DB_XREF=966789 /TID=BT.9589.1 /CNT=27 /FEA=EST /TIER=STACK /STK=9 /UG=BT.9589 /UG_TITLE=TRANSCRIBED	0.265971905	1.211098227
Bt.959.1.S1_at	FILAMIN A, ALPHA (ACTIN BINDING PROTEIN 280)	0.13674965	1.094806644
Bt.9591.2.S1_at	,GB:CB222709 /DB_XREF=GI:28293223 /DB_XREF=1IL31A08 /TID=BT.9591.2 /CNT=2	-0.28869452	0.867324641
Bt.9594.1.S1_at	,GB:BE685133 /DB_XREF=GI:10072757 /DB_XREF=187240 /TID=BT.9594.1 /CNT=9	-0.72230435	1.202289054
Bt.9629.2.S1_at	SIMILAR TO CG40127-PA.3	0.101877394	1.101308748
Bt.9662.1.S1_at	PROSTAGLANDIN E RECEPTOR 4 (SUBTYPE EP4)	-0.35811195	0.718362149
Bt.9667.1.A1_at	,GB:CK960385 /DB_XREF=GI:45474765 /DB_XREF=4101526 /CLONE=10BOV8_O21	-0.14021214	0.922041771
Bt.9676.1.S1_a_at	SIMILAR TO CG17059-PA	0.288993944	1.244240522
Bt.9698.1.S1_at	MITOGEN-ACTIVATED PROTEIN KINASE 14	0.261054855	1.289988086
Bt.9706.2.S1_at	SIMILAR TO RAB5-INTERACTING PROTEIN ISOFORM A	0.224794898	1.180100331
Bt.9725.1.A1_at	,GB:CK848549 /DB_XREF=GI:45211019 /DB_XREF=971328 /TID=BT.9725.1 /CNT=10 /FEA=EST /TIER=STACK /STK=7 /UG=BT.9725 /UG_TITLE=TRANSCRIBED	0.099867083	1.022698516

Bt.9728.1.S1_at	ATPASE, NA+/K+ TRANSPORTING, BETA 3 POLYPEPTIDE	0.158951962	1.123089072
Bt.9737.1.S1_at	SIMILAR TO LYMPHOCYTE ANTIGEN 6 COMPLEX LOCUS G6C PROTEIN	-0.17641765	1.099424913
Bt.9767.1.S1_a_at	,GB:CK949309 /DB_XREF=GI:45463689 /DB_XREF=4074569 /CLONE=10BOV26_L18 /TID=BT.9767.1 /CNT=12 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.9767	0.312032466	1.324450742
Bt.9774.1.S1_a_at	,GB:CK977109 /DB_XREF=GI:45495083 /DB_XREF=4108336 /CLONE=9BOV35_K15 /TID=BT.9774.1 /CNT=14 /FEA=EST /TIER=CONSEND /STK=3 /UG=BT.9774	0.271627047	1.240318041
Bt.981.1.S1_at	CHLORIDE INTRACELLULAR CHANNEL 4	0.281760628	1.105875682
Bt.9814.1.S1_at	RIBOSOMAL PROTEIN L36A	0.063911778	1.00509553
Bt.9826.1.S1_at	COX5A PROTEIN	0.139893342	1.071797398
Bt.983.1.S1_at	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE	0.288641472	1.197802062
Bt.9945.1.S1_at	SIMILAR TO GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) (R-	0.079856484	1.047306811
Bt.9947.1.S1_at	,GB:CB459802 /DB_XREF=GI:29266186 /DB_XREF=719606 /TID=BT.9947.1 /CNT=32	-0.14397952	0.914086668
Bt.9956.1.S1_at	PUTATIVE 42-9-9 PROTEIN	0.414827962	1.316680444
BtAffx.1.13.S1_at	TACHYKININ 3, NEUROKININ BETA	-0.28929525	0.830041749
BtAffx.1.20.S1_at	REGULATOR OF G-PROTEIN SIGNALING 20	0.91016286	1.731295976
BtAffx.29967.1.S1_at	,GI:45433264 /TID=BTAFFX.29967.1 /CNT=1 /FEA=MRNA /TIER=CONSEND /STK=0	-0.01656796	0.992679005
BtAffx.29968.1.S1_at	,GI:5823437 /TID=BTAFFX.29968.1 /CNT=1 /FEA=MRNA /TIER=CONSEND /STK=0	0.988434476	2.244508077