Table S1. Probe sets which are differentially regulated in atretic with respect to healthy follicles.

Probe set ID	**Gene Symbol**	**Gene Title**	**RefSeq Transcript ID**	**Fold Change**	***P* Value**
Bt.13326.1.S1_at	*A2M*	alpha-2-macroglobulin	NM_001109795	3.018	9.29E-03
Bt.19199.1.A1_at	*ABCC8*	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	XM_584132	2.046	3.84E-02
Bt.21471.1.S1_at	*ABCG1*	ATP-binding cassette, sub-family G (WHITE), member 1	XM_587930	2.475	1.49E-02
Bt.13293.1.S1_at	*ACOT7*	acyl-CoA thioesterase 7	NM_001075682	-2.308	1.57E-02
Bt.19884.2.S1_at	*ACP5*	acid phosphatase 5, tartrate resistant	XM_595165	3.212	5.24E-03
Bt.5215.1.S1_at	*ACP5*	acid phosphatase 5, tartrate resistant	XM_595165	2.385	6.10E-03
Bt.2657.1.S1_a_at	*ADCY8*	adenylate cyclase 8 (brain)	XM_001249965 /// XM_614987	2.387	1.95E-02
Bt.6202.1.S1_at	*ADM*	adrenomedullin	NM_173888	2.961	2.12E-02
Bt.23658.2.S1_at	*AIF1*	allograft inflammatory factor 1	NM_173985	2.244	6.36E-03

Bt.27319.1.A1_at	*ALG13*	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	NM_001080275	2.263	3.20E-02
Bt.5200.1.S1_at	*ALPL*	alkaline phosphatase, liver/bone/kidney	NM_176858	-2.211	2.30E-02
Bt.4507.1.S1_at	*AMY2A*	amylase, alpha 2A (pancreatic)	NM_001035016	2.208	2.47E-02
Bt.16232.1.S1_at	*ANGPT2*	angiopoietin 2	NM_001098855	2.812	1.82E-02
Bt.20272.1.S1_at	*ANLN*	Anillin, actin binding protein	XM_596461	-2.663	9.03E-03
Bt.4863.1.S1_at	*ANLN*	anillin, actin binding protein	XM_596461	-2.889	1.84E-02
Bt.2112.1.S1_at	*APCDD1*	Adenomatosis polyposis coli down-regulated 1	XM_585921	3.127	1.04E-02
Bt.24830.1.A1_at	*APLNR*	apelin receptor	NM_001102524	-2.084	4.53E-03
Bt.3686.1.S1_at	*APLNR*	apelin receptor	NM_001102524	-3.199	4.91E-03
Bt.11936.1.S1_a_at	*APOD*	Apolipoprotein D	NM_001076301	6.763	5.16E-03
Bt.16622.1.A1_at	*APOD*	Apolipoprotein D	NM_001076301	3.734	6.18E-03
Bt.8491.1.S1_at	*APOD*	apolipoprotein D	NM_001076301	2.808	6.94E-03

Bt.4733.1.S1_at	*APOE*	apolipoprotein E	NM_173991	2.553	5.84E-03
Bt.21513.2.S1_at	*AQP11*	aquaporin 11	NM_001110069	-2.196	1.36E-02
Bt.10007.1.A1_at	*ARHGEF11*	Rho guanine nucleotide exchange factor (GEF) 11	XM_588515	2.437	9.70E-03
Bt.26011.1.A1_at	*ARHGEF6*	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	XM_865157	2.191	1.40E-02
Bt.666.1.S1_at	*ASF1B*	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	NM_001075453	-2.950	7.64E-03
Bt.21523.1.S1_at	*ASF1B*	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	NM_001075453	-5.224	5.49E-03
Bt.6009.1.S1_at	*ASPA*	aspartoacylase (Canavan disease)	NM_001046033	2.631	5.16E-03
Bt.16721.1.A1_at	*ASPM*	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	XM_614763	-5.480	4.91E-03
Bt.26895.1.S1_at	*ASS1*	argininosuccinate synthase 1	NM_173892	-2.228	4.55E-03
Bt.21028.1.S1_at	*ATAD5*	ATPase family, AAA domain containing 5	XM_590682	-2.173	3.57E-02
Bt.11428.1.A1_at	*ATAD5*	ATPase family, AAA domain containing 5	XM_590682	-2.419	2.73E-02
Bt.16725.2.A1_at	*ATP2C2*	ATPase, Ca++ transporting, type 2C, member 2	XM_587457	3.561	5.02E-03

Bt.21433.2.S1_at	*AURKA*	aurora kinase A	NM_001038028	-3.167	7.03E-03
Bt.9510.2.A1_a_at	*AURKA*	aurora kinase A	NM_001038028	-3.459	9.47E-03
Bt.20521.3.A1_at	*AURKB*	aurora kinase B	NM_183084	-3.047	4.91E-03
Bt.16047.1.S1_at	*AURKB*	aurora kinase B	NM_183084	-5.310	4.83E-03
Bt.28185.1.S1_at	*BCL6*	B-cell CLL/lymphoma 6	XM_584289 /// XM_865691	2.502	1.25E-02
Bt.4198.1.S1_at	*BCS1L*	BCS1-like (yeast)	NM_001015671	-2.002	1.30E-02
Bt.10503.1.S1_at	*BDH1*	3-hydroxybutyrate dehydrogenase, type 1	NM_001034600	-2.027	3.26E-02
Bt.17939.1.S1_at	*BIRC5*	baculoviral IAP repeat-containing 5	NM_001001855	-5.720	5.24E-03
Bt.21540.1.S1_at	*BORA*	aurora borealis	XM_591968	-2.283	4.58E-03
Bt.21294.1.A1_at	*BRB*	brain ribonuclease	NM_173891	2.093	4.14E-02
Bt.12891.1.S1_at	*BRCA1*	Breast cancer 1, early onset	NM_178573	-2.650	1.46E-02
Bt.27757.1.S1_at	*BUB1*	budding uninhibited by benzimidazoles 1 homolog (yeast)	NM_001102011	-2.002	1.45E-02

Bt.17992.1.S1_at	*BUB1*	budding uninhibited by benzimidazoles 1 homolog (yeast)	NM_001102011	-5.208	5.35E-03
Bt.16875.1.A1_at	*BUB1B*	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	NM_001145173 /// XM_617181	-4.217	5.16E-03
Bt.13204.1.S1_at	*C13H20ORF108*	chromosome 20 open reading frame 108 ortholog	NM_001080278	2.109	5.63E-03
Bt.27043.1.A1_at	*C13H20ORF12*	chromosome 20 open reading frame 12 ortholog	NM_001076838	2.505	9.28E-03
Bt.21886.1.S1_at	*C1H21ORF7*	chromosome 21 open reading frame 7 ortholog	XM_613553	2.715	1.74E-02
Bt.1190.1.A1_at	*C1QA*	complement component 1, q subcomponent, A chain	NM_001014945	2.525	6.91E-03
Bt.24238.1.A1_at	*C1QB*	complement component 1, q subcomponent, B chain	NM_001046599	2.730	5.61E-03
Bt.23532.1.S1_at	*C1QC*	complement component 1, q subcomponent, C chain	XM_587039	2.786	6.22E-03
Bt.4872.1.S1_at	*C1QTNF7*	C1q and tumor necrosis factor related protein 7	NM_001076201	2.075	2.45E-02
Bt.20501.1.S1_at	*C1R*	complement component 1, r subcomponent	NM_001034407	4.172	5.49E-03
Bt.24446.1.A1_at	*C1S*	complement component 1, s subcomponent	NM_001076550	7.038	5.45E-03
Bt.9175.1.A1_at	*C28H10ORF10*	chromosome 10 open reading frame 10 ortholog	NM_001046515	4.122	6.99E-03

Bt.13796.1.S1_at	*C4A*	complement component 4A	NM_001166485 /// XM_584742	2.736	7.30E-03
Bt.23521.1.S1_at	*C7*	complement component 7	NM_001045966	4.378	6.92E-03
Bt.18895.1.A1_at	*C9orf100*	vav-like protein C9orf100 homolog	NM_001079800	-3.122	1.32E-02
Bt.7190.1.S1_at	*CABC1*	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	NM_001046419	2.031	1.08E-02
Bt.3191.1.A1_at	*CASC5*	cancer susceptibility candidate 5	XM_001790629	-4.950	5.45E-03
Bt.27207.1.A1_at	*CCDC115*	coiled-coil domain containing 115	NM_001034444	-2.024	7.74E-03
Bt.719.1.A1_at	*CCDC99*	coiled-coil domain containing 99	NM_001076854	-3.834	9.91E-03
Bt.2047.1.S1_at	*CCL25*	chemokine (C-C motif) ligand 25	NM_001046569	-2.892	1.95E-02
Bt.4310.1.A1_at	*CCNA2 /// LOC786906*	cyclin A2 /// similar to Cyclin A2	NM_001075123 /// XR_042775	-4.669	5.99E-03
Bt.20220.1.S1_at	*CCNB1*	cyclin B1	NM_001045872	-7.018	5.53E-03
Bt.28541.1.S1_at	*CCNB2*	cyclin B2	NM_174264	-5.139	4.91E-03
Bt.17994.1.S1_at	*CCNE2*	cyclin E2	NM_001015665	-2.296	8.91E-03

Bt.16886.1.A1_a_at	*CCNF*	cyclin F	NM_001098870	-3.611	5.24E-03
Bt.4873.1.S1_at	*CCR1*	chemokine (C-C motif) receptor 1	NM_001077839	2.834	4.55E-03
Bt.25823.1.A1_at	*CD14*	CD14 molecule	NM_174008	4.686	5.24E-03
Bt.24258.2.S1_at	*CD14*	CD14 molecule	NM_174008	2.393	6.36E-03
Bt.24707.1.S1_at	*CD36*	CD36 molecule (thrombospondin receptor)	NM_174010	3.546	1.09E-02
Bt.20827.1.A1_at	*CD48*	CD48 molecule	NM_001046002	2.418	1.89E-02
Bt.8834.1.S1_at	*CD53*	CD53 molecule	NM_001034232	2.912	1.21E-02
Bt.16094.1.S1_at	*CD5L*	CD5 molecule-like	NM_001102119	2.708	3.05E-02
Bt.18639.1.A1_at	*CD68*	CD68 molecule	NM_001045902	6.423	5.06E-03
Bt.26844.1.A1_at	*CD84*	CD84 molecule	XM_588136	2.116	2.22E-02
Bt.13798.1.S1_at	*CD86*	CD86 molecule	NM_001038017	2.236	4.55E-03
Bt.12685.1.S1_at	*CDC20*	cell division cycle 20 homolog (S. cerevisiae)	NM_001082436	-5.193	4.91E-03

Bt.18500.1.A1_at	*CDC25C*	cell division cycle 25 homolog C (S. pombe)	NM_001097996	-2.098	9.71E-03
Bt.7043.2.S1_a_at	*CDC6*	cell division cycle 6 homolog (S. cerevisiae)	XM_593299	-2.222	2.10E-02
Bt.28797.2.S1_at	*CDC6*	cell division cycle 6 homolog (S. cerevisiae)	XM_593299	-3.220	2.31E-02
Bt.546.1.S1_at	*CDCA2*	cell division cycle associated 2	NM_001046194	-5.729	4.91E-03
Bt.28379.1.S1_at	*CDCA3*	cell division cycle associated 3	NM_001035449	-5.264	4.83E-03
Bt.1181.1.S1_at	*CDCA5*	cell division cycle associated 5	NM_001076270	-5.371	5.86E-03
Bt.24288.2.S1_at	*CDCA7*	cell division cycle associated 7	NM_001037488	-3.853	1.67E-02
Bt.26844.2.S1_at	*CDCA8*	cell division cycle associated 8	NM_001083652	-2.701	1.05E-02
Bt.25924.1.A1_at	*CDCA8*	cell division cycle associated 8	NM_001083652	-6.156	6.57E-03
Bt.23453.1.S1_at	*CDK1*	cyclin-dependent kinase 1	NM_174016	-5.495	6.17E-03
Bt.29477.1.A1_at	*CDT1*	chromatin licensing and DNA replication factor 1	XM_597224	-2.413	1.20E-02
Bt.12565.1.S1_at	*CEBPD*	CCAAT/enhancer binding protein (C/EBP), delta	NM_174267	4.176	9.49E-03

Bt.18639.2.S1_at	*CEBPD*	CCAAT/enhancer binding protein (C/EBP), delta	NM_174267	3.270	1.06E-02
Bt.27849.2.S1_a_at	*CENP-A /// CENP-A /// LOC618307 /// LOC782601 /// LOC782634 /// LOC782883*	centromere protein-A /// CENP-A protein /// similar to Histone H3-like centromer	XM_001250060 /// XM_001250108 /// XM_001250161 /// XM_001250208 /// XM_001788955	-3.898	4.91E-03
Bt.29005.1.A1_at	*CENP-A /// LOC782601 /// LOC782883*	CENP-A protein /// similar to Histone H3-like centromeric protein A (Centromere	XM_001250060 /// XM_001250108 /// XM_001788955 /// XR_027462	-5.217	4.83E-03
Bt.1074.1.A1_a_at	*CENPF*	centromere protein F, 350/400ka (mitosin)	XM_612376	-4.666	4.91E-03
Bt.27798.1.A1_at	*CENPN*	centromere protein N	NM_001038099	-3.937	7.03E-03
Bt.26157.1.A1_at	*CENPN*	centromere protein N	NM_001038099	-4.915	5.45E-03
Bt.13670.1.S2_at	*CENPN*	centromere protein N	NM_001038099	-5.759	6.74E-03
Bt.24859.2.S1_at	*CENPO*	centromere protein O	NM_001077003	-2.198	1.78E-02
Bt.24266.1.A1_at	*CENPP*	centromere protein P	NM_001105615	-2.710	1.34E-02

Bt.17926.1.A1_at	*CFI*	complement factor I	NM_001038096	5.113	4.91E-03
Bt.18116.3.A1_s_at	*CH25H*	cholesterol 25-hydroxylase	NM_001075243	4.124	1.69E-02
Bt.12465.1.A1_at	*CHAF1A*	chromatin assembly factor 1, subunit A (p150)	NM_001101842	-3.311	1.08E-02
Bt.1052.1.A1_at	*CHAF1B*	chromatin assembly factor 1, subunit B (p60)	NM_001098014	-2.364	2.26E-02
Bt.13546.1.A1_at	*CHEK1*	CHK1 checkpoint homolog (S. pombe)	NM_001098023	-2.752	2.63E-02
Bt.7588.1.A1_at	*CHI3L2*	similar to chitinase 3-like 2	XR_042527	2.826	1.30E-02
Bt.24354.1.S1_at	*CHTF18*	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	XM_595170	-2.505	2.22E-02
Bt.4615.1.S1_at	*CITED2*	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	NM_001075819	2.209	2.18E-02
Bt.26029.1.A1_at	*CKAP2*	cytoskeleton associated protein 2	NM_001098032	-3.153	5.86E-03
Bt.22389.1.S1_at	*CKAP2L*	cytoskeleton associated protein 2-like	NM_001098901 /// XM_584116	-3.843	5.24E-03
Bt.19204.1.S1_at	*CKS1B*	CDC28 protein kinase regulatory subunit 1B	NM_001113311 /// XM_001789781	-2.502	2.07E-02
Bt.24370.1.A1_at	*CKS2*	CDC28 protein kinase regulatory subunit 2	NM_001113319 /// XM_001252074	-4.013	5.16E-03

Bt.393.1.S2_at	*CLDN11*	claudin 11	NM_001035055	4.562	4.84E-02
Bt.20428.2.S1_a_at	*CLDN5*	claudin 5	NM_001076460	2.525	1.14E-02
Bt.12916.1.S1_at	*CLU*	clusterin	NM_173902	2.062	2.69E-02
Bt.1185.2.S1_at	*CNDP2*	CNDP dipeptidase 2 (metallopeptidase M20 family)	NM_001035108	2.025	6.27E-03
Bt.986.1.A1_at	*COL4A6*	collagen, type IV, alpha 6	XM_601826	2.091	3.12E-02
Bt.26683.2.S1_at	*CORO1A*	coronin, actin binding protein, 1A	NM_174521	2.087	1.18E-02
Bt.20784.1.A1_at	*CP*	ceruloplasmin (ferroxidase)	XM_592003	3.176	1.94E-02
Bt.7331.1.S1_at	*CP*	ceruloplasmin (ferroxidase)	XM_592003	2.891	9.03E-03
Bt.13289.2.S1_at	*CP*	ceruloplasmin (ferroxidase)	XM_592003	2.435	7.52E-03
Bt.20836.1.S1_at	*CRYM*	crystallin, mu	NM_001045914	-2.202	3.71E-02
Bt.13413.2.A1_at	*CSTB*	cystatin B (stefin B)	NM_001100362	2.625	2.00E-02
Bt.28225.2.S1_at	*CTSB*	cathepsin B	NM_174031	2.936	4.53E-03

Bt.6800.1.A1_at	*CTSB*	cathepsin B	NM_174031	2.498	4.55E-03
Bt.9807.1.S1_at	*CTSB*	Cathepsin B	NM_174031	2.345	4.53E-03
Bt.27826.1.S1_at	*CTSF*	cathepsin F	NM_001075416	2.321	7.64E-03
Bt.13834.1.S1_at	*CTSW*	cathepsin W	NM_001110070	2.221	2.29E-02
Bt.284.1.S1_at	*CTSZ*	cathepsin Z	NM_001077835	2.103	5.16E-03
Bt.9863.1.S1_at	*CXCL14*	chemokine (C-X-C motif) ligand 14	NM_001034410	-3.679	5.06E-03
Bt.1185.1.A1_at	*CXCR4*	chemokine (C-X-C motif) receptor 4	NM_174301	3.909	6.84E-03
Bt.13387.1.S1_at	*CYB5R3*	cytochrome b5 reductase 3	NM_001103250	-2.165	5.02E-03
Bt.28366.2.S1_at	*CYBB*	cytochrome b-245, beta polypeptide	NM_174035	2.200	4.91E-03
Bt.16058.2.S1_at	*CYP11A1*	cytochrome P450, family 11, subfamily A, polypeptide 1	NM_176644	-2.485	1.17E-02
Bt.14371.1.A1_at	*DCK*	deoxycytidine kinase	NM_001034573	-2.349	2.59E-02
Bt.16538.2.A1_at	*DCLK1*	Doublecortin-like kinase 1	NM_001109962	2.357	4.91E-03

Bt.27600.1.A1_at	*DDX39*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	NM_001034752	-2.557	1.62E-02
Bt.24218.1.S1_at	*DSN1*	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_001100323	-3.164	1.51E-02
Bt.22672.1.A1_at	*DTYMK*	deoxythymidylate kinase (thymidylate kinase)	NM_001098893	-3.118	1.26E-02
Bt.1920.2.S1_at	*DUSP26*	dual specificity phosphatase 26 (putative)	NM_001076004	2.339	4.55E-03
Bt.5536.1.S1_at	*DUT*	deoxyuridine triphosphatase	NM_001077873	-2.586	4.55E-03
Bt.964.1.S1_at	*DUT*	deoxyuridine triphosphatase	NM_001077873	-2.708	4.53E-03
Bt.9807.2.S1_at	*DYNLRB2*	dynein, light chain, roadblock-type 2	NM_001077119	2.343	5.99E-03
Bt.18081.1.A1_at	*E2F8*	E2F transcription factor 8	XM_001254260	-3.813	9.95E-03
Bt.1088.1.S1_a_at	*ECT2*	epithelial cell transforming sequence 2 oncogene	NM_001097573	-3.206	7.36E-03
Bt.28826.1.A1_at	*ECT2*	epithelial cell transforming sequence 2 oncogene	NM_001097573	-3.508	5.16E-03
Bt.3863.1.S1_at	*EGR1*	early growth response 1	NM_001045875	2.297	2.71E-02
Bt.1296.2.S1_at	*ENPP2*	ectonucleotide pyrophosphatase/phosphodiesterase 2	NM_001080293	2.301	1.99E-02

Bt.13476.1.S1_at	*EPHX2 /// LOC785508*	epoxide hydrolase 2, cytoplasmic /// similar to epoxide hydrolase 2, cytoplasmic	NM_001075534 /// XM_001253506	2.388	1.95E-02
Bt.3371.1.S1_at	*ERCC6L*	excision repair cross-complementing rodent repair deficiency, complementation gr	NM_001102530	-3.228	1.46E-02
Bt.28243.2.S1_at	*ESPL1*	extra spindle pole bodies homolog 1 (S. cerevisiae)	NM_001045949 /// XM_001790117	-5.224	5.24E-03
Bt.12876.3.S1_a_at	*EZH2*	enhancer of zeste homolog 2 (Drosophila)	XM_585997 /// XM_865659	-2.122	5.74E-03
Bt.12295.1.S1_at	*FABP5*	fatty acid binding protein 5 (psoriasis-associated)	NM_174315	2.512	4.26E-02
Bt.29850.1.S1_at	*FAM83D*	Protein FAM83D	NM_001083393	-3.747	5.16E-03
Bt.7058.1.S1_at	*FAM84A*	family with sequence similarity 84, member A	NM_001034659	2.053	5.24E-03
Bt.13865.1.A1_at	*FANCI*	Fanconi anemia, complementation group I	XM_600723	-3.179	1.30E-02
Bt.1742.2.S1_a_at	*FBXO32*	F-box protein 32	NM_001046155	2.640	2.20E-02
Bt.4995.1.A1_at	*FBXO32*	F-box protein 32	NM_001046155	2.102	4.10E-02
Bt.5373.1.S1_at	*FBXO5*	F-box protein 5	NM_001082435	-3.238	9.90E-03
Bt.24600.1.S1_at	*FCER1A*	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	NM_001100310	2.073	5.24E-03

Bt.6687.1.S1_at	*FCGR1A*	Fc fragment of IgG, high affinity Ia, receptor (CD64)	NM_174538	2.470	9.27E-03
Bt.20677.1.S1_at	*FEN1*	flap structure-specific endonuclease 1	NM_001035113	-2.876	1.29E-02
Bt.28799.1.S1_at	*FERMT3*	fermitin family homolog 3 (Drosophila)	NM_001037606	2.220	6.18E-03
Bt.20262.1.S1_at	*FGFR2*	fibroblast growth factor receptor 2	XM_001789706	-2.251	1.59E-02
Bt.26683.1.S1_at	*FGL1*	fibrinogen-like 1	NM_001034313	2.259	8.70E-03
Bt.12744.1.S1_at	*FGL2*	fibrinogen-like 2	NM_001046097	2.731	1.48E-02
Bt.8718.1.S1_at	*FOLR2*	folate receptor 2 (fetal)	NM_001075325	3.294	4.91E-03
Bt.28225.1.A1_at	*FOS*	FBJ murine osteosarcoma viral oncogene homolog	NM_182786	3.101	3.25E-02
Bt.17915.1.S1_at	*FOS*	FBJ murine osteosarcoma viral oncogene homolog	NM_182786	3.083	4.14E-02
Bt.25478.1.A1_at	*FOSL2*	FOS-like antigen 2	XM_864138	3.101	6.90E-03
Bt.15682.1.A1_at	*FOXM1*	forkhead box M1	XM_001249704 /// XM_872119	-2.082	1.56E-02
Bt.28409.1.A1_at	*GABARAPL1*	GABA(A) receptor-associated protein like 1	NM_001033616	2.048	8.94E-03

Bt.20431.1.A1_at	*GAMT*	guanidinoacetate N-methyltransferase	NM_001038544	2.058	2.33E-02
Bt.6406.1.S3_at	*GAS7*	growth arrest-specific 7	NM_001102280	2.086	7.74E-03
Bt.1220.1.S1_at	*GEM*	GTP binding protein overexpressed in skeletal muscle	NM_001083732	2.248	2.05E-02
Bt.13336.2.S1_at	*GIMAP7*	GTPase, IMAP family member 7	NM_001080257	2.451	2.54E-02
Bt.2520.1.S1_at	*GIMAP7*	GTPase, IMAP family member 7	NM_001080257	2.263	3.09E-02
Bt.7620.1.S1_at	*GINS3*	GINS complex subunit 3 (Psf3 homolog)	NM_001076136	-2.142	8.03E-03
Bt.12961.1.A1_at	*GINS3*	GINS complex subunit 3 (Psf3 homolog)	NM_001076136	-2.165	1.33E-02
Bt.10510.1.S1_at	*GMFG*	glia maturation factor, gamma	NM_001024537	2.137	6.18E-03
Bt.4817.1.A1_at	*GPNMB*	glycoprotein (transmembrane) nmb	NM_001038065	14.505	6.44E-03
Bt.11936.1.S1_at	*GPNMB*	glycoprotein (transmembrane) nmb	NM_001038065	3.906	7.41E-03
Bt.26415.1.A1_at	*GPNMB*	glycoprotein (transmembrane) nmb	NM_001038065	2.139	1.84E-02
Bt.6397.1.S1_at	*GPR77*	G protein-coupled receptor 77	NM_001077947	2.265	4.04E-02

Bt.17488.1.A1_at	*GPX3*	glutathione peroxidase 3 (plasma)	NM_174077	3.394	6.17E-03
Bt.2111.1.S1_a_at	*H2AFX*	H2A histone family, member X	NM_001079780	-2.831	8.94E-03
Bt.21546.1.S1_at	*H2AFZ*	H2A histone family, member Z	NM_174809	-2.029	1.61E-02
Bt.7035.1.S1_at	*HJURP*	Holliday junction recognition protein	XM_869720	-5.629	4.91E-03
Bt.15733.1.A1_at	*HMGB2*	High-mobility group box 2	NM_001037616	-2.001	6.81E-03
Bt.11497.1.A1_at	*HMGB2*	high-mobility group box 2	NM_001037616	-2.345	5.49E-03
Bt.20499.1.S1_at	*HMMR*	hyaluronan-mediated motility receptor (RHAMM)	XM_590028	-2.058	1.33E-02
Bt.19819.1.S1_at	*HMMR*	hyaluronan-mediated motility receptor (RHAMM)	XM_590028	-3.575	5.84E-03
Bt.1343.2.A1_at	*HMOX1*	heme oxygenase (decycling) 1	NM_001014912	2.378	8.78E-03
Bt.21939.1.S1_at	*HN1*	hematological and neurological expressed 1	NM_001034734	-2.315	1.43E-02
Bt.9155.1.A1_at	*HPGD*	hydroxyprostaglandin dehydrogenase 15-(NAD)	NM_001034419	-2.402	2.10E-02
Bt.2556.1.S1_at	*HPGD*	hydroxyprostaglandin dehydrogenase 15-(NAD)	NM_001034419	-3.001	2.09E-02

Bt.9997.1.S1_at	*HRH1*	histamine receptor H1	NM_174083	2.068	6.84E-03
Bt.3560.1.S1_at	*HSD17B11*	hydroxysteroid (17-beta) dehydrogenase 11	NM_001046286	2.417	1.24E-02
Bt.2410.1.A1_at	*IL1R1*	interleukin 1 receptor, type I	XM_593695	2.265	4.55E-03
Bt.5193.1.S1_at	*IL6*	interleukin 6 (interferon, beta 2)	NM_173923	2.630	2.38E-02
Bt.15739.1.S1_at	*IQCA1*	IQ motif containing with AAA domain 1	XM_001790491 /// XM_870442	2.080	5.16E-03
Bt.17513.1.A1_at	*IQGAP3*	IQ motif containing GTPase activating protein 3	NM_001098880	-2.691	5.49E-03
Bt.2334.1.S1_at	*ISM1*	isthmin 1 homolog (zebrafish)	NM_001163935 /// XM_583413	2.799	2.27E-02
Bt.6456.1.A1_at	*ITGB2*	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	NM_175781	2.152	7.59E-03
Bt.10816.1.S1_s_at	*ITGB5*	integrin, beta 5	NM_174679	2.216	2.78E-02
Bt.26660.1.S1_at	*JUN*	jun oncogene	NM_001077827	2.609	1.51E-02
Bt.22083.2.S1_at	*JUN*	jun oncogene	NM_001077827	2.232	2.69E-02
Bt.28037.1.S1_at	*KANK1*	KN motif and ankyrin repeat domains 1	XM_614789	2.009	1.99E-02

Bt.22460.1.S2_at	*KCNMA1*	potassium large conductance calcium-activated channel, subfamily M, alpha member	NM_174680	-3.274	2.22E-02
Bt.4631.2.S1_at	*KIF20A*	kinesin family member 20A	NM_001046288	-3.719	4.94E-03
Bt.278.1.S1_at	*KIF20A*	kinesin family member 20A	NM_001046288	-5.109	5.24E-03
Bt.10253.1.A1_at	*KIF22*	kinesin family member 22	NM_001101868	-3.505	5.26E-03
Bt.19274.1.A1_at	*KIF23*	kinesin family member 23	NM_001098038	-3.013	5.84E-03
Bt.26952.1.S1_at	*KIF2C*	kinesin family member 2C	NM_001101147	-2.232	5.53E-03
Bt.22869.1.S1_at	*KIF2C*	kinesin family member 2C	NM_001101147	-5.024	6.17E-03
Bt.1978.1.S1_at	*KIF4A*	kinesin family member 4A	XM_617283	-3.753	5.31E-03
Bt.2353.1.S1_at	*KIFC1*	kinesin family member C1	NM_001101936	-3.286	5.49E-03
Bt.351.1.S1_at	*KLF15*	Kruppel-like factor 15	NM_001082425	2.106	1.37E-02
Bt.17821.3.A1_at	*KLHL24*	kelch-like 24 (Drosophila)	XM_866793	2.098	3.75E-02
Bt.6441.1.S1_at	*KNTC1*	kinetochore associated 1	XM_582786	-3.620	8.11E-03

Bt.12504.1.S1_at	*KPNA2*	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	NM_001034449	-3.723	5.16E-03
Bt.13975.2.A1_at	*LAPTM5*	lysosomal protein transmembrane 5	NM_001046118	2.369	6.94E-03
Bt.5193.2.S1_a_at	*LCP1*	lymphocyte cytosolic protein 1 (L-plastin)	NM_001034720	2.533	4.91E-03
Bt.12217.1.S1_at	*LGALS3*	lectin, galactoside-binding, soluble, 3	NM_001102341	4.954	4.91E-03
Bt.9807.3.S1_at	*LGMN*	legumain	NM_174101	2.010	5.06E-03
Bt.2515.1.S1_at	*LIG1*	ligase I, DNA, ATP-dependent	NM_001102548	-2.004	1.43E-02
Bt.28346.2.S1_a_at	*LIPG*	lipase, endothelial	XM_586851	-2.201	3.34E-02
Bt.2529.1.S1_at	*LMNB1*	lamin B1	NM_001103295	-3.670	6.90E-03
Bt.23106.1.S1_at	*LOC100138846 /// LOC784932 /// LOC784964 /// SERPINA3 /// SERPINA3-1 /// SERPINA3-2 /// SERPINA3-7*	similar to endopin 2C /// similar to endopin 2B /// similar to Endopin 1b /// se	NM_001012283 /// NM_001081744 /// NM_001146301 /// NM_174768 /// XM_001252646 //	-2.137	4.75E-02
Bt.28430.1.S1_at	*LOC100139092*	similar to Probable G-protein coupled receptor 34	XR_042936	2.090	2.12E-02

Bt.3681.1.S1_at	*LOC100139766 /// LOC507024 /// LOC510212 /// LOC618416 /// LOC783134*	similar to immunoglobulin-like transcript 5 protein /// similar to Leukocyte imm	XM_001787794 /// XM_001788788 /// XM_583568 /// XR_042676 /// XR_042799	2.159	9.69E-03
Bt.21159.1.S1_at	*LOC100302527*	hypothetical protein LOC100302527	NM_001163442	-2.066	7.71E-03
Bt.26604.2.S1_at	*LOC504773*	regakine 1	NM_001034220	4.946	4.91E-03
Bt.28741.2.S1_at	*LOC507141*	CE5 protein-like	XM_583699	2.298	2.03E-02
Bt.10391.1.S1_at	*LOC509513 /// TRB@*	hypothetical LOC509513 /// T cell receptor, beta cluster	NM_001080904	2.213	3.20E-02
Bt.23779.1.A1_at	*LOC513508*	similar to acyl-Coenzyme A dehydrogenase family, member 10	XM_001788744	2.123	2.61E-02
Bt.1440.1.S1_at	*LOC513587*	Similar to UPF0474 protein C5orf41	XM_876203	2.463	5.53E-03
Bt.26046.1.A1_at	*LOC513587*	Similar to UPF0474 protein C5orf41	XM_876203	2.101	8.57E-03
Bt.22120.1.S1_at	*LOC516579*	similar to ATPase, Class II, type 9A	XR_028542	2.519	1.31E-02
Bt.13458.1.S1_at	*LOC518821*	similar to Centromeric protein E (CENP-E)	XR_027308	-4.967	4.91E-03
Bt.3017.1.S1_at	*LOC521099*	similar to family with sequence similarity 20, member A	XM_599356	2.025	1.63E-02

Bt.11525.2.A1_at	*LOC529947*	similar to signal peptide, CUB domain, EGF-like 2	XM_608409	3.166	5.24E-03
Bt.28162.3.S1_at	*LOC530077*	similar to GTPase, IMAP family member 5	XM_864682	2.181	1.41E-02
Bt.25773.1.A1_at	*LOC535166*	similar to mKIAA1077 protein	XR_027912	2.621	1.13E-02
Bt.21087.1.A1_at	*LOC539596*	similar to Transforming growth factor-beta induced protein IG-H3 precursor (Beta	XR_028016	2.121	5.68E-03
Bt.1296.1.S1_at	*LOC540455*	hypothetical protein LOC540455	NM_001099109	-7.261	4.91E-03
Bt.15856.1.S1_at	*LOC614351*	similar to DNA replication complex GINS protein PSF2	XM_865829	-2.170	1.58E-02
Bt.26968.1.S1_at	*LOC615685*	UPF0452 protein C7orf41 homolog	NM_001101246	2.063	9.41E-03
Bt.14166.2.S1_at	*LOC617744*	hypothetical LOC617744	XR_043042	2.202	1.24E-02
Bt.24411.1.A1_at	*LOC618360*	similar to Nitric oxide-inducible gene protein	XM_870692	-2.261	2.07E-02
Bt.22390.2.S1_at	*LOC618591*	similar to NKp80 NK receptor	NM_001101276	2.249	4.91E-03
Bt.10236.1.S1_at	*LOC782922*	similar to prostaglandin F synthetase II	NM_001166224 /// XM_001250622	2.216	9.48E-03
Bt.20074.1.S1_a_at	*LOC783399*	major allergen Equ c 1-like	XM_001252015	3.292	1.65E-02

Bt.26604.1.S1_at	*LOC784007*	Similar to LOC496253 protein	XM_001252441	2.986	5.35E-03
Bt.20570.1.S1_at	*LOC784034*	similar to Uncharacterized protein C1orf112 homolog	XM_001252463	-2.371	1.95E-02
Bt.15587.1.S1_at	*LSM4*	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_001035436	-2.010	1.38E-02
Bt.24813.1.A1_at	*LTF*	lactotransferrin	NM_180998	2.303	2.95E-02
Bt.14379.2.S1_at	*LY9*	lymphocyte antigen 9	NM_001075918	2.179	1.03E-02
Bt.20778.3.A1_at	*MAD2 /// MAD2L1*	mitotic checkpoint component Mad2 /// MAD2 mitotic arrest deficient-like 1 (yeas	NM_001079796 /// XM_001254565	-3.409	1.09E-02
Bt.1929.1.S1_at	*MAGOHB*	mago-nashi homolog B (Drosophila)	NM_001076252	-2.096	7.45E-03
Bt.5819.1.S1_at	*MANF*	mesencephalic astrocyte-derived neurotrophic factor	NM_001101211	-2.191	6.90E-03
Bt.13413.1.S1_at	*MAOB*	monoamine oxidase B	NM_177944	2.567	2.33E-02
Bt.858.1.S1_at	*MCM2*	similar to KIAA0030	XM_864352	-2.501	2.94E-02
Bt.27090.1.S1_at	*MCM3*	minichromosome maintenance complex component 3	NM_001013586	-3.118	2.43E-02
Bt.25834.1.A1_at	*MCM4*	minichromosome maintenance complex component 4	NM_001075158	-3.387	1.63E-02

Bt.21607.1.S1_at	*MCM5*	minichromosome maintenance complex component 5	NM_001075290	-2.408	1.40E-02
Bt.13480.1.S1_at	*MCM6*	minichromosome maintenance complex component 6	NM_001046234	-2.159	2.45E-02
Bt.3804.1.S1_at	*MELK*	maternal embryonic leucine zipper kinase	NM_001111260 /// XM_001787811	-4.538	7.85E-03
Bt.639.1.S1_at	*MERTK*	c-mer proto-oncogene tyrosine kinase	XM_580552	2.767	4.53E-03
Bt.1416.1.S1_at	*MMP19*	matrix metallopeptidase 19	NM_001075983	2.974	8.58E-03
Bt.21408.1.S1_at	*MOBKL2B*	MOB1, Mps One Binder kinase activator-like 2B (yeast)	NM_001046491	2.186	1.68E-02
Bt.5993.1.S1_at	*MPEG1*	macrophage expressed 1	NM_001046464	2.591	5.16E-03
Bt.22117.1.S1_at	*MRC1L1*	mannose receptor, C type 1-like 1	XM_001252128	2.500	5.88E-03
Bt.6537.1.S1_at	*MRC1L1*	mannose receptor, C type 1-like 1	XM_001252128	2.419	1.46E-02
Bt.20574.1.S1_at	*MRPL15*	mitochondrial ribosomal protein L15	NM_001075445	-2.010	2.41E-02
Bt.12217.2.S1_at	*MSR1*	macrophage scavenger receptor 1	NM_001113240 /// NM_174113	3.375	4.91E-03
Bt.17179.1.S1_at	*MT2A*	metallothionein 2A	NM_001075140 /// XM_586929	2.740	2.73E-02

Bt.7670.1.A1_at	*MTHFD1*	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrof	NM_001083477	-2.034	1.24E-02
Bt.28142.1.S1_at	*MXD3*	MAX dimerization protein 3	XM_883278	-3.018	4.91E-03
Bt.29925.1.S1_at	*MXI1*	MAX interactor 1	NM_001076331	2.073	1.32E-02
Bt.27319.2.S1_at	*MXI1*	MAX interactor 1	NM_001076331	2.027	9.97E-03
Bt.29923.1.S1_at	*MXRA8*	matrix-remodelling associated 8	NM_001075830	2.511	9.50E-03
Bt.8803.1.A1_at	*MYBL2*	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	NM_001075448	-2.117	7.58E-03
Bt.2806.1.S1_at	*MYH11*	myosin, heavy chain 11, smooth muscle	NM_001102127	2.160	4.77E-02
Bt.1577.1.S1_at	*N4BP2L1*	NEDD4 binding protein 2-like 1	NM_001046574	2.222	1.80E-02
Bt.28266.1.A1_at	*NCAPD3*	non-SMC condensin II complex, subunit D3	XM_868423	-2.036	1.16E-02
Bt.6129.1.S1_at	*NCAPG*	non-SMC condensin I complex, subunit G	NM_001102376	-3.984	4.91E-03
Bt.11129.1.S1_at	*NCAPG2*	non-SMC condensin II complex, subunit G2	XM_594801	-3.184	1.73E-02
Bt.28960.1.A1_at	*NCAPH*	non-SMC condensin I complex, subunit H	NM_001034213	-2.104	1.52E-02

Bt.28797.1.A1_at	*NCAPH*	non-SMC condensin I complex, subunit H	NM_001034213	-4.593	5.90E-03
Bt.2913.1.A1_at	*NDC80*	NDC80 homolog, kinetochore complex component (S. cerevisiae)	XM_582722	-4.151	5.98E-03
Bt.7035.2.S1_at	*NDRG1*	N-myc downstream regulated 1	NM_001035009	2.214	4.91E-03
Bt.13330.2.A1_at	*NKG7*	natural killer cell group 7 sequence	NM_001035279	2.157	4.91E-03
Bt.20074.2.S1_at	*NOL3*	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_001083688	2.950	4.55E-03
Bt.22759.1.S1_at	*NOL3*	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_001083688	2.038	1.05E-02
Bt.9538.1.S1_at	*NPL*	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NM_001045978	2.238	4.66E-03
Bt.4374.1.S1_at	*NRM*	nurim (nuclear envelope membrane protein)	NM_001037596	-2.223	4.91E-03
Bt.28502.1.S1_at	*NRP2*	neuropilin 2	XM_614062 /// XM_865994 /// XM_877502	2.594	4.91E-03
Bt.4670.1.S1_at	*NRP2*	neuropilin 2	XM_614062 /// XM_865994 /// XM_877502	2.489	1.17E-02
Bt.4010.1.S1_at	*NRP2*	neuropilin 2	XM_614062 /// XM_865994 /// XM_877502	2.083	7.71E-03
Bt.14005.1.S1_at	*NSL1*	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_001101876	-2.002	2.73E-02

Bt.12217.3.A1_at	*NTRK2*	Neurotrophic tyrosine kinase, receptor, type 2	NM_001075225	4.448	3.11E-02
Bt.22430.1.A1_at	*NTRK2*	Neurotrophic tyrosine kinase, receptor, type 2	NM_001075225	3.828	3.02E-02
Bt.4902.1.S1_at	*NTRK2*	neurotrophic tyrosine kinase, receptor, type 2	NM_001075225	2.730	2.07E-02
Bt.26155.1.A1_at	*NUPR1*	nuclear protein, transcriptional regulator, 1	NM_001114515 /// XM_867457	3.544	6.27E-03
Bt.27531.1.A1_at	*NUSAP1*	nucleolar and spindle associated protein 1	NM_001046571	-5.067	5.06E-03
Bt.24844.1.S1_at	*OIP5*	Opa interacting protein 5	XM_588370	-3.765	8.94E-03
Bt.20397.1.S1_at	*OIT3*	oncoprotein induced transcript 3	NM_001046064	-3.856	5.16E-03
Bt.26309.1.A1_at	*ORC1L*	origin recognition complex, subunit 1-like (yeast)	NM_001014918	-2.617	2.18E-02
Bt.21343.2.A1_a_at	*OSMR*	oncostatin M receptor	NM_001080272	2.378	1.54E-02
Bt.23089.1.S1_at	*OSMR*	oncostatin M receptor	NM_001080272	2.342	1.24E-02
Bt.26855.1.S1_at	*PAF*	KIAA0101 protein	NM_001015678	-6.987	5.24E-03
Bt.3537.1.S1_at	*PARP12*	poly (ADP-ribose) polymerase family, member 12	XM_590833	2.033	4.55E-03

Bt.5278.2.S1_at	*PCDH7*	protocadherin 7	XM_864701	-2.115	3.38E-02
Bt.28062.1.S1_at	*PCNA*	proliferating cell nuclear antigen	NM_001034494	-2.596	1.58E-02
Bt.12606.1.S1_a_at	*PCOLCE2*	procollagen C-endopeptidase enhancer 2	NM_001075629	2.143	3.25E-02
Bt.26890.1.S1_at	*PDK4*	pyruvate dehydrogenase kinase, isozyme 4	NM_001101883	2.200	9.16E-03
Bt.16687.1.A1_at	*PDK4*	pyruvate dehydrogenase kinase, isozyme 4	NM_001101883	2.045	8.36E-03
Bt.1343.1.S1_at	*PDPN*	podoplanin	NM_001033120	2.138	5.84E-03
Bt.3532.1.A1_at	*PHGDH*	phosphoglycerate dehydrogenase	NM_001035017	-2.659	5.35E-03
Bt.22969.1.S1_at	*PID1*	phosphotyrosine interaction domain containing 1	NM_001079584	2.993	9.50E-03
Bt.16725.1.S1_at	*PKIB*	protein kinase (cAMP-dependent, catalytic) inhibitor beta	NM_001114518 /// XM_001788472 /// XM_001788483 /// XM_001788486 /// XM_001788495	4.523	6.90E-03
Bt.41.1.S1_at	*PLA1A*	phospholipase A1 member A	NM_001015610	2.801	4.91E-03
Bt.22385.2.S1_a_at	*PLA1A*	phospholipase A1 member A	NM_001015610	2.354	4.91E-03

Bt.13583.1.A1_at	*PLIN5*	perilipin 5	NM_001101136	-2.209	1.94E-02
Bt.14219.1.S1_at	*PLK1*	polo-like kinase 1 (Drosophila)	NM_001038173	-2.332	7.87E-03
Bt.23094.4.S1_at	*PLN*	phospholamban	NM_001103319	2.174	5.02E-03
Bt.13330.1.S1_at	*PLXNC1*	plexin C1	XM_596354	2.148	1.00E-02
Bt.4995.2.S1_at	*POLE2*	polymerase (DNA directed), epsilon 2 (p59 subunit)	NM_001105383	-2.562	2.69E-02
Bt.3734.1.A1_at	*PPA1*	pyrophosphatase (inorganic) 1	NM_001075118	-2.059	2.79E-02
Bt.12087.1.A1_at	*PRC1*	protein regulator of cytokinesis 1	NM_001076543	-4.719	5.24E-03
Bt.864.2.S1_at	*PRDM1*	PR domain containing 1, with ZNF domain	XM_618588	2.180	5.45E-03
Bt.4482.1.S1_at	*PSAT1*	phosphoserine aminotransferase 1	NM_001102150	-2.096	1.44E-02
Bt.15725.1.A1_at	*PSRC1*	proline/serine-rich coiled-coil 1	NM_001046501	-2.254	7.17E-03
Bt.18316.2.S1_at	*PTGDS*	prostaglandin D2 synthase 21kDa (brain)	NM_174791	2.199	2.04E-02
Bt.23668.1.A1_at	*PTGER4*	prostaglandin E receptor 4 (subtype EP4)	NM_174589	2.548	9.71E-03

Bt.18776.1.S1_at	*PTTG1*	pituitary tumor-transforming 1	NM_001034310	-6.471	5.16E-03
Bt.13134.1.S1_at	*RACGAP1*	Rac GTPase activating protein 1	XM_592496	-3.196	5.41E-03
Bt.25412.1.A1_at	*RAD51AP1*	RAD51 associated protein 1	NM_001076403	-5.508	7.64E-03
Bt.8939.1.S1_at	*RASGEF1B*	RasGEF domain family, member 1B	NM_001083649	2.664	5.99E-03
Bt.27087.1.A1_at	*RBM5*	RNA binding motif protein 5	NM_001046374	2.686	3.63E-02
Bt.18557.1.S1_at	*RBPMS*	RNA binding protein with multiple splicing	NM_001046535	2.299	4.83E-03
Bt.5506.1.A1_at	*RDM1*	RAD52 motif 1	XM_591173	-2.110	1.79E-02
Bt.29403.1.S1_at	*RENBP*	renin binding protein	NM_001046223 /// XM_594363	2.223	7.64E-03
Bt.19884.1.A1_at	*RGS1*	regulator of G-protein signaling 1	XM_001252887	3.006	3.63E-02
Bt.6980.1.S1_at	*RGS2*	regulator of G-protein signaling 2, 24kDa	NM_001075596	2.671	1.76E-02
Bt.27645.1.A1_at	*RMI2*	chromosome 16 open reading frame 75 ortholog	NM_001099720	-2.718	2.29E-02
Bt.6406.1.S2_at	*RNASE6*	ribonuclease, RNase A family, k6	NM_174594	2.031	2.64E-02

Bt.20027.1.S1_at	*RPA2*	replication protein A2, 32kDa	NM_001045984	-2.017	4.18E-02
Bt.19567.2.S1_at	*RPA3*	replication protein A3, 14kDa	NM_001034427	-2.309	6.27E-03
Bt.26507.1.S1_at	*RRAD*	Ras-related associated with diabetes	NM_001045913	2.171	2.20E-02
Bt.24859.1.A1_at	*RRM1*	ribonucleotide reductase M1	NM_001113296 /// XM_879432	-2.021	2.61E-02
Bt.20277.1.S1_at	*RRM2*	ribonucleotide reductase M2 polypeptide	XM_584910 /// XM_875690	-5.660	7.87E-03
Bt.2113.1.S1_at	*RTP4*	receptor (chemosensory) transporter protein 4	NM_001075961	2.302	4.55E-03
Bt.16049.1.S1_at	*RYR2*	ryanodine receptor 2 (cardiac)	XM_001788290	2.410	3.25E-02
Bt.8633.1.A1_at	*S100A13*	8KDa amlexanox-binding protein	NM_205800	2.527	6.41E-03
Bt.7467.1.S1_at	*S100A2*	S100 calcium binding protein A2	NM_001034367	-2.254	5.74E-03
Bt.27140.1.S1_at	*SAA3*	serum amyloid A 3	NM_181016	5.852	4.16E-02
Bt.12328.1.S1_at	*SAMSN1*	SAM domain, SH3 domain and nuclear localization signals 1	NM_001035404	2.855	4.83E-03
Bt.24258.1.S1_at	*SAMSN1*	SAM domain, SH3 domain and nuclear localization signals 1	NM_001035404	2.476	4.91E-03

Bt.1377.1.S1_at	*SERPING1*	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	NM_174821	3.931	4.91E-03
Bt.393.1.S1_at	*SERPING1*	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	NM_174821	3.662	4.91E-03
Bt.7962.1.S1_at	*SFRS1*	splicing factor, arginine/serine-rich 1	NM_001076394	-2.294	7.57E-03
Bt.7870.1.S1_at	*SGOL1*	shugoshin-like 1 (S. pombe)	NM_001081617	-3.793	7.72E-03
Bt.3756.1.A1_at	*SHCBP1*	SHC SH2-domain binding protein 1	XM_601664	-5.840	5.24E-03
Bt.15231.1.S1_at	*SHISA2*	shisa homolog 2 (Xenopus laevis)	NM_001101265	2.184	3.46E-02
Bt.6038.1.S1_at	*SIGLEC1*	sialic acid binding Ig-like lectin 1, sialoadhesin	XM_870818	2.234	7.41E-03
Bt.27212.1.A1_at	*SKA1*	spindle and kinetochore associated complex subunit 1	NM_001075327	-4.355	6.57E-03
Bt.1645.1.S1_at	*SKA3*	spindle and kinetochore associated complex subunit 3	NM_001110067	-2.962	1.95E-02
Bt.1088.2.S1_at	*SKA3*	spindle and kinetochore associated complex subunit 3	NM_001110067	-3.281	9.29E-03
Bt.6817.1.S1_at	*SLAMF7*	SLAM family member 7	XM_001790094	2.676	5.24E-03
Bt.27837.1.S1_at	*SLAMF9*	SLAM family member 9	XM_864973	2.077	4.55E-03

Bt.25039.1.S1_at	*SLC11A1*	solute carrier family 11 (proton-coupled divalent metal ion transporters), membe	NM_174652	2.189	2.54E-02
Bt.15731.1.A1_at	*SLC16A1*	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	NM_001037319	-2.264	1.79E-02
Bt.3100.1.A1_at	*SLC24A6*	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	NM_001177596 /// XM_585733	2.045	5.81E-03
Bt.7264.1.S1_at	*SLC31A2*	solute carrier family 31 (copper transporters), member 2	NM_001034556	2.177	4.55E-03
Bt.3211.1.S2_at	*SLC40A1*	solute carrier family 40 (iron-regulated transporter), member 1	NM_001077970	2.123	1.04E-02
Bt.6397.2.S1_at	*SLC7A7*	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	NM_001075151	2.650	5.16E-03
Bt.16538.1.S1_at	*SLCO2A1*	solute carrier organic anion transporter family, member 2A1	NM_174829	-2.210	7.87E-03
Bt.13537.1.A1_at	*SMC2*	structural maintenance of chromosomes 2	XM_585705	-2.504	3.59E-02
Bt.15534.1.S1_a_at	*SMC4*	structural maintenance of chromosomes 4	NM_001105326	-2.313	6.57E-03
Bt.1920.1.S1_at	*SMOC2*	SPARC related modular calcium binding 2	NM_001098134	2.585	2.08E-02
Bt.15730.1.S1_at	*SMOC2*	SPARC related modular calcium binding 2	NM_001098134	2.306	1.96E-02

Bt.20431.2.S1_at	*SNHG3-RCC1*	SNHG3-RCC1 readthrough transcript	NM_001105408	-2.064	1.02E-02
Bt.9517.1.S1_a_at	*SNX31*	sorting nexin 31	XM_001249966	2.493	1.82E-02
Bt.10696.1.S1_at	*SPAG5*	sperm associated antigen 5	XM_580731	-4.797	4.91E-03
Bt.12236.1.S1_at	*SPC24*	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	NM_001075391	-4.898	5.45E-03
Bt.1491.1.S1_at	*SPOCK2*	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	NM_001101115	3.051	1.32E-02
Bt.28366.1.A1_at	*STARD10*	StAR-related lipid transfer (START) domain containing 10	XM_592504	2.725	5.24E-03
Bt.20014.1.S1_at	*STARD10*	StAR-related lipid transfer (START) domain containing 10	XM_592504	2.432	6.57E-03
Bt.28741.1.A1_at	*STEAP1*	six transmembrane epithelial antigen of the prostate 1	XM_593128	2.449	3.34E-02
Bt.9363.1.A1_at	*STIL*	SCL/TAL1 interrupting locus	XR_028515	-3.203	1.20E-02
Bt.13352.2.S1_at	*STRA13*	stimulated by retinoic acid 13 homolog (mouse)	NM_001114527 /// XM_870351	-2.141	1.01E-02
Bt.24442.1.A1_at	*SULT1A1*	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	NM_177521	2.174	1.07E-02
Bt.12924.1.S1_at	*TACC3*	transforming, acidic coiled-coil containing protein 3	NM_001100305	-3.679	6.18E-03

Bt.13789.1.A1_at	*TAGLN3*	transgelin 3	NM_001034499	-2.168	1.95E-02
Bt.24202.1.S1_at	*TCF19*	transcription factor 19	NM_001083684	-3.431	8.60E-03
Bt.8003.1.A1_at	*TCP11L2*	t-complex 11 (mouse)-like 2	NM_001105431	2.187	4.00E-02
Bt.23216.1.S1_at	*TFF2*	trefoil factor 2	NM_001083521	-2.884	6.91E-03
Bt.2990.1.S1_at	*TGIF1*	TGFB-induced factor homeobox 1	NM_001128499 /// XM_587139	2.187	2.51E-02
Bt.196.1.S1_at	*TIMD4*	T-cell immunoglobulin and mucin domain containing 4	NM_001075320	2.281	2.42E-02
Bt.2899.1.S1_at	*TK1*	thymidine kinase 1, soluble	NM_001097572	-3.215	1.95E-02
Bt.8957.1.S1_at	*TLR7*	toll-like receptor 7	NM_001033761	2.230	5.16E-03
Bt.2551.1.S1_at	*TMEM150C*	transmembrane protein 150C	NM_001078001	2.327	1.14E-02
Bt.24687.1.A1_at	*TMEM150C*	transmembrane protein 150C	NM_001078001	2.092	8.91E-03
Bt.16786.1.A1_at	*TMEM156*	transmembrane protein 156	NM_001083469	2.349	5.24E-03
Bt.5573.1.S1_at	*TMEM88*	transmembrane protein 88	NM_001098378	-2.409	4.91E-03

Bt.2899.1.S2_at	*TOP2A*	topoisomerase (DNA) II alpha 170kDa	XM_001254457	-4.452	5.99E-03
Bt.5362.2.S1_a_at	*TOP2A*	topoisomerase (DNA) II alpha 170kDa	XM_001254457	-5.446	4.83E-03
Bt.22265.1.S1_at	*TPX2*	TPX2, microtubule-associated, homolog (Xenopus laevis)	NM_001098898	-3.787	5.49E-03
Bt.9777.1.S1_at	*TPX2*	TPX2, microtubule-associated, homolog (Xenopus laevis)	NM_001098898	-3.890	6.27E-03
Bt.19322.1.A1_at	*TRIP13*	thyroid hormone receptor interactor 13	XR_027559	-3.769	1.92E-02
Bt.16058.1.A1_at	*TROAP*	trophinin associated protein (tastin)	NM_001024477	-2.802	4.55E-03
Bt.4802.1.S1_at	*TUBA1A* /// *TUBA1B* /// *TUBA1C*	tubulin, alpha 1a /// tubulin, alpha 1b /// tubulin, alpha 1c	NM_001034204 /// NM_001114856 /// NM_001166505 /// XM_001790546 /// XM_876383	-2.326	1.74E-02
Bt.24966.1.S1_at	*TYMS*	thymidylate synthetase	NM_001037816	-2.366	1.70E-02
Bt.1048.1.S1_at	*TYROBP*	TYRO protein tyrosine kinase binding protein	NM_174627	3.474	5.16E-03
Bt.15980.1.A1_at	*UBE2C*	ubiquitin-conjugating enzyme E2C	NM_001037449	-6.077	4.91E-03
Bt.15720.1.S1_at	*UBE2L6*	ubiquitin-conjugating enzyme E2L 6	NM_001098917	2.702	4.55E-03

Bt.5934.1.S1_at	*UBE2L6*	ubiquitin-conjugating enzyme E2L 6	NM_001098917	2.515	4.53E-03
Bt.29203.1.A1_at	*UBE2S*	ubiquitin-conjugating enzyme E2S	NM_001076472	-2.437	7.61E-03
Bt.25661.1.A1_at	*UHRF1*	ubiquitin-like with PHD and ring finger domains 1	NM_001103098	-4.697	1.04E-02
Bt.21513.1.A1_at	*UHRF1*	ubiquitin-like with PHD and ring finger domains 1	NM_001103098	-7.020	7.17E-03
Bt.5578.1.S1_at	*VCAM1*	vascular cell adhesion molecule 1	NM_174484	2.527	1.57E-02
Bt.15925.1.S1_at	*VEGFA*	vascular endothelial growth factor A	NM_174216	-2.717	8.94E-03
Bt.28878.1.S1_at	*VNN1*	vanin 1	NM_001024556	2.886	4.85E-02
Bt.19567.1.A1_at	*VRK1*	vaccinia related kinase 1	NM_001038224	-2.749	1.77E-02
Bt.20606.2.S1_at	*VSIG4*	V-set and immunoglobulin domain containing 4	NM_001046529	2.889	1.54E-02
Bt.11159.1.S1_at	*WDFY4*	WDFY family member 4	XM_606192	2.164	4.55E-03
Bt.13336.1.A1_at	*WIPF3*	WAS/WASL interacting protein family, member 3	XM_001254241	2.207	5.81E-03
Bt.29462.1.S1_at	*YPEL3*	yippee-like 3 (Drosophila)	XR_042991	2.830	1.56E-02

Bt.17157.1.A1_at	*ZFP36*	zinc finger protein 36, C3H type, homolog (mouse)	NM_174493	2.269	6.90E-03
Bt.4441.1.S1_at	*ZSWIM7*	zinc finger, SWIM-type containing 7	XM_591893	2.282	1.30E-02
Bt.27172.1.A1_at	*ZWINT*	ZW10 interactor	NM_001040529	-3.083	1.21E-02
Bt.10855.1.S1_at	---	---	---	4.942	1.08E-02
Bt.22026.1.S1_at	---	---	---	4.608	9.10E-03
Bt.22366.1.S1_at	---	---	---	3.541	1.22E-02
Bt.1370.1.S1_at	---	---	---	3.462	7.41E-03
Bt.21238.1.S1_at	---	---	---	3.307	4.98E-03
Bt.7331.1.S2_at	---	---	---	3.170	1.50E-02
Bt.24247.1.S1_at	---	---	---	3.151	4.53E-03
Bt.11587.3.A1_a_at	---	---	---	3.088	6.32E-03
Bt.12500.2.S1_a_at	---	---	---	3.083	1.79E-02

Bt.26896.1.S1_at	---	---	---	3.058	1.41E-02
Bt.22969.1.S1_a_at	---	---	---	2.948	5.79E-03
Bt.26521.1.S1_at	---	---	---	2.936	2.07E-02
Bt.26636.1.S1_at	---	---	---	2.924	5.74E-03
Bt.6556.1.S1_at	---	---	---	2.884	2.24E-02
Bt.1537.1.S1_at	---	---	---	2.827	6.83E-03
Bt.22491.1.A1_at	---	---	---	2.791	1.71E-02
Bt.18081.2.S1_at	---	---	---	2.784	1.76E-02
Bt.7033.1.S1_at	---	---	---	2.752	6.92E-03
Bt.12619.1.S1_at	---	---	---	2.732	9.70E-03
Bt.8947.1.S1_at	---	---	---	2.695	1.94E-02
Bt.26722.1.A1_a_at	---	---	---	2.676	1.12E-02

Bt.12718.1.A1_at	---	---	---	2.670	8.51E-03
Bt.13573.1.A1_at	---	---	---	2.629	6.74E-03
Bt.13214.1.S1_at	---	---	---	2.581	1.95E-02
Bt.11271.1.S1_at	---	---	---	2.564	1.26E-02
Bt.5262.1.S1_at	---	---	---	2.560	2.03E-02
Bt.24872.1.S1_at	---	---	---	2.508	7.81E-03
Bt.15730.2.S1_at	---	---	---	2.469	5.74E-03
Bt.12550.1.S1_at	---	---	---	2.458	4.06E-02
Bt.1858.1.A1_at	---	---	---	2.420	2.85E-02
Bt.20164.1.S1_at	---	---	---	2.403	8.26E-03
Bt.5970.1.S1_a_at	---	---	---	2.372	5.79E-03
Bt.24461.1.A1_at	---	---	---	2.369	1.95E-02

Bt.1518.1.S1_at	---	---	---	2.368	1.53E-02
Bt.23278.1.S1_at	---	---	---	2.364	4.91E-03
Bt.10499.1.S1_at	---	---	---	2.353	1.27E-02
Bt.8308.2.S1_at	---	---	---	2.353	1.21E-02
Bt.11001.1.S1_at	---	---	---	2.344	9.03E-03
Bt.28346.1.A1_at	---	---	---	2.332	1.83E-02
Bt.8743.1.S1_at	---	---	---	2.319	4.66E-03
Bt.8308.1.A1_at	---	---	---	2.319	1.64E-02
Bt.4285.1.S1_at	---	---	---	2.314	8.58E-03
Bt.21576.1.S1_at	---	---	---	2.300	5.16E-03
Bt.4110.1.S1_at	---	---	---	2.293	2.26E-02
Bt.10092.1.S1_at	---	---	---	2.293	1.27E-02

Bt.23597.1.S1_at	---	---	---	2.264	6.57E-03
Bt.13975.1.S1_a_at	---	---	---	2.243	1.25E-02
Bt.7603.1.S1_at	---	---	---	2.200	4.91E-03
Bt.22390.3.A1_at	---	---	---	2.194	1.39E-02
Bt.9101.1.S1_at	---	---	---	2.194	5.16E-03
Bt.2810.1.A1_at	---	---	---	2.186	1.66E-02
Bt.16141.1.S1_at	---	---	---	2.177	8.51E-03
Bt.2629.1.S1_at	---	---	---	2.176	4.70E-02
Bt.25305.1.A1_at	---	---	---	2.147	4.55E-03
Bt.19267.1.A1_at	---	---	---	2.139	4.69E-02
Bt.20308.1.S1_at	---	---	---	2.123	3.56E-02
Bt.4001.1.S1_at	---	---	---	2.113	4.47E-02

Bt.23514.1.S1_at	---	---	---	2.097	6.65E-03
Bt.21047.1.A1_at	---	---	---	2.094	2.11E-02
Bt.24760.1.S1_at	---	---	---	2.084	5.16E-03
Bt.27356.1.S1_at	---	---	---	2.061	5.24E-03
Bt.22379.1.S1_at	---	---	---	2.058	1.58E-02
Bt.14576.1.A1_at	---	---	---	2.054	5.88E-03
Bt.28439.1.S1_a_at	---	---	---	2.053	1.31E-02
Bt.27328.1.S1_at	---	---	---	2.045	1.01E-02
Bt.9662.1.S1_at	---	---	---	2.038	1.91E-02
Bt.14379.1.A1_at	---	---	---	2.037	1.47E-02
Bt.19757.1.A1_at	---	---	---	2.023	8.51E-03
Bt.5392.1.S1_at	---	---	---	2.015	1.54E-02

Bt.12986.1.S1_at	---	---	---	2.011	1.31E-02
Bt.14166.1.A1_at	---	---	---	2.011	9.49E-03
Bt.29271.1.A1_at	---	---	---	2.007	5.53E-03
Bt.24927.1.A1_at	---	---	---	2.006	9.95E-03
Bt.13588.3.A1_at	---	---	---	2.001	2.77E-02
Bt.22314.1.S1_at	---	---	---	-2.021	7.41E-03
Bt.14026.1.A1_at	---	---	---	-2.024	1.08E-02
Bt.1130.1.S1_at	---	---	---	-2.036	6.74E-03
Bt.27997.1.S1_at	---	---	---	-2.056	6.44E-03
Bt.11993.1.S1_at	---	---	---	-2.057	2.00E-02
Bt.12576.3.S1_a_at	---	---	---	-2.081	5.26E-03
Bt.6133.2.A1_at	---	---	---	-2.090	1.85E-02

Bt.12610.1.A1_at	---	---	---	-2.096	3.77E-02
Bt.21820.1.S1_at	---	---	---	-2.127	2.30E-02
Bt.6404.1.S1_at	---	---	---	-2.161	1.51E-02
Bt.9202.1.S1_at	---	---	---	-2.171	1.14E-02
Bt.29327.1.A1_at	---	---	---	-2.181	1.44E-02
Bt.137.1.S1_at	---	---	---	-2.235	4.91E-03
Bt.13954.1.S1_at	---	---	---	-2.272	2.54E-02
Bt.17377.1.S1_at	---	---	---	-2.300	1.27E-02
Bt.12063.1.S1_at	---	---	---	-2.352	2.62E-02
Bt.24218.2.S1_a_at	---	---	---	-2.377	7.14E-03
Bt.287.1.S1_at	---	---	---	-2.512	4.53E-03
Bt.23854.1.A1_at	---	---	---	-2.610	7.87E-03

Bt.9841.1.S1_at	---	---	---	-2.757	6.81E-03
Bt.9577.1.S1_a_at	---	---	---	-2.890	7.58E-03
Bt.20890.1.S1_at	---	---	---	-3.257	6.74E-03
Bt.9455.1.A1_at	---	---	---	-3.607	5.24E-03
Bt.24288.1.A1_at	---	---	---	-3.667	6.57E-03
Bt.26530.1.S1_at	---	---	---	-3.724	5.30E-03
Bt.16925.1.A1_at	---	---	---	-4.071	5.30E-03
Bt.25837.1.S1_at	---	---	---	-4.201	9.31E-03
Bt.23271.1.A1_at	---	---	---	-4.345	4.83E-03
Bt.10648.1.S1_at	---	---	---	-4.461	5.24E-03
Bt.2725.1.S1_at	---	---	---	-4.564	6.27E-03
Bt.2.1.S1_at	---	---	---	-5.436	6.57E-03

Bt.23658.1.A1_at	---	---	---	-5.989	5.06E-03
Bt.4138.2.S1_at	---	---	---	-6.109	4.53E-03
Bt.24827.1.A1_at	---	---	---	-7.608	8.58E-03

Analysis by ANOVA in Partek, with > 2-fold change, $P < 0.05$ (n = 543), in alphabetical order. Probe sets which do not have gene assignations were placed at the end of the list. The P-value for multiple corrections was determined by the step-up FDR method.