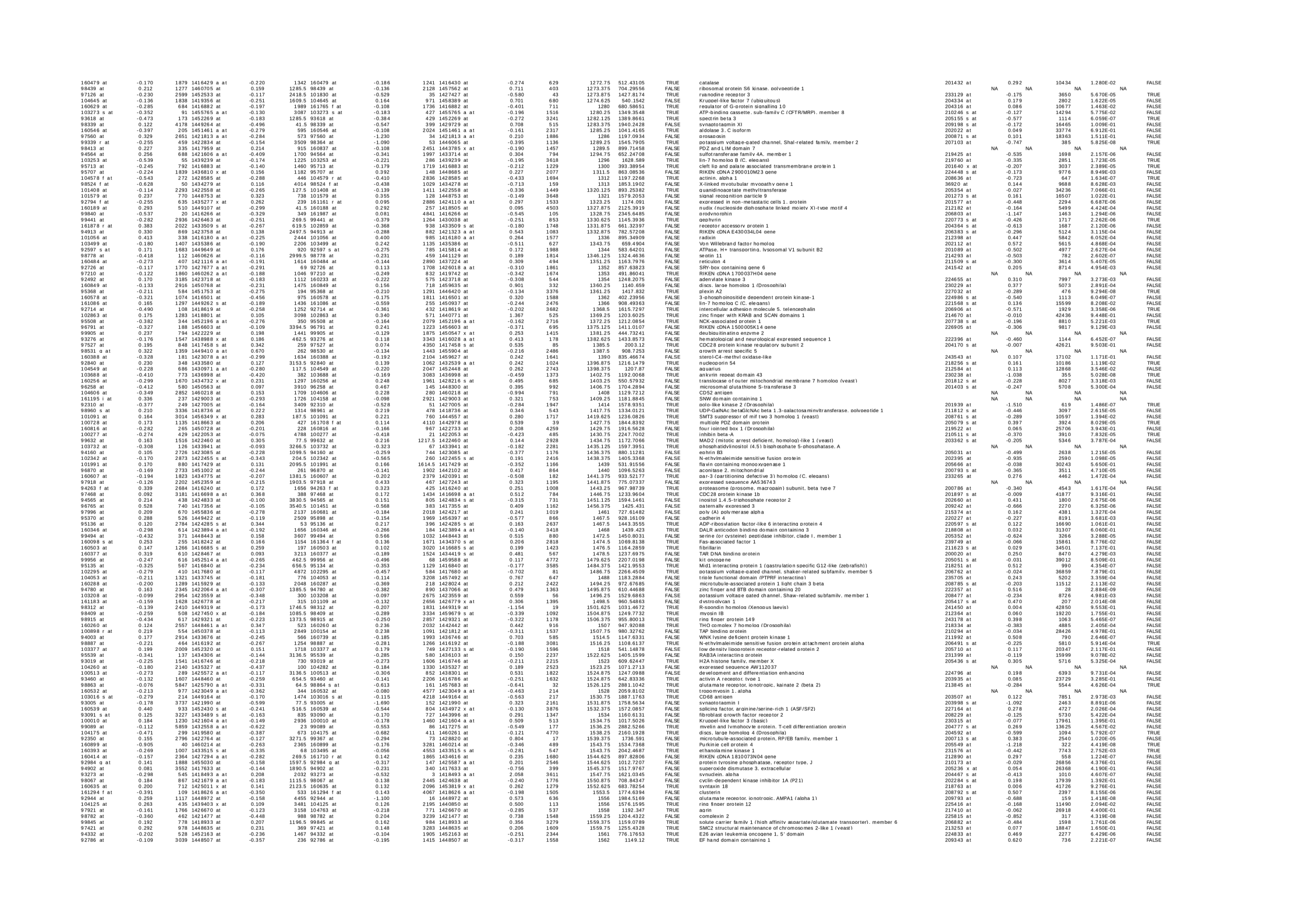
R6/1 24w PS	R6/1 M	R6/1 RANK	R6/2 6w PS	R6/2 6w M	R6/2 6w RANK	CHL2 15m PS	CHL2 15m M	CHL2 15m RANK	HdhO92 18m PS	HdhO92 18m M	Hdh O92 18m	Mean Rank Early	sdRank	concordance mice	Gene title	human HD PS	human HD M	human HD RANK	human HD FDR p	human-model concordance
100003 at	-1.147	7	1427306 at	-0.937	41.5	100003 at	-0.627	44	1427306 at	-1.697	6	24.625	20.957795	TRUE	ryanodine receptor 1, skeletal muscle	205485 at	0.564	1855	3.024E-06	FALSE
103282 at	-0.932	41	1417804 at	-0.833	77.5	103282 at	-0.943	27	1417804 at	-0.991	40	46.375	21.707813	TRUE	RAS, guanyl releasing protein 2	208206 s at	-0.804	387	5.846E-08	TRUE
96496 g at	-0.827	73	1421175 at	-0.506	35	96497 s at	-1.030	4	1460111 at	-0.510	115	56.75	48.002604	TRUE	myelin transcription factor 1-like	210016 at	-1.469	1202	7.254E-07	TRUE
103752 r at	-0.536	83	1422036 at	-0.446	77.5	100761 at	-0.472	172	1455156 at	-0.868	41	93.375	55.631788	TRUE	striatin, calmodulin binding protein	240969 at	-0.120	11077	1.776E-02	TRUE
98300 at	-0.634	29	1419225 at	-0.565	137	98300 at	-0.404	90	1419225 at	-0.540	158	103.5	57.227616	TRUE	calcium channel, voltage-dependent, alpha2/delta subunit 3	219714 s at	-1.042	577	1.294E-07	TRUE
94977 at	-0.870	39	1417279 at	-0.690	41.5	93895 s at	-0.767	28	1457189 at	-0.438	366	118.625	165.0209	TRUE	inositol 1,4,5-triphosphate receptor 1	211323 s at	-1.077	313	4.156E-08	TRUE
98457 at	-0.654	136	1452071 at	-0.385	124	98457 at	-0.631	122	1434096 at	-0.453	126	127	6.2182527	TRUE	solute carrier family 4 (anion exchanger), member 4	210738 s at	-0.236	7063	1.656E-03	TRUE
103905 at	-0.332	294	1428485 at	-0.705	25	103905 at	-0.369	42	1428485 at	-0.831	172	133.25	125.68048	TRUE	carbonic anyhydrase 12	204508 s at	-1.094	126	1.142E-08	TRUE
102711 at	-0.545	21	1419221 a at	-0.249	506.5	102711 at	-0.764	6	1419221 a at	-0.958	18	137.875	245.83544	TRUE	regulator of G-protein signaling 14	211021 s at	-1.067	37	3.440E-09	TRUE
92642 at	-0.529	154	1448752 at	-0.579	29	92642 at	-0.633	10	1448752 at	-0.359	400	148.25	179.57798	TRUE	carbonic anhydrase 2	209301 at	0.051	38737	8.429E-01	FALSE
102725 at	-0.530	134	1454043 a at	-0.676	97.5	162087 f at	-0.319	232	1448468 a at	-0.641	138	150.375	57.386664	TRUE	potassium voltage-gated channel, shaker-related subfamily, beta member 1	210471 s at	-1.595	50	4.008E-09	TRUE
101363 at	-1.119	26	1427519 at	-0.698	146.5	101364 at	-0.776	158	1427519 at	-1.081	283	153.375	105.03283	TRUE	adenosine A2a receptor	205013 s at	-1.233	79	5.363E-09	TRUE
99944 at	-0.792	34	1450930 at	-0.561	326	99944 at	-0.444	61	1450930 at	-0.495	204	156.25	135.53935	TRUE	hippocalcin	205454 at	-1.339	586	1.318E-07	TRUE
99892 at	-0.282	304	1419425 at	-0.546	77.5	99892 at	-0.305	191	1434172 at	-0.888	57	157.375	114.14127	TRUE	cannabinoid receptor 1 (brain)	213436 at	-1.714	134	1.219E-08	TRUE
97259 at	-1.420	5	1422609 at	-0.707	420.5	97259 at	-1.080	37	1422609 at	-0.839	170	158.125	188.9446	TRUE	cAMP-regulated phosphoprotein 19	214553 s at	-1.682	293	3.621E-08	TRUE
99342 at	-0.830	4	1449980 a at	-0.689	29	99342 at	-0.401	616	1449980 a at	-0.694	52	175.25	294.48642	TRUE	gamma-aminobutyric acid (GABA-A) receptor, subunit delta	208457 at	-0.772	33	3.329E-09	TRUE
99504 at	-0.509	324	1451008 at	-0.505	283	99504 at	-0.735	54	1451008 at	-0.928	61	180.5	143.03962	TRUE	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	208065 at	-0.832	1142	6.431E-07	TRUE
160822 at	-0.408	171	1428443 a at	-0.467	20	160822 at	-0.237	497	1428443 a at	-0.541	62	187.5	215.9236	TRUE	Rap1 GTPase-activating protein	203911 at	-1.026	541	1.161E-07	TRUE
93464 at	-0.337	339	1437082 at	-0.465	41.5	93464 at	-0.348	362	1435769 at	-0.519	84	206.625	167.29982	TRUE	A kinase (PRKA) anchor protein (yotiao) 9	215483 at	0.168	17773	1.342E-01	FALSE
96810 at	-0.759	9	1454086 a at	-0.317	777	93666 at	-0.654	22	1454086 a at	-0.854	31	209.75	378.27448	TRUE	LIM domain only 2	204249 s at	0.203	20416	2.136E-01	FALSE
100536 at	-0.531	409	1450088 a at	-0.826	1	99046 at	-0.788	62	1436263 at	-0.568	376	212	210.33782	TRUE	myelin-associated oligodendrocytic basic protein	235794 at	0.415	11345	1.981E-02	FALSE
102099 f at	-0.477	77	1435525 at	-0.367	117.5	101856 at	-0.318	124	1435525 at	-0.315	584	225.625	239.81985	TRUE	potassium channel tetramerisation domain containing 17	205561 at	-0.332	1970	3.591E-06	TRUE
97385 at	0.236	276	1419509 a at	0.336	251.5	97385 at	0.310	303	1419509 a at	0.512	75	226.375	103.08522	TRUE	N-acetylglucosamine kinase	218231 at	0.120	10678	1.463E-02	TRUE
160137 at	-0.329	208	1450026 a at	-0.481	276	160137 at	-0.458	279	1450026 a at	-0.632	169	233	53.808302	TRUE	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	219326 s at	-0.604	519	1.108E-07	TRUE
103317 at	-0.792	43	1423285 at	-0.829	10	103317 at	-0.633	887	1423285 at	-0.797	14	238.5	432.58333	TRUE	coagulation factor C homolog (Limulus polyphemus)	205229 s at	-1.684	1106	5.965E-07	TRUE
102652 at	-0.231	723	1460038 at	-0.332	116	102652 at	-0.377	57	1460038 at	-0.570	79	243.75	320.42615	TRUE	POU domain, class 3, transcription factor 1	210475 at	-0.291	3898	7.669E-05	TRUE
104499 at	-0.741	80	1421768 a at	-0.539	89.5	104499 at	-0.553	98	1437363 at	-0.481	712	244.875	311.50344	TRUE	homer homolog 1 (Drosophila)	226651 at	-0.719	1139	6.424E-07	TRUE
92734 at	-0.509	45	1423415 at	-0.347	195	92734 at	-0.830	738	1423415 at	-0.889	15	248.25	335.86046	TRUE	G protein-coupled receptor 83	222953 at	-0.154	18245	1.473E-01	FALSE
100044 at	-0.361	523	1416003 at	-0.621	51	100044 at	-0.821	312	1416003 at	-0.528	238	281	195.17001	TRUE	claudin 11	228335 at	0.393	13021	3.722E-02	FALSE
160841 at	-0.777	10	1418174 at	-0.396	160.5	160841 at	-0.345	916	1418174 at	-0.594	42	282.125	427.51304	TRUE	D site albumin promoter binding protein	209782 s at	-0.422	2746	1.487E-05	TRUE
95665 at	-0.852	14	1453412 a at	-0.369	416.5	95665 at	-0.532	18	1453412 a at	-0.480	684	283.125	327.21511	TRUE	SEC14-like 1 (S. cerevisiae)	202084 s at	-0.244	5069	2.856E-04	TRUE
100406 at	-0.538	86	1425130 a at	-0.752	52	100406 at	-0.312	847	1425131 at	-0.742	190	293.75	373.4759	TRUE	protein tyrosine phosphatase, non-receptor type 5	233471 at	-1.522	643	1.611E-07	TRUE
96662 at	-0.549	95	1429514 at	-0.373	127.5	96662 at	-0.258	728	1429514 at	-0.389	229	294.875	294.33608	TRUE	phosphatidic acid phosphatase type 2B	212226 s at	0.540	1587	1.740E-06	FALSE
99570 s at	-0.425	234	1427250 at	-0.574	2.5	99570 s at	-0.472	310	1443551 at	-0.345	638	296.125	262.77125	TRUE	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	212361 s at	-0.795	443	8.363E-08	TRUE
97776 at	-0.719	48	1418950 at	-0.533	213	97776 at	-0.505	92	1418950 at	-0.811	849	300.5	372.262	TRUE	dopamine receptor 2	206590 x at	-0.556	19	2.636E-09	TRUE
97463 g at	-0.320	789	1426679 at	-0.449	108.5	97462 at	-0.665	12	1426678 at	-0.355	293	300.625	345.82495	TRUE	zinc finger protein 706	227132 at	-0.333	4741	2.056E-04	TRUE
92237 at	-0.510	177	1418782 at	-0.371	846.5	92237 at	-0.803	106	1418782 at	-0.904	74	300.875	366.28777	TRUE	retinoid X receptor gamma	205954 at	-0.370	2289	6.606E-06	TRUE
94516 f at	-1.412	2	1427038 at	-0.809	77.5	94517 r at	-0.238	1194	1427038 at	-1.255	3	319.125	584.32074	TRUE	preproenkephalin 1	213791 at	-1.377	3182	2.940E-05	TRUE
96144 at	-0.568	118	1423259 at	-0.623	47.5	96144 at	-0.286	1110	1450928 at	-0.767	8	320.875	528.04709	TRUE	inhibitor of DNA binding 4	209292 at	0.999	2557	1.053E-05	FALSE
103605 g at	0.231	326	1417786 a at	0.341	119	103604 at	0.153	633	1417786 a at	0.520	210	322	223.97172	TRUE	regulator of G-protein signaling 19	204336 s at	0.099	16956	1.128E-01	FALSE
92730 at	-0.208	566	1418350 at	-0.299	170.5	92730 at	-0.446	14	1418350 at	-0.373	542	323.125	274.31563	TRUE	heparin-binding EGF-like growth factor	244857 at	0.032	27563	4.643E-01	FALSE
103009 at	-0.284	229	1436241 s at	0.221	745	103009 at	-0.226	235	1450050 at	0.421	98	326.75	285.90951	FALSE	histone cell cycle regulation defective homolog A (S. cerevisiae)	240451 at	0.102	12245	2.855E-02	FALSE
99804 at	-0.428	65	1422335 at	-0.373	656.5	99804 at	-0.272	324	1422335 at	-0.463	295	335.125	243.57284	TRUE	adrenergic receptor, alpha 2c	206128 at	-0.288	5077	2.918E-04	TRUE
102661 at	-0.347	167	1427683 at	-0.423	557.5	102661 at	-0.215	520	1427683 at	-1.010	120	341.125	229.51412	TRUE	early growth response 2	205249 at	-0.188	13567	4.490E-02	TRUE
99510 at	-0.608	18	1423478 at	-0.636	34	99511 at	-1.020	5	1460419 a at	-0.425	1321	344.5	651.10803	TRUE	protein kinase C, beta 1	228795 at	-1.110	192	1.846E-08	TRUE
96183 at	-0.607	161	1435222 at	-0.428	277.5	96183 at	-0.740	909	1456851 at	0.603	80	356.875	376.9037	FALSE	forkhead box P1	223287 s at	-0.581	550	1.192E-07	FALSE
92540 f at	-0.333	138	1421260 a at	-0.341	97.5	92540 f at	-0.401	36	1421260 a at	-0.218	1180	362.875	546.36166	TRUE	spermidine synthase	201516 at	-0.433	376	5.675E-08	TRUE
93602 at	-0.314	120	1448498 at	-0.201	1201	93602 at	-0.339	55	1448498 at	-0.592	77	363.25	559.15196	TRUE	ribosomal protein S6 kinase, polypeptide 4	204632 at	-0.139	9032	5.928E-03	TRUE
100706 f at	0.558	100	1434353 at	0.239	973.5	100706 f at	0.740	313	1434353 at	0.768	78	366.125	418.55513	TRUE	Scm-like with four mbt domains 2	232938 at	-0.020	36590	7.806E-01	FALSE
93382 at	-1.002	17	1449420 at	-0.617	160.5	93382 at	-0.264	1180	1449420 at	-0.751	147	376.125	539.80805	TRUE	phosphodiesterase 1B, Ca2+-calmodulin dependent	206444 at	-0.908	55	4.261E-09	TRUE
160522 at	-0.230	420	1436736 x at	-0.470	178	160522 at	-0.478	112	1450839 at	-0.472	818	382	319.40361	TRUE	DNA segment, human D4S114	230424 at	0.156	8340	4.043E-03	FALSE
95619 at	-0.853	8	1429122 a at	-0.270	939	95619 at	-0.572	456	1429122 a at	-0.598	130	383.25	415.97225	TRUE	RIKEN cDNA 1700040I03 gene	223312 at	-0.022	31441	6.105E-01	FALSE
93412 at	-0.298	222	1432273 a at	-0.254	855.5	93412 at	-0.213	200	1432273 a at	-0.560	279	389.125	312.69377	TRUE	Duffy blood group, chemokine receptor	208335 s at	0.054	34963	7.286E-01	FALSE
95324 at	-0.549	24	1420403 at	-0.637	25	95324 at	-0.605	540	1433888 at	-0.404	989	394.5	464.90178	TRUE	ATPase, Ca++ transporting, plasma membrane 2	211586 s at	-0.578	107	8.642E-09	TRUE
92484 at	-0.527	292	1422018 at	-0.337	557.5	92484 at	-0.905	109	1457932 at	0.454	620	394.625	237.65219	FALSE	human immunodeficiency virus type I enhancer binding protein 2	212642 s at	-0.387	1749	2.428E-06	FALSE
95092 at	-0.351	377	1438478 a at	-0.388	315	95092 at	-0.322	563	1438478 a at	-0.579	367	405.5	108.46044	TRUE	protein phosphatase 3, catalytic subunit, alpha isoform	202429 s at	-1.357	54	4.139E-09	TRUE
95033 at	-0.320	217	1426810 at	-0.230	1099.5	95033 at	-0.377	307	1426810 at	-0.505	65	422.125	462.49511	TRUE	jumonji domain containing 1A	212689 s at	0.360	6183	8.112E-04	FALSE
93411 at	-1.036	49	1459903 at	-0.335	89.5	93411 at	-0.259	789	1459903 at	-0.318	763	422.625	408.51507	TRUE	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	210083 at	-0.052	29963	5.556E-01	FALSE
104032 at	-0.651	56	1435666 at	-0.377	63	104032 at	-0.531	100	1435666 at	-0.540	1530	437.25	728.75573	TRUE	microtubule associated serine/threonine kinase 3	213045 at	-0.644	1302	8.952E-07	TRUE
92662 g at	-0.437	107	1449957 at	-0.210	1479	92662 g at	-0.310	113	1449957 at	-0.812	90	447.25	687.90231	TRUE	protein tyrosine phosphatase, receptor type, V		NA	NA	NA	NA
98553 at	-0.355	422	1421215 a at	-0.466	41.5	98553 at	-0.390	1051	1426457 at	-0.513	310	456.125	427.51499	TRUE	sarcolemma associated protein	225243 s at	-0.466	3353	3.705E-05	TRUE
103412 at	-0.354	1382	1435321 at	-0.268	286.5	103412 at	-0.536	74	1445398 at	-0.571	86	457.125	624.23959	TRUE	RIKEN cDNA 3732412D22 gene		NA	NA	NA	NA
97994 at	-0.262	432	1433471 at	-0.168	925	97994 at	-0.331	292	1433471 at	-0.589	189	459.5	325.92075	TRUE	transcription factor 7, T-cell specific	205255 x at	0.288	1327	9.405E-07	FALSE
100453 at	-0.457	148	1448676 at	-0.391	178	100453 at	-0.248	401	1448676 at	-0.363	1184	477.75	484.17103	TRUE	calcium/calmodulin-dependent protein kinase II, beta	213276 at	-0.659	144	1.355E-08	TRUE
160320 at	-0.336	649	1425826 a at	-0.250	307	160320 at	-0.161	902	1443983 at	-0.485	64	480.5	369.51725	TRUE	sorbin and SH3 domain containing 1	237026 at	0.495	3482	4.521E-05	FALSE
100523 r at	0.345	223	1451230 a at	0.318	615	100522 s at	0.552	81	1451230 a at	0.232	1028	486.75	425.67466	TRUE	WW domain binding protein 5	217975 at	0.421	6525	1.069E-03	TRUE
161616 f at	-0.393	315	1422552 at	0.194	1391.5	161616 f at	0.320	46	1422552 at	0.958	230	495.625	607.71065	FALSE	reprimo, TP53 dependent G2 arrest mediator candidate	219370 at	-0.070	24131	3.421E-01	FALSE
103438 at	-0.430	74	1426081 a at	-0.348	506.5	103438 at	-0.226	154	1418938 at	-0.253	1266	500.125	544.05581	TRUE	deiodinase, iodothyronine, type II	231240 at	-0.571	2322	6.983E-06	TRUE
98968 at	-0.526	174	1431320 a at	-0.348	170.5	100672 at	0.119	1643	1419754 at	-0.583	72	514.875	753.568	FALSE	myosin Va	227761 at	-0.845	1229	7.591E-07	FALSE
92369 at	-0.397	349	1450421 at	-0.206	485	92369 at	-0.596	320	1421942 s at	-0.327	939	523.25	286.34755	TRUE	transforming growth factor alpha	205015 s at	-0.035	28960	5.193E-01	FALSE
103032 at	-0.181	981	1421733 a at	-0.184	811	103032 at	-0.367	285	1421733 a at	-0.466	55	533	435.11531	TRUE	protein-tyrosine sulfotransferase 1	204140 at	0.327	15011	7.116E-02	FALSE
103787 at	-0.651	172	1417416 at	-0.413	182.5	103787 at	-0.682	216	1417416 at	0.397	1594	541.125	702.1674	FALSE	potassium voltage-gated channel, shaker-related subfamily, member 1	208479 at	-0.191	7833	2.932E-03	FALSE
92254 at	-0.250	535	1452298 a at	-0.237	1316.5	92254 at	-0.688	1	1437698 at	-0.557	347	549.875	556.88335	TRUE	myosin Vb	240006 at	0.057	19181	1.743E-01	FALSE
104123 at	-0.476	38	1428575 at	-0.219	570.5	104123 at	-0.173	1349	1436077 a at	-0.441	248	551.375	575.08309	TRUE	FCH domain only 1	213669 at	0.101	16182	9.486E-02	FALSE
103906 f at	-0.491	374	1423269 a at	-0.362	143	103906 f at	-0.463	421	1447171 at	0.226	1283	555.25	500.14823	FALSE	neural precursor cell expressed, developmentally down-regulated gene 4-like	212445 s at	-0.370	568	1.258E-07	FALSE
97297 at	-0.360	139	1452913 at	-0.407	86	160264 s at	-0.309	1742	1452913 at	-0.408	261	557	793.39061	TRUE	Purkinje cell protein 4-like 1		NA	NA	NA	NA
104566 at	0.190	872	1448350 at	0.281	696	104566 at	0.191	366	1448350 at	0.394	341	568.75	258.92776	TRUE	argininosuccinate lyase	204608 at	0.058	26132	4.087E-01	FALSE
92465 at	-0.228	320	1425600 a at	-0.384	627	92465 at	-0.444	76	1425781 a at	-0.491	1258	570.25	510.92359	TRUE	phospholipase C, beta 1	213222 at	-1.001	136	1.226E-08	TRUE
99449 at	-0.422	184	1451595 a at	-0.239	1677	99449 at	-0.371	140	1451595 a at	-0.356	280	570.25	740.1452	TRUE	potassium voltage-gated channel, subfamily Q, member 2	205737 at	-1.101	1295	8.786E-07	TRUE
94155 at	-0.251	2064	1448285 at	-1.175	13	94155 at	-1.350	190	1448285 at	-0.808	24	572.75	997.45856	TRUE	regulator of G-protein signaling 4	204337 at	-1.558	59	4.504E-09	TRUE
93159 at	-0.461	127	1449866 at	-0.211	828	101183 at	-0.241	1283	1449866 at	-0.753	59	574.25	586.5807	TRUE	synaptotagmin II		NA	NA	NA	NA
93634 at	0.254	666	1425461 at	-0.438	251.5	93634 at	-0.460	372	1438336 at	-0.290	1010	574.875	338.31306	FALSE	F-box and WD-40 domain protein 11	209456 s at	-0.282	5419	4.083E-04	FALSE
96302 at	-0.487	266	1436871 at	0.261	315	96302 at	-0.338	304	1424033 at	-0.221	1426	577.75	565.88949	FALSE	Splicing factor, arginine/serine-rich 7	213649 at	0.223	11299	1.945E-02	FALSE
103611 at	-0.366	753	1449507 a at	-0.243	228	97749 at	-0.353	32	1430997 at	-0.194	1323	584	579.11484	TRUE	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	226016 at	-0.336	7830	2.930E-03	TRUE
104652 at	-0.627	22	1449158 at	-0.330	717.5	104652 at	-0.490	476	1449158 at	-0.718	1127	585.625	461.94108	TRUE	potassium channel, subfamily K, member 2	210261 at	-0.385	585	1.313E-07	TRUE
102307 at	0.162	1064	1418141 at	0.251	127.5	102307 at	0.193	724	1448974 at	0.411	443	589.625	399.22704	TRUE	doublecortin	204850 s at	-0.460	2437	8.603E-06	FALSE
99337 at	-0.812	75	1435128 at	-0.442	77.5	103098 at	-0.195	590	1451027 at	-0.436	1621	590.875	728.20308	TRUE	brain-specific angiogenesis inhibitor 1-associated protein 2	205294 at	-0.750	308	4.038E-08	TRUE
100458 at	-0.254	490	1452444 at	-0.295	1204.5	92952 f at	-0.563	537	1452444 at	0.565	133	591.125	446.93892	FALSE	N-ethylmaleimide sensitive fusion protein attachment protein beta	225111 s at	-0.746	3745	6.264E-05	FALSE
92820 at	-0.486	69	1417168 a at	-0.438	77.5	92821 at	-0.281	1078	1417168 a at	-0.410	1177	600.375	610.02177	TRUE	ubiquitin specific peptidase 2	229337 at	-0.225	1412	1.166E-06	TRUE
97365 at	-0.518	105	1434326 x at	-0.290	151	97365 at	-0.300	302	1434755 at	-0.288	1887	611.25	854.65251	TRUE	coronin, actin binding protein, 2B	209789 at	-0.362	1442	1.258E-06	TRUE
104215 at	-0.365	359	1435444 at	-0.327	1089	104215 at	-0.457	40	1456021 at	-0.406	966	613.5	498.00569	TRUE	activating transcription factor 6	239825 at	-0.065	18433	1.532E-01	FALSE
96916 at	0.219	996	1448190 at	0.401	794	96916 at	0.262	369	1448190 at	0.337	312	617.75	331.40949	TRUE	mitochondrial ribosomal protein L33	203781 at	-0.176	5899	6.331E-04	FALSE
160580 at	-0.346	395	1417110 at	-0.334	1427	160580 at	-0.336	364	1417111 at	-0.402	303	622.25	537.85957	TRUE	mannosidase 1, alpha	221760 at	-0.802	1720	2.274E-06	TRUE
95754 at	-0.153	1909	1431385 a at	-0.379	211	95754 at	-0.254	171	1448240 at	-0.362	211	625.5	855.87441	TRUE	membrane-bound transcription factor peptidase, site 1	217543 s at	-0.285	838	2.971E-07	TRUE
104407 at	-0.463	231	1426300 at	-0.222	1849.5	104407 at	-0.864	24	1437466 at	-0.384	402	626.625	829.77019	TRUE	activated leukocyte cell adhesion molecule	201952 at	-0.134	19578	1.868E-01	FALSE
96490 at	-0.180	606	1427579 at	-0.315	865	96490 at	-0.201	939	1435941 at	-0.509	112	630.5	373.98975	TRUE	rhomboid, veinlet-like 3 (Drosophila)	230755 at	-0.117	8374	4.099E-03	TRUE
99146 at	-0.276	1667	1431646 a at	-0.280	374.5	99146 at	-0.333	238	1441133 at	-0.399	267	636.625	689.42166	TRUE	syntaxin 6	212799 at	-0.149	12426	3.064E-02	TRUE
99830 at	-1.320	3	1457899 at	-0.268	480	99830 at	-0.816	488	1457690 at	-0.596	1589	640	672.07986	TRUE	kalirin, RhoGEF kinase		NA	NA	NA	NA
103638 at	-0.324	1334	1426983 at	-0.387	20	103638 at	-0.387	648	1453746 at	-0.425	580	645.5	538.38617	TRUE	formin binding protein 1	230389 at	0.409	1967	3.589E-06	FALSE
98008 at	-0.730	23	1415803 at	-0.606	50	98008 at	-0.545	361	1415803 at	-0.396	2192	656.5	1035.0918	TRUE	chemokine (C-X3-C motif) ligand 1	823 at	-0.748	671	1.764E-07	TRUE
161750 f at	0.355	511	1450437 a at	-0.360	983.5	161750 f at	0.180	853	1426865 a at	0.459	319	666.625	305.61833	FALSE	neural cell adhesion molecule 1	216093 at	0.229	5136	3.137E-04	FALSE
95357 at	0.219	529	1453019 at	0.137	1684.5	95357 at	-0.353	264	1453018 at	-0.434	193	667.625	693.16513	FALSE	nuclear VCP-like	207877 s at	0.048	24115	3.416E-01	FALSE
99178 at	-0.225	1527	1425942 a at	-0.489	36	99178 at	-0.357	277	1423091 a at	-0.284	865	676.25	665.51302	TRUE	glycoprotein m6b	209167 at	0.283	1831	2.840E-06	FALSE
104244 at	-0.288	258	1415952 at	-0.312	766	99459 f at	-0.524	65	1435889 at	-0.436	1646	683.75	706.35325	TRUE	MAP/microtubule affinity-regulating kinase 2	203942 s at	-0.236	5451	4.237E-04	TRUE
101851 at	0.542	191	1448788 at	0.228	503.5	101851 at	0.304	1545	1448788 at	0.349	524	690.875	589.45206	TRUE	Cd200 antigen	209583 s at	-0.574	2097	4.536E-06	FALSE
104299 at	-0.376	772	1423668 at	-0.270	468	104299 at	-0.271	859	1437614 x at	-0.346	678	694.25	167.969	TRUE	zinc finger, DHHC domain containing 14	219247 s at	0.043	27105	4.467E-01	FALSE
104320 at	-0.201	1193	1427929 a at	-0.206	725	96519 at	-0.190	666	1427929 a at	-0.389	209	698.25	402.45031	TRUE	pyridoxal (pyridoxine, vitamin B6) kinase	218019 s at	-0.179	14351	5.897E-02	FALSE
99947 at	-0.166	1133	1421148 a at	-0.215	929	99947 at	-0.286	330	1455676 x at	-0.421	414	701.5	390.98892	TRUE	Tial1 cytotoxic granule-associated RNA binding protein-like 1	202406 s at	0.311	6633	1.167E-03	FALSE
98434 at	-0.413	116	1449066 a at	-0.158	1221.5	98434 at	-0.167	1219	1449066 a at	-0.487	269	706.375	596.65112	TRUE	Rho guanine nucleotide exchange factor (GEF7)	242999 at	-0.519	2921	1.901E-05	TRUE
102650 at	-0.345	115	1425245 a at	-0.181	1534	102650 at	-0.234	877	1425245 a at	-0.625	329	713.75	634.03332	TRUE	regulator of G-protein signaling 11	211872 s at	-0.066	18358	1.509E-01	FALSE
92757 at	-0.648	32	1427674 a at	-0.497	20	92757 at	-0.372	1840	1427674 a at	-0.566	996	722	874.43391	TRUE	seizure related gene 6	243430 at	-0.548	707	1.972E-07	TRUE
93614 at	-0.773	81	1431164 at	-0.150	1745	93614 at	-0.543	447	1434909 at	-0.342	616	722.25	717.46562	TRUE	Ras-related GTP binding D	221523 s at	-0.333	9175	6.479E-03	TRUE
96735 at	-0.429	98	1448956 at	-0.256	1020	96735 at	-0.213	1347	1448956 at	-0.455	460	731.25	558.89974	TRUE	START domain containing 10	223103 at	-0.101	19305	1.781E-01	FALSE
103678 at	-0.201	604	1451436 at	-0.181	1538	104106 at	-0.506	127	1457509 at	0.457	677	736.5	587.36388	FALSE	sno, strawberry notch homolog 1 (Drosophila)	216162 at	-0.067	23026	3.022E-01	FALSE
98478 at	-0.269	798	1448364 at	-0.308	189	98478 at	-0.327	320	1448364 at	-0.294	1645	738	658.88138	TRUE	cyclin G2	211559 s at	-0.361	5090	2.965E-04	TRUE
100004 at	-0.212	832	1428531 at	-0.301	309	100004 at	-0.202	1546	1443045 at	0.451	268	738.75	596.27699	FALSE	integrator complex subunit 7	218783 at	-0.161	12151	2.745E-02	FALSE
97243 at	-0.212	311	1438116 x at	-0.245	1064	97243 at	-0.123	1224	1450982 at	-0.366	359	739.5	472.0286	TRUE	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	201349 at	0.237	5524	4.555E-04	FALSE
92434 at	-0.402	61	1420707 a at	-0.193	2843	92434 at	-0.480	17	1420708 at	-0.627	38	739.75	1402.2818	TRUE	TRAF-interacting protein	205598 at	0.043	23832	3.321E-01	FALSE
96920 at	-0.455	197	1416749 at	-0.397	105	96920 at	-0.206	1888	1416749 at	-0.242	783	743.25	820.11884	TRUE	HtrA serine peptidase 1	201185 at	0.072	25615	3.915E-01	FALSE
161070 at	-0.340	1141	1434403 at	-0.213	957.5	161070 at	-0.750	144	1436892 at	0.675	795	759.375	433.915	FALSE	sprouty-related, EVH1 domain containing 2	212458 at	-0.094	21612	2.541E-01	FALSE
102835 at	0.130	1768	1455482 at	-0.277	133.5	102835 at	-0.317	229	1432007 s at	0.429	935	766.375	757.40559	FALSE	adaptor protein complex AP-2, alpha 2 subunit	215764 x at	-0.140	8559	4.516E-03	FALSE
97988 at	-0.545	25	1417129 a at	-0.324	1201	97988 at	-0.329	1074	1443926 at	-0.425	770	767.5	526.99684	TRUE	myeloid ecotropic viral integration site-related gene 1	207480 s at	-0.509	1756	2.452E-06	TRUE
94852 at	-0.498	253	1426235 a at	-0.631	89.5	94852 at	-1.010	1885	1426236 a at	-0.348	846	768.375	812.27247	TRUE	glutamate-ammonia ligase (glutamine synthetase)	217202 s at	-0.311	12856	3.536E-02	TRUE
93379 at	0.162	1282	1418298 s at	0.325	102	93379 at	0.272	198	1418299 at	0.201	1497	769.75	722.0528	TRUE	dihydropyrimidinase-like 4	205492 s at	-0.244	2813	1.632E-05	FALSE
96114 at	-0.298	121	1422605 at	-0.264	702	96114 at	-0.196	397	1422605 at	-0.276	1864	771	766.33022	TRUE	protein phosphatase 1, regulatory (inhibitor) subunit 1A	205478 at	-1.153	25	2.669E-09	TRUE
93619 at	-0.388	248	1449851 at	-0.182	1090	93619 at	-0.194	322	1449851 at	-0.410	1428	772	579.80916	TRUE	period homolog 1 (Drosophila)	244677 at	0.450	6252	8.773E-04	FALSE
104337 f at	0.537	1261	1449799 s at	-0.190	1301	162194 r at	0.210	291	1459358 at	-0.413	240	773.25	586.896	FALSE	plakophilin 2	207717 s at	-0.109	8687	4.864E-03	FALSE

102009 at	-0.555	264	1449273 at	-0.345	660	102009 at	-0.489	173	1442167 at	-0.319	2028	781.25	857.63293	TRUE	cytoplasmic FMR1 interacting protein 2	220999 s at	-0.617	1754	2.445E-06	TRUE
97383 at	-0.481	169	1421346 a at	-0.455	269.5	94405 at	-0.218	1198	1420148 at	-0.229	1491	781.875	661.85653	TRUE	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	228754 at	-0.240	14062	5.365E-02	FALSE
92426 at	-0.507	300	1431530 a at	-0.286	2178.5	92426 at	-0.598	352	1441467 at	0.648	306	784.125	929.8735	FALSE	tetraspanin 5	241060 x at	0.390	8556	4.495E-03	FALSE
160536 at	-0.432	63	1422407 s at	-0.233	1049	160536 at	-0.131	1755	1424132 at	-0.419	287	788.5	770.24563	TRUE	Harvey rat sarcoma virus oncogene 1	212983 at	-0.504	366	5.417E-08	TRUE
100122 at	-0.503	238	1422208 a at	-0.343	520	100122 at	-0.344	2244	1422208 a at	-0.386	154	789	982.54974	TRUE	guanine nucleotide binding protein, beta 5	207124 s at	-0.798	825	2.924E-07	TRUE
101509 at	0.351	642	1421750 a at	0.286	963	101509 at	0.487	311	1421750 a at	0.241	1241	789.25	401.94226	TRUE	von Hippel-Lindau binding protein 1	201472 at	-0.110	23633	3.249E-01	FALSE
160761 at	-0.143	2076	1417626 at	-0.296	89.5	160761 at	-0.272	182	1433761 at	-0.329	815	790.625	915.56607	TRUE	phosphodiesterase 4D interacting protein (myomegalin)	232615 at	0.666	375	5.674E-08	FALSE
104576 at	-0.416	532	1426373 at	-0.221	244	104576 at	-0.342	820	1444785 at	-0.258	1600	799	583.48265	TRUE	Sloan-Kettering viral oncogene homolog	NA	NA	NA	NA	
94793 at	0.244	381	1455511 at	0.183	692	94793 at	0.132	1178	1455511 at	0.261	953	801	343.2754	TRUE	selenophosphate synthetase 1	208940 at	0.301	3105	2.629E-05	TRUE
97984 i at	-0.228	924	1448541 at	-0.513	59	97984 i at	-0.122	1581	1428881 at	-0.380	641	801.25	632.37456	TRUE	kinesin 2	213656 s at	0.617	52	4.015E-09	FALSE
104139 at	-0.588	247	1426519 at	-0.428	64.5	104139 at	-0.335	105	1452094 at	-0.290	2816	808.125	1340.8686	TRUE	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	207543 s at	0.261	11150	1.836E-02	FALSE
94457 at	-0.242	278	1415792 at	-0.148	2575	94457 at	-0.498	31	1415792 at	-0.423	364	812	1183.7779	TRUE	expressed sequence AL033326	232150 at	0.252	2550	1.039E-05	FALSE
102273 at	-0.317	720	1449870 a at	-0.227	741	102273 at	-0.290	246	1434791 at	-0.180	1549	814	540.6829	TRUE	ATPase, H+ transporting, lysosomal V0 subunit A2	205704 s at	0.045	26160	4.097E-01	FALSE
97958 at	-0.550	164	1426614 at	-0.441	192.5	97958 at	-0.318	298	1426614 at	-0.180	2609	815.875	1196.8054	TRUE	protein kinase C binding protein 1	209049 s at	0.236	10764	1.524E-02	FALSE
93519 s at	-0.156	2047	1423715 a at	0.214	913	93519 s at	0.375	87	1440996 at	0.414	219	816.5	896.77552	FALSE	neural precursor cell expressed, developmentally down-regulated gene 8	201840 at	-0.282	4703	1.975E-04	FALSE
93789 s at	0.290	546	1455039 a at	0.554	32	93789 s at	0.256	1497	1455039 a at	0.348	1191	816.5	656.237	TRUE	transcriptional regulator, SIN3B (yeast)	209352 s at	-0.160	8555	4.495E-03	FALSE
99331 at	-0.479	62	1425968 s at	-0.216	1204.5	99331 at	-0.159	1088	1425968 s at	-0.347	912	816.625	517.25129	TRUE	SPEG complex locus	202222 s at	0.106	13075	3.795E-02	FALSE
98313 at	-0.249	1273	1451888 a at	-0.336	595	98313 at	-0.372	483	1446839 at	0.443	987	834.5	363.52487	FALSE	odd Oz/ten-m homolog 4 (Drosophila)	213273 at	0.092	18981	1.684E-01	FALSE
160552 at	-0.393	159	1416087 at	-0.247	1602	160552 at	-0.189	809	1416087 at	-0.266	812	845.5	590.48822	TRUE	adaptor protein complex AP-1, sigma 1	205196 s at	-0.703	1743	2.386E-06	TRUE
98477 s at	-0.359	1182	1425202 a at	-0.453	405	98477 s at	-0.280	1087	1451628 a at	-0.278	736	852.5	354.67779	TRUE	ankyrin 3, epithelial	207950 s at	-0.192	10113	1.067E-02	TRUE
96518 at	-0.465	113	1427261 at	-0.292	212	104643 at	-0.348	120	1420007 at	-0.148	2975	855	1414.053	TRUE	WW, C2 and coiled-coil domain containing 1	241950 at	0.102	13281	4.094E-02	FALSE
103824 at	-0.369	382	1448411 at	-0.370	114	103824 at	-0.268	2827	1448411 at	-0.583	103	856.5	1319.986	TRUE	Wolfram syndrome 1 homolog (human)	202908 at	0.253	13454	4.323E-02	FALSE
96936 at	-0.196	1958	1415670 at	-0.252	519	96936 at	-0.536	41	1415670 at	-0.255	923	860.25	815.80528	TRUE	coatomer protein complex, subunit gamma	217749 at	-0.086	16153	9.426E-02	FALSE
160185 at	-0.289	561	1450683 at	0.118	1924.5	160185 at	0.294	400	1450683 at	0.313	561	861.625	712.63635	FALSE	transgelin 3	204743 at	-0.849	1135	6.331E-07	FALSE
94214 at	-0.219	2080	1416023 at	0.374	192.5	94214 at	0.442	756	1416023 at	0.522	472	875.125	835.54397	FALSE	fatty acid binding protein 3, muscle and heart	205738 s at	-0.194	8840	5.314E-03	FALSE
161902 f at	-0.342	487	1421152 a at	-0.207	2069	161902 f at	-0.457	130	1448031 at	-0.327	876	890.5	842.66344	TRUE	guanine nucleotide binding protein, alpha o	204762 s at	-0.922	117	1.017E-08	TRUE
104590 at	-0.536	54	1451507 at	0.227	539.5	104591 g at	-0.388	2368	1421028 a at	0.704	626	896.875	1012.5442	FALSE	myocyte enhancer factor 2C	236395 at	0.097	13184	3.955E-02	FALSE
161788 f at	-0.264	478	1423571 at	-0.263	228	101953 at	0.200	2099	1423571 at	-0.295	788	898.25	832.62652	FALSE	endothelial differentiation sphingolipid G-protein-coupled receptor 1	204642 at	0.065	26614	4.283E-01	FALSE
94933 at	0.170	1236	1425323 a at	0.304	269.5	94933 at	0.167	494	1425323 a at	0.289	1608	901.875	626.23536	TRUE	cDNA sequence BC008155	219709 x at	0.364	1116	6.108E-07	TRUE
101008 at	0.294	810	1421033 a at	0.297	160.5	101008 at	0.202	2509	1450100 a at	0.422	136	903.875	1114.6714	TRUE	transcription elongation regulator 1 (CA150)	202396 at	-0.243	14120	5.469E-02	FALSE
96124 at	-0.163	1969	1428327 at	-0.234	477	96124 at	-0.206	743	1446015 at	0.297	428	904.25	723.19909	FALSE	trafficking protein, kinesin binding 1	214924 s at	0.447	1919	3.317E-06	FALSE
97520 s at	-0.285	1866	1423506 a at	-0.687	428	97520 s at	-0.419	440	1423506 a at	-0.735	910	911	675.06938	TRUE	neuronatin	204239 s at	-0.333	5546	4.629E-04	TRUE
93211 at	0.183	958	1460498 a at	-0.222	1014.5	93211 at	-0.313	1145	1448850 a at	0.384	527	911.125	267.78921	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 5	224613 s at	-0.275	3306	3.532E-05	FALSE
103054 at	0.205	494	1426242 at	0.263	600.5	103054 at	0.248	794	1426242 at	0.315	1791	919.875	593.87799	TRUE	polymerase (RNA) II (DNA directed) polypeptide A	217420 s at	0.029	23880	3.341E-01	FALSE
96047 at	-0.690	59	1426225 at	-0.377	1168.5	96047 at	-0.260	1891	1426225 at	-0.697	577	923.875	788.14195	TRUE	retinol binding protein 4, plasma	219140 s at	-1.127	1755	2.445E-06	TRUE
160337 at	-0.198	744	1415977 at	-0.295	214	160337 at	-0.284	97	1415977 at	-0.373	2650	926.25	1183.1434	TRUE	myo-inositol 1-phosphate synthase A1	222240 s at	0.073	24594	3.578E-01	FALSE
100958 at	-0.308	630	1454656 at	-0.155	2427	100958 at	-0.213	627	1454656 at	-0.554	58	935.5	1030.0616	TRUE	spermatogenesis associated 13	225564 at	0.046	33876	6.950E-01	FALSE
96592 at	-0.440	389	1425514 at	-0.217	2826	96592 at	-0.474	382	1425515 at	0.625	145	935.5	1265.4255	FALSE	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	NA	NA	NA	NA	
94719 at	0.283	257	1421568 at	-0.188	807	94719 at	-0.135	2640	1441049 at	-0.471	54	939.5	1177.4511	FALSE	potassium voltage-gated channel, shaker-related, subfamily, member 6	NA	NA	NA	NA	
94380 at	-0.169	1920	1453988 a at	-0.312	239	162160 at	0.188	339	1453988 a at	0.321	1269	941.75	800.25637	FALSE	insulin degrading enzyme	203327 at	0.133	9441	7.507E-03	FALSE
93178 at	-0.909	13	1448978 at	-0.408	269.5	93178 at	-0.235	1673	1448978 at	-0.381	1871	956.625	950.76175	TRUE	neuronal guanine nucleotide exchange factor	227240 at	-1.278	480	9.481E-08	TRUE
96310 at	-0.099	3390	1451961 a at	-0.723	2.5	96310 at	-0.226	468	1425263 a at	0.967	9	967.375	1629.7192	FALSE	myelin basic protein	210136 at	0.659	5466	4.316E-04	FALSE
97269 f at	-0.308	694	1417058 a at	0.260	627	97269 f at	0.313	349	1417059 at	0.172	2207	969.25	838.57672	FALSE	keratinocyte associated protein 2	224885 s at	0.294	1379	1.071E-06	FALSE
104745 at	-0.316	233	1416794 at	-0.463	105	104745 at	-0.256	1340	1416793 at	-0.158	2208	971.5	993.46683	TRUE	ADP-ribosylation factor-like 6 interacting protein 2	NA	NA	NA	NA	
95466 at	-0.303	386	1436838 x at	-0.221	2352.5	95466 at	-0.488	110	1436236 x at	-0.245	1049	974.375	999.68773	TRUE	coactosin-like 1 (Dictyostelium)	224583 at	0.603	3784	6.576E-05	FALSE
102259 at	0.386	193	1420816 at	-0.479	1756.5	102259 at	-0.575	1518	1420816 at	0.513	431	974.625	777.39966	FALSE	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	222985 at	-0.511	2785	1.565E-05	FALSE
93659 at	-0.548	196	1452453 a at	-0.688	1669	93659 at	-0.722	273	1443876 at	-0.351	1774	978	860.16394	TRUE	calcium/calmodulin-dependent protein kinase II alpha	213108 at	-0.443	4153	1.024E-04	TRUE
161619 f at	-0.190	709	1425679 a at	-0.396	182.5	161619 f at	0.165	671	1425679 a at	-0.304	2368	982.625	954.19158	FALSE	mitogen activated protein kinase 8 interacting protein 1	213014 at	-0.333	9233	6.644E-03	FALSE
92635 at	-0.452	94	1417373 a at	-0.326	160.5	161592 at	0.214	284	1417373 a at	0.144	3409	986.875	1616.6678	FALSE	tubulin, alpha 4	212242 at	-0.354	8434	4.193E-03	FALSE
103994 at	-0.326	907	1426366 at	-0.379	381	103994 at	-0.215	2265	1426366 at	1.217	401	988.5	885.11901	FALSE	eukaryotic translation initiation factor 2C, 2	213310 at	0.243	2807	1.626E-05	FALSE
95726 at	-0.227	985	1423916 s at	-0.202	583	95726 at	-0.271	463	1423916 s at	-0.186	1932	990.75	666.02421	TRUE	myeloid leukemia factor 2	200948 at	-0.349	340	4.749E-08	TRUE
160558 at	-0.174	715	1421324 a at	-0.404	178	160558 at	-0.142	1763	1424480 s at	-0.218	1335	997.75	695.52923	TRUE	thymoma viral proto-oncogene 2	225471 s at	0.163	2826	1.661E-05	FALSE
94947 g at	-0.275	260	1426687 at	-0.092	2958	94946 at	-0.190	577	1436522 at	-0.431	212	1001.75	1314.1822	TRUE	mitogen activated protein kinase kinase kinase 3	227131 at	0.170	6830	1.364E-03	FALSE
95670 at	0.203	2788	1423281 at	0.233	835	95670 at	0.531	377	1423281 at	0.673	26	1006.5	1232.9916	TRUE	stathmin-like 2	203000 at	-1.288	1762	2.472E-06	FALSE
93507 at	0.364	141	1420924 at	-0.298	881	161515 i at	0.230	2543	1420924 at	0.364	478	1010.75	1065.3501	FALSE	tissue inhibitor of metalloproteinase 2	231579 s at	0.421	6815	1.343E-03	FALSE
100593 at	0.170	1611	1424967 x at	0.402	41.5	100593 at	0.123	2387	1418726 a at	0.866	21	1015.125	1179.4544	TRUE	troponin T2, cardiac	215389 s at	-0.039	27273	4.526E-01	FALSE
95432 f at	-0.378	683	1417192 at	-0.288	1810	95431 at	-0.507	1190	1426675 at	-0.367	408	1022.75	616.73407	TRUE	translocase of outer mitochondrial membrane 70 homolog A (yeast)	201519 at	-1.005	196	1.949E-08	TRUE
160937 at	-0.560	79	1416776 at	-0.244	3969.5	160937 at	-0.677	19	1416776 at	-0.539	44	1027.875	1961.2377	TRUE	crystallin, mu	205489 at	-1.289	1430	1.224E-06	TRUE
103547 at	-0.259	979	1460565 at	-0.279	151	103547 at	-0.217	2909	1460565 at	-0.556	76	1028.75	1318.5842	TRUE	solute carrier family 41, member 1	225570 at	0.346	2876	1.794E-05	FALSE
103480 at	-0.144	1415	1419696 at	-0.220	1656	103480 at	-0.260	729	1419696 at	-0.771	315	1028.75	616.96049	TRUE	CD4 antigen	203547 at	0.065	20284	2.094E-01	FALSE
95889 at	-0.189	607	1421789 s at	-0.495	1561.5	95889 at	-0.254	516	1434787 at	-0.343	1436	1030.125	544.80981	TRUE	ADP-ribosylation factor 3	211622 s at	-0.620	56	4.411E-09	TRUE
104455 at	-0.123	3263	1421941 at	-0.396	244	104455 at	-0.681	132	1421941 at	-1.004	483	1030.5	1495.5152	TRUE	calcium/calmodulin-dependent protein kinase IV	241871 at	-1.140	163	1.425E-08	TRUE
93301 at	0.178	1005	1417199 at	0.187	434	93301 at	0.143	1899	1417200 at	0.274	802	1035	622.59832	TRUE	RIKEN cDNA 1300007B12 gene	212165 at	-0.330	3246	3.215E-05	FALSE
161610 at	-0.503	114	1448154 at	-0.403	218	161610 at	0.352	837	1448154 at	-0.212	2984	1038.25	1335.8509	FALSE	N-myc downstream regulated gene 2	206453 s at	0.369	2806	1.626E-05	FALSE
97339 at	-0.321	175	1454759 at	-0.390	122	97339 at	-0.143	3295	1454759 at	-0.494	582	1043.5	1515.0015	TRUE	G protein-coupled receptor kinase-interactor 1	218030 at	-0.154	8215	3.747E-03	TRUE
92654 at	0.129	2337	1437525 a at	0.260	1155.5	92654 at	0.189	408	1444310 at	0.628	278	1044.625	944.37487	TRUE	polymerase (RNA) III (DNA directed) polypeptide A	231763 at	-0.043	25032	3.739E-01	FALSE
102305 at	-0.240	541	1424146 at	-0.192	1306.5	102305 at	-0.206	363	1424146 at	-0.254	2016	1056.625	759.3468	TRUE	G protein-coupled receptor 37-like 1	207055 at	0.077	25077	3.754E-01	FALSE
98333 at	-0.288	949	1455572 x at	0.337	752.5	98333 at	0.276	532	1421838 at	0.170	1996	1057.375	648.51874	FALSE	ribosomal protein S18	201049 s at	-0.063	24222	3.447E-01	FALSE
103831 at	0.158	1626	1416733 at	0.202	480	103831 at	0.122	1393	1446203 at	0.253	755	1063.5	535.60589	TRUE	muskelin 1, intracellular mediator containing kelch motifs	233219 at	0.374	3395	3.975E-05	TRUE
101947 at	-0.404	215	1417734 at	-0.150	1774	101947 at	-0.247	1543	1417734 at	-0.323	822	1088.5	709.57851	TRUE	A kinase (PRKA) anchor protein 8-like	222160 at	0.080	15526	8.030E-02	FALSE
160941 at	-0.179	855	1418406 at	-0.267	466	160941 at	-0.180	2740	1418406 at	-0.498	305	1091.5	1122.9896	TRUE	phosphodiesterase 8A	215635 at	0.172	4321	1.233E-04	FALSE
93137 at	-0.197	1162	1417151 a at	-0.375	502	93137 at	-0.209	254	1417151 a at	-0.250	2449	1091.75	982.63129	TRUE	neurotensin receptor 2	206899 at	0.296	10367	1.234E-02	FALSE
92223 at	-0.354	1804	1449401 at	-0.286	332.5	92223 at	-0.123	1464	1449401 at	-0.721	768	1092.125	665.11758	TRUE	complement component 1, q subcomponent, C chain	225353 s at	0.522	9962	9.928E-03	FALSE
162492 at	0.298	1434	1420095 s at	0.135	1343	96707 at	0.185	940	1416370 at	0.245	671	1097	356.00094	TRUE	zinc finger proliferation 1	223424 s at	0.168	4717	2.002E-04	TRUE
93892 at	-0.307	1187	1423895 a at	-0.271	1781.5	93892 at	-0.417	1130	1458263 at	-0.510	290	1097.125	613.45421	TRUE	CUG triplet repeat, RNA binding protein 2	227178 at	-0.456	2408	8.196E-06	TRUE
97874 at	-0.345	782	1424628 a at	0.259	224	97874 at	0.270	1056	1424628 a at	0.168	2328	1097.5	890.39224	FALSE	RIKEN cDNA 1500032D16 gene	226209 at	-0.094	13334	4.157E-02	FALSE
93664 at	-0.136	2917	1422009 at	-0.612	187.5	93664 at	-0.716	441	1422009 at	-0.313	848	1098.375	1242.5672	TRUE	ATPase, Na+/K+ transporting, beta 2 polypeptide	204311 at	0.175	12965	3.660E-02	FALSE
93246 at	-0.280	852	1418022 at	0.158	2385	93246 at	-0.185	915	1418024 at	0.588	254	1101.5	906.02815	FALSE	NMDA receptor-regulated gene 1	226998 at	-0.064	19027	1.697E-01	FALSE
96117 r at	0.193	1148	1438865 at	0.201	2174.5	96116 at	0.235	405	1455631 at	0.610	691	1104.625	776.11741	TRUE	histocompatibility 13	230107 at	-0.061	18682	1.605E-01	FALSE
92555 at	0.236	452	1448501 at	0.325	661	92555 at	0.464	8	1448501 at	0.302	3300	1105.25	1488.2852	TRUE	tetraspanin 6	209108 at	0.606	4827	2.249E-04	TRUE
92703 at	0.139	1323	1426877 a at	-0.218	2409	104218 s at	-0.378	341	1427266 at	0.304	351	1106	983.21717	FALSE	polybromo 1	223238 s at	0.272	2935	1.942E-05	FALSE
92539 at	-0.286	204	1456642 x at	0.205	2050.5	92539 at	-0.170	1924	1456642 x at	-0.544	302	1120.125	1003.3986	FALSE	S100 calcium binding protein A10 (calpactin)	200872 at	0.259	15922	8.916E-02	FALSE
97974 at	-0.302	110	1451046 at	-0.231	812.5	97974 at	-0.251	1027	1451046 at	-0.305	2531	1120.125	1018.8599	TRUE	zinc finger protein, multitype 1	242282 at	-0.065	18641	1.593E-01	FALSE
104648 at	-0.144	1344	1435762 at	-0.145	2092	104648 at	-0.186	831	1440014 at	-0.500	216	1120.75	794.92028	TRUE	phosphofurin acidic cluster sorting protein 1	224658 x at	-0.171	6376	9.645E-04	TRUE
96785 at	-0.321	1107	1448839 at	-0.191	1535	96785 at	-0.199	1015	1456629 at	-0.355	838	1123.75	296.02182	TRUE	ankyrin repeat domain 47	208902 s at	-0.050	22720	2.924E-01	FALSE
98841 at	0.160	1519	1437382 at	0.199	1102.5	103500 at	0.268	1452	1439643 at	0.333	422	1123.875	502.2865	TRUE	activin receptor IIA	228416 at	-0.126	17772	1.342E-01	FALSE
98989 at	-0.325	128	1448619 at	-0.259	1016	98989 at	-0.164	501	1448619 at	-0.133	2871	1129	1217.0618	TRUE	7-dehydrocholesterol reductase	201791 s at	0.275	5893	6.317E-04	FALSE
104034 at	-0.157	1408	1435417 at	-0.222	648.5	104034 at	0.141	1094	1435417 at	-0.330	1381	1132.875	352.7937	FALSE	expressed sequence AI464131	232244 at	0.035	34743	7.233E-01	FALSE
99501 at	0.230	337	1455698 at	-0.207	1471	99501 at	-0.211	1958	1444811 at	0.808	780	1136.5	719.50098	FALSE	translocation protein 1	208942 s at	0.267	8275	3.868E-03	FALSE
99338 at	0.315	858	1428649 at	-0.175	1066.5	99338 at	-0.218	1986	1428648 at	0.283	676	1146.625	581.88277	FALSE	cullin associated and neddylation disassociated 1	239771 at	0.162	7607	2.481E-03	FALSE
102625 f at	0.175	550	1419239 at	0.144	2199.5	102626 r at	0.182	356	1419239 at	0.241	1506	1152.875	859.95914	TRUE	zinc finger protein 54	NA	NA	NA	NA	
100469 at	0.164	980	1452560 a at	0.219	742	100469 at	0.220	1132	1452560 a at	0.356	1762	1154	435.95413	TRUE	nuclear transcription factor-Y alpha	204108 at	0.138	6301	9.143E-04	TRUE
94986 at	0.131	2997	1417428 at	0.279	1394	94986 at	0.404	205	1417428 at	0.590	28	1156	1369.0276	TRUE	guanine nucleotide binding protein (G protein), gamma 3 subunit	222005 s at	-0.590	1400	1.138E-06	FALSE
95124 i at	-0.330	1172	1416577 a at	0.258	204.5	95125 f at	0.138	2036	1440061 at	0.267	1233	1161.375	749.62695	FALSE	ring-box 1	218117 at	-0.067	28308	4.938E-01	FALSE
98332 at	-0.216	790	1433029 at	0.110	2905	98332 at	0.224	950	1450712 at	2.027	2	1161.75	1233.8256	FALSE	potassium inwardly-rectifying channel, subfamily J, member 9	207527 at	-0.121	16435	1.003E-01	FALSE
93630 at	0.168	714	1425932 a at	-0.385	160.5	93630 at	-0.579	381	1427413 a at	-0.206	3392	1161.875	1504.0575	FALSE	CUG triplet repeat, RNA binding protein 1	209489 at	-0.301	1323	9.374E-07	FALSE
101068 at	0.149	1298	1434853 x at	-0.329	94	101068 at	-0.179	2333	1441879 x at	-0.307	933	1164.5	927.8608	FALSE	makorin, ring finger protein, 1	209845 at	-0.471	4277	1.183E-04	FALSE
97346 at	0.232	1256	1428552 at	0.338	412	97346 at	0.107	2553	1428552 at	0.318	438	1164.75	1005.0477	TRUE	RIKEN cDNA 2610001J05 gene	NA	NA	NA	NA	
162049 f at	-0.272	155	1424150 at	-0.235	539.5	161094 r at	0.142	3204	1424150 at	-0.353	767	1166.375	1381.698	FALSE	glycerophosphodiester phosphodiesterase domain containing 5	213343 s at	-0.132	11521	2.122E-02	FALSE
103600 at	-0.325	236	1460223 a at	-0.348	322.5	103600 at	-0.257	500	1438189 s at	-0.195	3610	1167.125	1632.2867	TRUE	erythrocyte protein band 4.9	204505 s at	-0.772	90	6.148E-09	TRUE
96502 at	0.094	2725	1421979 at	-0.287	420.5	96502 at	-0.118	1501	1421979 at	-1.168	23	1167.375	1211.7367	FALSE	phosphate regulating gene with homologies to endopeptidases on the X chromosome (hypophospha	210617 at	0.071	14638	6.390E-02	FALSE
161049 at	-0.352	651	1418357 at	-0.326	1656	161049 at	-0.606	179	1418357 at	-0.325	2228	1178.5	932.15038	TRUE	forkhead box G1	207658 s at	-0.269	3047	2.438E-05	TRUE
95390 at	-0.082	4015	1421037 at	-0.579	300	95390 at	-0.397	195	1421037 at	-0.963	215	1181.25	1889.715	TRUE	neuronal PAS domain protein 2	39548 at	-0.213	818	2.861E-07	TRUE
97273 at	-0.340	807	1417655 a at	-0.158	2394	97273 at	-0.303	1391	1417655 a at	-0.419	166	1189.5	946.0939	TRUE	arsenate resistance protein 2	222046 at	-0.041	26878	4.387E-01	FALSE
92294 at	0.257	281	1433951 at	0.128	3827	96751 at	0.339	143	1433951 at	0.295	516	1191.75	1763.5686	TRUE	ADP-ribosylation factor-like 5A	226617 at	-0.377	5528	4.562E-04	FALSE
95052 at	-0.108	2440	1417393 a at	-0.360	185	95052 at	-0.145	1979	1417393 a at	-0.457	191	1198.75	1182.193	TRUE	C1q domain containing 2	243292 at	0.009	41868	9.312E-01	FALSE
160655 at	-0.125	2280	1434547 at	-0.148	720	160655 at	-0.185	1334	1418018 at	0.596	470	1201	805.74024	FALSE	carboxypeptidase D	201942 s at	-0.148	14154	5.542E-02	FALSE
102425 at	-0.278	1115	1422751 at	-0.210	1462	102425 at	-0.328	1163	1434033 at	-0.222	1079	1204.75	174.91784	TRUE	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	228284 at	-0.322	6699	1.235E-03	TRUE
98057 at	-0.495	47	1436906 at	-0.190	1109	98057 at	-0.281	241	1436906 at	-0.166	3422	1204.75	1548.6085	TRUE	ring finger protein 166	227726 at	-0.011	41454	9.190E-01	FALSE
160270 at	-0.128	3093	1428129 at	-0.236	557.5	161288 r at	0.374	1076	1428130 at	0.531	116	1210.625	1314.8176	FALSE	lectin, mannose-binding, 1	224629 at	0.261	2263	6.183E-06	FALSE
92631 f at	-0.259	781	1426710 at	-0.262	1424.5	92631 f at	-0.568	300	1438825 at	-0.218	2369	1218.625	894.6386	TRUE	calmodulin 3	200623 s at	-0.990	563	1.255E-07	TRUE
95671 at	-0.160	1704	1415999 at	-0.172	1346	95671 at	-0.234	181	1415999 at	-0.244	1647	1219.5	709.92511	TRUE	hairy/enhancer-of-split related with YRPW motif 1	44783 s at	-0.358	2268	6.296E-06	TRUE
93285 at	-0.709	133	1415834 at	-0.232	2469.5	93285 at	-0.466	137	1415834 at	-0.287	2146	1221.375	1261.3718	TRUE	dual specificity phosphatase 6	208892 s at	-0.408	4763	2.095E-04	TRUE
92183 at	-0.171	1100	1419223 a at	-0.217	872	92183 at	-0.184	2287	1447280 at	0.302	633	1223	734.51254	FALSE	dystrobrevin alpha	227084 at	0.886	181	1.745E-08	FALSE
160100 at	-0.253	302	1431339 a at	-0.351	66	162427 r at	0.093	3733	1431339 a at	0.357	813	1228.5	1698.5257	FALSE	EF hand domain containing 2	222483 at	0.071	17490	1.266E-01	FALSE
97979 at	-0.398	400	1417919 at	-0.137	2284	97979 at	-0.212	1981	1448888 at	-0.360	258	1230.75	1050.1744	TRUE	protein phosphatase 1, regulatory (inhibitor) subunit 7	213465 s at	-0.919	377	5.708E-08	TRUE
161906 f at	0.094	2605	1420113 s at	0.257	557.5	96779 f at	0.290	346.5	1420114 s at	0.208	1422	1232.75	1026.3669	TRUE	RIKEN cDNA 2410022L05 gene	225096 at	-0.157	11105	1.802E-02	FALSE
99508 at	-0.183	663	1419200 at	0.156	2932.5	99508 at	0.266	572	1419200 at	0.462	787	1238.625	1132.6828	FALSE	FXYD domain-containing ion transport regulator 7	220131 at	-0.859	108	9.215E-09	FALSE
97859 at	-0.317	1758	1433605 at	-0.246	411	97858 at	0.172	864	1433605 at	-0.197	1973	1251.5	737.94783	FALSE	inositol polyphosphate-5-phosphatase A	203006 at	-1.125	212	2.100E-08	FALSE
92707 at	0.154	944	1452324 at	0.158	1912.5	92706 at	-0.139	2102	1450541 at	0.924	51	1252.375	947.98465	FALSE	plasmacytoma variant translocation 1	NA	NA	NA	NA	
93793 at	-0.245	267	1455470 x at	-0.216	823	93793 at	0.186	2055	1444947 at	0.200	1869	1253.5	852.39955	FALSE	LIM and SH3 protein 1	200618 at	0.115	13292	4.105E-02	FALSE
104608 at	-0.108	2437	1451996 at	0.169	1827.5	104608 at	0.368	45	1445244 at	0.351	718	1256.875	1076.6205	FALSE	TM2 domain containing 1	236524 at	0.486	2933	1.937E-05	FALSE
102082 at	0.183	1224	1450186 s at	-0.274	1311.5	102082 at	0.169	619	1453413 at	0.261	1877	1257.875	514.94342	FALSE	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	228173 at	0.322	1275	8.413E-07	FALSE
104684 at	-0.214	1073	1450202 at	-0.300	1494.5	104686 at	-0.780	645	1437968 at	-0.349	1828	1260.125	513.42256	TRUE	glutamate receptor, ionotropic, NMDA1 (zeta 1)	205915 x at	-0.773	531	1.156E-07	TRUE
102741 at	0.211	623	1425405 a at	-0.233	1073.5	96188 at	-0.614	865	1445596 at	-0.193	2483	1261.125	835.12478	FALSE	adenosine deaminase, RNA-specific	201786 s at	-0.045	29516	5.393E-01	FALSE
99623 s at	-0.882	11	1425784 a at	-0.286	576	99623 s at	-0.448	4140	1425784 a at	0.619	349	1269	1928.0261	FALSE	olfactomedin 1	205591 at	-0.550	5942	6.576E-04	FALSE
97263 s at	0.231	729	1437690 x at	0.162	1445	162001 f at	0.231	1148	1456727 a at	0.183	1757	1269.75	437.93407	TRUE	casein kinase 1, delta	208774 at	0.097	19807	1.946E-01	FALSE
103023 at	-0.177	1184	1417043 at	-0.131	1635	161759 r at	0.210	1253	1417043 at	-0.414	1015	1271.75	261.99412	FALSE	lecithin cholesterol acyltransferase	204428 s at	0.411	768	2.434E-07	FALSE

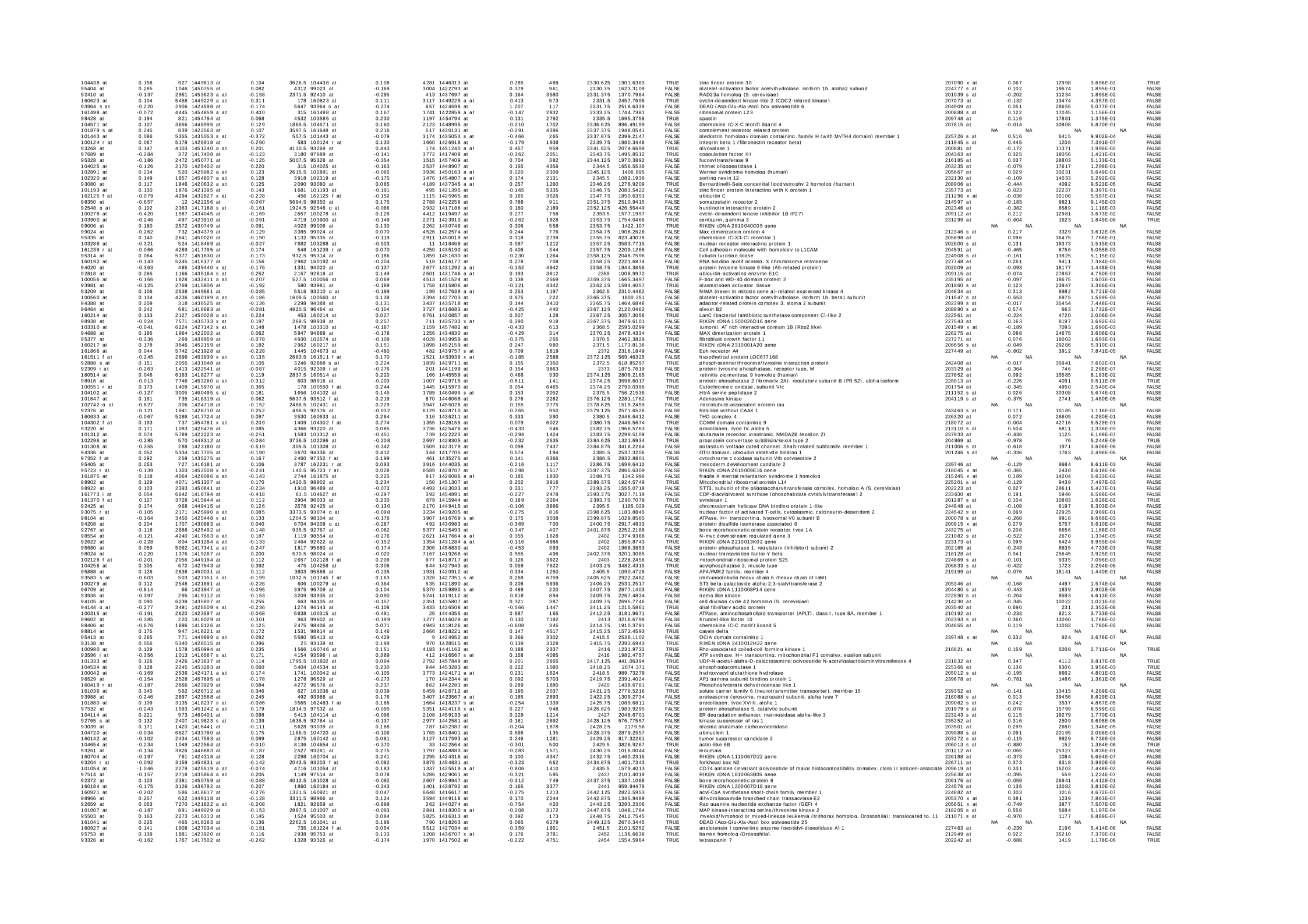


160117 at	-0.262	262	1450184 s at	-0.379	682	160117 at	-0.103	2130	1424175 at	-0.136	3184	1564.5	1343.8605	TRUE	thyrotroph embryonic factor	210167 s at	-0.201	5705	5.286E-04	TRUE
104177 at	-0.135	2494	1436058 at	0.104	2365	104177 at	-0.235	178	1421009 at	-0.716	1252	1572.25	1083.9079	FALSE	radical S-adenosyl methionine domain containing 2	213797 at	-0.123	14819	6.722E-02	FALSE
162011 f at	-0.077	4174	1449028 at	-0.208	1149	162011 f at	0.304	99	1449028 at	0.368	884	1576.5	1788.1392	FALSE	ras homolog gene family, member U	223168 at	0.311	10973	1.695E-02	FALSE
101476 at	-0.133	3255	1415728 at	0.200	394	101476 at	0.193	1199	1422849 a at	0.305	1463	1577.75	1207.0696	FALSE	poly(A) binding protein, nuclear 1	213046 at	0.153	7918	3.105E-03	FALSE
94535 at	-0.240	1127	1420954 a at	-0.383	77.5	94535 at	-0.181	2069	1439125 at	-0.142	3050	1580.875	1273.1501	TRUE	adducin 1 (alpha)	208030 s at	0.174	9732	8.787E-03	FALSE
161760 s at	0.341	366	1425115 at	0.132	2957	161760 s at	0.335	466	1425421 at	-0.166	2536	1581.25	1357.0619	FALSE	retinoblastoma binding protein 6	212781 at	0.119	10857	1.607E-02	FALSE
99621 s at	-0.262	2742	1436898 at	-0.211	2695	99621 s at	-0.657	93	1436898 at	0.639	809	1584.75	1341.5152	FALSE	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	214016 s at	0.318	5253	3.491E-04	FALSE
92802 s at	0.189	3843	1425467 a at	-0.666	6.5	92802 s at	-0.505	59	1425468 at	-0.190	2431	1584.875	1882.7832	FALSE	proteolipid protein (myelin) 1	210198 s at	0.133	16021	9.135E-02	FALSE
94001 at	-0.080	4027	1431037 a at	-0.333	290.5	94001 at	-0.232	993	1448151 at	-0.334	1033	1585.875	1662.7547	TRUE	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	227746 at	-0.345	4147	1.021E-04	TRUE
92381 at	0.107	2595	1420975 at	-0.195	905	92381 at	-0.228	1419	1434824 at	-0.188	1425	1586	715.46069	FALSE	bromodomain adjacent to zinc finger domain, 1B	208445 s at	0.173	5173	3.294E-04	FALSE
160964 at	-0.221	385	1420192 at	0.236	764	160964 at	-0.112	2191	1449770 x at	-0.138	3010	1587.5	1226.3601	FALSE	DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed	NA	NA	NA	NA	
99665 at	-0.215	1149	1416008 at	0.150	1808.5	99665 at	0.246	3086	1443284 at	0.405	318	1590.375	1168.7918	FALSE	special AT-rich sequence binding protein 1	203408 s at	0.268	7419	2.165E-03	FALSE
161196 r at	0.263	2077	1448329 at	0.192	1239.5	100526 f at	0.237	345	1448329 at	0.161	2701	1590.625	1023.7779	TRUE	a disintegrin and metallopeptidase domain 3 (cyritestin)	NA	NA	NA	NA	
92580 at	-0.178	3869	1438510 a at	0.286	699	92580 at	0.418	480	1438510 a at	0.337	1331	1594.75	1558.5049	FALSE	histidyl-tRNA synthetase	202042 at	-0.332	4852	2.331E-04	FALSE
97477 at	-0.265	938	1431665 a at	0.501	396	97477 at	0.271	1060	1431665 a at	0.135	3986	1595	1619.9132	FALSE	translocase of inner mitochondrial membrane 8 homolog b (yeast)	218357 s at	-0.081	21117	2.371E-01	FALSE
103885 at	-0.126	1722	1453005 at	0.302	498	103885 at	-0.089	3056	1453005 at	0.332	1126	1600.5	1091.4668	FALSE	PRP31 pre-mRNA processing factor 31 homolog (yeast)	202408 s at	0.191	7912	3.091E-03	FALSE
99393 at	0.206	758	1421282 at	0.111	3613	99393 at	-0.194	706	1444470 x at	0.268	1341	1604.5	1369.5947	FALSE	bone morphogenetic protein 5	205430 at	0.026	22936	2.992E-01	FALSE
97393 at	-0.131	1335	1425006 a at	-0.092	4555	97393 at	-0.254	530	1425006 a at	-0.848	10	1607.5	2039.2012	TRUE	vaccinia related kinase 1	203856 at	-0.391	2084	4.418E-06	TRUE
99347 f at	-0.107	3195	1427484 at	-0.199	1593	99347 f at	-0.246	579	1437791 s at	-0.348	1066	1608.25	1135.9869	TRUE	echinoderm microtubule associated protein like 5	242443 at	0.011	42057	9.366E-01	FALSE
160656 i at	-0.150	1690	1418323 at	-0.278	342	160656 i at	-0.151	1383	1418324 at	0.146	3022	1609.25	1104.4599	FALSE	feminization 1 homolog b (C. elegans)	212367 at	0.141	17831	1.360E-01	FALSE
97759 at	-0.537	89	1425987 a at	-0.099	3854.5	97759 at	-0.201	2073	1424848 at	0.929	424	1610.125	1729.3724	FALSE	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	228414 at	-0.794	2389	8.009E-06	FALSE
102811 at	-0.323	501	1417730 at	0.095	4350.5	102811 at	-0.253	1133	1458054 at	0.496	463	1611.875	1851.4269	FALSE	exostoses (multiple) 1	201995 at	0.135	10550	1.362E-02	FALSE
103315 at	0.072	4475	1425036 a at	-0.253	178	103315 at	0.254	1769	1459957 at	1.140	36	1614.5	2062.4843	FALSE	trinucleotide repeat containing 6a	234734 s at	0.201	2547	1.033E-05	FALSE
160128 at	0.206	1050	1450969 at	0.116	1924.5	160128 at	0.242	1564	1450969 at	0.251	1922	1615.125	413.06383	TRUE	propionyl Coenzyme A carboxylase, beta polypeptide	212694 s at	-0.045	32075	6.341E-01	FALSE
95334 at	-0.199	845	1422329 a at	-0.160	1396.5	95334 at	-0.210	3220	1426003 at	0.223	1026	1621.875	1089.8623	FALSE	neurotrophic tyrosine kinase, receptor, type 3	206462 s at	-0.451	641	1.601E-07	FALSE
93958 at	0.249	1517	1431030 a at	-0.568	244	93958 at	-0.335	536	1437035 x at	0.147	4191	1622	1797.1335	FALSE	ring finger protein 14	201823 s at	-0.239	15455	7.887E-02	FALSE
100902 at	-0.331	254	1428357 at	-0.233	1149	100902 at	-0.113	4831	1428357 at	-0.400	260	1623.5	2179.2865	TRUE	RIKEN cDNA 2610019F03 gene	230903 s at	-0.227	3986	8.460E-05	TRUE
92935 at	-0.094	3489	1427640 a at	-0.420	1121	92935 at	-0.341	204	1440310 at	-0.386	1689	1625.75	1384.6596	TRUE	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	205528 s at	-0.316	2486	9.451E-06	TRUE
94382 at	-0.142	2746	1437981 x at	0.200	787	94382 at	-0.226	1018	1428085 at	-0.199	1969	1630	902.87873	FALSE	RIKEN cDNA 1110057K04 gene	222192 s at	-0.181	6013	6.984E-04	FALSE
92958 at	-0.213	1170	1434832 at	-0.167	1137	92958 at	0.166	1647	1439598 at	-0.326	2567	1630.25	666.56001	FALSE	forkhead box O3a	242320 at	0.193	4096	9.577E-05	FALSE
160408 at	0.195	1195	1423689 a at	-0.360	511	160408 at	0.067	4112	1423689 a at	-0.368	724	1635.5	1675.5521	FALSE	G-protein signalling modulator 1 (AGS3-like, C. elegans)	226043 at	0.155	7993	3.269E-03	FALSE
92834 at	-0.183	2016	1433928 a at	0.215	706	92834 at	0.425	491	1433928 a at	0.131	3340	1638.25	1319.5859	FALSE	ribosomal protein L13a	200715 x at	0.043	29167	5.265E-01	FALSE
98077 at	-0.227	2476	1422884 at	0.239	3103.5	98077 at	-0.477	306	1449629 s at	-0.349	682	1641.875	1358.68	FALSE	small nuclear ribonucleoprotein D3	202567 at	0.050	27456	4.597E-01	FALSE
98560 at	-0.138	2445	1460740 at	-0.176	1519.5	98560 at	-0.154	1231	1456797 at	0.369	1392	1646.875	545.02024	FALSE	clathrin, light polypeptide (Lcb)	205172 x at	-0.381	6511	1.056E-03	FALSE
161956 at	0.138	3698	1416468 at	-0.321	1066.5	100068 at	-0.219	502	1416468 at	-0.533	1326	1648.125	1409.2128	FALSE	aldehyde dehydrogenase family 1, subfamily A1	212224 at	0.438	11011	1.724E-02	FALSE
97217 at	-0.145	3936	1425576 at	-0.477	133.5	97217 at	-0.174	688	1426831 at	-0.176	1840	1649.375	1681.9741	TRUE	S-adenosylhomocysteine hydrolase-like 1	200849 s at	0.670	530	1.149E-07	FALSE
99120 f at	-0.404	506	1436343 at	-0.394	664	99120 f at	-0.069	5273	1436343 at	0.566	157	1650	2424.6037	FALSE	chromodomain helicase DNA binding protein 4	201184 s at	0.094	15153	7.374E-02	FALSE
93374 at	-0.335	399	1418161 at	-0.132	2753	93374 at	-0.148	2383	1443724 at	-0.553	1070	1651.25	1103.8256	TRUE	junctophilin 3	220188 at	-0.822	172	1.617E-08	TRUE
99098 at	-0.331	652	1423418 at	-0.236	789.5	99098 at	0.081	4812	1423418 at	0.352	353	1651.625	2114.7818	FALSE	farnesyl diphosphate synthetase	201275 at	0.109	17538	1.275E-01	FALSE
97083 at	0.119	3370	1448820 a at	0.287	113	160365 at	0.118	1462	1417713 at	0.207	1678	1655.75	1336.2591	TRUE	eukaryotic translation initiation factor 2, subunit 2 (beta)	208726 s at	-0.154	18208	1.460E-01	FALSE
161096 at	-0.158	1655	1435669 at	-0.116	3246	161096 at	-0.223	188	1444851 at	-0.279	1568	1664.25	1250.4128	TRUE	zinc finger protein 532	NA	NA	NA	NA	
98579 at	-0.365	530	1417065 at	-0.461	1351.5	98579 at	-0.369	508	1417065 at	-0.409	4268	1664.375	1779.5846	TRUE	early growth response 1	201694 s at	-0.659	3479	4.498E-05	TRUE
93485 at	-0.246	1385	1429052 at	-0.291	89.5	93485 at	-0.149	4449	1443053 at	0.739	748	1667.875	1928.0484	FALSE	protein tyrosine phosphatase, receptor type, D	NA	NA	NA	NA	
101093 at	-0.428	145	1452035 at	-0.206	1882	101093 at	-0.119	3388	1452035 at	-0.265	1268	1670.75	1351.9979	TRUE	procollagen, type IV, alpha 1	233652 at	-0.046	23395	3.166E-01	FALSE
92592 at	-0.069	4328	1448249 at	-0.264	527.5	92592 at	-0.248	118	1448249 at	-0.278	1710	1670.875	1895.6592	TRUE	glycerol-3-phosphate dehydrogenase 1 (soluble)	204997 at	0.023	37579	8.081E-01	FALSE
99633 at	-0.164	1333	1416853 at	-0.256	321	99633 at	-0.120	4551	1416852 a at	-0.337	484	1672.25	1969.7806	TRUE	neurochondrin	209557 s at	-1.094	730	2.173E-07	TRUE
96647 at	-0.257	1192	1437256 at	0.115	2258	96647 at	-0.139	2358	1455769 at	-0.350	881	1672.25	746.11723	FALSE	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	223151 at	0.005	42955	9.591E-01	FALSE
104743 at	-0.218	846	1423551 at	-0.165	1217.5	104743 at	-0.274	1270	1459535 at	0.144	3360	1673.375	1140.1442	FALSE	cadherin 13	244091 at	-0.034	27242	4.518E-01	FALSE
100888 at	-0.371	731	1426258 at	-0.382	157	100888 at	-0.365	60	1453003 at	-0.106	5754	1675.5	2735.0762	TRUE	sortilin-related receptor, LDLR class A repeats-containing	203509 at	0.460	1904	3.287E-06	FALSE
98872 at	0.139	3418	1419063 at	-0.744	10	98872 at	-0.634	223	1419064 a at	-0.175	3055	1676.5	1809.509	FALSE	UDP galactosyltransferase 8A	208358 s at	0.132	30860	5.893E-01	FALSE
103276 at	-0.227	1242	1417435 at	-0.162	1915	103276 at	-0.257	2576	1443212 at	0.454	982	1678.75	715.79391	FALSE	like-glycosyltransferase	215543 s at	-0.638	70	4.928E-09	FALSE
93551 at	-0.183	1400	1428296 at	0.275	232.5	93551 at	0.076	3665	1428296 at	0.246	1420	1679.375	1435.4418	FALSE	polymerase (RNA) II (DNA directed) polypeptide L	202586 at	0.047	24392	3.502E-01	FALSE
100416 at	0.099	3172	1416558 at	-0.090	3133.5	100416 at	-0.184	287	1416558 at	-0.475	140	1683.125	1698.1103	FALSE	maternal embryonic leucine zipper kinase	204825 at	0.032	30383	5.706E-01	FALSE
94031 at	0.193	1543	1419946 s at	0.240	648.5	94031 at	0.135	3589	1418621 at	0.245	958	1684.625	1322.654	TRUE	RAB2, member RAS oncogene family	208732 at	-0.398	4764	2.099E-04	FALSE
95120 at	-0.259	1254	1460239 at	-0.246	332.5	95120 at	-0.154	4687	1460239 at	0.318	492	1691.375	2037.1637	FALSE	tetraspanin 13	217979 at	-1.011	1192	7.122E-07	FALSE
160230 at	-0.319	1554	1434435 s at	0.194	1681	160230 at	0.177	3089	1434871 at	-0.283	449	1693.25	1082.5613	FALSE	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	203880 at	-0.145	16567	1.033E-01	FALSE
92287 at	0.080	3583	1423349 at	-0.245	328	92287 at	-0.294	710	1423350 at	-0.201	2166	1696.75	1486.0784	FALSE	suppressor of cytokine signaling 5	209647 s at	-0.140	14532	6.189E-02	FALSE
98569 at	-0.075	3983	1424735 at	-0.208	346	98569 at	-0.215	515	1424735 at	-0.256	1945	1697.25	1684.2035	TRUE	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	225212 at	-0.199	5238	3.457E-04	TRUE
100002 at	-0.316	461	1449123 at	-0.507	940	100002 at	0.252	183	1449123 at	-0.441	5218	1700.5	2365.751	FALSE	inter-alpha trypsin inhibitor, heavy chain 3	205755 at	0.009	40499	8.926E-01	FALSE
102019 at	0.145	4012	1424204 at	0.201	533	102019 at	0.262	761	1435966 x at	0.242	1503	1702.25	1594.5472	TRUE	mitochondrial ribosomal protein L13	218049 s at	-0.091	22760	2.934E-01	FALSE
103858 at	-0.116	2374	1429806 at	0.147	2233	103858 at	-0.217	231	1429806 at	0.370	1978	1704	995.58124	FALSE	Era (G-protein)-like 1 (E. coli)	212087 s at	-0.067	14767	6.650E-02	FALSE
95563 at	0.247	332	1427188 at	-0.164	1519.5	95563 at	-0.241	2410	1436498 at	0.196	2575	1709.125	1028.4934	FALSE	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	242431 at	0.147	12506	3.135E-02	FALSE
94055 at	0.245	513	1433908 a at	0.113	3380.5	94055 at	-0.325	1260	1421314 at	0.188	1699	1713.125	1214.6277	FALSE	cortactin	201059 at	0.254	3002	2.219E-05	FALSE
161823 r at	0.147	2413	1451232 at	0.197	2123.5	97932 f at	0.144	1045	1427525 at	-0.272	1271	1713.125	658.30545	FALSE	CD151 antigen	204306 s at	0.144	9989	1.010E-02	FALSE
99829 at	0.298	428	1427839 at	0.181	1337.5	99829 at	0.107	2648	1437346 x at	-0.212	2456	1717.375	1035.7642	FALSE	immunoglobulin heavy chain (J558 family)	NA	NA	NA	NA	
99515 at	0.112	2546	1427077 a at	-0.215	2612	99515 at	-0.361	692	1445142 at	0.246	1027	1719.25	1002.492	FALSE	adaptor-related protein complex 2, beta 1 subunit	200615 s at	-0.214	9005	5.825E-03	FALSE
100595 at	-0.145	3284	1420613 at	-0.328	110	100595 at	-0.271	1860	1460707 at	-0.228	1627	1720.25	1299.5441	TRUE	protein tyrosine phosphatase 4a2	208615 s at	0.546	2323	6.983E-06	FALSE
99176 at	-0.134	2138	1438924 x at	0.160	1001	99176 at	-0.179	1402	1430171 at	-0.285	2345	1721.5	628.07245	FALSE	fibroblast growth factor (acidic) intracellular binding protein	202041 s at	-0.182	12335	2.957E-02	FALSE
92384 at	0.102	2763	1437320 s at	0.170	717.5	92384 at	0.297	1384	1437320 s at	-0.207	2024	1722.125	875.24267	FALSE	xeroderma pigmentosum, complementation group A	205672 at	0.064	28532	5.030E-01	FALSE
97847 at	-0.091	3467	1416354 at	-0.147	1401	97847 at	-0.109	1721	1416354 at	-0.303	311	1725	1308.8101	TRUE	RNA binding motif protein, X chromosome	213762 x at	-0.133	17073	1.164E-01	FALSE
97951 s at	-0.117	3293	1452105 a at	-0.233	727	97953 g at	-0.416	735	1452105 a at	-0.200	2151	1726.5	1240.4562	TRUE	tuberous sclerosis 2	215735 s at	-0.253	7397	2.125E-03	TRUE
96020 at	-0.535	1629	1417063 at	-0.265	828	96020 at	-0.210	2179	1417063 at	-0.535	2288	1731	667.52428	TRUE	complement component 1, q subcomponent, beta polypeptide	202953 at	0.442	15679	8.363E-02	FALSE
93232 at	-0.156	785	1435259 s at	0.140	1787.5	93232 at	0.161	783	1435259 s at	0.272	3571	1731.625	1314.3326	FALSE	transmembrane protein 141	225568 at	0.028	28398	4.972E-01	FALSE
95627 at	-0.314	696	1417818 at	-0.199	1445	103100 at	-0.083	3010	1417817 a at	0.284	1777	1732	964.53339	FALSE	WW domain containing transcription regulator 1	202133 at	0.986	3129	2.734E-05	FALSE
161113 at	0.204	1027	1421244 at	0.135	2069	93947 g at	-0.099	3192	1435663 at	0.309	644	1733	1143.9601	FALSE	estrogen receptor 1 (alpha)	211234 x at	0.073	20076	2.029E-01	FALSE
102382 at	-0.390	347	1425099 a at	-0.153	1980.5	102382 at	-0.108	3907	1457740 at	0.543	707	1735.375	1608.4342	FALSE	aryl hydrocarbon receptor nuclear translocator-like	210971 s at	-0.317	3312	3.545E-05	FALSE
98083 at	-0.211	1059	1427742 a at	-0.067	5067.5	98083 at	0.342	547	1427742 a at	0.664	272	1736.375	2244.5666	FALSE	Kruppel-like factor 6	208961 s at	0.379	2999	2.210E-05	FALSE
95911 at	-0.137	1868	1448144 at	-0.163	2311	94896 at	-0.092	2545	1426114 at	0.693	228	1738	1045.0802	FALSE	heterogeneous nuclear ribonucleoprotein A/B	201277 s at	0.107	22508	2.851E-01	FALSE
101447 at	-0.153	1592	1420956 at	-0.360	105	101447 at	-0.174	1886	1435543 at	0.119	3372	1738.75	1339.1369	FALSE	adenomatosis polyposis coli	215310 at	0.221	4836	2.297E-04	FALSE
98849 at	0.246	203	1439964 at	0.133	1862	98849 at	0.103	2236	1439964 at	0.187	2659	1740	1075.1481	TRUE	DNA segment, Chr 8, Brigham & Women's Genetics 1414 expressed	227586 at	0.417	1724	2.305E-06	TRUE
93062 at	0.101	5062	1448909 a at	0.350	55.5	93062 at	0.257	602	1417966 at	0.293	1259	1744.625	2265.6525	TRUE	mitochondrial ribosomal protein L39	236910 at	0.144	9794	9.008E-03	TRUE
100589 at	0.266	403	1429533 at	-0.313	300	100589 at	0.075	3438	1437126 at	-0.203	2840	1745.25	1628.3184	FALSE	Inner membrane protein, mitochondrial	200955 at	-0.212	9774	8.937E-03	FALSE
104678 at	-0.275	328	1417859 at	-0.175	2768.5	104678 at	-0.350	13	1417859 at	-0.389	3873	1745.625	1878.2658	TRUE	growth arrest specific 7	202192 s at	-0.528	1215	7.423E-07	TRUE
96156 at	-0.785	87	1436506 a at	0.711	324.5	161635 f at	0.192	368	1436506 a at	0.112	6204	1745.875	2974.6479	FALSE	RIKEN cDNA 1110008H02 gene	NA	NA	NA	NA	
103551 at	-0.201	2344	1425543 s at	-0.124	2303	103551 at	-0.240	1612	1425543 s at	-0.341	725	1746	759.00154	TRUE	pleckstrin homology domain containing, family A member 5	214989 x at	0.095	16189	9.496E-02	FALSE
101857 at	0.078	5756	1417135 at	-0.262	575	101857 at	-0.504	650	1447755 at	1.185	4	1746.25	2688.6875	FALSE	serine/arginine-rich protein specific kinase 2	239811 at	0.141	7115	1.731E-03	FALSE
103457 at	0.374	451	1424632 a at	0.154	2759.5	103457 at	0.209	1529	1426194 x at	0.214	2267	1751.625	1003.7614	TRUE	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	238736 at	0.232	8891	5.430E-03	TRUE
94505 at	-0.209	2872	1417372 a at	-0.197	3315	94505 at	-0.280	272	1444017 at	0.385	548	1751.75	1563.9037	FALSE	pellino 1	218319 at	-0.301	8053	3.375E-03	FALSE
95142 s at	-0.336	303	1453960 a at	-0.346	337	95141 at	0.132	1404	1417259 a at	0.112	4966	1752.5	2202.4778	FALSE	capping protein (actin filament) muscle Z-line, beta	232949 at	0.094	8072	3.431E-03	FALSE
96766 s at	-0.814	51	1425249 a at	-0.328	527.5	96766 s at	-0.360	1327	1425248 a at	-0.230	5105	1752.625	2296.0861	TRUE	TYRO3 protein tyrosine kinase 3	211431 s at	-0.087	18037	1.418E-01	FALSE
160556 at	0.127	3261	1450895 a at	0.298	315	160556 at	0.333	1286	1447629 at	0.228	2152	1753.5	1254.2191	TRUE	RIKEN cDNA 1810020G14 gene	217645 at	0.126	10990	1.711E-02	TRUE
103224 at	-0.194	854	1417529 at	0.071	5016	103224 at	0.426	449	1417529 at	0.367	698	1754.25	2180.887	FALSE	RAB33A, member of RAS oncogene family	216758 at	-0.026	18542	1.564E-01	FALSE
95938 at	0.118	1972	1415703 at	-0.151	1441	95938 at	-0.117	1870	1444279 at	0.258	1753	1759	230.10867	FALSE	HECT, UBA and WWE domain containing 1	236294 at	-0.371	7204	1.876E-03	FALSE
161232 r at	-0.063	4900	1448348 at	-0.250	639.5	92611 at	-0.331	378	1416461 at	-0.317	1123	1760.125	2115.8775	TRUE	GPI-anchored membrane protein 1	226289 at	-0.414	2626	1.163E-05	TRUE
95603 at	-0.291	144	1416049 at	-0.155	1162	95603 at	-0.239	266	1416049 at	-0.149	5469	1760.25	2513.8136	TRUE	glycine decarboxylase	204836 at	0.106	13823	4.937E-02	FALSE
92495 at	0.108	3433	1420999 at	-0.133	1632	92495 at	-0.227	1108	1450083 at	0.264	871	1761	1159.1281	FALSE	CCR4-NOT transcription complex, subunit 4	210866 s at	-0.107	9154	6.378E-03	FALSE
93984 at	-0.160	1663	1448770 a at	0.357	2011	93984 at	0.291	574	1434198 at	-0.150	2798	1761.5	923.11809	FALSE	ATPase inhibitory factor 1	223338 s at	-0.324	3976	8.419E-05	FALSE
161100 at	-0.219	592	1455040 s at	-0.120	3415	161100 at	-0.202	2408	1455040 s at	-0.474	642	1764.25	1387.204	TRUE	RIKEN cDNA 1110062M06 gene	NA	NA	NA	NA	
102677 at	-0.075	5162	1448660 at	0.165	1329	102677 at	0.321	490	1448660 at	0.463	96	1769.25	2319.5415	FALSE	Rho GDP dissociation inhibitor (GDI) gamma	206888 s at	-0.318	5928	6.516E-04	FALSE
100361 f at	0.255	388	1426196 at	0.113	3474.5	101752 f at	-0.234	1138	1425385 a at	0.325	2083	1770.875	1330.7434	FALSE	Immunoglobulin heavy chain 1a (serum IgG2a)	NA	NA	NA	NA	
103439 at	-0.189	1039	1435780 at	-0.189	1799.5	103439 at	-0.126	3006	1435780 at	-0.476	1248	1773.125	882.30233	TRUE	pleckstrin and Sec7 domain containing	208102 s at	-0.552	931	3.717E-07	TRUE
104504 at	-0.083	4439	1451894 a at	-0.307	1616.5	104504 at	-0.522	294	1439889 at	-0.299	750	1774.875	1858.8531	TRUE	sodium channel, voltage-gated, type VIII, alpha	207049 at	-0.393	337	4.682E-08	TRUE
160649 at	-0.250	483	1422977 at	-0.266	835	160649 at	0.121	1665	1422977 at	-0.178	4118	1775.25	1638.5576	FALSE	glycoprotein Ib, beta polypeptide	209768 s at	-0.521	194	1.902E-08	FALSE
96772 at	0.145	2631	1449061 a at	0.169	731	96772 at	0.079	3167	1449061 a at	0.298	575	1776	1316.6032	TRUE	DNA primase, p49 subunit	205053 at	-0.007	41466	9.195E-01	FALSE
102985 at	-0.116	1907	1454042 a at	-0.174	1180	102985 at	-0.123	2296	1455107 at	-0.182	1730	1778.25	463.63518	TRUE	serine/arginine-rich protein specific kinase 1	202200 s at	-0.259	3159	2.879E-05	TRUE
96951 at	-0.273	536	1438993 a at	0.260	1186.5	96951 at	0.135	3784	1438993 a at	0.207	1616	1780.625	1407.4432	FALSE	ATPase, H+ transporting, lysosomal V1 subunit D	208899 x at	-0.489	2386	7.971E-06	FALSE
162118 f at	-0.184	1484	1417153 at	-0.522	149	92525 i at	0.167	1309	1417152 at	-0.180	4186	1782	1708.6484	FALSE	BTB (POZ) domain containing 14A	243431 at	0.542	3373	3.820E-05	FALSE
96886 at	-0.155	1129	1450199 a at	-0.093	3910	96886 at	0.159	1323	1450199 a at	-0.236	769	1782.75	1436.6211	FALSE	stabilin 1	204150 at	0.209	14567	6.252E-02	FALSE
100023 at	0.198	673	1417656 at	0.266	277.5	161160 f at	0.112	1589	1454946 at	-0.118	4597	1784.125	1954.0434	FALSE	myeloblastosis oncogene-like 2	201710 at	-0.030	33464	6.804E-01	FALSE
102037 at	-0.128	2589	1426245 s at	-0.304	201.5	102037 at	-0.285	1795	1442553 at	0.261	2552	1784.375	1116.8819	FALSE	microtubule-associated protein, RP/EB family, member 2	213489 at	-0.291	6038	7.167E-04	FALSE
160468 at	-0.222	1034	1420474 at	-0.269	568.5	160468 at	-0.177	2862	1459597 at	-0.223	2674	1784.625	1153.8519	TRUE	myotrophin	224656 s at	-0.379	3686	5.835E-05	TRUE
95944 at	-0.187	3570	1424397 at	0.152	1656	95944 at	-0.120	1517	1424398 at	0.557	396	1784.75	1317.0688	FALSE	DEAH (Asp-Glu-Ala-His) box polypeptide 36	223140 s at	-0.256	6434	9.984E-04	FALSE
94087 at	-0.148	1208	1422673 at	-0.070	5716	94087 at	-0.237	115	1422673 at	-0.441	109	1787	2669.8034	TRUE	protein kinase C, mu	205880 at	0.121	18971	1.680E-01	FALSE
99882 at	0.268	393	1427813 at	0.120	2116.5	99882 at	-0.320	1805	1450166 at	0.312	2835	1787.375	1024.7656	FALSE	iduronate 2-sulfatase	206342 x at	-0.551	230	2.342E-08	FALSE
100572 at	0.184	1997	1460331 at	-0.202	2178.5	100572 at	-0.182	2006	1423295 at	-0.292	984	1791.375	544.69125	FALSE	transmembrane 9 superfamily member 2	201078 at	-0.304	10189	1.119E-02	FALSE
160871 at	0.190	1153	1451762 a at	-0.293	1436	94379 at	-0.084	4432	1425270 at	0.379	148	1792.25	1844.577	FALSE	kinesin family member 1B	226968 at	0.488	169	1.589E-08	FALSE
95541 at	-0.158	3091	1448904 at	0.117	3597.5	97770 s at	0.643	129	1417953 at	0.413	361	1794.625	1803.7492	FALSE	DNA segment, Chr 6, Wayne State University 176, expressed	201889 at	-0.588	4527	1.611E-04	FALSE
93694 at	-0.421	466	1417602 at	0.073	4662	93694 at	-0.414	899	1417602 at	-0.429	1156	1795.75	1931.9304	FALSE	period homolog 2 (Drosophila)	205251 at	0.158	17532	1.274E-01	FALSE
104356 at	-0.233	1281	1422778 at	0.385	209	104356 at	0.175	740	1451509 at	0.136	4959	1797.25	2152.7883	FALSE	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	202168 at	-0.557	2251	6.087E-06	FALSE
99031 at	0.144	2953	1421220 at	0.235	566	99031 at	-0.234	1753	1445826 at	0.284	1923	1798.75	978.00763	FALSE	ankyrin repeat domain 17	229858 at	0.205	4897	2.433E-04	FALSE
100720 at	-0.142	4126	1418883 a at	-0.247	814	100720 at	-0.314	142	1453840 at	-0.231	2117	1799.75	1754.2258	TRUE	poly A binding protein, cytoplasmic 1	215823 x at	0.218	9280	6.877E-03	FALSE
94821 at	-0.303	2272	1420886 a at	-0.201	1356	94821 at	-0.466	290	1420012 at	-0.128	3282	1800	1277.5424	TRUE	X-box binding protein 1	200670 at	-0.044	32705	6.543E-01	FALSE
92871 at	-0.221	1664	1425187 at	-0.291	133.5	92870 at	-0.434	274	1425188 s at	0.089	5134	1801.375	2326.653	FALSE	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	230265 at	-0.201	12715	3.382E-02	FALSE
97302 at	-0.754	37	1425718 a at	-0.412	781.5	97302 at	-0.172	5911	1425718 a at	-0.416	479	1802.125	2756.2568	TRUE	influenza virus NS1A binding protein	244235 at	-0.140	5994	6.873E-04	TRUE
99978 s at	-0.208	1076	1451927 a at	-0.201	820	99978 s at	-0.275	1796	1459617 at	-0.157	3535	1806.75	1224.0145	TRUE	mitogen activated protein kinase 14	210449 x at	-0.082	16666	1.052E-01	FALSE
97870 s at	0.149	2299	1419030 at	-0.191	1079	97870 s at	-0.167	1975	1449324 at	-0.161	1889	1810.5	518.63507	FALSE	ERO1-like (S. cerevisiae)	218498 s at	-0.123	6478	1.030E-03	FALSE
97774 at	0.149	1680	1425432 at	0.115	2356.5	97774 at	0.130	2783	1441791 at	0.329	429	1812.125	1027.8512	TRUE	opioid receptor, mu 1	207994 s at	-0.064	16140	9.388E-02	FALSE
102827 at	0.234	1121	1416816 at	0.095	4372	102827 at	0.330	348	1444447 at	0.225	1435	1819	1762.2249	TRUE	NIMA (never in mitosis gene a)-related expressed kinase 7	212530 at	0.665	848	3.061E-07	TRUE

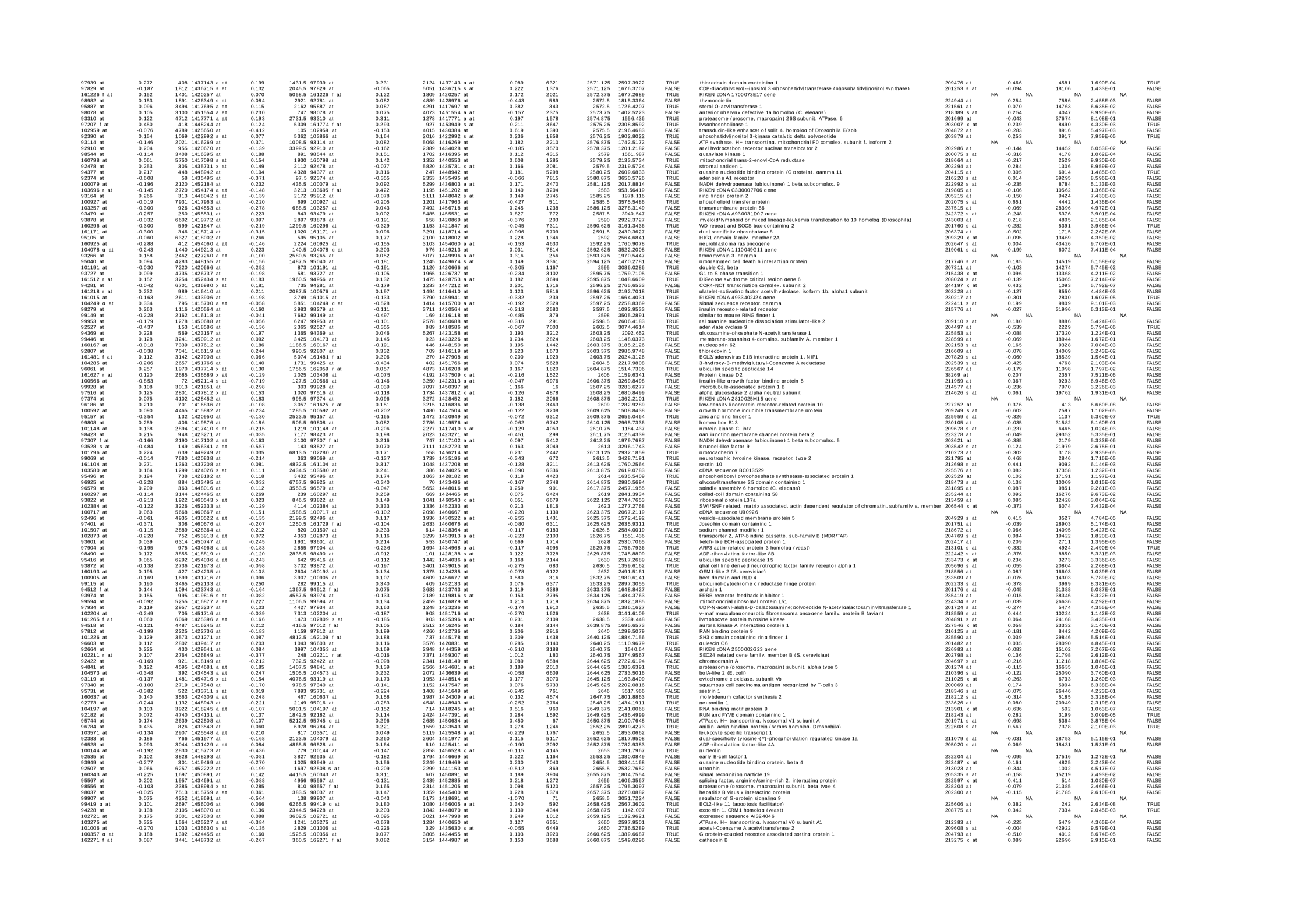
99196 at	0.198	3387	1452735 at	0.239	2338.5	99196 at	0.455	84	1452735 at	0.446	1469	1819.625	1397.7634	TRUE	PEST proteolytic signal containing nuclear protein	217816 s at	-0.062	28954	5.192E-01	FALSE
101923 at	-0.101	4827	1430700 a at	-0.343	186	101923 at	-0.345	687	1430700 a at	-0.346	1587	1821.75	2085.663	TRUE	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	206214 at	-0.120	9823	9.145E-03	TRUE
95895 at	0.082	4312	1451487 at	0.138	1131	95895 at	0.286	556	1433041 at	-0.231	1290	1822.25	1689.5128	FALSE	Rab9 effector protein with kelch motifs	203150 at	-0.263	1197	7.177E-07	FALSE
93366 r at	0.093	2926	1426424 at	0.177	670	93365 s at	0.250	949	1446757 at	0.152	2747	1823	1178.0874	TRUE	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	223329 x at	0.144	13525	4.440E-02	TRUE
161693 r at	0.209	357	1420246 at	0.141	3590	162090 i at	-0.118	1817	1419817 s at	-0.212	1529	1823.25	1336.4027	FALSE	DNA segment, Chr 1, ERATO Doi 161, expressed	218274 s at	0.187	4892	2.422E-04	FALSE
101057 at	-0.111	3705	1454682 at	0.155	2502	101057 at	0.209	439	1454682 at	0.410	648	1823.5	1559.8125	FALSE	RIKEN cDNA A430005L14 gene	222000 at	0.139	12914	3.602E-02	FALSE
161714 f at	-0.198	1120	1428667 at	0.060	5185	161714 f at	-0.171	766	1442676 at	0.692	226	1824.25	2270.4555	FALSE	monoamine oxidase A	212741 at	0.209	15545	8.074E-02	FALSE
101930 at	-0.226	3244	1451443 at	0.214	907	100307 at	-0.253	2182	1436363 a at	0.285	971	1826	1112.5116	FALSE	nuclear factor I/X	228278 at	0.533	23	2.669E-09	FALSE
95656 i at	0.180	1399	1424620 at	0.182	1724.5	95657 f at	0.287	2616	1451414 at	0.213	1569	1827.125	542.45589	TRUE	DNA segment, Chr 13, Wayne State University 177, expressed	203023 at	-0.113	9767	8.915E-03	FALSE
102994 at	0.108	2540	1448713 at	0.146	1817	102994 at	0.103	2590	1448713 at	0.425	380	1831.75	1030.268	TRUE	signal transducer and activator of transcription 4	206118 at	-0.382	2439	8.642E-06	FALSE
98362 s at	0.187	482	1439042 at	-0.332	779	98361 at	-0.155	1895	1429022 at	-0.155	4175	1832.75	1675.8008	FALSE	adenylate cyclase activating polypeptide 1 receptor 1	226690 at	0.656	177	1.697E-08	FALSE
98535 at	-0.409	824	1418701 at	-0.523	828	98535 at	0.136	4714	1418701 at	-0.573	973	1834.75	1920.7511	FALSE	catechol-O-methyltransferase	208818 s at	0.223	8776	5.108E-03	FALSE
100757 at	-0.028	7199	1452476 at	-0.388	61.5	100757 at	-0.502	30	1456401 at	-0.514	50	1835.125	3575.9404	TRUE	calcium channel, voltage-dependent, beta 2 subunit	213714 at	-0.912	888	3.390E-07	TRUE
94865 at	0.220	2104	1415788 at	0.099	4320	94865 at	0.195	338	1415790 at	0.303	579	1835.25	1831.7688	TRUE	ubiquitin-like domain containing CTD phosphatase 1	239489 at	0.087	13952	5.156E-02	FALSE
96806 at	0.138	1692	1452837 at	0.197	1323	161165 f at	-0.065	3660	1452837 at	0.404	674	1837.25	1285.9651	FALSE	lipin 2	202459 s at	-0.320	5408	4.029E-04	FALSE
161254 r at	-0.095	3376	1448149 at	-0.224	1381.5	161254 r at	0.112	2046	1437807 x at	-0.278	549	1838.125	1194.2391	FALSE	catenin (cadherin associated protein), alpha 1	240262 at	0.205	8312	3.970E-03	FALSE
101996 at	-0.100	3582	1417140 a at	0.146	1491	101996 at	0.125	1972	1417140 a at	0.342	324	1842.25	1350.5585	FALSE	protein tyrosine phosphatase, non-receptor type 2	213136 at	0.213	5919	6.473E-04	FALSE
104408 s at	-0.593	157	1449135 at	-0.275	322.5	104408 s at	-0.489	108	1449135 at	-0.072	6792	1844.875	3299.3599	TRUE	SRY-box containing gene 18	219568 x at	0.073	19581	1.868E-01	FALSE
100548 at	0.075	5385	1416407 at	-0.183	815.5	100548 at	0.225	1191	1459733 at	1.196	7	1849.625	2408.1351	FALSE	phosphoprotein enriched in astrocytes 15	200788 s at	0.218	5222	3.414E-04	FALSE
98790 s at	0.223	799	1450992 a at	0.229	592	98790 s at	0.065	5599	1459512 at	0.335	425	1853.75	2501.5152	TRUE	myeloid ecotropic viral integration site 1	204069 at	0.111	15767	8.545E-02	FALSE
98316 at	0.200	728	1427573 at	-0.115	4601.5	98316 at	-0.151	1856	1427573 at	0.651	242	1856.875	1950.6535	FALSE	cysteine-rich hydrophobic domain 1	NA	NA	NA	NA	
104219 f at	0.156	2503	1456340 at	0.126	2599	104219 f at	0.145	1004	1456340 at	-0.655	1325	1857.75	812.09826	FALSE	RIKEN cDNA 2610205E22 gene	223369 at	-0.130	9016	5.860E-03	FALSE
160614 at	-0.311	1260	1450655 at	-0.095	4495	94989 at	0.139	1410	1422553 at	0.773	271	1859	1828.5369	FALSE	phosphatase and tensin homolog	233254 x at	0.098	12078	2.671E-02	FALSE
101571 g at	-0.204	383	1437405 a at	-0.499	20	101571 g at	-0.329	1158	1421992 a at	0.145	5882	1860.75	2722.5242	FALSE	insulin-like growth factor binding protein 4	201508 at	0.138	20725	2.244E-01	FALSE
93968 at	-0.165	4259	1450638 at	0.369	173.5	93968 at	0.398	1206	1450638 at	0.171	1807	1861.375	1734.9352	FALSE	programmed cell death 5	219275 at	-0.140	12216	2.815E-02	FALSE
102808 at	-0.542	213	1418738 at	-0.237	394	102808 at	-0.313	1590	1418738 at	0.092	5249	1861.5	2339.514	FALSE	sodium channel, voltage-gated, type I, beta	205508 at	-0.282	3562	4.995E-05	FALSE
162277 r at	0.170	1098	1450816 at	0.167	1344	162277 r at	0.261	1229	1450816 at	-0.150	3777	1862	1280.6163	FALSE	polymerase (DNA directed), gamma 2, accessory subunit	205811 at	0.042	23107	3.051E-01	FALSE
104375 at	-0.159	2549	1435026 at	-0.233	957.5	104375 at	-0.290	1937	1450451 at	0.213	2005	1862.125	662.36022	FALSE	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	202524 s at	-0.319	4828	2.260E-04	FALSE
92839 f at	-0.103	2580	1452422 a at	0.196	927	92839 f at	0.083	3382	1426613 a at	0.293	560	1862.25	1341.0634	FALSE	U2 small nuclear ribonucleoprotein B	202505 at	-0.036	30490	5.752E-01	FALSE
93864 s at	0.242	252	1424800 at	-0.321	1149	161228 f at	0.072	3565	1431162 a at	0.342	2491	1864.25	1460.1711	FALSE	enabled homolog (Drosophila)	NA	NA	NA	NA	
95488 at	-0.143	3527	1427296 at	-0.209	627	95488 at	-0.221	1433	1427296 at	-0.193	1876	1865.75	1222.2426	TRUE	cDNA sequence BC010304	241242 at	0.110	9475	7.676E-03	FALSE
104425 at	0.175	898	1418983 at	-0.351	1903.5	104425 at	0.331	961	1442244 at	0.121	3719	1870.375	1315.4198	FALSE	InaD-like (Drosophila)	214705 at	-0.043	14495	6.131E-02	FALSE
102283 at	-0.411	398	1418057 at	-0.361	164.5	102283 at	-0.315	2330	1418057 at	-0.140	4594	1871.625	2058.0962	TRUE	T-cell lymphoma invasion and metastasis 1	206409 at	-0.227	4107	9.776E-05	TRUE
160875 at	-0.096	3428	1448166 a at	0.260	1047	98113 at	0.272	384	1420053 at	0.209	2639	1874.5	1402.8743	FALSE	Proteasome (prosome, macropain) subunit, beta type 1	214289 at	0.034	29798	5.496E-01	FALSE
161712 r at	0.116	3818	1422490 at	0.155	3307	93064 at	0.339	227	1441989 at	0.374	168	1880	1954.1005	TRUE	BCL2/adenovirus E1B interacting protein 1, NIP2	209308 s at	0.090	14016	5.259E-02	FALSE
102108 f at	-0.325	1214	1420171 s at	-0.153	2365	102108 f at	0.161	1454	1417472 at	0.210	2487	1880	639.97552	FALSE	myosin, heavy polypeptide 9, non-muscle	236455 at	-0.017	35788	7.548E-01	FALSE
94319 at	0.272	842	1420899 at	-0.175	3036	94319 at	0.318	1604	1420900 a at	0.171	2045	1881.75	916.00014	FALSE	RAB18, member RAS oncogene family	224377 s at	-0.244	10149	1.092E-02	FALSE
96058 s at	-0.252	1929	1434987 at	0.233	1814.5	96057 at	-0.111	3197	1437410 at	0.346	597	1884.375	1062.5743	FALSE	aldehyde dehydrogenase 2, mitochondrial	201425 at	0.074	24920	3.694E-01	FALSE
97327 at	-0.191	565	1421731 a at	0.161	785.5	97327 at	0.116	5084	1421731 a at	0.267	1112	1886.625	2143.3945	FALSE	flap structure specific endonuclease 1	204768 s at	-0.102	20833	2.278E-01	FALSE
96884 at	0.197	591	1415976 a at	-0.168	2170.5	96884 at	0.142	2093	1415975 at	-0.223	2699	1888.375	905.86251	FALSE	calcium regulated heat stable protein 1	218384 at	-0.157	8106	3.507E-03	FALSE
96115 at	0.147	3484	1419398 a at	-0.287	280.5	96115 at	-0.172	2998	1442128 at	0.498	801	1890.875	1585.8655	FALSE	receptor accessory protein 5	208873 s at	-0.365	2558	1.053E-05	FALSE
94801 at	-0.243	557	1428714 at	-0.160	1681	94801 at	0.094	3941	1452882 at	-0.200	1386	1891.25	1446.9716	FALSE	progesterone receptor membrane component 2	201701 s at	0.113	11045	1.752E-02	FALSE
93333 at	0.127	4677	1456205 x at	0.549	146.5	93333 at	0.550	335	1417652 a at	0.185	2408	1891.625	2120.8096	TRUE	tubulin cofactor a	216704 at	0.062	17401	1.241E-01	FALSE
160685 at	0.269	582	1452660 s at	0.145	4437.5	160685 at	-0.133	1390	1452660 s at	-0.251	1163	1893.125	1730.0395	FALSE	kelch-like 7 (Drosophila)	223250 at	-0.331	3214	3.086E-05	FALSE
99019 at	-0.224	671	1416933 at	-0.106	2914	99019 at	-0.190	1025	1416933 at	-0.177	2964	1893.5	1216.0303	TRUE	P450 (cytochrome) oxidoreductase	208928 at	0.097	20350	2.118E-01	FALSE
97927 at	-0.063	4545	1422572 at	-0.168	1385.5	97927 at	-0.173	514	1422572 at	-0.341	1132	1894.125	1804.7546	TRUE	ras homolog gene family, member G	203175 at	0.195	6918	1.490E-03	FALSE
97901 at	-0.213	1011	1460304 a at	-0.372	443	97901 at	-0.058	5044	1455490 at	-0.253	1088	1896.5	2117.9551	TRUE	upstream binding transcription factor, RNA polymerase I	202692 s at	0.123	13031	3.732E-02	FALSE
104633 at	0.178	825	1420498 a at	-0.089	4388.5	98045 s at	0.101	2188	1420498 a at	-0.486	188	1897.375	1858.5046	FALSE	disabled homolog 2 (Drosophila)	232898 at	-0.072	18268	1.481E-01	FALSE
97793 at	-0.586	140	1420563 at	-0.244	1756.5	97793 at	-0.644	928	1420563 at	0.252	4766	1897.625	2022.9442	FALSE	glutamate receptor, ionotropic, AMPA3 (alpha 3)	206730 at	-0.542	998	4.492E-07	FALSE
96220 at	0.196	805	1453986 at	0.077	4512.5	96220 at	-0.236	1014	1425865 a at	-0.251	1261	1898.125	1752.8533	FALSE	ligase III, DNA, ATP-dependent	204123 at	0.044	24643	3.591E-01	FALSE
93248 at	0.207	759	1438480 a at	0.289	204.5	93248 at	0.109	2936	1438769 a at	-0.227	3700	1899.875	1682.2502	FALSE	thymocyte nuclear protein 1	218491 s at	-0.185	8314	3.972E-03	FALSE
101405 at	-0.242	404	1448913 at	-0.307	394	101405 at	-0.110	3229	1448913 at	-0.334	3574	1900.25	1739.2114	TRUE	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member	203183 s at	-0.122	11041	1.751E-02	TRUE
95062 at	-0.171	1649	1426098 a at	0.106	3268	95062 at	0.238	606	1426098 a at	0.190	2080	1900.75	1101.7046	FALSE	calpastatin	208908 s at	0.349	2192	5.410E-06	FALSE
101634 at	0.184	3471	1420268 x at	0.173	1519.5	101634 at	0.339	829	1420267 at	0.171	1784	1900.875	1121.5042	TRUE	nucleophosmin 1	221923 s at	-0.106	14514	6.155E-02	FALSE
101530 at	-0.216	1240	1416557 a at	-0.100	3392	101530 at	-0.272	395	1438835 a at	-0.181	2581	1902	1340.4519	TRUE	elongation factor Tu GTP binding domain containing 2	222398 s at	0.047	28774	5.124E-01	FALSE
100112 at	-0.192	678	1417574 at	-0.200	1808.5	162234 f at	-0.110	3451	1417574 at	-0.237	1672	1902.375	1148.7992	TRUE	chemokine (C-X-C motif) ligand 12	209687 at	0.584	6046	7.262E-04	FALSE
101030 at	-0.183	1427	1449110 at	-0.234	391	101030 at	-0.114	4864	1449110 at	-0.265	929	1902.75	2018.9863	TRUE	ras homolog gene family, member B	226417 at	0.081	15735	8.487E-02	FALSE
99500 at	0.239	2619	1417622 at	-0.324	910	99500 at	0.267	3856	1443332 at	0.368	233	1904.5	1643.3507	FALSE	solute carrier family 12, member 2	225835 at	0.139	28124	4.856E-01	FALSE
95625 at	-0.346	751	1417116 at	-0.172	659	95625 at	0.203	2919	1448596 at	-0.179	3291	1905	1394.4442	FALSE	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	202219 at	0.347	2613	1.143E-05	FALSE
161436 s at	-0.317	1850	1421480 a at	-0.336	764	161436 s at	0.461	1536	1443968 at	0.165	3478	1907	1142.4214	FALSE	adenosine deaminase, RNA-specific, B1	203865 s at	-0.542	2124	4.726E-06	FALSE
101710 at	-0.183	1250	1421351 at	-0.137	1934	101710 at	-0.119	3526	1443285 at	0.231	921	1907.75	1158.4088	FALSE	glutamate receptor, ionotropic, AMPA4 (alpha 4)	208464 at	0.084	15628	8.277E-02	FALSE
96284 at	-0.285	1118	1423370 a at	-0.298	368	96284 at	-0.167	1653	1423370 a at	-0.143	4499	1909.5	1804.9928	TRUE	casein kinase 1, gamma 2	202574 s at	-0.032	30162	5.618E-01	FALSE
94021 at	-0.146	1177	1419630 a at	-0.069	4189	94021 at	-0.162	719	1419630 a at	-0.236	1556	1910.25	1557.2333	TRUE	tripartite motif protein 11	226566 at	-0.166	7778	2.819E-03	TRUE
160299 at	-0.120	3772	1427913 at	0.194	712	160299 at	0.165	1730	1427913 at	0.182	1432	1911.5	1311.8845	FALSE	RWD domain containing 1	219598 s at	0.041	33769	6.911E-01	FALSE
94899 at	-0.121	4131	1460342 s at	-0.129	2335.5	94899 at	-0.242	1101	1456763 at	-0.481	97	1916.125	1737.3535	TRUE	expressed sequence AA536749	225896 at	-0.192	9079	6.115E-03	TRUE
94346 at	0.382	589	1452401 at	0.188	1656	94346 at	0.111	5318	1452401 at	0.440	102	1916.25	2358.8648	TRUE	Wilms' tumour 1-associating protein	229630 s at	0.244	10835	1.589E-02	TRUE
95139 at	0.126	1875	1428882 at	-0.168	1978	95139 at	-0.233	1579	1429367 at	0.156	2234	1916.5	270.9348	FALSE	WD repeat domain, phosphoinositide interacting 2	226986 at	0.098	15359	7.735E-02	FALSE
103223 at	-0.346	531	1452878 at	-0.126	2293	94161 at	-0.569	157	1437860 at	0.096	4696	1919.25	2072.2607	FALSE	protein kinase C, epsilon	226101 at	-0.299	5520	4.539E-04	FALSE
161587 at	-0.574	402	1428326 s at	0.143	5104	96048 at	0.275	1820	1428326 s at	-0.417	368	1923.5	2225.6711	FALSE	heat-responsive protein 12	203790 s at	0.105	28910	5.176E-01	FALSE
100339 at	0.178	1070	1424898 at	0.172	1041.5	100340 at	0.065	3791	1450261 a at	-0.191	1804	1926.625	1292.0505	FALSE	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	207185 at	0.031	37057	7.926E-01	FALSE
104733 at	0.168	3655	1438647 x at	0.471	332.5	104733 at	0.195	1482	1418579 at	0.217	2241	1927.625	1393.441	TRUE	centrin 2	209194 at	0.283	16064	9.237E-02	FALSE
160896 at	-0.194	2207	1417090 at	-0.356	2829	160896 at	-0.357	2037	1417090 at	-0.526	643	1929	922.45036	TRUE	reticulocalbin 1	201063 at	-0.341	7525	2.346E-03	TRUE
99800 at	0.209	875	1450435 at	-0.191	714.5	99800 at	-0.171	4193	1450435 at	-0.179	1936	1929.625	1603.2955	FALSE	L1 cell adhesion molecule	204584 at	-0.743	949	3.879E-07	TRUE
93267 at	0.308	1347	1456386 at	-0.221	3486	93267 at	-0.227	1503	1438397 a at	0.300	1385	1930.25	1039.2912	FALSE	RNA-binding region (RNP1, RRM) containing 2	227223 at	0.151	15720	8.434E-02	FALSE
94963 at	-0.158	4321	1416157 at	-0.272	513	94963 at	-0.225	2753	1416157 at	-0.458	134	1930.25	1968.7318	TRUE	vinculin	200930 s at	0.034	24444	3.522E-01	FALSE
96712 at	0.306	99	1448321 at	0.125	3001	96712 at	0.139	1377	1448321 at	0.247	3246	1930.75	1476.1735	TRUE	SPARC related modular calcium binding 1	222784 at	0.274	2338	7.179E-06	TRUE
93590 at	-0.406	331	1460436 at	-0.183	963	92516 at	-0.185	1909	1442995 at	0.102	4521	1931	1844.4157	FALSE	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	202607 at	0.175	9924	9.706E-03	FALSE
93491 f at	0.241	1001	1455480 s at	-0.249	1357	93491 f at	-0.228	1298	1423113 a at	-0.113	4069	1931.25	1433.656	FALSE	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	243046 at	0.365	4652	1.848E-04	FALSE
104670 at	0.115	3210	1434846 at	-0.145	2194	104670 at	0.196	1300	1434846 at	-0.290	1030	1933.5	985.72258	FALSE	RIKEN cDNA 1700065A05 gene	234968 at	0.071	16467	1.010E-01	FALSE
97334 at	0.104	2789	1436050 x at	0.210	767	97334 at	0.197	704	1436050 x at	0.175	3485	1936.25	1415.5558	TRUE	hairy and enhancer of split 6 (Drosophila)	226446 at	0.361	2947	1.977E-05	TRUE
100032 at	-0.280	952	1418180 at	-0.159	2289	100032 at	-0.128	4114	1418180 at	0.592	397	1938	1653.789	FALSE	trans-acting transcription factor 1	224754 at	0.321	213	2.137E-08	FALSE
103261 at	0.183	1042	1418109 at	0.139	1319.5	103261 at	-0.070	3958	1418109 at	0.263	1433	1938.125	1356.5622	FALSE	G1 to S phase transition 2	205541 s at	-0.292	6490	1.039E-03	FALSE
104625 at	-0.168	1212	1429777 at	0.160	914	96120 at	0.084	5072	1435701 at	-0.333	563	1940.25	2104.615	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 6	209015 s at	0.300	13203	3.974E-02	FALSE
161170 r at	0.061	5124	1423065 at	-0.302	269.5	100479 at	-0.163	2304	1423065 at	0.929	66	1940.875	2350.3755	FALSE	DNA methyltransferase 3A	244428 at	-0.034	27431	4.589E-01	FALSE
160319 at	-0.270	538	1416114 at	-0.323	256	160319 at	0.057	5146	1416114 at	-0.175	1836	1944	2242.8143	FALSE	SPARC-like 1 (mast9, hevin)	200795 at	0.099	20269	2.089E-01	FALSE
95282 at	0.246	1982	1426645 at	-0.161	1642.5	95282 at	0.068	4106	1437497 a at	0.513	53	1945.875	1667.5788	FALSE	heat shock protein 90kDa alpha (cytosolic), class A member 1	214328 s at	0.070	24918	3.693E-01	FALSE
95758 at	-0.175	1345	1415823 at	-0.679	10	95758 at	-0.071	4341.5	1415823 at	-0.182	2098	1948.625	1813.9086	TRUE	stearoyl-Coenzyme A desaturase 2	NA	NA	NA	NA	
101890 f at	-0.203	1508	1448794 s at	-0.239	1228	104738 at	-0.167	3797	1417657 s at	-0.272	1275	1952	1236.0779	TRUE	DnaJ (Hsp40) homolog, subfamily C, member 2	NA	NA	NA	NA	
92880 at	-0.324	93	1420911 a at	-0.194	869	92880 at	-0.177	662	1420911 a at	0.082	6186	1952.5	2841.3392	FALSE	milk fat globule-EGF factor 8 protein	210605 s at	-0.050	26554	4.262E-01	FALSE
95722 at	0.087	4101	1416592 at	0.187	1597.5	95722 at	0.152	893	1416592 at	0.410	1220	1952.875	1460.7274	TRUE	glutaredoxin	206662 at	0.036	40564	8.945E-01	FALSE
93690 at	0.315	182	1425457 a at	-0.173	2335.5	95450 at	0.176	2567	1440935 at	0.185	2729	1953.375	1191.9059	FALSE	growth factor receptor bound protein 10	209409 at	-0.380	4407	1.373E-04	FALSE
161629 i at	0.192	1725	1436880 at	0.162	1210	161629 i at	0.186	1620	1436879 x at	-0.185	3265	1955	901.15666	FALSE	alpha fetoprotein	204694 at	0.047	20684	2.227E-01	FALSE
92418 at	-0.179	677	1430394 a at	-0.273	1639.5	92418 at	-0.146	1549	1430394 a at	-0.194	3955	1955.125	1402.1008	TRUE	ATP-binding cassette, sub-family B (MDR/TAP), member 9	214209 s at	-0.284	5997	6.883E-04	TRUE
92913 at	-0.174	1114	1419748 at	-0.097	5175	92913 at	-0.327	82	1446962 at	0.216	1468	1959.75	2222.6777	FALSE	ATP-binding cassette, sub-family D (ALD), member 2	207583 at	-0.050	20280	2.092E-01	FALSE
93253 at	-0.142	2399	1426585 s at	-0.211	971	93254 at	-0.272	551	1426585 s at	-0.190	3919	1960	1526.849	TRUE	mitogen activated protein kinase 1	212271 at	-0.859	1129	6.250E-07	TRUE
103582 r at	0.107	3301	1426398 at	0.178	2653	103582 r at	0.162	1471	1443188 at	0.895	418	1960.75	1277.4209	TRUE	ubiquitin-conjugating enzyme E2W (putative)	222657 s at	-0.298	2870	1.790E-05	FALSE
162245 f at	0.101	2898	1435559 at	-0.173	1133	92382 at	-0.149	1504	1433942 at	-0.147	2311	1961.5	794.75384	FALSE	myosin VI	203216 s at	0.462	6339	9.382E-04	FALSE
97390 at	0.118	2644	1417132 at	0.191	1193	97389 at	-0.095	2615	1417132 at	0.487	1406	1964.5	772.8745	FALSE	cell division cycle 25 homolog A (S. cerevisiae)	204695 at	-0.098	18801	1.635E-01	FALSE
92843 r at	0.543	481	1438686 at	-0.215	684.5	103926 at	-0.289	2494	1427037 at	0.426	4201	1965.125	1743.7004	FALSE	Eukaryotic translation initiation factor 4, gamma 1	208625 s at	0.229	6018	7.030E-04	FALSE
93844 at	-0.193	2115	1437134 at	0.126	1763	93844 at	0.243	371	1437134 at	0.181	3614	1965.75	1332.0834	FALSE	ubiquinol-cytochrome c reductase, complex III subunit VII	201568 at	-0.240	7140	1.780E-03	FALSE
160087 at	0.283	1063	1456037 x at	0.135	2625	161430 at	0.198	416	1455667 at	-0.137	3762	1966.5	1514.134	FALSE	prolactin regulatory element binding	217861 s at	0.023	33173	6.713E-01	FALSE
100449 g at	-0.231	244	1451604 a at	-0.053	6536	100450 r at	-0.231	1077	1451604 a at	-0.665	11	1967	3080.18	TRUE	activin A receptor, type II-like 1	210838 s at	0.050	29799	5.497E-01	FALSE
162377 f at	-0.479	42	1449511 a at	-0.122	5186	100974 at	-0.293	1525	1449511 a at	-0.291	1119	1968	2234.7297	TRUE	single stranded DNA binding protein 4	229269 x at	-0.359	1553	1.588E-06	TRUE
161665 at	-0.200	646	1425510 at	-0.242	999.5	161665 at	0.119	2585	1425510 at	-0.268	3643	1968.375	1399.0461	FALSE	MAP/microtubule affinity-regulating kinase 1	226653 at	-0.262	5030	2.766E-04	FALSE
160603 at	-0.208	2551	1453972 x at	0.181	648.5	160603 at	-0.090	4501	1421907 at	0.711	175	1968.875	1975.8462	FALSE	peroxisome proliferator activated receptor binding protein	203497 at	0.190	7562	2.425E-03	FALSE
96616 at	0.183	2370	1417555 at	0.084	3216	96616 at	0.178	1959	1446838 at	0.453	331	1969	1210.9162	TRUE	ATPase family, AAA domain containing 1	224850 at	-0.269	6105	7.631E-04	FALSE
101515 at	-0.138	2820	1416409 at	-0.210	699	101515 at	-0.188	2256	1416408 at	-0.160	2101	1969	901.27576	TRUE	acyl-Coenzyme A oxidase 1, palmitoyl	209600 s at	0.287	7988	3.264E-03	FALSE
161852 i at	-0.066	5918	1448287 at	0.291	978.5	161852 i at	0.251	453	1447320 x at	0.276	535	1971.125	2641.356	FALSE	RNA polymerase 1-3	218258 at	-0.060	31169	6.022E-01	FALSE
97412 at	-0.052	5900	1428004 at	0.221	462.5	97412 at	0.335	486	1428004 at	0.359	1044	1973.125	2631.6756	FALSE	RIKEN cDNA 3300001G02 gene	218493 at	-0.182	10375	1.238E-02	FALSE
98992 at	0.138	1513	1417596 at	0.250	200	98992 at	0.106	2503	1417596 at	0.149	3681	1974.25	1477.9814	TRUE	endothelial precursor protein B9	210534 s at	-0.334	5292	3.627E-04	FALSE
96652 at	-0.191	2350	1416284 at	0.107	2274.5	96652 at	0.334	617	1437622 x at	0.245	2667	1977.125	922.55717	FALSE	mitochondrial ribosomal protein L28	204599 s at	-0.109	16180	9.484E-02	FALSE
102704 at	-0.130	5096	1434449 at	-0.414	424	102704 at	-0.985	25	1434449 at	-0.362	2366	1977.75	2316.7213	TRUE	aquaporin 4	226228 at	0.479	2052	4.269E-06	FALSE
97711 at	0.120	2085	1448024 at	0.170	1115.5	97711 at	-0.192	2116	1448024 at	0.205	2603	1979.875	623.16669	FALSE	natriuretic peptide receptor 3	219790 s at	-0.025	33386	6.781E-01	FALSE
161320 r at	0.414	917	1425028 a at	-0.081	3143	100605 at	-0.094	2870	1419739 at	-0.404	1006	1984	1186.4864	FALSE	tropomyosin 2, beta	204083 s at	0.411	3366	3.801E-05	FALSE
160970 at	-0.337	437	1454735 at	-0.207	1856	100626 at	0.081	3696	1454735 at	-0.196	1951	1985	1334.369	FALSE	outer dense fiber of sperm tails 2	225617 at	0.146	11571	2.164E-02	FALSE
100628 at	-0.179	2281	1448284 a at	0.334	1134.5	100628 at	0.207	1963	1448284 a at	0.198	2564	1985.625	618.24744	FALSE	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	232146 at	-0.121	10563	1.368E-02	FALSE
161459 f at	-0.141	1734	1436198 at	0.158	924	161459 f at	0.058	4571	1439942 at	0.271	714	1985.75	1778.7221	FALSE	prolyl endopeptidase	204117 at	-0.106	11248	1.911E-02	FALSE
104255 at	-0.361	209	1435551 at	0.092	4456	104255 at	0.246	443	1435551 at	0.301	2836	1986	2029.9407	FALSE	formin homology 2 domain containing 3	236540 at	-0.158	5874	6.196E-04	FALSE
97449 at	0.103	2533	1448137 at	0.135	1574.5	97450 s at	-0.255	815	1448137 at	-0.164	3024	1986.625	986.10762	FALSE	aldehyde dehydrogenase family 7, member A1	213591 at	0.249	7492	2.289E-03	FALSE
97736 at	0.195	1119	1426590 at	-0.168	1223	97232 at	-0.136	1236	1426590 at	-0.129	4374	1988	1591.5282	FALSE	G elongation factor, mitochondrial 2	231917 at	-0.199	3453	4.301E-05	FALSE
96948 at	-0.191	2269	1437993 x at	-0.359	108.5	96948 at	-0.311	956	1423664 at	-0.118	4624	1989.375	1968.5014	TRUE	quinoid dihydropteridine reductase	209123 at	0.230	15099	7.265E-02	FALSE
104020 at	-0.449	512	1439548 at	-0.089	4892	104020 at	-0.258	332	1439548 at	-0.379	2222	1989.5	2114.1488	TRUE	RAP2B, member of RAS oncogene family	238622 at	-0.257	1280	8.535E-07	TRUE
93806 at	0.402	469	1436997 x at	0.417	184	93806 at	0.124	4912	1421871 at	0.169	2397	1990.5	2181.6514	TRUE	SH3-binding domain glutamic acid-rich protein like	201311 s at	-0.165	14650	6.408E-02	FALSE
160173 at	0.159	3225	1426758 s at	-0.144	3387.5	160172 at	-0.281	1243	1429257 at	0.925	111	1991.625	1588.172	FALSE	GTL2, imprinted maternally expressed untranslated mRNA	NA	NA	NA	NA	
103250 at	0.060	5595	1421534 at	-0.334	235	97124 at	-0.457	1429	1421534 at	-0.284	713	1993	2450.9497	FALSE	deafness, autosomal dominant 5 homolog (human)	203695 s at	0.158	13655	4.613E-02	FALSE
96915 f at	-0.213	1963	1428464 at	0.305	648.5	102097 f at	0.287	477	1428464 at	0.118	4886	1993.625	2039.3041	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	218563 at	-0.279	6624	1.159E-03	FALSE
101786 at	0.100	2813	1422255 at	-0.181	2817	101786 at	-0.422	644	1438613 at	-0.369	1713	1996.75	1040.7563	FALSE	potassium voltage-gated channel, shaker-related subfamily, member 4	207248 at	-0.398	720	2.087E-07	FALSE
160833 at	-0.115	3718	1425803 a at	-0.312	473	160833 at	-0.086	2955	1417165 at	-0.303	841	1996.75	1585.1937	TRUE	methyl-CpG binding domain protein 2	202484 s at	0.066	29839	5.512E-01	FALSE

102700 at	-0.611	68	1416711 at	0.106	2638	102700 at	0.626	2132	1416711 at	0.979	3154	1998	1352.6261	FALSE	T-box brain gene 1	220025 at	-0.029	32427	6.452E-01	FALSE
96954 at	0.163	932	1426247 at	-0.309	336	96954 at	-0.108	3258	1426248 at	0.160	3470	1999	1597.1829	FALSE	serine/threonine kinase 24 (STE20 homolog, yeast)	208854 s at	-0.394	1479	1.342E-06	FALSE
100887 at	-0.127	3720	1448829 at	0.134	2235	100887 at	-0.149	1520	1417736 at	0.322	521	1999	1345.5435	FALSE	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	218781 at	0.142	7649	2.559E-03	FALSE
104444 at	-0.135	2975	1425191 at	0.158	1137	104444 at	0.239	1372	1425191 at	0.212	2517	2000.25	886.39095	FALSE	RIKEN cDNA 9430098E02 gene	205441 at	0.120	7615	2.497E-03	FALSE
161001 at	0.158	1656	1455180 at	0.067	5323.5	161001 at	0.316	91	1455180 at	-0.230	931	2000.375	2305.8642	FALSE	expressed sequence AA407270	212244 at	0.381	513	1.080E-07	FALSE
95392 at	0.049	5664	1421415 s at	-0.306	662	95392 at	-0.435	816	1421415 s at	-0.567	872	2003.5	2441.9481	FALSE	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	215595 x at	0.181	4664	1.879E-04	FALSE
93251 at	0.273	1234	1456748 a at	0.195	682	93251 at	0.091	3537	1448465 at	0.235	2570	2005.75	1292.4159	TRUE	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	201708 s at	-0.345	744	2.281E-07	FALSE
94845 at	-0.196	2456	1426361 at	-0.224	1456.5	94845 at	-0.313	1353	1426359 at	-0.174	2768	2008.375	709.80765	TRUE	zinc finger CCCH type containing 11A	NA	NA	NA	NA	
93116 at	-0.081	4884	1420610 at	-0.557	379.5	93116 at	0.186	898	1420610 at	0.262	1883	2011.125	2014.2057	FALSE	protein kinase, cAMP dependent, catalytic, beta	202742 s at	-0.601	1954	3.527E-06	FALSE
103234 at	-0.189	2418	1424847 at	-0.518	47.5	103234 at	0.366	599	1424847 at	-0.309	4984	2012.125	2225.1179	FALSE	neurofilament, heavy polypeptide	33767 at	-0.621	4164	1.041E-04	FALSE
95473 s at	-0.217	1666	1433611 s at	0.173	2649	95473 s at	0.220	910	1439466 s at	0.211	2830	2013.75	896.10281	FALSE	BUD31 homolog (yeast)	NA	NA	NA	NA	
161062 r at	0.081	4391	1455605 at	0.222	1052.5	161062 r at	0.164	2516	1424402 at	0.504	99	2014.625	1870.2797	TRUE	RUN and FYVE domain containing 3	213437 at	0.331	4176	1.056E-04	TRUE
103092 at	-0.153	3449	1455012 s at	-0.254	280.5	103092 at	-0.478	422	1435604 at	0.118	3918	2017.375	1934.2425	FALSE	tripartite motif protein 37	213009 s at	-0.476	2669	1.333E-05	FALSE
92403 at	-0.117	2759	1419420 at	-0.139	3231	92403 at	-0.840	125	1449468 at	-0.180	1958	2018.25	1367.1745	TRUE	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialylt	220979 s at	-0.644	2941	1.958E-05	TRUE
94743 f at	0.310	367	1425999 at	0.135	2155	94743 f at	0.239	79	1425999 at	-0.077	5475	2019	2480.2645	FALSE	complement factor H-related protein	NA	NA	NA	NA	
103855 at	-0.333	190	1419835 s at	-0.263	324.5	103855 at	-0.042	5967	1419835 s at	-0.234	1620	2025.375	2705.6924	TRUE	plectin 1	201373 at	0.214	8345	4.058E-03	FALSE
95486 at	0.171	662	1420056 s at	0.199	1052.5	95486 at	0.083	3275	1420057 at	0.176	3114	2025.875	1360.3851	TRUE	phosphatidylserine receptor	212723 at	0.375	6479	1.030E-03	TRUE
104701 at	-0.602	46	1418025 at	-0.332	557.5	104701 at	-0.472	531	1418025 at	-0.054	6969	2025.875	3303.7941	TRUE	basic helix-loop-helix domain containing, class B2	201169 s at	-0.064	31696	6.208E-01	FALSE
160115 at	-0.148	2724	1437906 x at	0.084	3398	160115 at	0.581	251	1423299 at	0.196	1731	2026	1367.1428	FALSE	thioredoxin-like 1	201588 at	-0.105	18299	1.489E-01	FALSE
103800 at	-0.103	2908	1435684 at	0.155	1144	103800 at	-0.085	3664	1447384 at	0.418	413	2032.25	1510.0226	FALSE	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	209380 s at	-0.289	4736	2.041E-04	FALSE
160954 at	0.058	6015	1449030 at	-0.396	228	160954 at	-0.420	1285	1460230 at	0.395	604	2033	2690.4705	FALSE	synapsin II	210315 at	-0.901	1509	1.419E-06	FALSE
96911 at	-0.096	4857	1450623 at	-0.246	612	96911 at	-0.195	1039	1450623 at	-0.267	1635	2035.75	1927.0553	TRUE	guanine nucleotide binding protein, beta 2	200852 x at	-0.149	8189	3.674E-03	TRUE
103226 at	-0.050	5676	1450430 at	0.164	1616.5	103226 at	0.255	117	1450430 at	-0.307	745	2038.625	2501.6524	FALSE	mannose receptor, C type 1	204438 at	-0.035	37734	8.125E-01	FALSE
160570 at	-0.167	1291	1448327 at	-0.318	665.5	160570 at	-0.043	5943	1448327 at	-0.795	288	2046.875	2630.1442	TRUE	actinin alpha 2	203862 s at	-0.640	53	4.015E-09	TRUE
160122 at	-0.214	1084	1424396 a at	-0.153	1600	160122 at	-0.322	50	1424395 at	-0.134	5454	2047	2360.991	TRUE	asparaginase like 1	222764 at	0.178	9247	6.734E-03	FALSE
96207 at	-0.256	1062	1418703 at	-0.151	2086	94972 at	-0.061	4130	1434005 at	-0.260	913	2047.75	1482.8563	TRUE	RNA binding motif, single stranded interacting protein 1	207266 x at	-0.350	306	4.010E-08	TRUE
94180 s at	0.109	2521	1420694 a at	-0.103	4480.5	94180 s at	-0.186	691	1433743 at	-0.540	504	2049.125	1858.8675	FALSE	dachshund 1 (Drosophila)	228915 at	-1.087	216	2.138E-08	FALSE
92615 at	-0.159	4003	1434057 at	0.211	1468.5	92615 at	0.239	1149	1434057 at	0.243	1590	2052.625	1313.4845	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	203613 s at	-0.306	4923	2.490E-04	FALSE
96606 at	0.527	534	1450007 at	-0.379	357	96606 at	-0.299	3393	1420810 at	0.158	3941	2056.25	1874.7336	FALSE	RIKEN cDNA 1500003O03 gene	207993 s at	-0.154	9612	8.248E-03	FALSE
98775 at	0.165	1567	1418512 at	0.158	3774	98775 at	-0.178	1625	1418513 at	0.312	1270	2059	1153.8582	FALSE	serine/threonine kinase 3 (Ste20, yeast homolog)	204068 at	0.401	2504	9.599E-06	FALSE
93451 at	-0.283	1602	1455056 at	-0.135	4031	93451 at	-0.474	1294	1455056 at	-0.415	1309	2059	1322.2907	TRUE	LIM domain only 7	NA	NA	NA	NA	
161252 r at	0.353	1355	1425974 a at	-0.106	4675.5	100475 at	0.141	999	1419879 s at	-0.525	1211	2060.125	1749.7035	FALSE	tripartite motif protein 25	224806 at	0.107	14171	5.558E-02	FALSE
104253 at	-0.131	1715	1434805 at	-0.166	1656	104253 at	-0.220	907	1434805 at	-0.173	3965	2060.75	1321.7	TRUE	myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	224993 at	-0.080	17742	1.333E-01	FALSE
100291 at	0.199	492	1450457 at	-0.109	3503	100291 at	-0.086	3949	1455886 at	0.929	304	2062	1931.555	FALSE	Casitas B-lineage lymphoma	225234 at	0.210	2465	8.940E-06	FALSE
96280 at	-0.209	2727	1417368 s at	0.400	228	96280 at	0.324	585	1417368 s at	0.107	4715	2063.75	2083.7232	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	209224 s at	-0.143	16034	9.172E-02	FALSE
104241 at	-0.416	327	1434487 at	-0.200	1242.5	104241 at	-0.173	4385	1458901 at	0.199	2314	2067.125	1745.6167	FALSE	myocyte enhancer factor 2D	225641 at	-0.248	5148	3.167E-04	FALSE
92522 at	-0.245	321	1451808 at	-0.427	658	92522 at	-0.395	214	1451808 at	-0.139	7077	2067.5	3345.0214	TRUE	potassium inwardly-rectifying channel, subfamily J, member 4	211451 s at	-0.521	870	3.269E-07	TRUE
160454 at	0.181	1523	1423949 at	0.077	3972	160454 at	-0.181	1812	1423949 at	0.227	963	2067.5	1317.6748	FALSE	ubiquitin-conjugating enzyme E2Z (putative)	222395 s at	0.306	3557	4.972E-05	FALSE
93716 at	-0.133	1925	1460568 at	-0.174	1164	93716 at	-0.259	733	1460568 at	-0.209	4461	2070.75	1667.9637	TRUE	tripartite motif protein 46	238147 at	-0.199	4390	1.344E-04	TRUE
97967 at	-0.522	57	1451475 at	-0.338	320	97967 at	-0.055	6754	1451475 at	-0.607	1154	2071.25	3156.6636	TRUE	Plexin D1	38671 at	0.410	1026	4.803E-07	FALSE
93352 at	-0.098	3389	1433428 x at	-0.135	2264.5	93352 at	0.125	2187	1417500 a at	-0.613	453	2073.375	1211.8751	FALSE	transglutaminase 2, C polypeptide	201042 at	0.247	14982	7.075E-02	FALSE
96908 at	-0.079	5196	1428781 at	-0.547	234	96908 at	-0.163	2829	1428781 at	-1.455	35	2073.5	2439.9473	TRUE	RIKEN cDNA 1110014F24 gene	226926 at	-0.136	12348	2.977E-02	TRUE
160444 at	0.073	4842	1455284 x at	0.200	364	160444 at	0.105	2538	1455284 x at	0.433	552	2074	2091.0686	TRUE	phosphatidylinositol glycan, class X	227403 at	-0.089	17442	1.252E-01	FALSE
101853 f at	0.152	3059	1423153 x at	-0.081	4281	101853 f at	0.245	472	1450876 at	-0.349	487	2074.75	1908.4064	FALSE	complement component factor h	213800 at	0.347	6837	1.372E-03	FALSE
92353 at	-0.126	2007	1448982 at	-0.185	1029.5	92353 at	-0.433	23	1448982 at	0.151	5253	2078.125	2266.2777	FALSE	kallikrein 6	204733 at	0.254	19261	1.764E-01	FALSE
103619 at	-0.203	2384	1417767 at	-0.258	201.5	96878 at	-0.505	248	1417767 at	-0.084	5480	2078.375	2485.7857	TRUE	cytochrome b5 type B	238554 at	-0.478	290	3.474E-08	TRUE
96799 at	-0.163	2448	1417476 at	-0.109	4185	96799 at	-0.330	716	1417476 at	-0.339	967	2079	1598.5108	TRUE	F-box and WD-40 domain protein 5	223050 s at	-0.067	19750	1.928E-01	FALSE
103451 at	-0.728	67	1434653 at	-0.113	5063	103451 at	-0.801	159	1442437 at	0.411	3040	2082.25	2419.5233	FALSE	PTK2 protein tyrosine kinase 2 beta	203110 at	-0.476	1230	7.591E-07	FALSE
94056 at	-0.186	1949	1415965 at	-0.391	77.5	94057 g at	0.375	47	1415964 at	0.086	6256	2082.375	2921.1419	FALSE	stearoyl-Coenzyme A desaturase 1	211162 x at	-0.286	11090	1.787E-02	FALSE
162013 f at	0.065	4463	1437997 x at	0.308	251.5	96059 at	0.129	1966	1437997 x at	0.222	1652	2083.125	1752.9254	TRUE	Mitochondrial ribosomal protein L48	218281 at	0.001	44336	9.927E-01	FALSE
104562 at	0.126	1618	1434343 at	0.145	2746.5	104562 at	0.093	2945	1434343 at	0.418	1032	2085.375	913.61547	TRUE	RIKEN cDNA 5730403M16 gene	NA	NA	NA	NA	
97367 at	-0.222	1442	1418279 a at	-0.217	2048	97369 g at	-0.253	673	1449019 at	-0.108	4180	2085.75	1505.2779	TRUE	A kinase (PRKA) anchor protein 1	210625 s at	-0.113	18082	1.428E-01	FALSE
93886 at	0.151	1771	1423048 a at	-0.281	123	160809 at	0.109	4029	1423047 at	0.161	2426	2087.25	1616.935	FALSE	toll interacting protein	217930 s at	-0.241	5985	6.853E-04	FALSE
101090 at	0.146	1311	1425896 a at	0.175	674	162170 r at	0.118	3613	1458593 at	-0.164	2756	2088.5	1338.5282	FALSE	fibrillin 1	202766 s at	0.209	3032	2.365E-05	FALSE
161553 i at	0.171	2310	1418100 at	-0.140	5060	161553 i at	0.230	149	1448952 at	0.276	839	2089.5	2175.7589	FALSE	RIKEN cDNA A030009H04 gene	238096 at	0.029	27322	4.545E-01	FALSE
94927 at	0.211	619	1417076 at	0.098	3818	160729 f at	-0.137	3121	1421804 at	0.275	805	2090.75	1619.0541	FALSE	fatty acid binding protein 9, testis	NA	NA	NA	NA	
100514 at	-0.178	2686	1422555 s at	-0.222	871	104316 at	-0.087	4611	1422556 at	0.391	196	2091	1981.9056	FALSE	guanine nucleotide binding protein, alpha 13	224761 at	0.612	928	3.691E-07	FALSE
93426 at	0.645	70	1428982 at	0.341	639.5	93426 at	0.045	6084	1428982 at	0.211	1575	2092.125	2732.6174	TRUE	RIKEN cDNA D530031C13 gene	NA	NA	NA	NA	
94433 at	-0.229	2137	1426722 at	-0.400	294	162233 r at	0.234	504	1429594 at	0.107	5442	2094.25	2379.0091	FALSE	solute carrier family 38, member 2	222982 x at	0.378	11182	1.857E-02	FALSE
94232 at	-0.150	1653	1417420 at	-0.122	4725.5	94232 at	-0.228	1176	1417419 at	0.432	827	2095.375	1785.8032	FALSE	cyclin D1	208712 at	0.173	17597	1.293E-01	FALSE
94238 at	-0.393	129	1431057 a at	-0.046	6393	94238 at	-0.290	177	1430956 at	-0.198	1709	2102	2953.2741	TRUE	protease, serine, 23	229441 at	-0.120	11691	2.274E-02	TRUE
97358 at	-0.338	411	1428510 at	-0.228	636	97358 at	-0.188	1306	1428510 at	-0.089	6058	2102.75	2664.0938	TRUE	latrophilin 1	47560 at	-0.436	1811	2.699E-06	TRUE
100364 at	0.135	2181	1426106 a at	-0.324	682	100364 at	-0.430	1639	1420188 at	0.131	3912	2103.5	1355.6181	FALSE	synaptotagmin VI	244227 at	-0.298	5147	3.166E-04	FALSE
101519 at	-0.120	4713	1454615 x at	0.333	530	101519 at	0.296	187	1454615 x at	0.168	2992	2105.5	2140.6993	FALSE	signal recognition particle 14	200007 at	0.086	23853	3.330E-01	FALSE
161925 at	0.243	2028	1451797 at	-0.130	3914	97992 at	-0.244	963	1434546 at	-0.240	1518	2105.75	1281.5538	FALSE	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	34868 at	0.078	13989	5.209E-02	FALSE
96211 at	-0.268	509	1428698 at	-0.091	4840	96211 at	-0.259	1290	1428698 at	-0.403	1785	2106	1896.8449	TRUE	RIKEN cDNA 2310004I03 gene	NA	NA	NA	NA	
161527 r at	-0.079	3742	1448335 s at	-0.108	3461.5	94819 f at	0.339	484	1458536 at	-0.290	739	2106.625	1733.3443	FALSE	cyclin I	239804 at	0.206	8601	4.650E-03	FALSE
94262 at	0.263	207	1427408 a at	-0.097	5341.5	94262 at	-0.200	1423	1452125 at	0.457	1459	2107.625	2233.0658	FALSE	thyroid hormone receptor associated protein 3	222440 s at	0.067	18466	1.541E-01	FALSE
102407 at	-0.229	453	1449456 a at	0.153	1423	102407 at	0.346	211	1449456 a at	0.070	6345	2108	2872.8051	FALSE	chymase 1, mast cell	214533 at	-0.019	36665	7.824E-01	FALSE
92361 at	-0.266	595	1452894 at	-0.129	5555.5	92361 at	0.217	2009	1428741 at	0.380	275	2108.625	2418.2717	FALSE	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	234904 x at	-0.039	26876	4.387E-01	FALSE
99886 at	-0.175	2224	1451813 at	-0.083	4646.5	99886 at	-0.282	856	1446394 at	-0.681	716	2110.625	1822.3226	TRUE	opioid receptor, kappa 1	207553 at	-0.541	1519	1.461E-06	TRUE
102671 at	0.146	1847	1452529 a at	0.082	5676.5	102673 at	0.238	221	1421582 a at	0.389	699	2110.875	2473.077	TRUE	cAMP responsive element binding protein 1	204314 s at	0.227	5743	5.469E-04	TRUE
160627 at	0.171	1510	1434608 at	0.275	292	160627 at	0.084	4121	1434607 at	0.237	2530	2113.25	1621.2755	TRUE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	212834 at	0.065	22203	2.749E-01	FALSE
101725 at	0.111	1979	1450530 at	-0.280	196	101725 at	-0.075	5181	1455234 at	-0.358	1099	2113.75	2170.5347	FALSE	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	220829 s at	-0.044	30770	5.852E-01	FALSE
101475 at	0.453	76	1448733 at	0.157	4053	101475 at	0.268	544	1417493 at	0.120	3784	2114.25	2094.9912	TRUE	B lymphoma Mo-MLV insertion region 1	202265 at	0.221	11760	2.348E-02	TRUE
93850 at	0.100	3461	1417380 at	-0.177	1346	104300 at	0.152	1213	1445724 at	0.262	2439	2114.75	1052.2447	FALSE	IQ motif containing GTPase activating protein 1	213446 s at	0.250	3185	2.953E-05	FALSE
103418 at	0.075	4093	1438161 s at	0.140	2027	103418 at	0.226	215	1438161 s at	0.247	2126	2115.25	1584.3346	TRUE	replication factor C (activator 1) 4	204023 at	0.022	33423	6.787E-01	FALSE
160707 at	0.130	2836	1454648 s at	0.150	2206	160707 at	0.153	1006	1454648 s at	0.190	2415	2115.75	784.85683	TRUE	DNA segment, Chr 10, Wayne State University 102, expressed	226349 at	-0.109	10558	1.365E-02	FALSE
93632 g at	-0.037	6235	1421043 s at	-0.283	488.5	93632 g at	-0.566	77	1421043 s at	-0.315	1665	2116.375	2827.003	TRUE	rho/rac guanine nucleotide exchange factor (GEF) 2	207629 s at	-0.246	3895	7.640E-05	TRUE
92567 at	0.115	2294	1450625 at	0.153	1559	92567 at	0.219	2131	1450625 at	0.585	2489	2118.25	400.52746	TRUE	procollagen, type V, alpha 2	221729 at	0.137	11655	2.239E-02	TRUE
99916 at	-0.084	4114	1422079 at	-0.417	101	99916 at	-0.147	4161	1422079 at	-0.572	104	2120	2329.6877	TRUE	protein kinase C, eta	218764 at	-0.562	2325	6.991E-06	TRUE
161818 f at	-0.199	820	1448949 at	-0.182	2105	103046 at	-0.131	1791	1418094 s at	0.249	3776	2123	1230.2799	FALSE	carbonic anhydrase 4	206208 at	0.045	30500	5.756E-01	FALSE
97227 at	0.061	6229	1450097 s at	-0.410	10	97227 at	-0.519	498	1421026 at	-0.253	1766	2125.75	2833.846	FALSE	guanine nucleotide binding protein, alpha 12	221737 at	0.303	4867	2.376E-04	FALSE
104005 at	-0.115	2960	1448941 at	-0.234	2028	104005 at	-0.319	618	1418080 at	-0.234	2898	2126	1091.6666	TRUE	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	209413 at	-0.054	27143	4.479E-01	FALSE
103841 at	0.156	1167	1451696 at	0.089	5055	103841 at	0.158	589	1440251 s at	-0.215	1695	2126.5	2003.9004	FALSE	zinc finger protein 64	218968 s at	-0.092	10407	1.255E-02	FALSE
98799 g at	-0.143	2343	1434679 at	-0.233	374.5	98798 at	-0.120	2045	1423604 at	-0.131	3751	2128.375	1385.8818	TRUE	chondroitin sulfate proteoglycan 3	205143 at	-0.669	2617	1.153E-05	TRUE
94944 at	-0.071	4141	1416754 at	-0.270	2077.5	101927 at	-0.366	1097	1416754 at	0.332	1206	2130.375	1410.4068	FALSE	protein kinase, cAMP dependent regulatory, type I beta	212555 at	-0.403	892	3.418E-07	FALSE
104358 at	-0.172	690	1449687 at	0.142	1647.5	104358 at	-0.124	5378	1426855 at	0.356	806	2130.375	2206.7235	FALSE	DNA segment, Chr 10, ERATO Doi 610, expressed	227427 at	-0.045	27158	4.487E-01	FALSE
92208 at	0.157	1581	1427944 at	0.165	1501	92208 at	0.290	165	1427944 at	0.126	5276	2130.75	2195.1143	TRUE	C1q domain containing 1	218456 at	-0.321	5760	5.650E-04	FALSE
101023 f at	0.116	3008	1433936 at	0.181	632.5	101023 f at	0.224	1681	1433936 at	-0.161	3207	2132.125	1207.6012	FALSE	RIKEN cDNA 0610010E21 gene	NA	NA	NA	NA	
161372 f at	-0.099	2946	1449039 a at	-0.149	2715	96083 s at	-0.304	1830	1420093 s at	-0.217	1041	2133	872.53768	TRUE	heterogeneous nuclear ribonucleoprotein D-like	209067 s at	-0.138	25365	3.856E-01	FALSE
161275 at	0.105	3539	1420375 at	-0.076	4227	100398 at	-0.249	708	1420375 at	0.528	60	2133.5	2056.666	FALSE	kinesin family member 3A	228680 at	-0.253	8647	4.748E-03	FALSE
97541 f at	-0.705	2454	1425545 x at	-0.195	3604	97541 f at	0.285	651	1451934 at	0.208	1841	2137.5	1231.3122	FALSE	histocompatibility 2, D region locus 1	NA	NA	NA	NA	
98827 i at	0.035	7012	1450804 at	-0.610	204.5	92433 at	-0.513	1304	1422945 a at	1.043	33	2138.375	3297.5182	FALSE	kinesin family member 5C	NA	NA	NA	NA	
95497 at	0.264	668	1426612 at	0.251	228	95497 at	0.229	1003	1426612 at	0.054	6655	2138.5	3027.6786	TRUE	timeless interacting protein	219258 at	0.090	10665	1.456E-02	TRUE
95480 at	-0.131	2246	1421050 at	0.087	3942	95480 at	-0.209	962	1421050 at	0.273	1407	2139.25	1314.4594	FALSE	vacuolar protein sorting 25 (yeast)	224608 s at	-0.025	32788	6.574E-01	FALSE
161790 at	0.198	1101	1422589 at	0.089	3568	161790 at	0.262	263	1422589 at	0.157	3626	2139.5	1717.5592	TRUE	RAB3A, member RAS oncogene family	204974 at	-0.617	1152	6.522E-07	FALSE
99144 s at	0.222	525	1423308 at	-0.361	328	99144 s at	-0.188	1092	1418520 at	0.084	6613	2139.5	2999.8667	FALSE	trans-golgi network protein	212040 at	0.207	15425	7.840E-02	FALSE
101063 at	-0.354	201	1418370 at	-0.072	4725.5	101063 at	0.077	3435	1418370 at	0.500	197	2139.625	2301.9415	FALSE	troponin C, cardiac/slow skeletal	209904 at	0.019	32026	6.326E-01	FALSE
99489 at	0.342	1529	1418253 a at	-0.201	1210	99489 at	-0.157	1813	1449010 at	0.129	4007	2139.75	1268.9679	FALSE	heat shock protein 4 like	205543 at	-0.147	19544	1.862E-01	FALSE
160069 at	-0.069	4419	1417506 at	0.248	160.5	160069 at	0.127	2437	1417506 at	0.232	1547	2140.875	1784.3875	FALSE	geminin	218350 s at	0.644	7503	2.314E-03	FALSE
101695 at	0.101	3216	1439268 x at	0.375	215	160554 at	0.242	2813	1434523 x at	0.148	2321	2141.25	1335.3008	TRUE	Eukaryotic translation initiation factor 3, subunit 6	235429 at	0.237	2704	1.388E-05	TRUE
101587 at	-0.086	3919	1422438 at	-0.305	365	101587 at	-0.066	4167	1422438 at	-0.665	124	2143.75	2197.6044	TRUE	epoxide hydrolase 1, microsomal	202017 at	0.408	6776	1.309E-03	FALSE
160791 at	0.348	857	1424802 a at	0.117	4084	160791 at	0.124	3360	1451485 at	0.431	276	2144.25	1860.8286	TRUE	RIKEN cDNA 3300001P08 gene	203804 s at	0.329	4337	1.261E-04	TRUE
97838 at	0.110	4058	1433675 at	0.421	218	97838 at	0.305	1113	1454703 x at	-0.199	3195	2146	1783.2945	FALSE	small nucleolar RNA, C/D box 22	NA	NA	NA	NA	
96130 at	-0.082	5437	1449336 a at	-0.222	749.5	101437 at	-0.412	900	1441262 at	0.445	1498	2146.125	2217.6048	FALSE	STE20-like kinase (yeast)	206875 s at	-0.202	20937	2.314E-01	FALSE
99645 at	0.194	4316	1428127 at	-0.145	4025	99163 at	-0.287	104	1428127 at	0.474	146	2147.75	2338.7527	FALSE	RIKEN cDNA 4921506J03 gene	NA	NA	NA	NA	
98134 at	0.218	1223	1454914 at	0.072	4200.5	98134 at	-0.111	1723	1444131 at	0.353	1445	2147.875	1383.6203	FALSE	RIKEN cDNA 2610101N10 gene	236696 at	0.237	5714	5.324E-04	FALSE
94337 at	0.102	2700	1438564 at	0.236	1034	94337 at	0.099	1893	1450112 a at	-0.209	2965	2148	871.43827	FALSE	growth arrest specific 2	205848 at	-0.069	18695	1.610E-01	FALSE
100977 at	0.059	4931	1423748 at	0.156	704.5	100977 at	0.094	2349	1435836 at	0.455	623	2151.875	2016.1636	TRUE	pyruvate dehydrogenase kinase, isoenzyme 1	239798 at	0.120	12945	3.634E-02	TRUE
162182 f at	-0.346	103	1416956 at	-0.271	77.5	102892 at	-0.298	4356	1425885 a at	-0.314	4079	2153.875	2385.5735	TRUE	potassium voltage-gated channel, shaker-related subfamily, beta member 2	211791 s at	-0.529	229	2.342E-08	TRUE
94966 at	-0.165	1526	1448354 at	-0.070	4384	94966 at	-0.145	1712	1448354 at	-0.273	1000	2155.5	1515.9546	TRUE	glucose-6-phosphate dehydrogenase X-linked	202275 at	0.041	28525	5.027E-01	FALSE
93831 at	0.254	1647	1415820 x at	0.078	4885	93831 at	-0.194	1357	1431239 at	0.280	734	2155.75	1858.943	FALSE	non-POU-domain-containing, octamer binding protein	200057 s at	0.097	11834	2.411E-02	FALSE
97504 at	-0.129	3421	1416123 at	-0.122	3209	97504 at	-0.255	825	1434745 at	-0.413	1168	2155.75	1348.6708	TRUE	cyclin D2	200953 s at	-0.181	15355	7.730E-02	FALSE
160931 at	0.237	1599	1452638 s at	-0.382	1091	160931 at	0.179	4276	1428087 at	0.226	1658	2156	1436.0685	FALSE	dynamin 1-like	203105 s at	-0.480	1501	1.409E-06	FALSE
94882 at	0.133	2938	1416446 at	0.116	3370	95613 at	-0.299	1181	1448339 at	0.214	1135	2156	1165.9597	FALSE	transmembrane protein 30A	217743 s at	-0.468	5877	6.239E-04	FALSE
104597 at	-0.740	2492	1435906 x at	0.110	2995	104597 at	0.186	1171	1418240 at	-0.799	1972	2157.5	779.0783	FALSE	guanylate nucleotide binding protein 2	NA	NA	NA	NA	
100494 at	0.276	185	1423136 at	-0.172	2394	100494 at	0.260	186	1441042 at	0.125	5867	2158	2682.902	FALSE	fibroblast growth factor 1	205117 at	0.535	2332	7.071E-06	FALSE
99423 at	0.161	1366	1422145 at	-0.210	1361.5	99423 at	-0.269	697	1428801 at	0.082	5211	2158.875	2058.8835	FALSE	mannoside acetylglucosaminyltransferase 3	244104 at	-0.064	25108	3.765E-01	FALSE
99932 at	-0.132	1809	1416224 at	-0.088	3163.5	99932 at	-0.094	2554	1416224 at	-0.248	1110	2159.125	892.17827	TRUE	zinc finger and BTB domain containing 17	203602 s at	0.109	13403	4.253E-02	FALSE
103067 at	-0.294	1870	1456049 at	-0.070	4942.5	103067 at	-0.203	943	1456049 at	0.307	886	2160.375	1908.8016	FALSE	v-ral simian leukemia viral oncogene homolog A (ras related)	224880 at	0.120	13215	3.989E-02	FALSE
161326 f at	0.151	2871	1448506 at	0.177	1803.5	161326 f at	0.204	781	1448506 at	0.191	3186	2160.375	1093.4547	TRUE	serine (or cysteine) peptidase inhibitor, clade A, member 6	206325 at	0.008	41424	9.183E-01	FALSE
99451 at	0.081	4783	1426894 s at	-0.193	1085.5	99451 at	0.126	2449	1426893 at	-0.405	326	2160.875	1956.3361	FALSE	RIKEN cDNA C230093N12 gene	212400 at	-0.111	20046	2.017E-01	FALSE
96046 at	0.134	1227	1448246 at	0.131	1722	96046 at	0.167	2015	1448246 at	0.196	3685	2162.25	1065.9835	TRUE	histone deacetylase 1	201209 at	0.528	703	1.961E-07	TRUE
160480 at	-0.412	135	1426794 at	-0.166	1032.5	160480 at	-0.032	7322	1436855 at	0.407	163	2163.125	3464.3949	FALSE	protein tyrosine phosphatase, receptor type, S	210823 s at	-0.070	21772	2.607E-01	FALSE
103536 at	-0.190	1274	1419073 at	-0.337	248	103536 at	-0.280	49	1419073 at	0.055	7096	2166.75	3329.7134	FALSE	transmembrane protein with EGF-like and two follistatin-like domains 2	233910 at	-0.140	6162	7.999E-04	FALSE
102735 at	0.141	2338	1453360 a at	0.130	1967	102735 at	0.088	3706	1453360 a at	0.266	656	2166.75	1254.4431	TRUE	testis expressed gene 9	243198 at	0.270	12639	3.303E-02	TRUE
160880 at	-0.098	4293	1416437 a at	-0.383	1396.5	160880 at	-0.178	2463	1460628 at	-0.301	519	2167.875	1624.5064	TRUE	mitogen-activated protein kinase 8 interacting protein 3	216139 s at	-0.310	5636	4.954E-04	TRUE

100383 at	-0.046	6324	1418360 at	-0.308	77.5	100383 at	-0.525	288	1418360 at	-0.286	1983	2168.125	2898.9165	TRUE	zinc finger protein 179	223603 at	-0.468	925	3.676E-07	TRUE
101456 at	0.150	1759	1425331 at	-0.292	1592	95792 at	0.103	2326	1425332 at	-0.191	3016	2173.25	643.69111	FALSE	zinc finger protein 106	217781 s at	-0.248	5770	5.695E-04	FALSE
100064 f at	-0.324	941	1415801 at	-0.695	49	100065 r at	-0.114	4704	1415801 at	-0.181	3001	2173.75	2091.3108	TRUE	gap junction membrane channel protein alpha 1	201667 at	0.777	1209	7.392E-07	FALSE
104545 at	-0.295	1179	1419034 at	-0.111	4180.5	104545 at	-0.083	3230	1419034 at	0.768	108	2174.375	1861.8592	FALSE	casein kinase II, alpha 1 polypeptide	206075 s at	-0.161	6646	1.177E-03	FALSE
162092 f at	-0.102	2910	1422969 s at	-0.257	347.5	162092 f at	0.076	3265	1422968 at	0.255	2176	2174.625	1299.754	FALSE	inositol hexaphosphate kinase 1	212439 at	-0.069	18377	1.515E-01	FALSE
102972 s at	-0.185	1024	1427308 at	-0.139	2380.5	102972 s at	-0.242	2115	1427307 a at	0.517	3190	2177.375	894.58253	FALSE	disabled homolog 1 (Drosophila)	226020 s at	0.344	5712	5.308E-04	FALSE
160928 at	0.097	3071	1418064 at	0.201	1106.5	160928 at	0.157	1332	1418064 at	0.121	3201	2177.625	1111.7262	TRUE	TCF3 (E2A) fusion partner	218996 at	-0.088	23401	3.168E-01	FALSE
96217 at	-0.152	2010	1434229 a at	-0.275	1406	96217 at	-0.118	1459	1434229 a at	-0.214	3847	2180.5	1144.0724	TRUE	polymerase (DNA directed), beta	203616 at	-0.175	7854	2.976E-03	TRUE
98818 at	-0.066	5036	1421866 at	-0.306	406	98818 at	-0.414	663	1453860 s at	0.204	2621	2181.5	2144.7279	FALSE	nuclear receptor subfamily 3, group C, member 1	216321 s at	0.292	5756	5.601E-04	FALSE
161347 r at	0.270	2751	1449648 s at	0.302	77.5	160426 at	0.085	3119	1417041 at	0.184	2783	2182.625	1413.2527	TRUE	RNA polymerase 1-1	209317 at	0.089	21237	2.413E-01	FALSE
99366 at	0.231	1687	1424906 at	0.094	4842	99366 at	0.382	226	1424906 at	0.268	1985	2185	1930.9181	TRUE	PO loop repeat containing	225579 at	0.232	12850	3.528E-02	TRUE
99987 at	0.110	2768	1456486 at	-0.206	967	92432 at	-0.160	455	1435202 at	-0.135	4553	2185.75	1864.0221	FALSE	zinc finger protein 574	218762 at	-0.028	35182	7.361E-01	FALSE
160935 at	-0.109	4023	1427289 at	-0.188	1196.5	160935 at	-0.174	2378	1455321 at	-0.235	1146	2185.875	1350.5731	TRUE	DDHD domain containing 1	243705 at	0.018	35564	7.484E-01	FALSE
160549 at	0.158	993	1415741 at	0.104	2980	160549 at	0.176	979	1415741 at	0.143	3799	2187.75	1427.3858	TRUE	TPA regulated locus	242306 at	0.370	6281	8.998E-04	TRUE
96273 at	-0.539	101	1423231 at	-0.246	2107	96273 at	-0.626	342	1423231 at	-0.232	6207	2189.25	2823.839	TRUE	neurogranin	204081 at	-1.300	343	4.785E-08	TRUE
101887 at	-0.140	1807	1423396 at	-0.385	533	101887 at	0.137	1910	1423396 at	-0.705	4508	2189.5	1667.7191	FALSE	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	202834 at	0.666	1816	2.741E-06	FALSE
102059 at	-0.041	6433	1449377 at	0.192	860	102059 at	0.163	1310	1449376 at	0.429	155	2189.5	2868.6567	FALSE	nicolin 1	223442 at	-0.142	13057	3.765E-02	FALSE
160794 at	-0.119	2409	1424760 a at	0.089	4356	162269 at	0.291	359	1424760 a at	0.399	1634	2189.5	1673.4409	FALSE	SET and MYND domain containing 2	233713 at	0.135	18282	1.484E-01	FALSE
102922 at	-0.197	1993	1455204 at	-0.349	127.5	102922 at	0.062	6014	1428025 s at	-0.364	632	2191.625	2667.2736	FALSE	phosphatidylinositol transfer protein, cytoplasmic 1	239808 at	0.648	521	1.116E-07	FALSE
98129 at	0.045	6734	1436682 at	0.147	973.5	98129 at	0.543	52	1437185 s at	0.242	1018	2194.375	3058.9955	TRUE	thymosin, beta 10	NA	NA	NA	NA	
161122 f at	-0.118	5345	1447919 x at	0.244	1656	161122 f at	0.274	1020	1428160 at	0.671	759	2195	2133.5215	FALSE	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	202077 at	-0.429	5657	5.044E-04	FALSE
100534 at	-0.329	518	1430045 at	0.239	390	100534 at	0.066	6650	1423395 at	0.261	1222	2195	2992.4409	FALSE	translin-associated factor X	203983 at	-0.176	19204	1.748E-01	FALSE
162315 f at	0.112	3497	1434651 a at	0.205	1124	94493 at	0.076	2973	1453258 at	-0.242	1188	2195.5	1219.505	FALSE	claudin 3	203953 s at	0.065	20471	2.151E-01	FALSE
94008 at	-0.338	640	1427914 a at	0.290	1196.5	94010 g at	-0.115	1438	1452593 a at	-0.144	5509	2195.875	2233.8807	FALSE	transcription elongation factor B (SIII), polypeptide 1	202824 s at	-0.421	4467	1.486E-04	FALSE
95557 at	-0.183	976	1427458 at	0.107	2264.5	92701 at	-0.069	5067	1427457 a at	-0.309	497	2201.125	2051.1971	FALSE	bone morphogenetic protein 1	206725 x at	-0.061	27136	4.478E-01	FALSE
98356 at	-0.490	33	1419811 at	-0.149	1756.5	98356 at	-0.213	3760	1419811 at	-0.312	3256	2201.375	1677.4296	TRUE	DNA segment, Chr 16, Wayne State University 65, expressed	NA	NA	NA	NA	
95702 at	-0.294	1075	1426343 at	-0.243	408.5	95702 at	-0.194	1362	1431541 at	0.088	5963	2202.125	2538.8641	FALSE	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	238303 at	0.155	6163	8.004E-04	FALSE
92288 at	0.181	1780	1460658 at	-0.178	869	92288 at	-0.444	1055	1423388 at	0.102	5109	2203.25	1976.6322	FALSE	adaptor protein complex AP-1, gamma 1 subunit	241294 at	0.125	7886	3.035E-03	FALSE
103767 f at	0.115	3602	1433773 at	0.148	2454	103767 f at	0.159	2255	1437222 x at	0.443	502	2203.25	1280.1441	TRUE	ribonucleotide reductase M2 B (TP53 inducible)	223342 at	0.139	14660	6.425E-02	FALSE
103720 at	0.153	3375	1425564 at	0.166	2513.5	103720 at	-0.142	1116	1425565 at	0.306	1811	2203.875	966.99262	FALSE	RE1-silencing transcription factor	204535 s at	-0.043	31170	6.022E-01	FALSE
160483 at	-0.253	2013	1416723 at	-0.231	1424.5	160483 at	-0.238	4539	1416723 at	0.308	843	2204.875	1627.7432	FALSE	transcription factor 4	203753 at	0.612	410	6.578E-08	FALSE
97511 at	-0.402	97	1431331 at	0.134	2293	97511 at	0.195	2409	1431331 at	0.159	4024	2205.75	1612.6358	FALSE	monoglyceride lipase	211026 s at	-0.107	23879	3.340E-01	FALSE
97989 at	-0.113	3684	1433835 at	-0.090	4687	97989 at	-0.380	15	1446149 at	0.360	451	2209.25	2325.2461	FALSE	protein phosphatase 3, catalytic subunit, beta isoform	202432 at	-0.747	2810	1.627E-05	FALSE
103385 at	-0.055	4945	1448126 at	-0.179	2095.5	103385 at	-0.181	1068	1448126 at	-0.358	729	2209.375	1914.0584	TRUE	teratocarcinoma expressed, serine rich	220147 s at	-0.173	9523	7.828E-03	TRUE
97935 at	-0.137	1390	1428872 at	-0.217	1595	97935 at	-0.127	1189	1428872 at	-0.185	4676	2212.5	1650.6763	TRUE	RIKEN cDNA 4121402D02 gene	212708 at	-0.277	14083	5.400E-02	FALSE
161307 f at	-0.122	2197	1452959 a at	0.233	539.5	97331 at	-0.087	3740	1452959 a at	0.165	2384	2215.125	1311.7177	FALSE	calpain 10	221040 at	0.012	35095	7.331E-01	FALSE
101011 at	0.176	3302	1456082 x at	0.161	1003	101011 at	0.252	626	1438560 x at	0.218	3958	2222.25	1654.6171	TRUE	chaperonin subunit 4 (delta)	200877 at	-0.082	26768	4.340E-01	FALSE
92671 f at	0.189	796	1418535 at	0.072	5235	92671 f at	-0.184	301	1440662 at	-0.279	2565	2224.25	2230.0609	FALSE	ral guanine nucleotide dissociation stimulator,-like 1	209568 s at	0.170	11628	2.218E-02	FALSE
95409 at	-0.137	1942	1415733 a at	0.242	1525.5	95409 at	0.188	541	1415733 a at	0.144	4896	2226.125	1874.3427	FALSE	RIKEN cDNA 1110019J04 gene	NA	NA	NA	NA	
100155 at	-0.107	4966	1415798 at	-0.359	488.5	100155 at	-0.122	2477	1437619 x at	-0.254	978	2227.375	2012.213	TRUE	discoidin domain receptor family, member 1	1007 s at	0.495	658	1.714E-07	FALSE
101837 g at	0.253	1520	1425330 a at	-0.343	143	101836 at	0.169	2137	1425330 a at	0.121	5113	2228.25	2096.0276	FALSE	protein phosphatase 1B, magnesium dependent, beta isoform	232580 x at	0.188	11035	1.746E-02	FALSE
96590 f at	0.317	564	1429139 at	-0.039	7589	96590 f at	0.497	269	1429139 at	0.360	495	2229.25	3575.3872	FALSE	zinc finger, A20 domain containing 1	227436 at	0.320	1414	1.167E-06	FALSE
102559 at	0.221	749	1423635 at	-0.039	6568.5	102559 at	-0.149	1516	1423635 at	-0.454	94	2231.875	2948.9106	FALSE	bone morphogenetic protein 2	205290 s at	0.128	14220	5.668E-02	FALSE
96836 r at	0.154	1503	1437585 x at	0.094	2855	96836 r at	-0.104	3426	1420864 at	-0.277	1149	2233.25	1082.911	FALSE	zinc finger protein 161	208199 s at	0.052	19694	1.903E-01	FALSE
100470 at	-0.230	1403	1448342 at	-0.145	2043.5	100470 at	-0.171	3588	1458002 at	-0.214	1904	2234.625	943.23304	TRUE	mitogen activated protein kinase 10	204813 at	-0.044	28093	4.846E-01	FALSE
162130 r at	-0.154	1748	1427345 a at	0.087	4655.5	103087 at	0.247	131	1427345 a at	-0.203	2413	2236.875	1875.6755	FALSE	sulfotransferase family 1A, phenol-preferring, member 1	211385 x at	-0.016	37044	7.922E-01	FALSE
103031 g at	-0.267	687	1427754 a at	-0.493	688.5	103031 g at	0.301	2583	1456346 at	-0.167	4992	2237.625	2042.0653	FALSE	dynamin 1	215116 s at	-0.869	2527	9.925E-06	FALSE
102976 at	0.330	92	1424629 at	0.066	5421.5	102976 at	0.187	638	1424630 a at	0.139	2804	2238.875	2423.5196	TRUE	breast cancer 1	211851 x at	0.085	15256	7.564E-02	FALSE
101888 at	0.100	3866	1424035 at	-0.106	4441	101889 s at	0.255	503	1424035 at	0.421	153	2240.75	2225.6844	FALSE	RAR-related orphan receptor alpha	233449 at	0.170	12730	3.402E-02	FALSE
161126 at	0.328	885	1435998 at	0.114	2629.5	161126 at	0.101	3809	1435998 at	0.242	1654	2244.375	1263.9641	TRUE	gene model 288, (NCBI)	217988 at	0.070	25497	3.888E-01	FALSE
98623 g at	0.328	1134	1415931 at	0.120	3730	98623 g at	0.108	2893	1415931 at	-0.208	1223	2245	1278.5322	FALSE	insulin-like growth factor 2	239939 at	-0.030	30958	5.932E-01	FALSE
95003 at	0.178	3930	1452596 at	0.474	1144	95003 at	0.349	1648	1452596 at	-0.158	2266	2247	1212.1964	FALSE	polymerase (RNA) II (DNA directed) polypeptide K	202635 s at	-0.397	5461	4.302E-04	FALSE
160706 at	-0.037	6350	1453004 at	-0.287	425.5	160706 at	-0.138	1365	1453004 at	-0.295	851	2247.875	2761.5942	TRUE	RIKEN cDNA 3110004L20 gene	242055 at	0.294	5063	2.839E-04	FALSE
103043 at	0.138	1905	1455710 x at	0.070	4276	103043 at	0.218	275	1456207 at	0.327	2541	2249.25	1654.1871	TRUE	mature T-cell proliferation 1	244790 at	-0.158	6435	1.001E-03	FALSE
96729 at	0.196	2818	1417084 at	-0.166	1365	96729 at	-0.080	4328	1417084 at	0.820	490	2250.25	1685.3815	FALSE	eukaryotic translation initiation factor 4E binding protein 2	224653 at	0.351	1195	7.153E-07	FALSE
102287 at	0.196	742	1428059 at	0.195	1339	102288 at	0.052	5648	1426079 at	-0.243	1274	2250.75	2280.5674	FALSE	CD247 antigen	210031 at	0.010	40407	8.899E-01	FALSE
160766 at	0.128	2324	1417223 at	0.104	2089	160766 at	-0.224	1249	1417223 at	0.170	3349	2252.75	864.32416	FALSE	CD2 antigen (cytoplasmic tail) binding protein 2	202256 at	0.068	18413	1.525E-01	FALSE
96554 r at	0.328	130	1419846 at	0.059	5714	95291 r at	0.185	1019	1438130 at	0.266	2171	2258.5	2450.5108	TRUE	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	227891 s at	0.223	5613	4.856E-04	TRUE
103399 at	-0.119	2267	1426241 a at	-0.083	4321	103399 at	-0.158	1554	1439554 at	0.641	899	2260.25	1483.0741	FALSE	sex comb on midleg homolog 1	232858 at	0.078	14368	5.934E-02	FALSE
97311 at	-0.311	225	1423189 at	-0.123	4923	97311 at	-0.119	3134	1446299 at	-0.623	762	2261	2178.7359	TRUE	RIKEN cDNA 6720456B07 gene	224575 at	-0.128	12359	2.984E-02	TRUE
161903 f at	0.130	2425	1448728 a at	0.110	2982	98988 at	-0.122	2696	1417483 at	-0.485	954	2264.25	902.62003	FALSE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	223218 s at	0.262	15673	8.352E-02	FALSE
96016 at	-0.024	7227	1436349 at	0.329	499.5	96016 at	0.171	451	1436349 at	0.397	882	2264.875	3313.6948	FALSE	RIKEN cDNA 2700094K13 gene	231045 x at	-0.328	4875	2.388E-04	FALSE
100772 g at	-0.268	218	1451780 at	0.020	7773	100772 g at	0.163	549	1451780 at	0.433	523	2265.75	3674.5744	FALSE	B-cell linker	207655 s at	0.102	25518	3.894E-01	FALSE
98059 s at	-0.295	1029	1426868 x at	0.170	1494.5	98059 s at	0.181	3328	1457670 s at	-0.193	3234	2271.375	1181.8254	FALSE	lamin A	203411 s at	0.235	7659	2.578E-03	FALSE
99475 at	-0.209	767	1449109 at	-0.237	752.5	99475 at	0.057	6942	1438470 at	-0.422	625	2271.625	3114.2369	FALSE	suppressor of cytokine signaling 2	203372 s at	-0.039	27568	4.645E-01	FALSE
95456 r at	-0.245	1505	1418575 at	0.295	1008.5	95456 r at	0.317	493	1418575 at	-0.065	6081	2271.875	2572.8093	FALSE	split hand/foot malformation (ectrodactyly) type 1	202276 at	-0.103	21461	2.482E-01	FALSE
96004 at	0.135	2242	1450878 at	0.112	3332.5	96004 at	0.094	3034	1450878 at	0.322	480	2272.125	1280.2953	TRUE	sorcin	208920 at	0.171	19233	1.759E-01	FALSE
104085 at	0.094	4392	1453016 at	0.504	105	104085 at	0.125	1962	1453016 at	0.226	2630	2272.25	1771.4921	TRUE	RIKEN cDNA 2900042B11 gene	NA	NA	NA	NA	
94064 at	-0.129	3283	1429615 at	-0.187	1141	94064 at	-0.145	2745	1426326 at	0.516	1921	2272.5	939.54085	FALSE	zinc finger protein 91	224631 at	0.244	5984	6.852E-04	FALSE
160782 at	-0.146	2579	1451631 at	-0.204	1455	160782 at	-0.078	4368	1443166 at	0.456	690	2273	1597.6727	FALSE	cDNA sequence BC021395	218209 s at	-0.213	11524	2.122E-02	FALSE
100131 at	0.315	179	1423150 at	0.110	6208	100131 at	0.328	379	1446755 at	0.367	2327	2273.25	2796.3794	TRUE	secretogranin V	203889 at	-1.051	1531	1.503E-06	FALSE
99964 at	0.150	2041	1418175 at	0.162	1498.5	99965 at	-0.061	4599	1418176 at	-0.305	956	2273.625	1612.2901	FALSE	vitamin D receptor	204255 s at	-0.054	19126	1.726E-01	FALSE
98590 at	-0.045	6930	1417654 at	-0.310	300	98590 at	0.602	914	1417654 at	0.660	955	2274.75	3117.9251	FALSE	syndecan 4	202071 at	0.792	1529	1.497E-06	FALSE
101196 at	0.103	2408	1426981 at	-0.166	1295	101196 at	-0.140	1967	1426981 at	-0.193	3431	2275.25	896.15638	FALSE	proprotein convertase subtilisin/kexin type 6	242662 at	0.257	15430	7.846E-02	FALSE
95348 at	0.128	3885	1419209 at	0.142	2708.5	95349 g at	-0.219	391	1457644 s at	-0.173	2121	2276.375	1455.2419	FALSE	chemokine (C-X-C motif) ligand 1	206336 at	-0.005	41349	9.163E-01	FALSE
97909 at	-0.206	1072	1415849 s at	0.032	7427.5	97909 at	0.396	343	1415849 s at	0.426	274	2279.125	3451.1844	FALSE	stathmin 1	217714 x at	0.134	8208	3.723E-03	FALSE
102368 at	0.155	2033	1427935 at	0.241	1003	102368 at	0.101	4132	1427934 at	-0.180	1949	2279.25	1320.505	FALSE	RIKEN cDNA 2610208E05 gene	227712 at	0.117	9587	8.149E-03	FALSE
94862 i at	-0.139	3876	1428257 s at	0.268	725	94862 i at	0.136	2434	1428257 s at	-0.222	2082	2279.25	1294.6246	FALSE	dynein light chain roadblock-type 1	217917 s at	-0.145	12035	2.633E-02	FALSE
160565 at	-0.404	689	1432418 a at	-0.363	343	160565 at	0.036	6550	1417089 a at	-0.226	1552	2283.5	2889.4108	FALSE	creatine kinase, mitochondrial 1, ubiquitous	NA	NA	NA	NA	
100607 at	-0.346	285	1416013 at	-0.262	418.5	100607 at	-0.379	649	1416013 at	0.032	7783	2283.875	3669.1651	FALSE	phospholipase D family, member 3	201050 at	-0.572	3048	2.441E-05	FALSE
92700 at	-0.112	3877	1416718 at	-0.173	1718	92700 at	-0.171	1142	1416718 at	-0.197	2404	2285.25	1179.91	TRUE	brevican	221623 at	0.359	4182	1.070E-04	FALSE
160391 at	-0.268	1374	1423680 at	-0.317	610	160391 at	-0.054	5381	1423680 at	-0.171	1779	2286	2119.4963	TRUE	fatty acid desaturase 1	208963 x at	0.508	1618	1.818E-06	FALSE
96198 at	-0.220	1665	1418085 at	-0.169	812.5	96571 at	-0.296	901	1454902 at	-0.100	5775	2288.375	2355.7141	TRUE	protein kinase C, zeta	202178 at	-0.679	1157	6.587E-07	TRUE
92853 at	-0.152	1642	1422943 a at	-0.140	1494.5	92853 at	-0.159	2091	1453914 at	-0.135	3928	2288.875	1121.8087	TRUE	heat shock protein 1	201841 s at	0.961	4959	2.567E-04	FALSE
95044 at	-0.168	2973	1416508 at	0.202	1727	95044 at	0.129	3429	1448374 at	-0.401	1031	2290	1105.42	FALSE	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	228992 at	0.387	1877	3.137E-06	FALSE
104680 at	-0.400	228	1417481 at	-0.113	5450	104680 at	-0.334	66	1417481 at	-0.125	3419	2290.75	2611.4018	TRUE	receptor (calcitonin) activity modifying protein 1	204916 at	0.229	9191	6.526E-03	FALSE
96281 at	0.096	4873	1423255 at	0.292	1035	96281 at	0.365	601	1423255 at	0.221	2663	2293	1935.5213	TRUE	ATPase, H+ transporting, lysosomal V1 subunit G1	208737 at	0.068	24836	3.669E-01	FALSE
102787 at	0.073	5277	1421118 a at	-0.266	332.5	102787 at	0.091	2479	1421118 a at	-0.274	1085	2293.375	2178.8128	FALSE	G protein-coupled receptor 56	212070 at	0.375	9173	6.462E-03	FALSE
161013 f at	-0.392	643	1420150 at	-0.195	1358.5	161013 f at	0.149	3066	1428472 at	-0.123	4109	2294.125	1580.2078	FALSE	splA/ryanodine receptor domain and SOCS box containing 1	226075 at	0.195	7394	2.119E-03	FALSE
102046 at	0.139	2692	1418527 a at	-0.208	2623	102046 at	0.118	2232	1423982 at	-0.227	1631	2294.5	486.50351	FALSE	FUS interacting protein (serine-arginine rich) 1	206095 s at	0.226	8992	5.764E-03	FALSE
102933 at	0.137	2036	1420995 at	0.098	2469.5	102933 at	-0.121	1943	1420995 at	0.170	2732	2295.125	370.76686	FALSE	plexin A3	203623 at	0.112	14471	6.081E-02	FALSE
98483 at	-0.489	44	1448656 at	-0.294	521.5	98483 at	-0.282	240	1448656 at	-0.012	8376	2295.375	4058.4845	TRUE	calcium channel, voltage-dependent, beta 3 subunit	209530 at	-0.401	748	2.316E-07	TRUE
92992 i at	-0.178	1205	1421504 at	0.084	3805.5	92992 i at	0.197	1209	1421504 at	0.130	2962	2295.375	1303.0726	FALSE	trans-acting transcription factor 4	236265 at	0.157	7288	1.979E-03	FALSE
95165 at	0.072	4162	1448060 at	-0.226	1025	95165 at	-0.111	1994	1448060 at	-0.237	2006	2296.75	1325.7323	FALSE	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	233882 s at	-0.238	10289	1.190E-02	FALSE
93676 at	0.135	2286	1417940 s at	0.127	1235.5	93676 at	0.094	2418	1417939 at	0.191	3248	2296.875	825.82185	TRUE	RAD51 associated protein 1	204146 at	-0.013	29993	5.568E-01	FALSE
93857 at	0.219	533	1450385 at	-0.092	4038	96010 at	0.101	3690	1445527 at	0.386	932	2298.25	1820.8464	FALSE	karyopherin (importin) alpha 3	233224 at	0.066	21513	2.502E-01	FALSE
102292 at	-0.116	2695	1449519 at	-0.097	2987	102292 at	0.128	2518	1449519 at	-0.235	995	2298.75	890.41877	FALSE	growth arrest and DNA-damage-inducible 45 alpha	203725 at	-0.218	25143	3.774E-01	FALSE
95698 at	-0.211	1402	1448331 at	0.234	831	162323 at	0.163	1584	1448331 at	0.114	5381	2299.5	2079.2291	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	202839 s at	-0.080	25604	3.913E-01	FALSE
102335 at	-0.112	3407	1455896 a at	-0.320	146.5	102335 at	-0.227	641	1448690 at	-0.104	5008	2300.625	2305.6853	TRUE	potassium channel, subfamily K, member 1	204678 s at	-0.733	886	3.384E-07	TRUE
92263 at	-0.157	1861	1449531 at	-0.155	2922.5	92263 at	-0.131	1951	1449531 at	-0.279	2471	2301.375	493.71439	TRUE	leprecan-like 2	204854 at	-0.045	27253	4.522E-01	FALSE
162098 i at	-0.082	4503	1427928 s at	0.146	844.5	93183 at	-0.088	3016	1459134 at	0.401	845	2302.125	1788.9804	FALSE	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	225903 at	0.082	19055	1.704E-01	FALSE
92502 at	0.166	1994	1426208 x at	-0.304	3346	92502 at	-0.335	1764	1450533 a at	-0.224	2110	2303.5	709.71802	FALSE	pleiomorphic adenoma gene-like 1	NA	NA	NA	NA	
93402 i at	0.186	1779	1421394 a at	-0.084	5322	93401 g at	-0.147	1366	1450231 a at	0.273	751	2304.5	2055.5292	FALSE	baculoviral IAP repeat-containing 4	225859 at	-0.088	21516	2.505E-01	FALSE
99481 at	-0.225	1968	1452308 a at	-0.537	57.5	99481 at	-0.041	7074	1455136 at	0.879	121	2305.125	3300.4061	FALSE	ATPase, Na+/K+ transporting, alpha 2 polypeptide	203296 s at	0.418	3888	7.601E-05	FALSE
103878 at	-0.231	1515	1450915 at	-0.162	2621.5	103878 at	-0.152	1873	1423235 at	-0.127	3216	2306.375	761.75449	FALSE	adaptor-related protein complex 3, beta 1 subunit	240600 at	0.249	2497	9.562E-06	FALSE
96121 at	0.134	1632	1417887 at	-0.161	1175	161444 f at	0.105	2446	1417887 at	0.135	3974	2306.75	1229.5336	TRUE	integrator complex subunit 5	53968 at	0.098	11227	1.890E-02	FALSE
98085 f at	-0.137	2412	1454778 x at	0.265	1005	98085 f at	0.092	2927	1431708 a at	-1.589	2883	2306.75	898.59237	FALSE	Cytotoxic granule-associated RNA binding protein 1	201449 at	0.099	15705	8.408E-02	FALSE
93852 at	-0.280	1340	1425426 a at	-0.177	2052	93852 at	-0.434	38	1427185 at	-0.084	5802	2308	2474.0989	TRUE	myocyte enhancer factor 2A	239571 at	0.120	14762	6.635E-02	FALSE
160971 at	0.180	844	1436528 at	-0.016	7947	160971 at	0.352	72	1436528 at	0.659	377	2310	3771.386	FALSE	Kazal-type serine peptidase inhibitor domain 1	217511 at	0.040	29955	5.555E-01	FALSE
96875 r at	0.362	1775	1420175 at	0.148	1977	96875 r at	0.132	2935	1442901 at	0.288	2554	2310.25	531.43665	TRUE	Tax1 (human T-cell leukemia virus type I) binding protein 1	200976 s at	0.057	26428	4.220E-01	FALSE
95601 at	0.307	542	1419385 a at	-0.326	121	95601 at	-0.409	1240	1450345 at	0.036	7350	2313.25	3389.3954	FALSE	ubiquilin 1	222990 at	-0.252	13028	3.726E-02	FALSE
100134 at	-0.268	436	1432176 a at	0.100	3421	100134 at	0.137	1720	1432176 a at	-0.113	3677	2313.5	1523.476	FALSE	endoglin	201809 s at	0.154	15770	8.548E-02	FALSE
96725 at	-0.152	1621	1415746 at	-0.136	2307.5	96725 at	-0.214	1403	1415746 at	-0.141	3923	2313.625	1140.0428	TRUE	capicua homolog (Drosophila)	212784 at	-0.070	20397	2.130E-01	FALSE
102233 at	0.135	2365	1427202 at	0.138	1250.5	102233 at	0.151	1566	1427202 at	0.148	4078	2314.875	1265.5473	TRUE	RIKEN cDNA 4833442J19 gene	NA	NA	NA	NA	
104038 at	0.084	4160	1448463 at	0.153	1204.5	102141 f at	0.355	757	1453733 a at	0.157	3157	2319.625	1609.7078	TRUE	RIKEN cDNA 4933434E20 gene	223034 s at	-0.200	7804	2.876E-03	FALSE
95434 at	-0.168	2428	1448279 at	0.171	2953	95434 at	-0.181	1814	1448279 at	0.310	2084	2319.75	491.28564	FALSE	actin related protein 2/3 complex, subunit 3	208736 at	-0.293	12854	3.533E-02	FALSE
97096 at	0.152	986	1427414 at	-0.117	2870	97096 at	-0.157	2110	1452915 at	0.133	3316	2320.5	1019.5049	FALSE	protein kinase, cAMP dependent regulatory, type II alpha	225000 at	0.410	67	4.782E-09	FALSE
94348 f at	-0.136	3507	1431086 s at	0.239	648.5	94348 f at	0.149	2639	1431086 s at	0.196	2494	2322.125	1202.0677	FALSE	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	208857 s at	-0.722	3689	5.857E-05	FALSE
160237 at	-0.214	1914	1448427 at	0.330	947	160237 at	0.294	707	1448427 at	0.091	5723	2322.75	2326.0921	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	202000 at	-0.169	9555	7.990E-03	FALSE
92293 at	-0.234	1630	1434709 at	-0.088	4629	92293 at	-0.422	121	1458833 at	0.275	2915	2323.75	1914.6062	FALSE	RIKEN cDNA C130076O07 gene	243240 at	0.200	10761	1.522E-02	FALSE
160652 at	0.245	1856	1435759 at	0.066	5701	160652 at	0.185	431	1448111 at	0.251	1314	2325.5	2325.7037	TRUE	cytidine 5'-triphosphate synthase 2	222819 at	0.063	21841	2.626E-01	FALSE
94561 at	0.294	150	1422499 at	0.101	3785.5	94561 at	-0.062	4828	1425654 a at	0.326	540	2325.875	2332.0175	FALSE	LIM domain and actin binding 1	217892 s at	0.171	6255	8.794E-04	FALSE
97808 at	-0.245	1917	1449138 at	0.069	5222	97808 at	-0.452	116	1418562 at	0.323	2050	2326.25	2122.4493	FALSE	splicing factor 3b, subunit 1	211185 s at	0.202	5812	5.922E-04	FALSE
102240 at	0.119	3112	1456395 at	-0.327	146.5	102240 at	-0.067	5212	1460336 at	-0.320	835	2326.375	2303.627	FALSE	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	219195 at	0.037	31922	6.283E-01	FALSE
96627 at	-0.183	1097	1416667 at	-0.184	762	96627 at	-0.161	1759	1416667 at	0.068	5690	2327	2279.9501	FALSE	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	213787 s at	-0.186	6565	1.104E-03	FALSE
104451 at	-0.207	1595	1417584 at	0.100	2932.5	104451 at	0.120	4532	1426441 at	-0.511	253	2328.125	1831.7524	FALSE	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	203124 s at	0.231	13305	4.117E-02	FALSE
99988 at	-0.141	1308	1437141 x at	0.099	3158	99988 at	-0.104	2498	1437141 x at	-0.182	2355	2329.75	765.70594	FALSE	dymeclin	220774 at	0.116	4791	2.150E-04	FALSE
100095 at	-0.225	480	1416050 a at	-0.083	4955	100095 at	-0.218	597	1455820 x at	-0.154	3288	2330	2178.2392	TRUE	scavenger receptor class B, member 1	201819 at	-0.282	2312	6.821E-06	TRUE



162169 r at	0.211	1259	1427762 x at	-0.201	1836	161394 f at	-0.057	5165	1427762 x at	-0.350	1564	2456	1821.314	FALSE	Histone 1. H2bp	209911 x at	0.121	17079	1.167E-01	FALSE
98603 s at	0.092	4846	1423749 s at	0.142	1020	98602 at	0.140	1976	1451092 a at	0.254	1986	2457	1655.8474	TRUE	RAN GTPase activating protein 1	212125 at	-0.247	10269	1.181E-02	FALSE
93387 at	0.111	3007	1418063 at	0.175	1309.5	93387 at	0.106	2610	1418063 at	0.149	2905	2457.875	783.87205	TRUE	keratocan	220504 at	-0.009	38112	8.255E-01	FALSE
97666 r at	0.200	537	1457588 at	0.111	3822	97665 i at	-0.081	3294	1457588 at	0.257	2180	2458.25	1452.2301	FALSE	expressed sequence C76213	NA	NA	NA	NA	
160589 at	0.092	3589	1435341 at	0.232	378	160589 at	-0.068	5786	1436505 at	0.681	83	2459	2727.7442	FALSE	peptidyl-prolyl isomerase G (cyclophilin G)	208993 s at	0.253	10652	1.442E-02	FALSE
97886 at	0.079	4406	1432372 a at	0.209	509.5	97886 at	-0.076	3753	1432372 a at	0.331	1170	2459.625	1908.5173	FALSE	sepiapterin reductase	203458 at	0.190	9010	5.845E-03	FALSE
99779 at	0.018	7633	1446244 at	-0.411	120	99779 at	0.211	705	1447207 at	0.232	1383	2460.25	3486.9032	FALSE	RIKEN cDNA 2810482G21 gene	225350 s at	-0.167	9921	9.681E-03	FALSE
160920 at	-0.123	2974	1430453 a at	-0.132	2724.5	160920 at	0.158	1192	1430454 x at	0.179	2958	2462.125	854.39378	FALSE	Bcl2-like 2	241848 x at	0.094	7807	2.884E-03	FALSE
92771 at	0.158	3067	1455092 at	0.152	1560	92771 at	0.126	5156	1438515 at	1.038	70	2463.25	2172.4735	TRUE	zinc finger protein 207	231848 x at	0.257	5798	5.871E-04	TRUE
103338 at	-0.287	657	1428931 a at	-0.123	3211	103338 at	-0.172	1496	1440644 at	0.098	4490	2463.5	1719.0072	FALSE	poly (ADP-ribose) polymerase family. member 6	241867 at	0.429	1413	1.167E-06	FALSE
98626 at	0.118	5508	1417105 at	0.325	935.5	98626 at	0.297	233	1417105 at	0.206	3179	2463.875	2386.8273	TRUE	RIKEN cDNA 1810017G16 gene	218354 at	-0.199	12476	3.110E-02	FALSE
102858 at	0.275	329	1421137 a at	0.148	2034.5	102858 at	0.098	3490	1421137 a at	0.221	4008	2465.375	1651.1915	TRUE	protein kinase inhibitor beta. cAMP dependent. testis specific	223551 at	-0.082	20267	2.089E-01	FALSE
98026 g at	0.168	2575	1450241 a at	-0.103	5803	98026 g at	0.392	365	1458788 at	0.384	1121	2466	2406.2887	FALSE	ecotropic viral integration site 2a	204774 at	0.114	32378	6.441E-01	FALSE
104557 at	-0.060	5829	1421013 at	-0.295	1052.5	102696 s at	-0.832	114	1420307 a at	-0.158	2870	2466.375	2516.8016	TRUE	phosphatidylinositol transfer protein. beta	235985 at	0.264	2452	8.784E-06	FALSE
160550 i at	0.087	4907	1416212 at	0.514	423	160550 i at	0.200	1921	1416212 at	0.158	2617	2467	1866.5612	TRUE	mago-nashi homolog. proliferation-associated (Drosophila)	210093 s at	0.080	22692	2.914E-01	FALSE
94376 s at	0.104	2482	1416748 a at	0.112	2870	94376 s at	-0.128	2682	1458509 at	0.233	1839	2468.25	448.41824	FALSE	meiotic recombination 11 homolog A (S. cerevisiae)	242456 at	0.151	8718	4.965E-03	FALSE
92770 at	-0.291	1103	1421375 a at	0.243	2159	92770 at	0.248	2641	1421375 a at	-0.236	3972	2468.75	1190.3289	FALSE	S100 calcium binding protein A6 (calcyclin)	217728 at	0.761	1245	7.959E-07	FALSE
92628 at	-0.258	2359	1433510 x at	0.273	1269.5	92628 at	0.243	1226	1416519 at	-0.104	5030	2471.125	1784.6243	FALSE	similar to ribosomal protein L36	NA	NA	NA	NA	
103744 at	-0.120	2709	1434109 at	-0.095	4997	103744 at	-0.257	94	1434211 at	-0.251	2088	2472	2019.4169	TRUE	SH3 domain binding glutamic acid-rich protein like 2	225354 s at	-0.146	11654	2.238E-02	TRUE
95444 at	-0.264	1012	1421491 a at	-0.193	1268	95444 at	-0.198	2467	1444820 at	0.128	5143	2472.5	1889.9278	FALSE	transmembrane protein 49	220990 s at	-0.209	18421	1.528E-01	FALSE
94455 at	0.086	5102	1448536 at	0.327	800	94455 at	0.192	2661	1448536 at	0.259	1328	2472.75	1919.8037	TRUE	LSM3 homolog. U6 small nuclear RNA associated (S. cerevisiae)	202209 at	-0.137	13205	3.975E-02	FALSE
162336 r at	0.154	1951	1448445 at	0.095	3652	162336 r at	0.139	1603	1444410 at	0.199	2700	2476.5	907.54339	TRUE	Acid phosphatase 6. lysophosphatidic	218795 at	0.218	5039	2.782E-04	TRUE
162378 r at	-0.149	1003	1451133 s at	0.060	5657.5	162378 r at	-0.165	765	1423822 a at	0.167	2481	2476.625	2252.3481	FALSE	RIKEN cDNA 8430437G11 gene	234726 s at	-0.097	21675	2.570E-01	FALSE
103501 at	0.160	3102	1420628 at	-0.190	2527	103501 at	-0.246	2497	1456898 at	-0.264	1783	2477.25	540.11133	FALSE	purine rich element binding protein A	204020 at	0.187	5443	4.183E-04	FALSE
160807 at	-0.144	2514	1450504 a at	-0.122	3044	160807 at	-0.105	1887	1433818 at	-0.169	2465	2477.5	472.9697	TRUE	1-acylglycerol-3-phosphate O-acyltransferase 3	225440 at	0.247	3055	2.459E-05	FALSE
101861 at	0.184	552	1420688 a at	0.065	5410	101861 at	-0.100	2650	1443518 at	0.543	1298	2477.5	2139.1652	FALSE	sarcoglycan. epsilon	204688 at	-0.016	41276	9.146E-01	FALSE
98004 at	0.484	717	1420859 at	0.192	2695	98005 at	0.333	2332	1420858 at	0.122	4169	2478.25	1417.6279	TRUE	protein kinase inhibitor. alpha	226864 at	-0.816	2195	5.414E-06	FALSE
94890 at	0.171	2194	1416810 at	0.348	111.5	94890 at	0.096	4588	1416810 at	0.206	3028	2480.375	1865.0787	TRUE	male enhanced antigen 1	218061 at	-0.127	10969	1.690E-02	FALSE
94694 at	0.137	1367	1421396 at	0.059	6067	94694 at	0.145	2140	1421396 at	0.506	352	2481.5	2499.9542	TRUE	proprotein convertase subtilisin/kexin type 1	205825 at	-0.554	1783	2.564E-06	FALSE
99856 r at	-0.426	212	1422592 at	-0.116	3441	99856 r at	-0.126	3231.5	1456116 at	-0.209	3045	2482.375	1522.2023	TRUE	catenin (cadherin associated protein). delta 2	209617 s at	0.362	3095	2.613E-05	FALSE
99618 at	-0.204	2451	1448292 at	0.281	1420.5	99618 at	0.176	1137	1448292 at	0.107	4923	2482.875	1721.9414	FALSE	ubiquinol-cytochrome c reductase (6.4kD) subunit	202090 s at	-0.108	18941	1.670E-01	FALSE
100066 at	-0.123	2131	1416283 at	0.097	3289.5	100066 at	0.273	134	1424435 a at	0.131	4379	2483.375	1815.3937	FALSE	phosphoribosylglycinamide formyltransferase	230097 at	0.164	8762	5.064E-03	FALSE
102217 at	-0.107	2985	1449514 at	-0.150	1829.5	102217 at	0.109	4418	1449514 at	-0.249	709	2485.375	1588.5365	FALSE	G protein-coupled receptor kinase 5	204395 s at	-0.059	20535	2.176E-01	FALSE
92949 at	-0.291	284	1449381 a at	-0.405	360.5	92949 at	-0.132	3155	1449380 at	-0.106	6147	2486.625	2781.9079	TRUE	protein kinase C and casein kinase substrate in neurons 1	227053 at	-0.788	2735	1.455E-05	TRUE
98366 at	0.080	4560	1452784 at	0.246	869	104385 i at	0.274	228	1432296 a at	0.097	4292	2487.25	2256.5725	TRUE	integrin alpha V	241769 at	0.226	11096	1.795E-02	TRUE
160301 at	-0.087	3372	1419981 at	0.157	1321.5	160301 at	0.111	3535	1419981 at	0.237	1722	2487.625	1129.18	FALSE	RIO kinase 3 (yeast)	215588 x at	0.293	2943	1.971E-05	FALSE
98996 at	0.095	4944	1419838 s at	0.146	1594	98996 at	0.396	206	1419838 s at	0.274	3209	2488.25	2046.0154	TRUE	polo-like kinase 4 (Drosophila)	204887 s at	-0.028	27801	4.725E-01	FALSE
94459 at	0.022	7468	1455152 at	0.176	462.5	94459 at	0.292	754	1455152 at	0.290	1282	2491.625	3334.8758	TRUE	expressed sequence AI462493	NA	NA	NA	NA	
160138 at	-0.236	1648	1425732 a at	-0.196	1210	160138 at	0.304	1919	1425732 a at	-0.108	5191	2492	1822.8906	FALSE	Max interacting protein 1	202364 at	0.359	1372	1.048E-06	FALSE
162438 f at	-0.080	3581	1460278 a at	-0.281	190.5	104141 at	-0.182	538	1460278 a at	-0.100	5680	2497.375	2611.7789	TRUE	DNA segment. Chr 15. Wayne State University 75. expressed	212527 at	-0.043	27257	4.524E-01	FALSE
97089 at	0.646	275	1450154 at	-0.001	8507	97089 at	0.349	295	1450154 at	0.582	915	2498	4017.0017	FALSE	folate hydrolase	215363 x at	0.194	26064	4.063E-01	FALSE
98390 at	0.127	2677	1423239 at	0.088	3320	98390 at	-0.185	879	1423239 at	-0.129	3123	2499.75	1113.4778	FALSE	inosine 5'-phosphate dehydrogenase 1	204169 at	-0.181	7682	2.633E-03	FALSE
101939 at	0.167	1031	1449086 at	-0.148	1892	101939 at	0.147	2154	1449087 at	0.126	4922	2499.75	1684.5795	FALSE	ring finger protein 141	226106 at	0.171	17007	1.145E-01	FALSE
95074 at	0.086	5153	1416425 at	0.149	825	95074 at	-0.105	3457	1455208 at	-0.331	566	2500.25	2198.5024	FALSE	peroxisome biogenesis factor 19	201707 at	-0.154	7949	3.178E-03	FALSE
98586 at	-0.211	1640	1420479 a at	-0.205	3553.5	98587 at	-0.200	2485	1420477 at	-0.193	2323	2500.375	791.83662	TRUE	nucleosome assembly protein 1-like 1	204528 s at	0.123	13431	4.296E-02	FALSE
104554 at	-0.228	489	1460648 at	-0.198	573	104554 at	0.032	6881	1460648 at	-0.191	2067	2502.5	3007.6611	FALSE	nuclear receptor subfamily 2. group F. member 6	209261 s at	-0.082	16131	9.369E-02	FALSE
101903 at	0.134	3137	1450203 at	0.117	2491.5	101904 at	-0.170	2113	1450203 at	-0.216	2269	2502.625	450.53438	FALSE	SET and MYND domain containing 1	228406 at	-0.026	32173	6.375E-01	FALSE
102371 at	-0.313	605	1416505 at	-0.270	2232	102371 at	-0.166	4164	1416505 at	-0.624	3013	2503.5	1493.8613	TRUE	nuclear receptor subfamily 4. group A. member 1	202340 x at	0.090	24271	3.461E-01	FALSE
162288 f at	0.089	3776	1416383 a at	-0.097	4336	AFFX-PyruCarbM	-0.171	860	1416383 a at	-0.319	1047	2504.75	1807.3729	FALSE	pyruvate carboxylase	204476 s at	0.070	21109	2.370E-01	FALSE
104317 at	-0.197	908	1448809 at	0.073	4243.5	104317 at	0.151	2942	1448809 at	0.168	1931	2506.125	1425.1586	FALSE	chromosome segregation 1-like (S. cerevisiae)	210765 at	0.049	25080	3.755E-01	FALSE
100037 at	0.235	419	1416070 a at	0.101	2834	100037 at	-0.258	1325	1416070 a at	-0.078	5450	2507	2200.3822	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	208895 s at	0.168	10773	1.537E-02	FALSE
100473 at	-0.200	748	1460444 at	-0.180	2011	100473 at	-0.068	3700	1460444 at	-0.157	3581	2510	1404.3725	TRUE	arrestin. beta 1	222912 at	0.524	729	2.173E-07	FALSE
92691 at	-0.202	2342	1426621 a at	-0.187	2683.5	92691 at	-0.145	1505	1426621 a at	0.176	3518	2512.125	833.54608	FALSE	protein phosphatase 2 (formerly 2A). regulatory subunit B (PR 52). beta isoform	213849 s at	-0.530	2543	1.025E-05	FALSE
93466 at	0.066	5083	1422684 a at	-0.149	2553	93466 at	-0.377	135	1431062 a at	0.188	2279	2512.5	2026.1737	FALSE	exocyst complex component 4	239264 at	0.147	8264	3.827E-03	FALSE
101593 at	-0.498	82	1417311 at	-0.259	932.5	101593 at	-0.002	8436	1417311 at	-0.307	602	2513.125	3964.0716	TRUE	cysteine rich protein 2	208978 at	-0.029	38784	8.437E-01	FALSE
97206 at	-0.179	997	1416627 at	-0.035	7070.5	97206 at	-0.230	1614.5	1416627 at	-0.487	371	2513.25	3080.2883	TRUE	serine protease inhibitor. Kunitz type 1	235546 at	-0.025	29941	5.551E-01	FALSE
92477 at	0.354	1792	1460164 at	-0.295	469	99528 at	-0.573	764	1436809 a at	0.043	7033	2514.5	3065.2444	FALSE	spindlin	217813 s at	-0.157	14869	6.815E-02	FALSE
97304 at	-0.181	1130	1455222 a at	0.132	3295	97304 at	-0.135	3780	1460655 a at	-0.169	1856	2515.25	1233.0357	FALSE	upstream binding protein 1	218082 s at	-0.253	9677	8.594E-03	FALSE
94792 at	0.198	3024	1425435 at	0.121	3594.5	94140 at	0.165	1099	1422062 at	-0.165	2347	2516.125	1073.5729	FALSE	macrophage scavenger receptor 1	214770 at	0.076	15842	8.690E-02	FALSE
100442 at	0.099	2990	1448796 s at	0.082	2876	95341 at	-0.200	570	1417658 at	-0.220	3631	2516.75	1339.7033	FALSE	transforming growth factor beta regulated gene 4	220789 s at	-0.045	24881	3.682E-01	FALSE
103869 at	-0.080	3757	1416623 at	-0.146	1983	103869 at	0.074	3860	1416623 at	-0.320	474	2518.5	1612.4769	FALSE	thrombospondin 3	209561 at	-0.112	13682	4.649E-02	FALSE
161256 at	0.167	1285	1415830 at	0.197	2199.5	100894 at	0.164	1802	1415830 at	-0.104	4795	2520.375	1561.9532	FALSE	origin recognition complex. subunit 5-like (S. cerevisiae)	204957 at	-0.355	3578	5.096E-05	FALSE
94473 at	-0.164	1528	1420131 s at	-0.166	3215	94473 at	0.072	5183	1420131 s at	-0.435	161	2521.75	2169.7563	FALSE	pituitary tumor-transforming 1 interacting protein	200677 at	0.626	771	2.475E-07	FALSE
102870 at	-0.584	454	1455748 at	0.055	6149.5	102870 at	0.242	1431	1435948 at	0.621	2055	2522.375	2506.2422	FALSE	G protein-coupled receptor 178	225127 at	-0.303	5003	2.708E-04	FALSE
103309 at	-0.143	2851	1436267 a at	0.082	4088	103309 at	0.153	3026	1459625 at	0.418	129	2523.5	1687.3108	FALSE	FK506 binding protein 12-rapamycin associated protein 1	202288 at	-0.123	7200	1.872E-03	FALSE
160065 s at	-0.356	571	1425810 a at	-0.532	6.5	160065 s at	-0.221	3355	1425811 a at	-0.096	6165	2524.375	2834.2816	TRUE	cysteine and glycine-rich protein 1	200621 at	0.610	154	1.384E-08	FALSE
100973 i at	-0.532	125	1430375 a at	0.120	3764.5	100972 s at	0.269	222	1434962 x at	-0.157	5991	2525.625	2864.3396	FALSE	chemokine (C-C motif) ligand 27	230327 at	-0.162	6759	1.289E-03	FALSE
160261 i at	0.354	1178	1419678 at	-0.069	4854	160261 i at	-0.352	1693	1419678 at	0.219	2380	2526.25	1628.0758	FALSE	large tumor suppressor 2	227013 at	0.759	655	1.714E-07	FALSE
162473 r at	0.297	2702	1448483 a at	0.312	543.5	95131 f at	0.163	2080	1416834 x at	0.129	4783	2527.125	1756.3449	TRUE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex. 2	226391 at	-0.315	911	3.604E-07	FALSE
98562 at	-0.485	1582	1417381 at	-0.099	3360	98562 at	-0.259	920	1417381 at	-0.390	4254	2529	1544.0073	TRUE	complement component 1. q subcomponent. alpha polypeptide	218232 at	0.465	12830	3.516E-02	FALSE
93252 at	0.082	4674	1451049 at	0.178	891	93252 at	0.282	244	1456279 a at	0.194	4312	2530.25	2286.5095	TRUE	B-cell receptor-associated protein 31	200837 at	-0.128	17201	1.198E-01	FALSE
101315 at	0.066	5145	1427832 at	0.113	2668	101315 at	-0.138	799	1452571 at	0.304	1510	2530.5	1905.6083	FALSE	tubulin alpha. related sequence 1	NA	NA	NA	NA	
101865 at	0.078	4479	1419279 at	-0.228	587	101865 at	-0.118	2541	1442310 at	0.192	2518	2531.25	1588.9314	FALSE	phosphatidylinositol-4-phosphate 5-kinase. type II. alpha	241155 at	0.441	3073	2.525E-05	FALSE
96902 at	-0.103	4282	1452721 a at	0.153	3165.5	96902 at	0.142	2085	1457628 at	-0.289	596	2532.125	1571.8065	FALSE	coiled-coil domain containing 53	218628 at	-0.072	27503	4.615E-01	FALSE
103753 at	-0.283	2024	1434332 at	-0.116	2750	103753 at	-0.081	4037	1438487 s at	0.306	1319	2532.5	1160.7442	FALSE	zinc finger. ZZ domain containing 3	212893 at	0.301	4560	1.646E-04	FALSE
98819 at	0.198	899	1420573 at	0.142	3257	98819 at	0.174	1511	1420573 at	-0.146	4464	2532.75	1629.6602	FALSE	homeo box D1	205974 at	-0.066	18964	1.679E-01	FALSE
94339 at	0.177	669	1426715 s at	0.124	2887.5	94339 at	0.067	4683	1426715 s at	-0.224	1894	2533.375	1696.1709	FALSE	DNA segment. Chr 11. ERATO Doi 18. expressed	233531 at	0.004	42550	9.484E-01	FALSE
96861 at	0.346	658	1451266 at	0.095	4797	96861 at	-0.196	624	1451266 at	-0.132	4057	2534	2206.6697	FALSE	mitochondrial ribosomal protein L50	225581 s at	-0.023	36108	7.660E-01	FALSE
102221 at	0.149	2588	1419289 a at	-0.126	3287.5	102221 at	-0.166	1733	1434661 at	0.154	2528	2534.125	635.69258	FALSE	synaptogyrin 1	204287 at	-0.250	6917	1.489E-03	FALSE
101099 at	-0.187	2349	1423055 at	-0.167	1149	161463 f at	0.081	4974	1423056 at	-0.183	1668	2535	1698.6271	FALSE	neuron specific gene family member 1	209570 s at	-0.920	1262	8.197E-07	FALSE
94271 at	-0.159	1447	1456697 x at	0.129	4909	94271 at	0.112	2092	1422636 at	-0.198	1692	2535	1604.8383	FALSE	cyclin D binding myb-like transcription factor 1	203301 s at	0.079	20058	2.020E-01	FALSE
103833 at	-0.062	6709	1424863 a at	-0.207	1008.5	103833 at	0.195	1242	1458520 at	0.225	1181	2535.125	2784.3397	FALSE	homeodomain interacting protein kinase 2	NA	NA	NA	NA	
93798 at	-0.690	53	1423653 at	-0.164	2716.5	93797 g at	-0.595	1320	1423653 at	0.172	6052	2535.375	2584.4909	FALSE	ATPase. Na+/K+ transporting. alpha 1 polypeptide	220948 s at	-0.635	1095	5.809E-07	FALSE
162391 r at	0.127	2043	1419692 a at	-0.089	3491	162391 r at	0.079	3494	1419692 a at	-0.380	1116	2536	1167.5099	FALSE	leukotriene C4 synthase	206480 at	-0.056	25845	3.987E-01	FALSE
161202 r at	0.076	4750	1421916 at	-0.219	899.5	95079 at	-0.164	1824	1421917 at	-0.197	2671	2536.125	1643.6846	FALSE	platelet derived growth factor receptor. alpha polypeptide	215305 at	0.073	10642	1.433E-02	FALSE
93595 at	-0.299	730	1448313 at	-0.051	5413	93595 at	-0.155	2344	1434768 at	-0.199	1660	2536.75	2028.3822	TRUE	tripeptidyl peptidase I	200743 s at	0.283	5016	2.732E-04	FALSE
95507 at	0.139	5251	1416052 at	0.156	2189	95507 at	0.134	2347	1416052 at	0.304	360	2536.75	2021.7425	TRUE	phosphoribosyl pyrophosphate synthetase 1	208447 s at	-0.212	17113	1.173E-01	FALSE
104168 at	0.299	396	1452587 at	-0.097	4049.5	104168 at	-0.371	2882	1452587 at	-0.135	2821	2537.125	1535.2761	FALSE	ARP2 actin-related protein 2 homolog (yeast)	200728 at	-0.220	10142	1.088E-02	FALSE
95129 at	-0.154	3642	1448893 at	-0.270	527.5	95129 at	-0.188	3169	1451841 a at	-0.305	2811	2537.375	1382.4633	TRUE	nuclear receptor co-repressor 2	207760 s at	0.290	3600	5.259E-05	FALSE
161631 f at	-0.112	2018	1417117 at	0.108	3671.5	161631 f at	0.138	1778	1417117 at	0.201	2685	2538.125	847.43361	FALSE	Cleavage stimulation factor. 3' pre-RNA. subunit 1	32723 at	-0.039	16469	1.010E-01	FALSE
95356 at	-0.087	3350	1432466 a at	-0.300	296.5	95356 at	0.089	3065	1432466 a at	-0.187	3444	2538.875	1503.5766	FALSE	apolipoprotein E	203382 s at	0.193	14933	6.955E-02	FALSE
103436 at	-0.098	2541	1450023 at	-0.090	3360	103436 at	-0.196	265	1450023 at	-0.123	3993	2539.75	1628.8273	TRUE	GTP binding protein 1	219357 at	0.150	7661	2.579E-03	FALSE
97356 at	-0.132	3553	1460424 at	0.091	4234	97356 at	0.249	192	1460424 at	0.248	2182	2540.25	1782.9818	FALSE	RIKEN cDNA 1810008O21 gene	219219 at	-0.298	4946	2.531E-04	FALSE
160440 at	-0.129	3272	1422487 at	-0.223	1656	160440 at	-0.131	3955	1422486 a at	-0.201	1284	2541.75	1277.6318	TRUE	MAD homolog 4 (Drosophila)	202527 s at	0.130	19170	1.738E-01	FALSE
94511 at	0.303	1262	1448843 at	-0.177	1190	94511 at	-0.175	1451	1448843 at	0.083	6264	2541.75	2483.9397	FALSE	similar to signal sequence receptor. alpha	NA	NA	NA	NA	
95064 at	-0.089	6106	1455061 a at	-0.411	680	95064 at	0.225	2103	1428145 at	-0.234	1280	2542.25	2446.3922	FALSE	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	202003 s at	0.209	8210	3.728E-03	FALSE
103360 at	0.080	5560	1417989 at	0.150	2023	103360 at	0.232	849	1417989 at	0.246	1739	2542.75	2072.739	TRUE	testis-specific serine kinase 1	211694 at	0.003	43395	9.696E-01	FALSE
160750 at	0.174	1453	1452062 at	0.122	2080	160750 at	-0.125	2027	1452062 at	-0.107	4612	2543	1408.2478	FALSE	phosphoribosyl pyrophosphate synthetase-associated protein 2	239696 at	0.079	19054	1.703E-01	FALSE
162172 f at	0.076	4204	1451109 a at	-0.431	67	93101 s at	-0.179	2632	1421955 a at	0.277	3271	2543.5	1772.7005	FALSE	neural precursor cell expressed. developmentally down-regulted gene 4	213012 at	0.041	22427	2.827E-01	FALSE
98532 at	-0.440	160	1435509 x at	-0.270	255	98532 at	0.004	8373	1426885 a at	-0.215	1387	2543.75	3925.9337	FALSE	CDK2 (cyclin-dependent kinase 2)-associated protein 1	201938 at	0.430	3649	5.662E-05	FALSE
94499 at	-0.144	2988	1422901 at	-0.270	198.5	94499 at	-0.183	3839	1439081 at	-0.168	3153	2544.625	1606.9029	TRUE	meningioma expressed antigen 5 (hyaluronidase)	214972 at	-0.148	11554	2.152E-02	TRUE
103708 at	0.113	3215	1424344 s at	0.181	413	103708 at	0.276	407	1424344 s at	0.072	6152	2546.75	2743.2222	TRUE	eukaryotic translation initiation factor 1A	244482 at	0.155	9040	5.955E-03	TRUE
100397 at	-0.424	486	1450792 at	0.191	1168.5	100397 at	0.073	5301	1450792 at	-0.389	3236	2547.875	2176.1753	FALSE	TYRO protein tyrosine kinase binding protein	204122 at	0.380	12320	2.939E-02	FALSE



160218 at	-0.073	4821	1451385 at	0.188	863	160218 at	-0.145	4152	1443339 at	0.426	811	2661.75	2124.7731	FALSE	RIKEN cDNA 2310056P07 gene	220942 x at	-0.376	2000	3.855E-06	FALSE
95886 g at	-0.092	4508	1434633 at	0.078	3426	95886 g at	0.250	2599	1436983 at	1.175	118	2662.75	1867.9146	FALSE	CREB binding protein	202160 at	0.282	4700	1.970E-04	FALSE
101631 at	-0.047	7150	1436790 a at	0.209	3344	101631 at	0.777	2	1436790 a at	0.627	156	2663	3364.6644	FALSE	SRY-box containing gene 11	204915 s at	-0.271	4451	1.451E-04	FALSE
161764 r at	0.092	3295	1418957 at	0.166	2870	161764 r at	0.130	1033	1445344 at	0.165	3456	2663.5	1114.7527	TRUE	src homology three (SH3) and cysteine rich domain	205743 at	-0.063	27785	4.720E-01	FALSE
102767 at	-0.065	5463	1455089 at	-0.191	600.5	102767 at	0.076	4021	1421947 at	0.345	574	2664.625	2469.9515	FALSE	guanine nucleotide binding protein (G protein), gamma 12	212294 at	0.575	1822	2.790E-06	FALSE
95323 at	0.204	1065	1427654 a at	-0.044	6830	95321 at	0.127	2736	1443365 at	-0.944	37	2667	2989.9071	FALSE	5 hydroxytryptamine (serotonin) receptor 4	207577 at	-0.520	1086	5.706E-07	FALSE
92599 at	-0.196	812	1418373 at	0.009	8136	92599 at	-0.418	180	1418373 at	-0.444	1542	2667.5	3687.8982	FALSE	phosphoglycerate mutase 2	205736 at	0.340	3167	2.906E-05	FALSE
93212 at	0.377	368	1433706 a at	0.083	4879	93212 at	-0.508	1587	1452427 s at	0.198	3844	2669.5	2059.9392	FALSE	protein tyrosine phosphatase-like A domain containing 1	217777 s at	-0.318	11933	2.514E-02	FALSE
100570 at	-0.076	4773	1420535 a at	-0.083	3854.5	161580 f at	0.125	1684	1420535 a at	-0.346	373	2671.125	2006.1613	FALSE	RIKEN cDNA 6330412F12 gene	222512 at	0.313	1727	2.314E-06	FALSE
99103 at	0.049	5801	1435271 at	0.141	1821	99103 at	0.185	1315	1416898 a at	-0.276	1750	2671.75	2098.1241	FALSE	interferon regulatory factor 3	202621 at	0.252	1386	1.087E-06	FALSE
101486 at	-0.036	6597	1448632 at	0.215	746	101486 at	0.306	268	1448632 at	0.279	3077	2672	2890.1178	FALSE	proteasome (prosome, macropain) subunit, beta type 10	202659 at	-0.149	14731	6.564E-02	FALSE
103262 at	0.109	2714	1421298 a at	-0.135	1882	103262 at	-0.231	2580	1424540 at	-0.218	3514	2672.5	669.15145	FALSE	homeodomain interacting protein kinase 1	212291 at	0.386	3513	4.716E-05	FALSE
101065 at	0.083	5550	1417947 at	0.154	1756.5	101065 at	0.226	1640	1417947 at	0.214	1745	2672.875	1918.7995	TRUE	proliferating cell nuclear antigen	201202 at	0.092	25195	3.794E-01	FALSE
100499 at	0.059	4942	1425536 at	-0.094	3764.5	100497 at	-0.190	1143	1425536 at	-0.327	842	2672.875	2002.7643	FALSE	syntaxin 3	216985 s at	-0.022	34254	7.068E-01	FALSE
99087 at	0.106	2977	1455382 at	0.085	3080	99087 at	0.126	1274	1427539 a at	0.226	3362	2673.25	946.92252	TRUE	ZW10 interactor	204026 s at	-0.184	9285	6.898E-03	FALSE
96041 at	0.357	1085	1422660 at	0.524	60	96041 at	0.574	1389	1422660 at	0.025	8159	2673.25	3701.0973	TRUE	similar to Putative RNA-binding protein 3 (RNA-binding motif protein 3)	NA	NA	NA	NA	
95904 at	0.235	282	1455628 at	0.047	6579	95904 at	0.285	250	1455628 at	0.172	3590	2675.25	3037.8454	TRUE	RIKEN cDNA 6430543G08 gene	NA	NA	NA	NA	
160993 at	0.083	4251	1459894 at	-0.120	3106	160993 at	-0.144	2216	1433885 at	-0.462	1130	2675.75	1325.046	FALSE	IQ motif containing GTPase activating protein 2	NA	NA	NA	NA	
92725 at	0.197	1319	1418361 at	0.136	3536	92725 at	-0.163	1409	1418361 at	0.129	4446	2677.5	1561.9677	FALSE	growth arrest specific 8	204921 at	0.121	8562	4.517E-03	FALSE
93938 at	-0.158	895	1422786 at	0.040	7120	93938 at	-0.132	2150	1422786 at	-0.378	546	2677.75	3040.5406	FALSE	solute carrier family 30 (zinc transporter), member 1	212907 at	0.367	5909	6.393E-04	FALSE
102232 at	0.106	3547	1421249 at	0.211	2165	102232 at	0.228	980	1421249 at	0.165	4029	2680.25	1381.6313	TRUE	similar to solute carrier family 39 (zinc transporter), member 9	NA	NA	NA	NA	
98580 at	-0.200	2100	1451943 a at	-0.223	627	98580 at	-0.183	3928	1417221 at	-0.128	4068	2680.75	1636.5874	TRUE	protein phosphatase 1A, magnesium dependent, alpha isoform	210407 at	0.146	11330	1.970E-02	FALSE
162052 i at	-0.112	2901	1448615 at	0.137	1246	162052 i at	0.263	611	1448615 at	0.077	5972	2682.5	2396.0521	FALSE	copper chaperone for superoxide dismutase	203522 at	0.165	4740	2.049E-04	FALSE
93966 at	-0.130	1806	1448410 at	-0.184	2218	93966 at	0.150	1165	1444465 at	0.133	5549	2684.5	1958.1986	FALSE	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	215533 s at	-0.143	11282	1.937E-02	FALSE
99577 at	-0.203	2486	1448117 at	-0.284	97.5	99577 at	0.096	5751	1440621 at	-0.264	2414	2687.125	2324.4022	FALSE	kit ligand	226534 at	0.117	20481	2.155E-01	FALSE
92247 at	0.059	7063	1423194 at	-0.274	774	92247 at	-0.512	1421	1423194 at	0.242	1495	2688.25	2934.4255	FALSE	Rho GTPase activating protein 5	235635 at	0.648	732	2.176E-07	FALSE
98092 at	-0.143	4484	1451335 at	0.128	1354	98092 at	0.078	3750	1451335 at	-0.330	1165	2688.25	1678.5455	FALSE	placenta-specific 8	219014 at	0.208	15945	8.968E-02	FALSE
95455 at	-0.035	6679	1416127 a at	-0.248	218	95455 at	0.089	3213	1460579 at	-0.406	649	2689.75	2969.9672	FALSE	aspartyl aminopeptidase	201937 s at	-0.034	28187	4.887E-01	FALSE
93784 at	0.103	4235	1416742 at	0.309	16.5	93784 at	0.181	1942	1416742 at	0.098	4572	2691.375	2131.9825	TRUE	craniofacial development protein 1	210701 at	0.118	8860	5.364E-03	TRUE
161116 at	0.143	2442	1450821 at	0.073	5657.5	161116 at	0.171	2012	1445105 at	0.443	658	2692.375	2117.8799	TRUE	p300/CBP-associated factor	239585 at	0.433	2548	1.038E-05	TRUE
92594 at	0.097	3114	1419113 at	-0.077	4294	92594 at	0.176	2275	1419113 at	-0.238	1089	2693	1352.5263	FALSE	adaptor protein complex AP-1, gamma 2 subunit	201613 s at	-0.334	6476	1.029E-03	FALSE
99998 at	0.091	3712	1436542 at	-0.164	1201	99998 at	0.090	4504	1445445 s at	-0.204	1358	2693.75	1665.9701	FALSE	prostaglandin E receptor 1 (subtype EP1)	207650 x at	0.049	25507	3.890E-01	FALSE
92449 at	-0.195	1414	1423007 a at	0.069	5177.5	92449 at	0.166	2519	1459847 x at	0.472	1670	2695.125	1720.985	FALSE	glial cell line derived neurotrophic factor family receptor alpha 2	205721 at	0.070	23092	3.049E-01	FALSE
103374 at	-0.085	3754	1428401 at	0.180	474	103374 at	-0.054	5876	1428402 at	0.958	681	2696.25	2596.7462	FALSE	zinc finger, CCHC domain containing 3	229993 at	-0.101	10703	1.473E-02	FALSE
102664 at	0.070	5041	1421123 at	-0.298	969	102664 at	-0.331	1754	1421124 at	0.230	3026	2697.5	1777.4334	FALSE	cyclin-dependent kinase 5, regulatory subunit (p35) 1	204995 at	-0.913	3056	2.462E-05	FALSE
100601 at	-0.073	4697	1417533 a at	-0.176	1349.5	162218 f at	0.063	4472	1417534 at	-0.373	277	2698.875	2222.8186	FALSE	integrin beta 5	201125 s at	0.327	1101	5.924E-07	FALSE
104237 at	0.146	2860	1452621 at	0.422	15	104237 at	0.289	351	1452621 at	0.049	7570	2699	3486.6183	TRUE	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alph	240846 at	0.130	11665	2.248E-02	TRUE
96713 at	0.008	8254	1434510 at	-0.221	643	96713 at	-0.248	1107	1434510 at	-0.316	793	2699.25	3708.2098	FALSE	3'-phosphoadenosine 5'-phosphosulfate synthase 2	203060 s at	0.481	7465	2.230E-03	FALSE
162432 f at	0.219	1252	1455099 at	0.200	545	161107 r at	0.196	1183	1455099 at	0.027	7819	2699.75	3427.6415	TRUE	monoacylglycerol O-acyltransferase 2	232428 at	-0.050	20824	2.276E-01	FALSE
93818 g at	0.164	2003	1420867 at	-0.245	536	93818 g at	-0.164	891	1436451 a at	-0.039	7374	2701	3177.3919	FALSE	transmembrane emp24 domain trafficking protein 2	204426 at	-0.216	10042	1.033E-02	FALSE
98875 at	-0.145	1761	1423793 at	-0.054	5560	98875 at	-0.127	2114	1423793 at	-0.344	1369	2701	1930.1359	TRUE	DNA segment, Chr 2, ERATO Doi 391, expressed	203364 s at	0.099	11636	2.224E-02	FALSE
101010 at	0.206	806	1423431 a at	0.136	2456	101010 at	0.092	3891	1423430 at	0.164	3653	2701.5	1411.0815	TRUE	MYB binding protein (P160) 1a	219098 at	-0.134	8525	4.420E-03	FALSE
93839 at	0.081	5717	1425539 a at	-0.182	1824	93839 at	-0.139	3115	1443220 at	0.450	151	2701.75	2347.9976	FALSE	reticulon 3	244418 at	-0.304	5598	4.802E-04	FALSE
162448 f at	-0.078	3719	1417014 at	-0.101	4581.5	160139 at	-0.181	826	1417013 at	-0.529	1682	2702.125	1744.1889	TRUE	heat shock protein 8	221667 s at	0.818	1287	8.571E-07	FALSE
102332 at	-0.092	3681	1416504 at	-0.113	2085	102332 at	0.304	234	1416504 at	0.099	4818	2704.5	1992.2839	FALSE	Unc-51 like kinase 1 (C. elegans)	209333 at	-0.564	2487	9.453E-06	FALSE
102299 at	-0.105	3947	1427562 a at	0.052	6243.5	102299 at	-0.379	43	1427562 a at	-0.349	586	2704.875	2923.4655	FALSE	protein kinase C, alpha	213093 at	0.359	2596	1.102E-05	FALSE
103783 at	-0.126	4340	1450130 at	-0.302	154	103783 at	0.086	5958	1452271 at	-0.664	370	2705.5	2899.1412	FALSE	xenotropic and polytropic retrovirus receptor 1	222581 at	0.141	8369	4.088E-03	FALSE
93421 at	-0.208	2210	1419249 at	-0.330	1340.5	93422 at	0.035	7087	1419250 a at	0.497	187	2706.125	3035.8485	FALSE	PFTAIRE protein kinase 1	204604 at	-0.309	3727	6.134E-05	FALSE
160724 at	0.093	4715	1448478 at	0.122	3133.5	162114 f at	0.136	969	1459413 at	0.238	2007	2706.125	1604.6399	TRUE	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	212872 s at	0.082	13339	4.168E-02	TRUE
160726 at	-0.154	3645	1429318 a at	-0.521	29	95096 at	-0.085	5465	1444698 at	0.315	1693	2708	2358.4094	FALSE	quaking	241938 at	0.594	386	5.825E-08	FALSE
102685 at	0.096	5864	1421782 a at	0.221	879	102684 at	0.169	1871	1451953 at	-0.189	2220	2708.5	2179.0127	FALSE	submaxillary gland androgen regulated protein 2	NA	NA	NA	NA	
95689 at	-0.060	4899	1460718 s at	-0.156	1152.5	95689 at	-0.130	1688	1460718 s at	-0.140	3097	2709.125	1674.4927	TRUE	mitochondrial carrier homolog 1 (C. elegans)	221619 s at	-0.176	10219	1.139E-02	TRUE
103070 at	-0.255	493	1448534 at	-0.192	1216	95803 at	-0.522	694	1416986 a at	0.005	8434	2709.25	3828.6444	FALSE	signal-regulatory protein alpha	202897 at	0.177	12162	2.756E-02	FALSE
161881 f at	0.206	634	1419281 a at	0.119	2553	161881 f at	0.172	772.5	1428294 at	-0.070	6878	2709.375	2913.2201	FALSE	zinc finger protein 259	200054 at	0.024	33654	6.869E-01	FALSE
92272 at	-0.138	2139	1455310 at	0.103	4364	92272 at	0.079	3877	1455310 at	0.297	458	2709.5	1779.0586	FALSE	RNA binding motif protein 16	NA	NA	NA	NA	
96608 at	0.214	1928	1460194 at	0.097	4111	96608 at	0.320	2222	1460194 at	0.165	2578	2709.75	971.23508	TRUE	phytanoyl-CoA hydroxylase	203335 at	0.186	13920	5.105E-02	FALSE
101952 at	-0.083	3676	1425239 at	0.098	3094.5	101952 at	0.156	960	1435405 at	-0.247	3110	2710.125	1197.7056	FALSE	SET domain containing 4	219482 at	0.070	18329	1.498E-01	FALSE
97557 at	-0.134	1802	1438547 x at	0.203	1113	97557 at	0.148	1669	1423783 at	-0.062	6257	2710.25	2383.2585	FALSE	torsin family 2, member A	NA	NA	NA	NA	
101518 at	-0.267	644	1451412 a at	-0.171	4945	101518 at	0.172	3014	1451412 a at	0.296	2240	2710.75	1786.7004	FALSE	intraflagellar transport 20 homolog (Chlamydomonas)	NA	NA	NA	NA	
104355 at	0.126	1955	1455831 at	-0.135	2686	104355 at	-0.043	5753	1455831 at	0.512	450	2711	2231.4454	FALSE	fusion, derived from t(12:16) malignant liposarcoma (human)	231108 at	0.117	9329	7.084E-03	FALSE
101511 at	0.048	6329	1427096 s at	0.125	2469.5	101511 at	0.269	635	1427096 s at	0.229	1413	2711.625	2526.0526	TRUE	signal sequence receptor, delta	242108 at	0.269	2152	4.952E-06	TRUE
161781 at	0.180	1432	1416092 a at	-0.236	557.5	161781 at	-0.041	6264	1443702 at	0.222	2602	2713.875	2510.5816	FALSE	microtubule-associated protein 4	212566 at	0.569	184	1.780E-08	FALSE
97530 at	-0.181	2317	1425478 x at	0.102	2940	97530 at	-0.081	3528	1453189 at	0.456	2073	2714.5	653.74842	FALSE	ubiquitin-conjugating enzyme E2I	233360 at	0.092	10808	1.568E-02	FALSE
162410 s at	0.161	2519	1426170 a at	0.178	1407.5	162410 s at	0.097	3024	1448569 at	-0.122	3909	2714.875	1043.8852	FALSE	CD8 antigen, beta chain 1	230037 at	-0.021	33509	6.826E-01	FALSE
94510 at	0.202	1165	1434552 at	0.129	2334	94510 at	-0.042	6213	1430289 a at	0.315	1150	2715.5	2396.7262	FALSE	WD repeat domain 77	201420 s at	-0.053	23312	3.126E-01	FALSE
93902 at	0.099	3415	1417694 at	-0.441	133.5	93902 at	-0.028	6795	1417694 at	-0.369	522	2716.375	3088.1377	FALSE	growth factor receptor bound protein 2-associated protein 1	242572 at	0.670	796	2.729E-07	FALSE
96313 at	0.015	8015	1422600 at	-0.311	501	96313 at	-0.665	1043	1459056 at	-0.293	1311	2717.5	3547.7021	FALSE	RAS protein-specific guanine nucleotide-releasing factor 1	210550 s at	-0.232	9313	7.012E-03	FALSE
101554 at	-0.055	5866	1420089 at	0.199	2140.5	101554 at	0.274	1303	1449731 s at	-0.241	1562	2717.875	2127.7509	FALSE	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	201502 s at	0.817	3223	3.120E-05	FALSE
160854 at	-0.064	6086	1455441 at	0.142	2325	160854 at	-0.124	1561	1425795 a at	0.358	902	2718.5	2319.0786	FALSE	mitogen activated protein kinase kinase kinase 7	206854 s at	0.155	17218	1.202E-01	FALSE
94979 at	-0.234	1238	1451221 at	-0.087	4990.5	94979 at	-0.179	3639	1451221 at	-0.268	1013	2720.125	1924.3964	TRUE	cDNA sequence BC018507	209654 at	0.199	10921	1.649E-02	FALSE
160740 at	0.013	7737	1454921 at	0.376	769	160740 at	0.421	48	1454921 at	0.241	2333	2721.75	3476.8775	TRUE	gene model 561, (NCBI)	NA	NA	NA	NA	
101097 at	-0.042	6741	1452580 a at	0.204	881	101097 at	0.158	748	1452580 a at	0.174	2522	2723	2797.5176	FALSE	mitochondrial ribosomal protein L21	225315 at	-0.191	6935	1.510E-03	FALSE
104267 at	-0.099	2777	1417329 at	-0.158	1553	104267 at	-0.057	5904	1442983 at	-0.357	661	2723.75	2290.7363	TRUE	solute carrier family 23 (nucleobase transporters), member 2	209236 at	-0.118	14273	5.743E-02	FALSE
102687 at	0.092	3234	1422979 at	0.202	616.5	102687 at	0.054	5504	1433996 at	0.260	1541	2723.875	2147.0558	TRUE	suppressor of variegation 3-9 homolog 2 (Drosophila)	219262 at	-0.010	36454	7.762E-01	FALSE
160394 at	-0.464	455	1427244 at	0.018	7880	160394 at	-0.560	911	1441528 at	0.238	1655	2725.25	3471.9073	FALSE	tetratricopeptide repeat domain 15	229556 at	-0.053	22840	2.962E-01	FALSE
93134 at	-0.261	333	1434877 at	-0.150	4365	93134 at	-0.528	1444	1422130 at	0.429	4760	2725.5	2175.1206	FALSE	neuronal pentraxin 1	204684 at	-0.845	803	2.769E-07	FALSE
93339 at	0.212	1739	1460542 s at	0.043	6671	93339 at	0.173	1531	1460542 s at	0.261	962	2725.75	2650.5921	TRUE	transformed mouse 3T3 cell double minute 4	225740 x at	0.477	254	2.849E-08	TRUE
103739 at	-0.213	1576	1428374 at	-0.122	2267	103739 at	-0.092	4429	1440386 at	-0.147	2635	2726.75	1216.7811	TRUE	glucuronyl C5-epimerase	213552 at	-0.225	5809	5.906E-04	TRUE
102237 at	0.189	1263	1417597 at	0.087	4124	102237 at	0.107	3409	1443703 at	0.195	2115	2727.75	1282.5198	TRUE	CD28 antigen	211856 x at	0.095	14036	5.295E-02	FALSE
103733 at	0.094	2815	1448019 at	0.241	239	103733 at	0.049	5787	1448019 at	0.178	2074	2728.75	2308.5266	TRUE	RIKEN cDNA 2900006A08 gene	NA	NA	NA	NA	
93284 at	0.256	279	1416332 at	0.292	170.5	93284 at	0.167	3458	1416332 at	0.081	7008	2728.875	3234.6924	TRUE	cold inducible RNA binding protein	228519 x at	0.174	6343	9.400E-04	TRUE
103369 at	-0.085	3604	1436316 at	-0.223	358	103369 at	0.288	612	1436316 at	0.093	6344	2729.5	2824.7229	FALSE	RIKEN cDNA 9430029L20 gene	NA	NA	NA	NA	
104400 at	-0.218	1206	1460191 at	-0.199	1533	104400 at	-0.306	111	1448464 at	-0.016	8072	2730.5	3612.548	TRUE	YKT6 homolog (S. Cerevisiae)	217785 s at	-0.372	1898	3.248E-06	TRUE
94875 at	-0.103	5132	1416093 a at	0.232	512	94875 at	0.166	2298	1416093 a at	0.172	2980	2730.5	1909.4721	FALSE	mitochondrial ribosomal protein L20	220527 at	0.031	23093	3.049E-01	FALSE
92688 at	0.184	847	1424654 at	0.100	2600	92688 at	-0.133	1574	1424655 at	0.094	5905	2731.5	2234.5425	FALSE	acid phosphatase 2, lysosomal	202767 at	-0.082	16706	1.065E-01	FALSE
101354 at	0.018	7803	1422203 at	-0.300	484	101354 at	-0.148	1392	1422203 at	-0.543	1247	2731.5	3404.378	FALSE	solute carrier family 18 (vesicular monoamine), member 3	207150 at	-0.060	23872	3.339E-01	FALSE
161570 r at	-0.078	4338	1416668 at	0.312	729	100400 at	0.207	2474	1416668 at	0.121	3386	2731.75	1536.8284	FALSE	RIKEN cDNA 4921531G14 gene	203584 at	0.176	19322	1.786E-01	FALSE
104598 at	-0.385	391	1448830 at	-0.327	432.5	104598 at	0.011	8257	1448830 at	-0.369	1848	2732.125	3744.9994	FALSE	dual specificity phosphatase 1	201041 s at	0.445	12186	2.780E-02	FALSE
92358 at	-0.318	517	1423561 at	0.189	1942.5	92358 at	-0.265	3896	1423560 at	0.201	4575	2732.625	1851.2229	FALSE	NEL-like 2 (chicken)	203413 at	-0.701	1675	2.056E-06	FALSE
103467 g at	-0.136	3521	1419284 at	0.132	1451	103467 g at	0.160	2381	1435328 at	-0.128	3584	2734.25	1018.5884	FALSE	cysteine and histidine rich 1	NA	NA	NA	NA	
95658 at	-0.005	8434	1424122 s at	0.325	488.5	95658 at	0.453	414	1446787 at	-0.186	1602	2734.625	3838.2328	FALSE	COMM domain containing 1	234020 x at	0.082	14089	5.423E-02	FALSE
97731 at	-0.260	356	1420437 at	-0.084	6760	161824 r at	0.099	3625	1420437 at	-0.623	201	2735.5	3113.065	FALSE	indoleamine-pyrrole 2,3 dioxygenase	210029 at	0.044	29739	5.480E-01	FALSE
95897 at	-0.128	3536	1437738 at	-0.146	2123.5	161574 r at	0.063	4334	1439215 at	0.296	949	2735.625	1501.347	FALSE	ATPase, Ca++-sequestering	209934 s at	-0.205	3324	3.598E-05	FALSE
162055 f at	-0.165	970	1433786 x at	0.120	2859.5	162055 f at	-0.095	2947	1433786 x at	0.124	4166	2735.625	1319.5237	FALSE	small EDRK-rich factor 2	226692 at	0.215	4468	1.488E-04	FALSE
160521 at	0.123	1736	1426813 at	0.165	1772	160521 at	-0.030	6336	1426813 at	0.219	1100	2736	2419.7653	FALSE	LTV1 homolog (S. cerevisiae)	239212 at	0.119	18335	1.501E-01	FALSE
101362 at	0.062	5316	1421877 at	-0.272	347.5	101362 at	-0.498	1351	1421878 at	0.111	3931	2736.375	2288.2003	FALSE	mitogen activated protein kinase 9	210570 x at	-0.348	556	1.203E-07	FALSE
99615 at	0.123	3221	1423133 at	0.247	223	99616 s at	0.241	973	1423133 at	0.051	6530	2736.75	2831.5483	TRUE	RIKEN cDNA 0610040D20 gene	223067 at	-0.059	28444	4.989E-01	FALSE
99544 at	-0.075	5475	1425228 a at	-0.119	3103.5	99543 s at	-0.095	698	1425228 a at	-0.285	1671	2736.875	2075.6399	TRUE	deoxyguanosine kinase	203816 at	-0.377	2030	4.048E-06	TRUE
160789 at	-0.047	6213	1423695 at	-0.146	1674	160789 at	-0.123	1599	1444335 at	0.214	1462	2737	2318.995	FALSE	ER degradation enhancer, mannosidase alpha-like 2	218282 at	0.080	14397	5.983E-02	FALSE
100051 at	0.122	2527	1419097 a at	0.085	4610.5	100052 at	-0.180	1718	1419099 x at	-0.260	2094	2737.375	1291.7574	FALSE	stomatin	201061 s at	0.430	7072	1.665E-03	FALSE
101382 at	-0.341	200	1418893 at	-0.156	1013	101382 at	0.013	7667	1418893 at	-0.203	2070	2737.5	3374.3312	FALSE	pre B-cell leukemia transcription factor 2	202876 s at	-0.096	16629	1.045E-01	FALSE
93496 at	0.026	7970	1415840 at	-0.256	422	93496 at	-0.310	767	1415840 at	-0.210	1792	2737.75	3536.3558	FALSE	ELOVL family member 5, elongation of long chain fatty acids (yeast)	214153 at	0.156	10668	1.458E-02	FALSE
97276 at	0.019	7903	1448533 at	0.207	1319.5	97276 at	0.288	259	1448533 at	0.230	1479	2740.125	3484.2441	TRUE	cytoskeleton-associated protein 1	216194 s at	0.105	23156	3.072E-01	FALSE
101966 s at	0.355	764	1420620 a at	-0.151	2403	101966 s at	-0.119	4469	1451074 at	-0.158	3327	2740.75	1565.4768	FALSE	ring finger protein 13	NA	NA	NA	NA	
161238 f at	0.140	3392	1426067 x at	0.145	1326	98446 s at	-0.142	3105	1439679 at	0.153	3142	2741.25	952.07191	FALSE	chaperonin subunit 3 (gamma)	200910 at	0.092	26697	4.315E-01	FALSE
100970 at	-0.120	3330	1425711 a at	-0.202	2540	100970 at	0.156	2659	1442759 at	0.223	2438	2741.75	402.43126	FALSE	thymoma viral proto-oncogene 1	207163 s at	-0.046	25629	3.921E-01	FALSE
94464 at	-0.365	1858	1433487 at	-0.097	3733	102786 at	0.193	3013	1416610 a at	0.207	2364	2742	812.37553	FALSE	chloride channel 3	201733 at	-0.090	21142	2.381E-01	FALSE
97936 at	0.064	5019	1435243 at	0.083	3071	97936 at	0.120	1577	1441041 at	-0.204	1301	2742	1705.5474	FALSE	zinc finger protein 746	225848 at	-0.041	23762	3.295E-01	FALSE
96064 at	0.199	1088	1448872 at	0.169	828	162187 f at	0.185	1296	1448872 at	0.030	7759	2742.75	3349.6425	TRUE	regenerating islet-derived 3 gamma	NA	NA	NA	NA	
160912 i at	0.160	971	1426456 a at	-0.140	1547.5	100941 at	-0.130	2972	1426456 a at	0.075	5485	2743.875	2011.6499	FALSE	protein inhibitor of activated STAT 2	214442 s at	-0.302	325	4.515E-08	FALSE
102726 at	-0.544	342	1416783 at	0.147	3864.5	102726 at	0.221	4406	1416783 at	-0.216	2374	2746.625	1818.8129	FALSE	tachykinin 1	206552 s at	-1.730	611	1.436E-07	FALSE
95436 at	-0.643	60	1417954 at	-0.234	1214.5	95436 at	-0.242	2264	1417954 at	0.041	7452	2747.625	3262.8637	FALSE	somatostatin	213921 at	-0.530	13444	4.305E-02	FALSE
98331 at	0.168	1911	1427883 a at	-0.106	3926	102990 at	0.143	876	1427884 at	-0.105	4280	2748.25	1626.8232	FALSE	procollagen, type III, alpha 1	232458 at	-0.079	15584	8.181E-02	FALSE
97201 s at	-0.167	3286	1417286 at	0.422	470	97201 s at	0.202	2380	1417285 a at	-0.109	4870	2751.5	1836.3902	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	201304 at	-0.462	6225	8.540E-04	FALSE
98287 at	0.113	2833	1451394 at	-0.140	3472	98287 at	-0.442	217	1451394 at	0.139	4488	2752.5	1822.5331	FALSE	dipeptidylpeptidase 6	207789 s at	-0.578	701	1.932E-07	FALSE
96224 at	-0.125	2441	1417325 at	0.036	7019	160790 s at	-0.448	56	1417325 at	-0.229	1494	2752.5	3008.5982	FALSE	beta-transducin repeat containing protein	224471 s at	-0.247	6783	1.314E-03	FALSE
161879 r at	0.120	1930	1423660 at	-0.154	1482	161879 r at	0.073	3289	1451075 s at	-0.098	4321	2755.5	1295.9765	FALSE	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	NA	NA	NA	NA	
92637 at	-0.119	1900	1450269 a at	-0.068	5387	92637 at	-0.304	1317	1453541 at	0.205	2420	2756	1810.9403	FALSE	phosphofructokinase, liver, B-type	211065 x at	0.085	14681	6.482E-02	FALSE
162421 r at	0.110	3946	1448471 a at	0.085	3605.5	162421 r at	-0.178	797	1448471 a at	-0.369	2678	2756.625	1412.0332	FALSE	cytotoxic T lymphocyte-associated protein 2 alpha	NA	NA	NA	NA	
160535 at	-0.233	724	1416331 a at	-0.071	5105	101757 at	-0.288	1598	1416331 a at	-0.149	3601	2757	1974.9945	TRUE	nuclear factor, erythroid derived 2,-like 1	200759 x at	0.091	11499	2.099E-02	FALSE
100434 s at	0.188	2223	1425924 at	0.130	2887.5	100432 f at	-0.152	1435	1425924 at	-0.113	4483	2757.125	1294.726	FALSE	MyoD family inhibitor	NA	NA	NA	NA	
96879 at	-0.211	2493	1451274 at	-0.325	2713	96879 at	-0.192	4187	1445632 at	-0.286	1643	2759	1057.9086	TRUE	oxoglutarate dehydrogenase (lipoamide)	201282 at	0.138	11197	1.866E-02	FALSE
96953 at	-0.379	380	1418457 at	-0.058	6983	96953 at	-0.103	2057	1418456 a at	-0.411	1618	2759.5	2903.8194	TRUE	chemokine (C-X-C motif) ligand 14	222484 s at	-0.391	9863	9.384E-03	TRUE
100427 at	0.346	242	1417676 a at	0.143	3128	100427 at	0.076	6133	1425863 a at	0.382	1540	2760.75	2539.1124	TRUE	protein tyrosine phosphatase, receptor type, O	208121 s at	-0.776	3587	5.174E-05	FALSE
98431 at	0.037	6454	1430891 at	-0.116	2909	98431 at	-0.125	1299	1430891 at	-0.365	384	2761.5	2673.8066	FALSE	dual specificity phosphatase 12	218576 s at	0.103	16440	1.005E-01	FALSE
160205 f at	0.235	1749	1452058 a at	0.065	6593.5	160205 f at	0.285	812	1439685 at	0.170	1902	2764.125	2597.9892	TRUE	ring finger protein 11	208924 at	-0.178	13120	3.861E-02	FALSE
93499 at	0.303	988	1439455 x at	0.117	4347	93499 at	0.292	207	1439455 x at	0.156	5519	2765.25	2568.2895	TRUE	capping protein (actin filament) muscle Z-line, alpha 1	242125 at	0.197	3813	6.759E-05	TRUE
101138 at	0.057	4988	1450319 at	-0.095	3618	101138 at	-0.233	2070	1450319 at	0.495	386	2765.5	1984.2717	FALSE	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 2	207352 s at	-0.051	23276	3.112E-01	FALSE

93735 f at	-0.111	4695	1416282 at	0.164	1712	93735 f at	0.211	2143	1416282 at	0.145	2513	2765.75	1327.1642	FALSE	proteasome (prosome, macropain) 26S subunit, ATPase 3	201267 s at	-0.568	962	4.080E-07	FALSE
161215 at	0.181	2169	1427728 at	0.091	4624	95639 at	0.112	1508	1427728 at	-0.220	2762	2765.75	1340.5413	FALSE	cholinergic receptor, nicotinic, gamma polypeptide	221355 at	0.105	8492	4.336E-03	FALSE
101500 at	0.059	4916	1433492 at	-0.261	648.5	101500 at	0.051	5055	1459619 at	0.626	447	2766.625	2564.0844	FALSE	Erythrocyte protein band 4.1-like 2	201718 s at	-0.324	7582	2.449E-03	FALSE
101867 at	-0.180	1348	1425834 a at	-0.187	677	101867 at	-0.016	7634	1419499 at	-0.294	1412	2767.75	3261.1538	TRUE	glycerol-3-phosphate acyltransferase, mitochondrial	225424 at	0.259	13828	4.940E-02	FALSE
103533 at	0.123	2951	1437810 a at	0.226	1829.5	103533 at	0.105	3090	1450736 a at	-0.190	3206	2769.125	635.03128	FALSE	hemoglobin Z, beta-like embryonic chain	213515 x at	-0.117	23708	3.277E-01	FALSE
101701 at	-0.220	1430	1422052 at	-0.006	8370	101701 at	-0.297	126	1455365 at	-0.364	1151	2769.25	3775.6896	TRUE	cadherin 8	210518 at	-0.324	1360	1.013E-06	TRUE
98455 at	-0.033	7310	1426582 at	-0.332	367	98455 at	-0.221	2461	1437777 at	0.439	943	2770.25	3152.7458	FALSE	activating transcription factor 2	205446 s at	-0.132	9864	9.384E-03	FALSE
160291 at	-0.320	915	1434986 a at	-0.156	757	160291 at	-0.052	7334	1416190 a at	-0.174	2076	2770.5	3098.6516	TRUE	Sec61 alpha 1 subunit (S. cerevisiae)	217716 s at	0.304	1427	1.215E-06	FALSE
94823 at	-0.233	1343	1426660 x at	0.196	2485	94823 at	0.224	1234	1426660 x at	0.063	6020	2770.5	2238.999	FALSE	ribosomal protein L23a	208825 x at	-0.089	13091	3.826E-02	FALSE
100151 at	-0.156	3095	1456080 a at	-0.442	55.5	100151 at	-0.047	7160	1434548 at	0.763	774	2771.125	3200.5336	FALSE	serine incorporator 3	221471 at	-0.207	12167	2.765E-02	FALSE
92893 at	-0.105	2969	1421163 a at	0.094	3688	92893 at	0.104	4120	1438236 at	0.784	309	2771.5	1708.9311	FALSE	nuclear factor I/A	224970 at	0.620	46	3.628E-09	FALSE
99062 at	0.069	4078	1423331 a at	-0.110	4350.5	161415 r at	0.104	2524	1423331 a at	0.482	137	2772.375	1932.3584	FALSE	poliovirus receptor-related 3	227503 at	0.281	4969	2.602E-04	FALSE
103251 at	0.040	6770	1429186 a at	-0.115	2841	103251 at	0.269	435	1458339 at	-0.237	1056	2775.5	2851.6043	FALSE	cytidine and dCMP deaminase domain containing 1	221015 s at	0.137	7673	2.611E-03	FALSE
94078 at	-0.177	3152	1424364 a at	0.183	3064	94078 at	0.332	252	1424364 a at	0.148	4635	2775.75	1830.3713	FALSE	RIKEN cDNA 1110020P15 gene	228142 at	-0.346	1207	7.378E-07	FALSE
94435 at	-0.028	7859	1420646 at	-0.273	1673	94435 at	-0.266	1075	1434304 s at	-0.323	498	2776.25	3422.2888	TRUE	DNA segment, Chr 10, ERATO Doi 438, expressed		NA	NA	NA	NA
102349 at	-0.063	4520	1427449 a at	0.157	1505.5	102349 at	-0.144	1946	1427449 a at	0.175	3147	2779.625	1351.8129	FALSE	ADP-ribosylhydrolase like 2	223097 at	0.174	4953	2.545E-04	FALSE
95659 at	0.092	3232	1456730 x at	0.118	3353	95659 at	-0.091	3513	1456730 x at	-0.270	1021	2779.75	1178.1345	FALSE	actin-like 6A	202666 s at	0.295	3989	8.465E-05	FALSE
161114 i at	-0.113	2999	1453324 at	-0.046	5569	161114 i at	-0.185	2313	1453324 at	-0.387	245	2781.5	2196.2686	TRUE	RIKEN cDNA 6330509M23 gene		NA	NA	NA	NA
98007 at	-0.306	291	1417542 at	-0.237	891	98007 at	-0.012	7908	1417542 at	-0.225	2039	2782.25	3493.2739	TRUE	ribosomal protein S6 kinase, polypeptide 2	240732 at	-0.072	19418	1.818E-01	FALSE
160225 at	0.082	4400	1451135 at	0.171	1942.5	160225 at	0.188	1230	1451135 at	0.126	3557	2782.375	1452.8148	TRUE	general transcription factor IIB	208066 s at	-0.042	33540	6.838E-01	FALSE
97438 r at	0.086	4776	1429193 at	-0.165	1974	97437 f at	0.124	1995	1447312 at	-0.252	2392	2784.25	1341.6841	FALSE	ankyrin repeat and IBR domain containing 1	224687 at	0.328	5249	3.473E-04	FALSE
99590 at	-0.094	3562	1437510 x at	0.390	595	99590 at	0.119	3605	1438501 at	0.058	3378	2785	1463.3156	FALSE	ribosomal protein S17	216348 at	0.129	11486	2.092E-02	FALSE
97907 at	-0.234	1325	1417313 at	0.126	1563	97907 at	0.269	1752	1417313 at	-0.139	6500	2785	2482.8208	FALSE	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	204559 s at	-0.173	14642	6.395E-02	FALSE
95587 at	0.140	2357	1438153 x at	0.260	354	95587 at	0.054	4658	1433628 at	0.128	3771	2785	1877.3448	TRUE	coenzyme Q10 homolog A (yeast)	225747 at	0.006	41601	9.235E-01	FALSE
99933 at	0.127	2711	1424456 at	0.099	2676	99933 at	0.123	2603	1424456 at	0.196	3151	2785.25	247.94942	TRUE	poliovirus receptor-related 2		NA	NA	NA	NA
97271 at	-0.260	853	1428526 at	0.337	366	161860 f at	0.117	3796	1428526 at	0.077	6127	2785.5	2694.1461	FALSE	LSM domain containing 1	224512 s at	-0.276	6494	1.040E-03	FALSE
96226 at	-0.064	5317	1430559 at	0.138	2736.5	162046 at	0.141	1341	1451180 a at	0.232	1749	2785.875	1786.2256	FALSE	5'-nucleotidase, cytosolic III-like	225044 at	-0.426	1865	3.065E-06	FALSE
160316 at	0.097	5695	1434390 at	0.140	2716.5	160316 at	0.241	1118	1423050 s at	-0.227	1615	2786.125	2051.0628	FALSE	Heterogeneous nuclear ribonucleoprotein U	235603 at	-0.178	5151	3.176E-04	FALSE
98619 at	0.099	4150	1449116 a at	0.217	480	98619 at	0.167	594	1438096 a at	0.110	5922	2786.5	2696.7568	TRUE	deoxythymidylate kinase	203270 at	0.102	15717	8.431E-02	FALSE
103294 at	0.040	6723	1420941 at	-0.182	2926	103294 at	-0.231	1486	1420941 at	1.053	12	2786.75	2881.2406	FALSE	regulator of G-protein signaling 5	209070 s at	-0.341	11931	2.511E-02	FALSE
94483 at	0.112	2326	1419936 at	0.132	3280.5	94483 at	-0.125	2555	1453100 at	-0.180	2986	2786.875	427.97515	FALSE	casein kinase II, alpha 2, polypeptide	203575 at	-0.045	26648	4.298E-01	FALSE
103355 at	-0.217	1932	1440213 a at	-0.006	8349	103355 at	-0.534	29	1440213 a at	-0.266	847	2789.25	3787.5679	TRUE	RIKEN cDNA 2010001M06 gene		NA	NA	NA	NA
98766 at	-0.101	3393	1421923 at	0.061	6350.5	98766 at	-0.387	751	1444346 at	0.293	664	2789.625	2690.6112	FALSE	SH3-domain binding protein 5 (BTK-associated)	201811 x at	-0.334	7133	1.767E-03	FALSE
102039 at	-0.082	3964	1437163 x at	0.113	3578	102039 at	-0.174	881	1417093 a at	-0.193	2738	2790.25	1371.8849	FALSE	general transcription factor II H, polypeptide 4	203577 at	-0.148	9270	6.857E-03	FALSE
99035 at	0.166	2193	1438011 at	-0.112	3122.5	99035 at	-0.062	5592	1421957 a at	0.445	259	2791.625	2215.4096	FALSE	phosphate cytidylyltransferase 1, choline, alpha isoform	225069 at	0.333	397	6.077E-08	FALSE
98481 at	0.132	1776	1451759 at	0.096	2142	98481 at	0.106	3846	1420524 a at	0.142	3414	2794.5	992.05695	TRUE	mannan-binding lectin serine peptidase 2	207041 at	-0.020	30921	5.912E-01	FALSE
98942 r at	-0.197	3236	1429144 at	-0.176	3793	98942 r at	-0.305	3555	1429144 at	-0.288	603	2796.75	1480.1956	TRUE	preimplantation protein 4	230492 s at	-0.129	12380	3.007E-02	TRUE
161399 r at	0.164	1778	1418050 at	-0.095	3910	95566 at	0.187	689	1418050 at	-0.185	4814	2797.75	1896.4072	FALSE	glycosylphosphatidylinositol specific phospholipase D1	238752 at	-0.222	3529	4.808E-05	FALSE
97443 at	-0.147	3806	1460701 a at	0.434	33	97443 at	0.231	3242	1455366 at	-0.111	4115	2799	1879.0875	FALSE	mitochondrial ribosomal protein L52	221997 s at	0.076	19016	1.696E-01	FALSE
92908 at	-0.163	2485	1422742 at	-0.205	1460	92908 at	0.258	997	1422742 at	0.127	6255	2799.25	2386.2563	FALSE	human immunodeficiency virus type I enhancer binding protein 1	204512 at	0.107	14290	5.774E-02	FALSE
100959 at	-0.143	2082	1418704 at	0.205	835	161121 f at	0.268	763	1418704 at	0.058	7520	2800	3204.399	FALSE	S100 calcium binding protein A13	202598 at	0.265	11406	2.027E-02	FALSE
103052 r at	0.334	793	1416160 at	-0.140	3486	103052 r at	0.242	1944	1416160 at	0.316	4978	2800.25	1823.4642	FALSE	nuclear receptor subfamily 2, group F, member 2	209121 x at	0.323	4521	1.607E-04	FALSE
93868 at	-0.230	1405	1416222 at	-0.055	5596.5	98631 g at	-0.213	954	1451799 at	0.268	3250	2801.375	2111.6065	FALSE	NAD(P) dependent steroid dehydrogenase-like	209279 s at	-0.072	16733	1.069E-01	FALSE
101585 at	0.243	1620	1423451 at	0.131	5235	101585 at	0.232	1513	1423451 at	0.137	2841	2802.25	1730.092	TRUE	progesterone receptor membrane component 1	201120 s at	-0.593	5298	3.640E-04	FALSE
99102 at	0.161	3688	1450038 s at	-0.160	1285.5	99102 at	-0.140	2658	1428193 at	0.140	3582	2803.375	1112.639	FALSE	ubiquitin specific peptidase 9, X chromosome	229573 at	-0.152	6856	1.399E-03	FALSE
94481 at	0.104	4182	1434486 x at	-0.211	1585	94481 at	-0.073	3744	1451742 a at	-0.179	1708	2804.75	1350.2665	FALSE	UDP-glucose pyrophosphorylase 2	205480 s at	-0.690	527	1.141E-07	FALSE
99656 at	-0.143	2255	1437314 a at	-0.278	732.5	99656 at	-0.126	2411	1437314 a at	-0.077	5828	2806.625	2151.8605	TRUE	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	203701 s at	0.090	14922	6.936E-02	FALSE
102857 at	-0.135	2473	1419019 a at	0.149	815.5	102857 at	0.041	6008	1419019 a at	0.186	1937	2808.375	2242.0914	FALSE	A kinase (PRKA) anchor protein 4	207019 s at	-0.037	31535	6.142E-01	FALSE
94286 at	-0.143	4642	1426646 at	-0.079	4035.5	94286 at	-0.292	1701	1426647 at	-0.351	857	2808.875	1816.7883	TRUE	RIKEN cDNA 9130011J15 gene		NA	NA	NA	NA
94304 at	-0.184	965	1429246 a at	-0.129	3376	94304 at	-0.137	1324	1429247 at	0.098	5577	2810.5	2128.2908	FALSE	annexin A6	200982 s at	-0.438	1439	1.257E-06	FALSE
98575 at	-0.272	336	1423828 at	-0.280	557.5	98575 at	-0.025	7666	1423828 at	-0.162	2684	2810.875	3405.4388	TRUE	fatty acid synthase	212218 s at	-0.349	5587	4.757E-04	TRUE
94073 at	0.093	5158	1416270 at	0.166	1849.5	94073 at	0.173	2160	1416270 at	0.185	2079	2811.625	1569.768	TRUE	polymerase (RNA) II (DNA directed) polypeptide G	202306 at	0.210	10390	1.246E-02	TRUE
93130 at	0.157	931	1452118 at	0.097	3733	93130 at	-0.101	4617	1456117 at	-0.236	1966	2811.75	1669.3455	FALSE	RIKEN cDNA 2600005C20 gene	212846 at	-0.027	36956	7.896E-01	FALSE
102370 at	0.190	3269	1434642 at	0.174	654.5	102370 at	0.393	759	1443059 at	-0.050	6565	2811.875	2778.6971	FALSE	dehydrogenase/reductase (SDR family) member 8	217989 at	0.321	11513	2.113E-02	FALSE
161778 i at	0.162	3816	1460634 at	-0.228	432.5	100530 at	-0.125	2491	1460634 at	-0.113	4513	2813.125	1795.037	FALSE	ral guanine nucleotide dissociation stimulator	209050 s at	0.436	3043	2.418E-05	FALSE
160345 at	-0.129	2884	1438014 at	0.183	1027	160345 at	0.121	2456	1416349 at	0.119	4895	2815.5	1597.6008	FALSE	mitochondrial ribosomal protein L34	221692 s at	-0.282	3552	4.956E-05	FALSE
103397 at	-0.155	2942	1452237 at	-0.348	305.5	100954 at	-0.094	4516	1452237 at	-0.161	3502	2816.375	1796.2073	TRUE	HIV-1 Rev binding protein	218092 s at	0.142	15428	7.845E-02	FALSE
103972 at	0.247	788	1418614 at	0.096	4725.5	103973 at	0.089	3303	1418614 at	-0.201	2453	2817.375	1645.9956	FALSE	potassium inwardly-rectifying channel, subfamily J, member 1	210402 at	-0.120	11298	1.945E-02	FALSE
95705 s at	0.219	4248	1436722 a at	-0.067	6626	AFFX-b-ActinMur	-0.275	102	1440365 at	0.680	300	2819	3176.0951	FALSE	actin, beta, cytoplasmic	213867 x at	-0.108	15401	7.793E-02	FALSE
160286 at	-0.102	4396	1452659 at	-0.123	5450	160286 at	-0.286	1098	1452659 at	-0.327	333	2819.25	2486.7064	TRUE	DEK oncogene (DNA binding)	200934 at	0.299	8607	4.655E-03	FALSE
101790 f at	0.117	2457	1422408 at	0.131	5532	101789 i at	0.171	1633	1422408 at	0.195	1656	2819.5	1848.4748	TRUE	interferon alpha family, gene 4	208344 x at	-0.062	23429	3.179E-01	FALSE
102090 f at	-0.084	4272	1451722 s at	0.078	4172.5	93916 at	-0.406	88	1447749 at	-0.236	2746	2819.625	1949.9453	FALSE	SET and MYND domain containing 5	209516 at	-0.126	8670	4.817E-03	FALSE
94218 at	0.193	918	1448122 at	0.041	6654	162443 at	0.085	3048	1442317 at	0.405	668	2822	2768.8886	TRUE	t-complex protein 1	222010 at	-0.197	8782	5.121E-03	FALSE
92265 f at	0.103	2982	1423433 at	-0.050	6423	92265 f at	0.202	1576	1436533 at	0.843	308	2822.25	2637.2658	FALSE	TROVE domain family, member 2	212852 s at	0.630	109	9.215E-09	FALSE
94925 at	-0.228	456	1423625 a at	0.155	4089.5	94925 at	0.148	3216	1423625 a at	-0.116	3530	2822.875	1618.7453	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 19		NA	NA	NA	NA
103311 at	0.141	1703	1425391 a at	0.063	5955	103311 at	0.209	375	1425391 a at	0.201	3259	2823	2397.6811	TRUE	oxysterol binding protein-like 5	223464 at	0.085	13396	4.247E-02	TRUE
161694 f at	-0.112	2816	1436448 a at	0.029	7222.5	161694 f at	0.242	630	1423414 at	0.254	624	2823.125	3109.1531	FALSE	prostaglandin-endoperoxide synthase 1	205128 x at	0.083	18531	1.561E-01	FALSE
95686 at	-0.075	4561	1419244 a at	-0.250	2123.5	104442 at	-0.282	770	1415686 at	-0.153	3851	2826.375	1710.8956	TRUE	RAB14, member RAS oncogene family	211503 s at	0.193	10320	1.212E-02	FALSE
99014 at	-0.222	959	1423892 at	-0.079	5141	99014 at	-0.151	1934	1423892 at	0.159	3273	2826.75	1811.1124	FALSE	amyloid beta (A4) precursor protein-binding, family B, member 1	202652 at	-0.011	40318	8.869E-01	FALSE
97130 at	0.327	142	1420652 at	-0.065	6408	97130 at	-0.343	357	1420036 at	0.206	4404	2827.75	3088.7221	FALSE	arginine-tRNA-protein transferase 1	225497 at	-0.187	10513	1.334E-02	FALSE
101984 at	-0.073	4563	1460639 a at	0.224	1505.5	101984 at	0.179	587	1460640 at	0.094	4656	2827.875	2091.4824	FALSE	ATX1 (antioxidant protein 1) homolog 1 (yeast)	203454 s at	0.111	16463	1.009E-01	FALSE
99164 at	-0.139	3942	1435729 at	0.159	1712	99164 at	0.178	2149	1435729 at	0.165	3515	2829.5	1067.6224	FALSE	mitogen activated protein binding protein interacting protein	218291 at	0.011	39773	8.717E-01	FALSE
100014 at	-0.135	3060	1431827 a at	-0.143	1285.5	100014 at	0.096	4798	1457357 at	0.454	2175	2829.625	1498.9361	FALSE	tousled-like kinase 2 (Arabidopsis)	228627 at	0.049	19357	1.797E-01	FALSE
104303 i at	0.036	6470	1439266 a at	0.328	557.5	104303 i at	0.098	3460	1422753 a at	0.328	836	2830.875	2756.011	TRUE	polymerase (RNA) III (DNA directed) polypeptide K	218866 s at	-0.283	2449	8.765E-06	FALSE
161597 r at	0.121	3528	1423219 a at	0.132	2797.5	161597 r at	0.135	1539	1423218 a at	0.161	3462	2831.625	922.74133	TRUE	mitochondrial ribosomal protein L49	201717 at	-0.052	22604	2.882E-01	FALSE
101914 at	-0.277	925	1431606 a at	-0.150	1199	101914 at	0.070	6841	1448360 s at	-0.214	2362	2831.75	2744.4683	FALSE	angel homolog 2 (Drosophila)	221825 at	-0.292	4882	2.397E-04	FALSE
160988 r at	0.129	2325	1433640 at	0.150	4045	94395 at	0.220	4283	1437544 at	0.575	675	2832	1681.9104	TRUE	far upstream element (FUSE) binding protein 1	240307 at	0.352	3561	4.992E-05	TRUE
102635 at	0.116	2295	1419190 at	-0.241	857	102635 at	-0.081	4845	1446365 at	0.190	3333	2832.5	1682.4747	FALSE	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	233323 at	0.130	5715	5.325E-04	FALSE
93163 at	0.293	1832	1418177 at	-0.019	7905	93163 at	-0.328	593	1418177 at	0.298	1003	2833.25	3420.2185	FALSE	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 2	206849 at	-0.885	763	2.403E-07	FALSE
103955 at	0.083	3128	1416795 at	0.125	1933	161779 r at	0.179	2000	1430681 at	0.126	4272	2833.25	1104.7827	TRUE	crystallin, lamda 1	220753 s at	0.229	7657	2.577E-03	TRUE
100381 at	-0.492	85	1427735 a at	-0.110	4078	100381 at	-0.290	261	1427735 a at	0.095	6910	2833.5	3283.222	FALSE	actin, alpha 1, skeletal muscle	203872 at	-0.119	8342	4.044E-03	FALSE
101001 at	0.355	802	1423824 at	-0.123	3862	101001 at	0.283	2071	1423825 at	0.154	4609	2836	1724.1989	FALSE	G protein-coupled receptor 177	221958 s at	0.643	2223	5.707E-06	FALSE
94116 at	0.174	1459	1422265 at	0.139	2110	94116 at	0.124	2548	1422265 at	0.079	5231	2837	1657.5253	TRUE	bombesin-like receptor 3		NA	NA	NA	NA
96887 at	-0.113	5003	1416056 a at	0.266	986.5	96887 at	0.183	1745	1455911 x at	0.134	3615	2837.375	1817.8425	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	218320 s at	-0.168	9517	7.803E-03	FALSE
102395 at	-0.042	6109	1417133 at	-0.237	1244	102395 at	-0.325	1071	1417133 at	-0.225	2927	2837.75	2335.9856	TRUE	peripheral myelin protein	243050 at	0.300	1204	7.267E-07	FALSE
162460 f at	-0.266	457	1460737 at	-0.097	5701	162460 f at	-0.163	2471	1449700 at	0.152	2726	2838.75	2161.262	FALSE	immunoglobulin (CD79A) binding protein 1	202105 at	-0.097	13611	4.559E-02	FALSE
161101 r at	0.195	1886	1425660 at	-0.355	707	95393 at	-0.381	2280	1425660 at	0.198	6485	2839.5	2520.5442	FALSE	BTB (POZ) domain containing 3	243462 s at	0.475	1373	1.055E-06	FALSE
161277 r at	0.068	4262	1450454 at	0.102	4911	161277 r at	0.170	1530	1428660 s at	-0.431	657	2840	2065.0031	FALSE	torsin family 3, member A	233851 s at	0.084	15902	8.863E-02	FALSE
96640 at	0.142	1485	1416893 at	0.066	6136	96640 at	0.213	406	1416892 s at	-0.198	3342	2842.25	2508.3847	FALSE	RIKEN cDNA 3110001A13 gene	223059 s at	0.838	409	6.575E-08	FALSE
98596 s at	-0.187	974	1460241 a at	-0.322	1008.5	98596 s at	-0.002	8444	1460241 a at	0.379	944	2842.625	3734.343	FALSE	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	203217 s at	-0.292	5254	3.491E-04	FALSE
94868 at	0.141	2066	1453237 at	0.130	2642.5	94868 at	0.121	4495	1453237 at	-0.209	2169	2843.125	1129.4998	FALSE	glutaminyl-tRNA synthetase	217846 at	0.182	11020	1.735E-02	FALSE
101558 s at	-0.210	3518	1415676 a at	0.164	1834	101558 s at	-0.149	3492	1415676 a at	0.152	2529	2843.25	815.16926	FALSE	proteasome (prosome, macropain) subunit, beta type 5	208799 at	-0.175	11652	2.237E-02	FALSE
100538 at	0.017	7962	1435304 at	0.157	1237	100538 at	0.443	1695	1440222 at	0.775	482	2844	3448.4595	TRUE	superoxide dismutase 1, soluble	200642 at	-0.114	20509	2.168E-01	FALSE
93318 at	0.178	1805	1448417 at	0.069	4771	93318 at	0.079	3397	1448417 at	0.264	1405	2844.5	1545.8955	TRUE	ninjurin 1	203045 at	0.278	2039	4.128E-06	TRUE
162380 r at	-0.121	1589	1452633 s at	0.104	2527	104176 at	0.177	1667	1420025 s at	0.115	5595	2844.5	1882.2719	FALSE	hypothetical protein LOC637741		NA	NA	NA	NA
99940 at	0.189	1772	1416324 s at	0.207	966	99940 at	0.096	4608	1416324 s at	0.129	4033	2844.75	1751.3312	TRUE	RIKEN cDNA 2410004N11 gene	228299 at	0.311	435	7.867E-08	TRUE
101505 at	-0.046	6217	1452140 at	-0.209	1519.5	101505 at	-0.082	2848	1426644 at	-0.322	797	2845.375	2402.8904	TRUE	TBC1 domain family, member 20	226409 at	0.090	19794	1.943E-01	FALSE
99052 at	-0.081	5327	1418926 at	-0.081	4285.5	99052 at	-0.201	968	1418926 at	-0.235	804	2846.125	2303.922	TRUE	zinc finger homeobox 1a	212758 s at	0.237	10672	1.460E-02	FALSE
92205 at	0.091	3984	1443969 at	-0.137	2168.5	92205 at	-0.129	3009	1443969 at	0.320	2225	2846.625	849.75657	FALSE	insulin receptor substrate 2	209184 s at	0.282	8245	3.803E-03	FALSE
98806 s at	0.165	1237	1420925 at	-0.132	2546.5	98805 at	-0.169	2426	1420925 at	0.098	5180	2847.375	1663.5835	FALSE	tubby candidate gene	210737 at	-0.031	32408	6.447E-01	FALSE
99183 at	-0.221	3858	1450368 a at	-0.408	41.5	99183 at	-0.252	162	1433591 at	-0.071	7332	2848.375	3474.5452	TRUE	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	204507 s at	-0.931	349	4.861E-08	TRUE
94982 f at	-0.527	199	1448905 at	0.155	2087.5	94981 i at	0.122	3118	1448905 at	0.095	5995	2849.875	2420.1967	FALSE	expressed in non-metastatic cells 3	204862 s at	0.178	7662	2.579E-03	FALSE
93393 at	0.234	1025	1419597 at	0.118	3298.5	93393 at	-0.103	2619	1449524 at	0.119	4457	2849.875	1433.8279	FALSE	ectodysplasin-A	211127 x at	0.113	15188	7.431E-02	FALSE
99493 at	-0.090	5548	1423990 at	0.231	801	99493 at	0.178	690	1453406 a at	0.144	4362	2850.25	2478.5311	FALSE	RAB28, member RAS oncogene family	227003 at	0.373	1760	2.462E-06	FALSE
93742 at	0.079	3635	1449933 a at	0.341	57.5	93742 at	-0.030	6952	1449933 a at	0.280	766	2852.625	3140.2608	FALSE	RIKEN cDNA 5730449L18 gene	225400 at	-0.059	22417	2.824E-01	FALSE
160812 at	-0.061	5202	1428141 at	-0.119	2204	160812 at	-0.076	3142	1428141 at	-0.315	863	2852.75	1824.1548	TRUE	golgi associated, gamma adaptin ear containing, ARF binding protein 2	208914 at	-0.141	6884	1.447E-03	TRUE
93006 at	-0.191	911	1435527 at	-0.265	435.5	93006 at	0.021	7209	1429148 at	-0.182	2856	2852.875	3087.0922	FALSE	nuclear factor I/C	226895 at	0.504	75	5.244E-09	FALSE
103814 at	0.067	4341	1420460 a at	0.123	1505.5	103814 at	-0.105	2303	1420460 a at	0.216	3263	2853.125	1224.8129	FALSE	peroxisomal biogenesis factor 11b	202658 at	-0.413	4587	1.702E-04	FALSE
103015 at	-0.157	1309	1450381 a at	0.125	3890	103015 at	-0.089	5444	1450381 a at	0.314	773	2854	2198.4072	FALSE	B-cell leukemia/lymphoma 6	203140 at	0.908	3108	2.631E-05	FALSE
92461 at	-0.427	211	1448598 at	-0.114	3932	92461 at	-0.455	119	1448598 at	-0.117	7157	2854.75	3373.6017	TRUE	matrix metallopeptidase 17	206234 s at	-0.218	4291	1.199E-04	TRUE
103991 at	0.114	2691	1450636 s at	0.101	4008	102132 i at	-0.135	1892	1450636 s at	-0.155	2844	2858.75	872.49427	FALSE	alkaline phosphatase 5	211619 s at	-0.016	37154	7.954E-01	FALSE
102225 at	0.067	5088	1421488 at	-0.146	1167	102225 at	-0.087	4981	1429197 s at	-0.572	206	2860.5	2541.167	FALSE	RAB GTPase activating protein 1-like	203020 at	-0.388	5923	6.477E-04	FALSE
161472 r at	0.226	1728	1423075 at	-0.095	3504	93993 at	-0.261	545	1423074 at	-0.079	5668	2861.25	2231.6095	FALSE	lectin, mannose-binding 2	200805 at	0.046	24221	3.447E-01	FALSE
102941 at	-0.115	2640	1448009 at	-0.084	4490.5	102941 at	-0.200	1657	1432318 at	0.178	2658	2861.375	1182.5024	FALSE	UDP-glucose ceramide glucosyltransferase-like 1	222569 at	0.030	32089	6.346E-01	FALSE
103532 at	-0.051	5886	1426001 at	0.150	1285.5	103532 at	0.125	2087	1435172 at	-0.352	2195	2863.375	2055.5157	FALSE	eomesodermin homolog (Xenopus laevis)	231776 at	0.052	18787	1.633E-01	FALSE
160806 at	0.093	5655	1419550 a at	-0.166	1974	160806 at	-0.252	869	1419550 a at	0.143	2960	2864.5	2047.0321	FALSE	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	202786 at	-0.019	39554	8.657E-01	FALSE
92838 at	-0.197	761	1416516 at	-0.445	1527.5	92838 at	-0.038	5957	1457739 at	0.244	3213	2864.625	2301.9767	FALSE	fascin homolog 1, actin bundling protein (Strongylocentrotus) purpuratus)	210933 s at	-0.204	13464	4.346E-02	FALSE
102348 at	-0.258	2422	1424607 a at	-0.091	4420	102348 at	0.396	1528	1424609 a at	0.247	3089	2864.75	1218.198	FALSE	similar to hypothetical protein MGC37588		NA	NA	NA	NA
101847 at	0.085	3245	1451821 a at	0.109	3060	101848 g at	0.126	2301	1451821 a at	-0.231	2853	2864.75	408.51958	FALSE	nuclear antigen Sp100		NA	NA	NA	NA
93697 at	0.234	2052	1419583 at	0.023	7868	93697 at	0.491	1177	1419583 at	0.342	365	2865.5	3405.4036	TRUE	chromobox homolog 4 (Drosophila Pc class)	206724 at	-0.120	15993	9.071E-02	FALSE
98952 at	-0.096	4219	1424053 a at	-0.184	4172.5	98951 at	-0.195	2892	1437204 a at	0.761	179	2865.625	1893.6909	FALSE	transcription factor 25 (basic helix-loop-helix)	221495 s at	-0.285	4607	1.737E-04	FALSE
97353 at	-0.212	851	1433558 at	-0.154	1377	97353 at	-0.010	8129	1433558 at	-0.277	1107	2866	3515.2333	TRUE	disabled homolog 2 (Drosophila) interacting protein	225020 at	-0.421	354	4.953E-08	TRUE
96677 at	-0.200	1221	1460687 at	-0.161	1581.5	96677 at	0.062	4257	1441557 at	0.121	4405	2866.125	1698.9572	FALSE	SET domain containing (lysine methyltransferase) 8	225118 at	0.097	8814	5.234E-03	FALSE
99851 at	0.185	1394	1419575 s at	0.161	2123.5	99851 at	-0.041	5841	1457842 at	-0.165	2113	2867.875	2011.2774	FALSE	zinc finger protein 292	236435 at	0.160	4286	1.190E-04	FALSE
160575 at	0.160	2526	1454641 at	0.126	2880.5	160575 at	0.204	2504	1455658 at	0.157	3564	2868.625	494.64825	TRUE	CGG triplet repeat binding protein 1	224600 at	-0.182	10912	1.645E-02	FALSE
95483 at	-0.096	5400	1429291 at	0.089	3231	95483 at	0.230	1376	1429291 at	0.265	1471	2869.5	1890.3665	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	201199 s at	-0.197	7414	2.160E-03	FALSE
95448 at	-0.132	4119	1435859 x at	0.240	533	95448 at	0.104	5502	1435859 x at	0.243	1336	2872.5	2331.1031	FALSE	proteasome (prosome, macropain) 26S subunit, ATPase 2	201068 s at	-0.202	13773	4.810E-02	FALSE
160671 at	-0.071	4230	1448456 at	-0.187	619.5	160671 at	-0.099	3268	1455745 at	0.183	3374	2872.875	1562.7686	FALSE	ceroid-lipofuscinosis, neuronal 8	219341 at	0.236	10774	1.537E-02	FALSE

97828 at	-0.138	1384	1418377 a at	0.047	6267.5	97828 at	0.135	1514	1426323 x at	-0.156	2326	2872.875	2301.1476	FALSE	Cd27 binding protein (Hindu God of destruction)	210792 x at	0.147	11897	2.479E-02	FALSE
104261 at	0.154	1152	1435077 at	-0.076	4797	104261 at	-0.146	1348	1435077 at	0.098	4195	2873	1891.818	FALSE	additional sex combs like 1 (Drosophila)	212234 at	0.283	1051	5.230E-07	FALSE
94930 at	0.076	4157	1450663 at	0.078	4581.5	94930 at	0.130	1956	1447862 x at	0.255	803	2874.375	1797.5362	TRUE	thrombospondin 2	203083 at	0.311	13144	3.898E-02	TRUE
160134 at	0.138	3000	1451311 a at	-0.082	4126	160134 at	0.077	3070	1424312 at	-0.226	1305	2875.25	1166.6977	FALSE	adiponectin receptor 1	217748 at	-0.210	3382	3.886E-05	FALSE
99136 at	-0.053	5598	1438621 x at	0.298	339	99136 at	0.086	4113	1423586 at	-0.290	1455	2876.25	2407.9772	FALSE	AXL receptor tyrosine kinase	202686 s at	0.322	5763	5.661E-04	FALSE
102910 at	0.259	445	1419758 at	-0.119	2893.5	102910 at	-0.016	7288	1419758 at	-0.386	879	2876.375	3128.5683	FALSE	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	243951 at	0.085	13045	3.751E-02	FALSE
97363 at	-0.164	1036	1423059 at	-0.089	4921	97363 at	0.100	4573	1440082 at	0.531	976	2876.5	2164.6734	FALSE	PTK2 protein tyrosine kinase 2	241387 at	0.404	3790	6.606E-05	FALSE
93670 at	-0.592	106	1422114 at	0.064	5269.5	93670 at	-0.100	4369	1435561 at	-0.272	1764	2877.125	2371.1692	FALSE	Ets2 repressor factor	203643 at	0.011	39402	8.615E-01	FALSE
98436 s at	-0.117	2748	1449839 at	0.122	2332	98437 at	0.032	6153	1449839 at	0.394	286	2879.75	2433.0429	FALSE	caspase 3	202763 at	0.114	8231	3.773E-03	FALSE
102667 at	0.147	2371	1422093 at	0.058	5544.5	102667 at	0.164	1151	1446764 at	0.241	2455	2880.375	1873.3843	TRUE	wingless-related MMTV integration site 3A	NA	NA	NA	NA	
93529 at	0.287	1522	1419041 at	-0.132	3054	93529 at	-0.341	267	1419041 at	-0.054	6682	2881.25	2778.3332	FALSE	integrin alpha FG-GAP repeat containing 1	221449 s at	-0.960	1476	1.335E-06	FALSE
160990 r at	0.069	5784	1424243 at	-0.279	1632	160990 r at	-0.171	2228	1424244 at	0.220	1884	2882	1950.0277	FALSE	RWD domain containing 4A	225574 at	0.145	15682	8.368E-02	FALSE
93098 at	-0.077	4365	1434231 x at	0.228	1085.5	93098 at	0.209	448	1436840 x at	0.098	5630	2882.125	2510.1501	FALSE	ribosomal protein L35	200002 at	-0.027	36330	7.725E-01	FALSE
92896 s at	0.098	4609	1419438 at	0.208	1261.5	92896 s at	0.097	3007	1419437 at	0.165	2652	2882.375	1375.63	TRUE	single-minded homolog 2 (Drosophila)	206558 at	0.014	39460	8.631E-01	FALSE
92299 at	0.185	1327	1452360 a at	-0.113	5041.5	92299 at	0.133	5076	1441318 at	-0.401	87	2882.875	2563.0141	FALSE	jumonji, AT rich interactive domain 1A (Rbp2 like)	202040 s at	0.409	3372	3.818E-05	FALSE
97706 at	0.266	648	1437226 x at	0.199	2371.5	97706 at	0.059	5674	1435415 x at	0.243	2838	2882.875	2085.5505	TRUE	MARCKS-like 1	200644 at	0.135	20297	2.098E-01	FALSE
161323 f at	0.131	1548	1452829 at	0.050	5897	161323 f at	-0.144	2374	1452830 s at	0.220	1715	2883.5	2040.4023	FALSE	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	202715 at	0.118	11300	1.948E-02	FALSE
162142 f at	0.089	2920	1432763 at	0.194	1049	162142 f at	0.152	2054	1432763 at	0.079	5512	2883.75	1911.7012	TRUE	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	205617 at	-0.018	38118	8.255E-01	FALSE
97106 at	0.150	1971	1419208 at	0.127	2474	97106 at	-0.070	5032	1419208 at	-0.165	2060	2884.25	1448.5106	FALSE	mitogen activated protein kinase kinase kinase 8	235421 at	0.403	6590	1.122E-03	FALSE
103217 at	-0.055	5960	1449317 at	0.111	2295.5	103217 at	-0.103	2430	1425686 at	0.374	854	2884.875	2170.6467	FALSE	CASP8 and FADD-like apoptosis regulator	239629 at	0.712	395	6.019E-08	FALSE
101163 at	0.076	4498	1418065 at	0.202	1381.5	101163 at	0.129	3542.5	1418065 at	-0.224	2119	2885.25	1400.1599	FALSE	recombination activating gene 2	215117 at	-0.019	27836	4.746E-01	FALSE
96588 at	0.157	1104	1425251 at	0.103	3526	96588 at	0.090	2665	1440369 at	-0.129	4248	2885.75	1352.6528	FALSE	prostaglandin E receptor 3 (subtype EP3)	210834 s at	0.048	24265	3.460E-01	FALSE
97733 at	0.128	1999	1434772 at	0.096	2347	99864 at	0.067	4580	1434430 s at	0.167	2619	2886.25	1157.3266	TRUE	adenosine A2b receptor	205891 at	-0.104	18810	1.640E-01	FALSE
161051 at	-0.193	2029	1456010 x at	-0.093	3402	161051 at	-0.251	1430	1456010 x at	0.201	4688	2887.25	1456.919	FALSE	hairy and enhancer of split 5 (Drosophila)	239230 at	-0.129	15616	8.240E-02	FALSE
161718 at	0.224	577	1425693 at	-0.037	7260.5	161718 at	-0.115	2628	1456505 at	0.428	1084	2887.375	3043.1065	FALSE	Braf transforming gene	NA	NA	NA	NA	
104647 at	-0.218	446	1417263 at	0.154	2950	104647 at	0.093	5026	1417262 at	0.431	3131	2888.25	1879.4769	FALSE	prostaglandin-endoperoxide synthase 2	204748 at	0.040	25822	3.976E-01	FALSE
93320 at	0.155	1786	1460409 at	-0.198	714.5	93320 at	-0.024	7163	1460409 at	-0.244	1890	2888.375	2898.8581	FALSE	carnitine palmitoyltransferase 1a, liver	203633 at	0.227	8282	3.887E-03	FALSE
97825 at	0.178	1912	1416271 at	0.034	7295.5	97825 at	0.206	1749	1416271 at	-0.469	599	2888.875	2995.3003	FALSE	PERP, TP53 apoptosis effector	222392 x at	0.146	18035	1.418E-01	FALSE
93520 at	0.160	1156	1450045 at	0.061	4872	93521 at	0.072	5180	1459828 at	0.349	350	2889.5	2492.0393	TRUE	serine/arginine repetitive matrix 1	201224 s at	0.127	9447	7.538E-03	TRUE
160220 at	0.265	245	1437237 x at	0.163	1736	160220 at	0.086	4544	1450998 at	-0.135	5035	2890	2285.0589	FALSE	zinc finger protein 110	232436 at	0.160	4608	1.737E-04	FALSE
103434 at	0.077	4505	1418758 a at	-0.111	3097	103434 at	-0.168	1658	1431707 a at	0.232	2302	2890.5	1226.7356	FALSE	pleckstrin homology, Sec7 and coiled-coil domains 3	243752 s at	-0.139	9917	9.666E-03	FALSE
103435 at	0.143	1316	1434184 s at	-0.185	1095	103435 at	0.058	5490	1445739 at	-0.140	3662	2890.75	2086.1034	FALSE	RIKEN cDNA 9430080K19 gene	NA	NA	NA	NA	
162459 f at	-0.692	28	1448590 at	-0.116	4949.5	162459 f at	-0.187	3993	1448590 at	-0.450	2595	2891.375	2139.7983	TRUE	procollagen, type VI, alpha 1	213428 s at	0.361	3360	3.749E-05	FALSE
97182 at	0.138	1716	1422535 at	0.092	3883.5	97182 at	0.122	2309	1422535 at	-0.286	3657	2891.375	1047.4032	FALSE	cyclin E2	211814 s at	-0.100	20835	2.278E-01	FALSE
103779 at	-0.180	1113	1434900 at	-0.104	3650	103779 at	-0.074	3735	1434900 at	-0.253	3073	2892.75	1222.4037	TRUE	MKL (megakaryoblastic leukemia)/myocardin-like 1	241207 at	-0.040	28012	4.812E-01	FALSE
97781 at	0.082	4077	1422089 at	0.126	2478	97781 at	0.126	1592	1422089 at	0.154	3425	2893	1087.7662	TRUE	natural cytotoxicity triggering receptor 1	217095 x at	-0.017	38620	8.398E-01	FALSE
103472 at	0.223	413	1447604 at	0.031	7132	103472 at	0.128	2067	1447604 at	0.174	1961	2893.25	2925.202	TRUE	cDNA sequence BC053393	NA	NA	NA	NA	
98967 at	0.384	756	1450779 at	0.514	875.5	98967 at	0.334	2203	1450779 at	-0.068	7744	2894.625	3298.7556	FALSE	fatty acid binding protein 7, brain	205030 at	0.145	26343	4.178E-01	FALSE
97647 at	-0.288	1183	1416404 s at	0.087	5827	97647 at	0.135	2022	1455835 at	-0.137	2547	2894.75	2033.9453	FALSE	ribosomal protein S16	226130 at	0.086	15088	7.249E-02	FALSE
99863 at	-0.161	1204	1433467 at	0.111	2835.5	99863 at	0.123	2433	1433467 at	0.086	5107	2894.875	1629.868	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	203580 s at	-0.035	30204	5.640E-01	FALSE
104206 at	-0.168	2143	1453287 at	0.119	3646	104206 at	-0.060	5561	1453287 at	0.899	231	2895.25	2260.8226	FALSE	RIKEN cDNA 5730557B15 gene	NA	NA	NA	NA	
160306 at	-0.263	183	1424737 at	0.029	7338	160306 at	-0.339	742	1424737 at	-0.289	3324	2896.75	3261.6269	FALSE	thyroid hormone responsive SPOT14 homolog (Rattus)	229476 s at	-0.029	32435	6.453E-01	FALSE
162243 f at	-0.153	951	1425601 a at	-0.112	3904.5	162243 f at	0.046	5323	1425601 a at	-0.240	1411	2897.375	2073.294	FALSE	rhotekin	239653 at	0.348	2812	1.631E-05	FALSE
96242 at	-0.125	2263	1415753 at	-0.304	139	96242 at	-0.059	4461	1415753 at	-0.121	4730	2898.25	2145.8874	TRUE	DNA segment, Chr 10, Brigham & Women's Genetics 1364 expressed	NA	NA	NA	NA	
99056 at	0.256	296	1418713 at	0.198	855.5	99056 at	0.107	2904	1418713 at	-0.123	7539	2898.625	3290.4471	FALSE	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alph	203557 s at	0.098	12575	3.228E-02	FALSE
96256 at	0.108	3747	1416292 at	0.242	1684.5	96256 at	0.096	3832	1416292 at	0.153	2336	2899.875	1061.6919	TRUE	peroxiredoxin 3	201619 at	-0.231	10101	1.060E-02	FALSE
160711 at	0.141	3120	1419367 at	0.152	1982	160711 at	-0.059	4690	1419367 at	-0.179	1808	2900	1327.6154	FALSE	2,4-dienoyl CoA reductase 1, mitochondrial	236432 at	-0.042	23309	3.124E-01	FALSE
100486 at	-0.196	1449	1418290 a at	-0.105	2522	100486 at	-0.137	4403	1429629 at	0.174	3232	2901.5	1240.6328	FALSE	enhancer of zeste homolog 1 (Drosophila)	32259 at	0.180	2398	8.156E-06	FALSE
96736 at	0.095	4233	1425673 at	0.111	3004	96736 at	0.098	2711	1437235 x at	0.262	1662	2902.5	1057.6775	TRUE	LIM domain containing preferred translocation partner in lipoma	202822 at	0.434	798	2.740E-07	TRUE
103359 at	0.095	3143	1451141 at	0.257	399	160625 f at	0.067	3872	1442636 at	-0.139	4196	2902.5	1726.1156	FALSE	methyltransferase like 8	220007 at	-0.053	22377	2.809E-01	FALSE
97713 at	0.235	1060	1452705 at	0.405	2116.5	160163 at	0.136	1172	1419327 at	0.063	7263	2902.875	2945.1198	TRUE	RIKEN cDNA 2210010A19 gene	212053 at	-0.109	10715	1.483E-02	FALSE
101044 at	0.118	2123	1424877 a at	0.284	3588	101044 at	-0.177	1054	1424877 a at	0.177	4854	2904.75	1663.612	FALSE	aminolevulinate, delta-, dehydratase	218487 at	0.230	6541	1.083E-03	FALSE
96730 at	-0.042	6978	1430575 a at	-0.234	896	161537 f at	0.141	2106	1421894 a at	0.192	1639	2904.75	2760.8312	FALSE	tripeptidyl peptidase II	203374 s at	-0.066	22010	2.686E-01	FALSE
94340 at	0.218	1035	1428772 at	0.087	6027.5	94340 at	0.176	3371	1441682 s at	0.227	1190	2905.875	2338.467	TRUE	exportin, tRNA (nuclear export receptor for tRNAs)	212160 at	0.177	16651	1.048E-01	FALSE
160680 at	0.044	5956	1417960 at	-0.220	1894.5	160680 at	0.085	3473	1417960 at	0.369	301	2906.125	2410.6117	FALSE	cytoplasmic polyadenylation element binding protein 1	222903 s at	-0.060	27023	4.436E-01	FALSE
161681 i at	0.160	2129	1448522 at	0.072	5096	161681 i at	0.146	2707	1448522 at	-0.236	1698	2907.5	1516.4306	FALSE	seryl-aminoacyl-tRNA synthetase 2	218702 at	-0.075	15267	7.586E-02	FALSE
102776 at	-0.189	1514	1428592 s at	0.104	3119	160605 s at	-0.272	208	1428592 s at	0.047	6791	2908	2849.295	FALSE	ubiquitin specific peptidase 38	223288 at	0.110	24995	3.722E-01	FALSE
161371 r at	-0.100	3162	1431680 a at	0.094	3282	161371 r at	-0.049	5110	1443491 at	0.727	82	2909	2084.8236	FALSE	protein tyrosine phosphatase, receptor type, K	203038 at	0.592	2068	4.358E-06	FALSE
98330 at	0.215	838	1423424 at	0.182	2315.5	98330 at	0.128	2834	1438737 at	-0.183	5652	2909.875	2014.1958	FALSE	zinc finger protein of the cerebellum 3	207197 at	-0.048	29406	5.357E-01	FALSE
98475 at	-0.302	198	1455978 a at	-0.052	6036	161776 at	0.179	1381	1445580 at	0.110	4026	2910.25	2627.4269	FALSE	matrilin 2	202350 s at	0.619	6868	1.415E-03	FALSE
97972 at	-0.152	1884	1448434 at	-0.128	4935	97972 at	-0.180	4458	1442414 at	-0.461	374	2912.75	2158.7705	TRUE	ring finger protein 103	202636 at	-0.063	24015	3.387E-01	FALSE
92974 at	0.165	1004	1449391 at	0.163	1106.5	161605 f at	0.267	1461	1449391 at	0.018	8080	2912.875	3450.3099	TRUE	zinc finger protein 37	207068 at	0.013	36582	7.801E-01	FALSE
102838 at	0.192	2520	1419480 at	0.160	2084	102838 at	0.062	4582	1419481 at	-0.178	2467	2913.25	1129.3312	FALSE	selectin, lymphocyte	204563 at	0.217	8939	5.589E-03	FALSE
103734 at	0.206	2239	1455177 at	0.125	5375	103734 at	0.199	3194	1439083 at	0.523	856	2916	1899.6398	TRUE	Abelson helper integration site	244699 at	0.104	20273	2.090E-01	FALSE
95530 at	0.464	593	1433511 at	0.159	1955	95530 at	0.210	1880	1454631 at	-0.040	7236	2916	2947.0633	FALSE	RIKEN cDNA 6330549H03 gene	NA	NA	NA	NA	
161900 f at	-0.136	2067	1455918 at	0.117	2909	92536 at	0.141	1527	1455918 at	0.092	5162	2916.25	1601.5291	FALSE	adrenergic receptor, beta 3	206812 at	-0.028	32795	6.576E-01	FALSE
100049 at	-0.123	2376	1416184 s at	-0.088	3896	100049 at	0.087	3064	1416184 s at	-0.172	2332	2917	733.70203	FALSE	high mobility group AT-hook 1	206074 s at	-0.249	1301	8.941E-07	FALSE
102954 at	-0.036	6727	1423500 a at	-0.170	941	102954 at	0.116	2879	1432189 a at	0.459	1125	2918	2685.3541	FALSE	SRY-box containing gene 5	242025 at	0.439	657	1.714E-07	FALSE
104150 at	0.047	5923	1451522 s at	0.086	4001.5	104151 at	-0.160	1109	1424879 at	-0.418	640	2918.375	2494.3778	FALSE	leucine-rich repeats and calponin homology (CH) domain containing 4	90610 at	0.138	7826	2.924E-03	FALSE
95701 at	-0.571	119	1448960 at	-0.212	1049	95701 at	0.056	6407	1431469 a at	0.168	4099	2918.5	2880.7084	FALSE	CXXC finger 5	224516 s at	0.658	918	3.641E-07	FALSE
103265 r at	0.776	1043	1434575 at	-0.245	483	103265 r at	0.008	7973	1460592 at	-0.220	2183	2920.5	3441.8055	FALSE	erythrocyte protein band 4.1-like 1	212339 at	-0.613	1038	5.029E-07	FALSE
93873 s at	0.158	1284	1452400 a at	0.110	3435	161670 f at	0.185	1023	1452400 a at	0.078	5940	2920.5	2284.7851	TRUE	homeo box A11, opposite strand transcript	NA	NA	NA	NA	
103400 at	0.206	3345	1456398 at	-0.323	1299.5	161749 r at	0.066	4911	1426771 at	-0.264	2128	2920.875	1570.3489	TRUE	taurine upregulated gene 1	NA	NA	NA	NA	
104694 at	0.210	1139	1451902 at	0.129	2569	104694 at	-0.142	5090	1451902 at	-0.291	2887	2921.25	1633.5182	FALSE	cDNA sequence BC021442	NA	NA	NA	NA	
93234 at	0.258	439	1418417 at	0.165	1644	93234 at	-0.030	6548	1418417 at	0.229	3066	2924.25	2643.6821	FALSE	musculin	209928 s at	-0.012	39060	8.521E-01	FALSE
104634 at	0.092	5117	1418230 a at	-0.099	4465	104634 at	0.280	1649	1443947 at	0.279	467	2924.5	2224.5901	FALSE	LIM and senescent cell antigen-like domains 1	212687 at	0.288	7300	1.992E-03	FALSE
104501 at	-0.163	2358	1436079 s at	-0.076	4655.5	104501 at	0.286	564	1458501 at	0.111	4123	2925.125	1855.2308	FALSE	vesicle-associated membrane protein, associated protein B and C	202550 s at	-0.108	14921	6.930E-02	FALSE
99888 at	0.170	621	1421614 at	0.131	2246.5	99888 at	0.067	5049	1421614 at	0.148	3786	2925.625	1916.7223	TRUE	zonadhesin	NA	NA	NA	NA	
98307 at	-0.083	5293	1421176 at	-0.697	20	98307 at	-0.667	360	1421176 at	-0.174	6031	2926	3176.6285	TRUE	RAS guanyl releasing protein 1	205590 at	-1.090	452	8.556E-08	TRUE
93944 r at	-0.052	5442	1437626 at	-0.208	1175	160273 at	0.079	3686	1437626 at	-0.288	1403	2926.5	2024.3011	FALSE	zinc finger protein 36, C3H type-like 2	201369 s at	0.364	6455	1.018E-03	FALSE
104112 at	0.102	3015	1437741 at	0.059	6254	104112 at	0.197	281	1447497 at	-0.174	2158	2927	2494.6175	FALSE	RAB21, member RAS oncogene family	226268 at	0.047	33315	6.760E-01	FALSE
104639 i at	0.142	1199	1430147 a at	0.086	3428	104639 i at	0.077	3918	1452987 at	0.218	3165	2927.5	1193.8326	TRUE	Josephin domain containing 3	218750 at	0.239	6006	6.956E-04	TRUE
97724 at	0.096	3319	1426383 at	-0.160	2614	97724 at	-0.411	806	1426383 at	-0.106	4972	2927.75	1725.5238	FALSE	cryptochrome 2 (photolyase-like)	212695 at	-0.105	13940	5.131E-02	FALSE
92724 at	-0.259	1226	1455305 x at	-0.119	2176	92724 at	0.041	7286	1423531 a at	-0.266	1034	2930.5	2946.2792	FALSE	heterogeneous nuclear ribonucleoprotein A1	234122 at	0.276	1691	2.122E-06	FALSE
98549 at	-0.069	5007	1420484 a at	-0.166	2932.5	98549 at	-0.111	3312	1420484 a at	-0.353	471	2930.625	1871.4111	TRUE	vitronectin	204534 at	0.001	44406	9.945E-01	FALSE
103286 at	0.092	2740	1453338 at	0.177	1110.5	103286 at	-0.040	6978	1440034 at	0.585	906	2933.625	2818.3629	FALSE	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	209649 at	0.090	22887	2.974E-01	FALSE
95612 at	-0.161	990	1452917 at	-0.008	8226.5	95612 at	-0.162	1276	1452917 at	-0.272	1245	2934.375	3530.4096	TRUE	replication factor C (activator 1) 5	NA	NA	NA	NA	
94739 at	0.121	4202	1421095 a at	-0.258	796.5	94740 g at	-0.306	640	1421096 at	-0.112	6110	2937.125	2678.6877	FALSE	transient receptor potential cation channel, subfamily C, member 1	211602 s at	-0.090	16525	1.024E-01	FALSE
101490 at	-0.162	2970	1423652 at	-0.273	578.5	101490 at	-0.310	1406	1423651 at	-0.052	6798	2938.125	2757.7097	TRUE	HESB like domain containing 2	209273 s at	-0.363	3432	4.205E-05	TRUE
101050 at	0.230	641	1415737 at	0.093	4744	97104 g at	-0.399	1000	1416230 at	0.144	5369	2938.5	2463.2938	FALSE	riboflavin kinase	NA	NA	NA	NA	
99042 s at	0.785	122	1420559 a at	-0.112	3694	99042 s at	1.100	646	1438042 at	-0.593	7293	2938.75	3302.5585	FALSE	short stature homeobox 2	210135 s at	0.091	14320	5.817E-02	FALSE
103497 at	0.120	3499	1424232 a at	0.105	2202	103497 at	0.163	3165	1451273 x at	0.187	2889	2938.75	550.86137	TRUE	cDNA sequence BC025546	222811 at	0.142	15718	8.431E-02	FALSE
103381 at	-0.187	3388	1453014 a at	-0.123	2742.5	103381 at	-0.158	1164	1453014 a at	-0.105	4462	2939.125	1379.6578	TRUE	SEC31-like 1 (S. cerevisiae)	210616 s at	0.086	15117	7.288E-02	FALSE
99127 at	0.410	1476	1456466 x at	0.120	4097	99127 at	-0.167	3276	1438653 x at	0.195	2911	2940	1094.788	FALSE	ataxin 10	208833 s at	-0.283	5658	5.049E-04	FALSE
97160 at	-0.061	7280	1416589 at	-0.367	1025	97160 at	0.612	437	1448392 at	-0.639	3023	2941.25	3097.0264	FALSE	secreted acidic cysteine rich glycoprotein	200665 s at	0.504	7310	2.008E-03	FALSE
97478 at	-0.069	4618	1454657 s at	0.188	735	97478 at	0.037	5807	1445410 at	0.273	605	2941.25	2667.6842	FALSE	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	219362 at	0.076	16846	1.099E-01	FALSE
100877 at	-0.077	4589	1436339 at	0.113	3176	100877 at	0.256	189	1442129 at	0.123	3816	2942.5	1924.4262	FALSE	RIKEN cDNA 1810058I24 gene	NA	NA	NA	NA	
103590 at	0.199	505	1423554 at	0.054	6109	103590 at	0.102	4445	1445898 at	-0.351	717	2944	2779.5969	FALSE	gamma-glutamyl carboxylase	214006 s at	-0.049	23625	3.245E-01	FALSE
95347 at	0.167	960	1422773 at	0.087	3048	95347 at	0.138	1481	1439365 at	0.062	6287	2944	2398.8254	TRUE	myelin transcription factor 1	215822 x at	-0.046	27342	4.557E-01	FALSE
103232 at	-0.051	5561	1454732 at	-0.184	1616.5	103232 at	-0.107	2821	1454732 at	-0.258	1786	2946.125	1822.7287	TRUE	BPY2 interacting protein 1	218522 s at	-0.422	2105	4.581E-06	TRUE
97162 at	0.277	987	1426906 at	0.147	2039	97162 at	-0.027	6825	1426906 at	-0.461	1934	2946.25	2628.7586	FALSE	Interferon activated gene 203	NA	NA	NA	NA	
95309 at	0.180	2188	1424936 a at	0.081	5387	161398 at	-0.124	1448	1425692 a at	0.167	2763	2946.5	1713.7228	FALSE	Dynein, axonemal, heavy chain 8	233052 at	-0.013	38400	8.340E-01	FALSE
104419 at	0.198	1682	1426903 at	0.122	3740	104419 at	0.163	4785	1443863 at	-0.204	1584	2947.75	1577.4541	FALSE	fibronectin type III domain containing 3a	215910 s at	-0.177	6043	7.205E-04	FALSE
93092 at	-0.142	2218	1422527 at	0.007	8297	93092 at	-0.174	667	1422527 at	-0.434	614	2949	3642.1246	FALSE	histocompatibility 2, class II, locus DMa	217478 s at	0.397	10005	1.013E-02	FALSE
94814 at	0.146	1483	1437225 x at	0.086	4085	94814 at	0.166	418	1437225 x at	0.100	5811	2949.25	2451.9827	TRUE	guanine nucleotide binding protein, alpha inhibiting 3	201180 s at	0.525	1557	1.599E-06	TRUE
101003 at	0.171	779	1416150 a at	0.244	2145	101003 at	-0.018	7774	1416151 at	-0.226	1102	2950	3268.4015	FALSE	splicing factor, arginine/serine-rich 3 (SRp20)	208673 s at	-0.309	14482	6.103E-02	FALSE
96011 at	0.399	1787	1434888 a at	0.112	4933	96011 at	-0.493	567	1438368 a at	-0.117	4515	2950.5	2114.4559	FALSE	matrin 3	228012 at	-0.352	477	9.294E-08	FALSE
104056 at	0.160	1762	1433995 s at	0.089	4655.5	104056 at	0.468	354	1433995 s at	0.093	5032	2950.875	2265.2455	TRUE	DNA segment, Chr 16, Brigham & Women's Genetics 1543 expressed	NA	NA	NA	NA	
94761 at	-0.213	325	1421228 at	0.116	3470	94761 at	0.177	309	1421228 at	-0.035	7700	2951	3497.5421	FALSE	chemokine (C-C motif) ligand 7	208075 s at	-0.003	43222	9.655E-01	FALSE
99581 at	-0.100	4960	1424017 a at	0.370	781.5	99581 at	0.144	1428	1424017 a at	0.151	4636	2951.375	2152.6391	FALSE	histidine triad nucleotide binding protein 1	208826 x at	-0.441	2410	8.196E-06	FALSE
92201 at	0.241	1811	1419874 x at	-0.066	6153	92202 g at	-0.330	3609	1439163 at	0.624	234	2951.75	2540.8302	FALSE	zinc finger and BTB domain containing 16	205883 at	0.787	1429	1.215E-06	FALSE
94886 at	0.167	2739	1422845 at	-0.320	377	160180 at	-0.122	3521	1428935 at	-0.116	5182	2954.75	1997.7174	TRUE	calnexin	238034 at	-0.286	4455	1.456E-04	FALSE
95514 at	-0.075	4165	1426897 at	-0.191	627	160206 at	-0.199	1490	1426897 at	-0.141	5537	2954.75	2287.4027	FALSE	regulator of chromosome condensation 2	224578 at	0.062	21782	2.610E-01	FALSE
93237 s at	0.149	1395	1426119 at	0.066	4298	100756 r at	0.100	2620	1426119 at	0.133	3506	2954.75	1245.4015	TRUE	thymidylate synthase, pseudogene	NA	NA	NA	NA	
102077 at	0.088	4036	1450646 at	-0.361	1182	94916 at	-0.098	3046	1422534 at	-0.136	3562	2956.5	1250.1748	FALSE	Cytochrome P450, family 51	216607 s at	-0.285	9855	9.311E-03	FALSE
102885 at	0.124	3438	1426269 at	0.238	1952	102885 at	-0.139	2888	1452007 at	0.158	3552	2957.5	730.33577	FALSE	synaptobrevin like 1	202829 s at	0.004	43660	9.762E-01	FALSE
93495 at	-0.034	7065	1416167 at	0.270	978.5	93495 at	0.503	136	1431269 at	0.124	3652	2957.875	3121.4948	FALSE	peroxiredoxin 4	201923 at	-0.065	34768	7.241E-01	FALSE
160821 r at	0.235	1244	1424346 at	0.052	5993	103947 at	0.162	3462	1424346 at	0.256	1134	2958.25	2289.8335	TRUE	protein phosphatase 6, catalytic subunit	203529 at	0.138	10608	1.403E-02	TRUE
101052 g at	-0.083	4705	1421856 at	0.087	4304.5	101052 g at	-0.108	2246	1421856 at	-0.336	587	2960.625	1914.2996	FALSE	S100 calcium binding protein A3	206027 at	0.047	24751	3.634E-01	FALSE
95564 at	0.145	1329	1460399 at	0.059	6058	95564 at	0.126	3107	1452218 at	0.296	1349	2960.75	2226.7085	TRUE	cDNA sequence BC018601	225644 at	0.277	8984	5.728E-03	TRUE
162251 f at	0.207	1686	1437394 at	0.050	6659	92397 at	0.162	3045	1435433 at	0.865	454	2961	2682.8426	TRUE	centaurin, gamma 2	240758 at	0.445	2693	1.364E-05	TRUE
92676 at	0.094	5131	1424704 at	0.184	1712	92676 at	0.090	2507	1424704 at	0.410	2496	2961.5	1493.457	TRUE	runt related transcription factor 2	232231 at	0.230	12193	2.792E-02	FALSE
96663 at	-0.199	1016	1416864 at	0.113	2846.5	96663 at	0.086	5499	1416864 at	0.170	2485	2961.625	1867.6325	FALSE	surfeit gene 6	225038 s at	0.081	15654	8.322E-02	FALSE
93737 at	0.070	4643	1421900 at	-0.133	2403	93737 at	-0.065	4349	1436006 at	0.430	452	2961.75	1946.1167	FALSE	eukaryotic translation initiation factor 2 alpha kinase 1	217735 s at	-0.067	23854	3.330E-01	FALSE
160487 at	-0.895	19	1422580 at	0.099	3932	160487 at	0.081	3314	1422580 at	0.611	4591	2964	2031.3934	FALSE	myosin, light polypeptide 4	210088 x at	0.050	24070	3.402E-01	FALSE
160060 at	-0.048	5942	1452880 at	0.342	699	160060 at	-0.174	1379	1452880 at	0.155	3843	2965.75	2400.2474	FALSE	zinc finger, HIT type 3	212544 at	-0.391	5954	6.652E-04	FALSE
93489 at	-0.057	5254	1450970 at	-0.125	3087	93489 at	0.160	1479	1450970 at	0.180	2044	2966	1664.4156	FALSE	glutamate oxaloacetate transaminase 1, soluble	208813 at	-0.720	1892	3.187E-06	FALSE
97660 s at	0.110	2564	1429427 s at	-0.754	41.5	97660 s at	0.036	6338	1447071 at	0.267	2922	2966.375	2587.5744	FALSE	transcription factor 7-like 2, T-cell specific, HMG-box	212761 at	0.712	992	4.374E-07	FALSE

101769 at	0.089	4909	1427687 at	0.049	5792	101769 at	-0.176	701	1427687 at	0.372	464	2966.5	2777.9941	FALSE	protocadherin alpha 10	223435 s at	-0.445	1814	2.731E-06	FALSE
161521 at	0.042	5863	1431092 at	-0.115	3058.5	161521 at	0.098	2533	1454848 at	-0.440	415	2967.375	2243.2304	FALSE	protein phosphatase 1, regulatory (inhibitor) subunit 12C	223152 at	-0.121	9445	7.535E-03	FALSE
100439 i at	-0.176	1788	1425677 a at	-0.118	3947	100440 f at	0.083	2793	1452512 a at	0.126	3346	2968.5	917.30566	FALSE	ankyrin 1, erythroid	236393 at	-0.095	11352	1.987E-02	FALSE
92727 at	-0.299	707	1427288 at	-0.131	2787	92727 at	0.026	7922	1427288 at	0.453	459	2968.75	3463.2392	FALSE	amyloid beta (A4) precursor protein-binding, family A, member 2	209871 s at	0.111	19324	1.787E-01	FALSE
94555 at	0.067	4622	1430527 a at	-0.149	1627.5	94555 at	-0.107	1982	1430527 a at	-0.201	3646	2969.375	1410.027	FALSE	ring finger protein 167	212047 s at	-0.043	28690	5.089E-01	FALSE
160953 at	0.110	2402	1422710 a at	-0.174	1979	160953 at	-0.065	4917	1422710 a at	-0.373	2582	2970	1322.3789	FALSE	calcium channel, voltage-dependent, T type, alpha 1H subunit	205845 at	-0.283	915	3.630E-07	FALSE
98629 f at	0.380	387	1448183 a at	-0.124	5143	98629 f at	0.317	2008	1431981 at	0.150	4343	2970.25	2175.9588	FALSE	hypoxia inducible factor 1, alpha subunit	200989 at	0.197	16379	9.920E-02	FALSE
102678 at	0.273	583	1448940 at	0.157	2210	102678 at	0.060	5187	1448940 at	-0.332	3903	2970.75	2005.0723	FALSE	tripartite motif protein 21	204804 at	0.084	10757	1.514E-02	FALSE
101429 at	-0.276	235	1417516 at	-0.030	7269	101429 at	0.080	4332	1443897 at	0.495	48	2971	3481.1277	FALSE	DNA-damage inducible transcript 3	209383 at	-0.090	19307	1.782E-01	FALSE
101842 g at	0.082	5290	1432647 at	0.055	5359.5	101841 at	-0.173	941	1424932 at	-0.363	296	2971.625	2730.0315	FALSE	epidermal growth factor receptor	201983 s at	0.418	7404	2.136E-03	FALSE
102797 at	-0.158	1067	1448390 a at	-0.103	3746	102797 at	-0.073	5316	1448390 a at	-0.199	1758	2971.75	1931.8586	TRUE	dehydrogenase/reductase (SDR family) member 3	238032 at	0.203	3859	7.234E-05	FALSE
104469 at	0.262	703	1419309 at	0.089	3219	104469 at	-0.048	5012	1419309 at	-0.188	2956	2972.5	1767.411	FALSE	podoplanin	221898 at	0.257	10752	1.510E-02	FALSE
102943 at	0.212	414	1428612 at	0.115	3275.5	102943 at	0.048	5337	1428612 at	0.182	2867	2973.375	2019.8778	TRUE	autophagy-related 7 (yeast)	222709 at	0.111	7150	1.794E-03	TRUE
99558 at	0.045	6919	1428570 at	0.308	1604	99558 at	0.128	1358	1417861 at	-0.264	2015	2974	2643.9278	FALSE	cyclin C	201955 at	-0.261	11125	1.821E-02	FALSE
99582 at	0.145	2037	1416579 a at	-0.291	4637	99582 at	0.171	1106	1416579 a at	-0.163	4119	2974.75	1677.6953	FALSE	tumor-associated calcium signal transducer 1	201839 s at	-0.503	974	4.187E-07	FALSE
160068 at	0.023	7550	1417719 at	0.229	791.5	160068 at	0.162	1169	1417719 at	0.191	2394	2976.125	3125.0328	TRUE	sin3 associated polypeptide	204900 x at	0.388	7507	2.322E-03	TRUE
93623 at	0.207	1310	1417307 at	0.049	6296	93623 at	-0.076	3728	1430320 at	0.707	572	2976.5	2591.1822	FALSE	dystrophin, muscular dystrophy	203881 s at	0.312	12591	3.256E-02	FALSE
93954 at	-0.363	900	1420871 at	-0.206	1439	93954 at	-0.225	3335	1420871 at	0.090	6233	2976.75	2408.9467	FALSE	guanylate cyclase 1, soluble, beta 3	211555 s at	-1.057	333	4.659E-08	FALSE
160409 at	-0.198	659	1423283 at	-0.232	450	160409 at	0.074	5317	1423282 at	0.091	5481	2976.75	2799.0754	FALSE	phosphatidylinositol transfer protein, alpha	201192 s at	-0.129	23702	3.273E-01	FALSE
160551 at	0.158	4087	1416175 a at	0.132	4415.5	160551 at	0.190	1636	1416175 a at	0.199	1771	2977.375	1478.0729	TRUE	voltage-dependent anion channel 3	208846 s at	-0.271	9023	5.887E-03	FALSE
92583 at	0.103	3794	1423866 at	0.203	521.5	92583 at	0.193	380	1457263 at	0.037	7214	2977.375	3234.8903	TRUE	serine (or cysteine) peptidase inhibitor, clade A, member 3K	NA	NA	NA	NA	
161847 r at	0.137	2925	1433690 at	0.173	1388.5	161847 r at	-0.063	5389	1433690 at	0.182	2221	2980.875	1723.877	FALSE	RIKEN cDNA 2210016L21 gene	219022 at	-0.195	4615	1.757E-04	FALSE
96136 at	0.071	4237	1423587 a at	-0.103	2147	96136 at	-0.079	3666	1423587 a at	-0.178	1879	2982.25	1148.4359	FALSE	exosome component 10	207541 s at	0.197	9070	6.078E-03	FALSE
97436 at	-0.063	4953	1423688 at	0.121	1706.5	97436 at	-0.095	2982	1423688 at	-0.179	2291	2983.125	1412.9422	FALSE	mannosidase, alpha, class 2C, member 1	238089 at	0.066	21459	2.481E-01	FALSE
103406 at	-0.213	2214	1417390 at	0.099	3626.5	103406 at	0.188	3420	1417390 at	0.194	2673	2983.375	656.38446	FALSE	XPA binding protein 1	209313 at	0.002	43839	9.808E-01	FALSE
93463 at	0.213	1090	1455205 a at	-0.106	4202	93463 at	-0.173	2061	1438812 x at	-0.152	4581	2983.5	1680.5849	FALSE	ubiquitin specific peptidase 19	226357 at	0.108	5310	3.674E-04	FALSE
161911 f at	0.196	2629	1435803 a at	0.183	676	161911 f at	-0.076	3800	1435804 at	-0.131	4832	2984.25	1782.6804	FALSE	eukaryotic translation initiation factor 4E member 2	213571 s at	0.135	7552	2.406E-03	FALSE
95021 at	-0.127	3985	1433597 at	0.097	3697	95021 at	0.152	4010	1433598 at	0.773	249	2985.25	1829.6871	FALSE	RIKEN cDNA 9430010O03 gene	228477 at	-0.085	21971	2.674E-01	FALSE
103684 at	0.159	1959	1418484 at	0.131	2593.5	103684 at	0.058	5261	1418484 at	0.159	2129	2985.625	1540.4392	TRUE	tektin 2	210323 at	0.210	9301	6.970E-03	TRUE
95732 at	-0.222	3401	1451185 at	0.156	1388.5	95732 at	0.182	4353	1439370 x at	0.145	2806	2987.125	1241.681	FALSE	splicing factor 3b, subunit 5	221263 s at	-0.027	36706	7.834E-01	FALSE
161706 f at	0.112	3360	1423885 at	-0.124	3500	102404 at	0.066	3689	1423885 at	-0.208	1401	2987.5	1066.2234	FALSE	laminin, gamma 1	200771 at	0.216	10920	1.649E-02	FALSE
104468 at	-0.093	2688	1423092 at	0.176	875.5	104468 at	-0.071	5776	1423093 at	0.170	2615	2988.625	2038.3594	FALSE	inner centromere protein	244862 at	0.063	19226	1.756E-01	FALSE
98447 at	-0.038	6744	1418982 at	-0.117	3306	98447 at	-0.164	1121	1418982 at	-0.319	785	2989	2741.5053	TRUE	CCAAT/enhancer binding protein (C/EBP), alpha	204039 at	-0.032	34404	7.108E-01	FALSE
160980 at	-0.065	5577	1428810 at	0.212	356	160980 at	0.133	1005	1428810 at	-0.099	5020	2989.5	2688.9681	FALSE	RIKEN cDNA 2700097O09 gene	NA	NA	NA	NA	
93771 at	0.157	1229	1448766 at	-0.220	2274.5	93771 at	-0.151	659	1448766 at	-0.045	7797	2989.875	3273.8291	FALSE	gap junction membrane channel protein beta 1	204973 at	-0.002	44099	9.865E-01	FALSE
92874 f at	-0.119	2159	1423245 at	-0.077	3589	92875 s at	-0.405	83	1423245 at	0.079	6129	2990	2539.9037	FALSE	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana)	209029 at	-0.060	24386	3.499E-01	FALSE
161522 i at	-0.300	822	1426195 a at	-0.069	6695	161522 i at	0.167	3894	1426195 a at	-0.301	551	2990.5	2897.8834	FALSE	cystatin C	201360 at	0.083	26765	4.339E-01	FALSE
162129 f at	0.103	2309	1417801 a at	-0.067	5811.5	162129 f at	0.181	1851	1444516 at	0.181	1995	2991.625	1889.6171	FALSE	protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2	212841 s at	0.281	7546	2.387E-03	FALSE
96676 at	0.100	3409	1454640 at	0.224	993	96676 at	0.061	4862	1444318 at	-0.183	2703	2991.75	1607.3073	FALSE	coiled-coil-helix-coiled-coil-helix domain containing 7	222701 s at	-0.155	13556	4.478E-02	FALSE
92500 at	-0.112	3235	1449315 at	-0.057	6611.5	92500 at	-0.235	2078	1442997 at	0.548	47	2992.875	2748.8329	FALSE	odd Oz/ten-m homolog 3 (Drosophila)	233291 at	-0.066	21357	2.456E-01	FALSE
96421 at	0.124	2556	1420470 at	0.215	2226.5	96421 at	0.192	1458	1420470 at	-0.124	5732	2993.125	1882.9797	FALSE	sulfotransferase family, cytosolic, 1C, member 1	NA	NA	NA	NA	
98593 at	-0.047	6719	1426662 at	0.112	2757	98593 at	0.249	888	1426662 at	0.211	1610	2993.5	2600.1593	FALSE	cytidine monophospho-N-acetylneuraminic acid synthetase	241065 x at	0.131	6378	9.680E-04	FALSE
102318 at	0.120	3098	1419186 a at	0.189	2718	102318 at	0.245	982	1446617 at	0.090	5178	2994	1722.8844	TRUE	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	242943 at	-0.060	17946	1.393E-01	FALSE
94710 g at	0.154	1588	1420455 at	0.104	3701	94710 g at	-0.082	3448	1420456 at	0.148	3239	2994	956.17746	FALSE	glial cells missing homolog 2 (Drosophila)	220799 at	0.008	38815	8.449E-01	FALSE
160830 at	-0.249	685	1417524 at	-0.161	2843	160830 at	-0.269	2060	1417524 at	-0.089	6401	2997.25	2438.1854	TRUE	cornichon homolog 2 (Drosophila)	230070 at	-0.308	2909	1.865E-05	TRUE
93007 at	-0.092	4432	1426054 at	0.082	3833.5	93128 at	0.079	2876	1421471 at	0.535	850	2997.875	1568.7792	FALSE	neuropeptide Y receptor Y1	205440 s at	-0.717	2093	4.517E-06	FALSE
102476 f at	-0.180	1842	1415682 at	-0.075	4874	95526 at	-0.080	4995	1435814 at	-0.524	281	2998	2325.6404	TRUE	Exportin 7	212166 at	-0.199	5911	6.409E-04	TRUE
103550 at	-0.232	708	1423594 a at	-0.238	891	103550 at	0.006	8196	1426314 at	-0.310	2200	2998.75	3527.9623	FALSE	endothelin receptor type B	206701 x at	-0.197	17280	1.215E-01	FALSE
161075 at	-0.090	3346	1456481 at	-0.155	1510.5	161075 at	0.055	5537	1456481 at	-0.232	1605	2999.625	1890.3897	FALSE	DNA segment, Chr 9, ERATO Doi 280, expressed	239770 at	-0.112	12725	3.400E-02	FALSE
94794 at	-0.127	3692	1448771 a at	-0.142	2160	161913 r at	0.091	3002	1448771 a at	-0.147	3146	3000	633.97792	FALSE	ferritin heavy chain 1	214211 at	0.156	19905	1.977E-01	FALSE
93025 at	0.129	2804	1424820 a at	0.162	2593.5	93025 at	0.086	4936	1451493 at	0.202	1667	3000.125	1381.8639	TRUE	Nedd4 family interacting protein 1	222423 at	-0.452	5886	6.284E-04	FALSE
104453 at	-0.011	8034	1415718 at	0.145	1314	104453 at	0.131	1453	1460071 at	0.204	1201	3000.5	3357.2489	FALSE	SAP30-like	219129 s at	0.116	8638	4.740E-03	FALSE
96577 i at	-0.232	1840	1454643 at	0.153	2214	96577 i at	0.027	7408	1454643 at	0.391	545	3001.75	3023.2914	FALSE	ubiquitin associated protein 2-like	201377 at	0.150	8630	4.715E-03	FALSE
102653 at	-0.523	162	1450123 at	0.063	6317	102653 at	-0.565	924	1445498 at	0.168	4613	3004	2942.1202	FALSE	ryanodine receptor 2, cardiac	207557 s at	-0.686	3699	5.947E-05	FALSE
94011 at	-0.092	5393	1454183 at	0.109	3353	94011 at	-0.165	2805	1415739 at	-0.299	465	3004	2026.1	FALSE	RIKEN cDNA 3100004P22 gene	205740 s at	0.095	16170	9.458E-02	FALSE
94225 at	-0.044	6355	1418236 s at	0.184	2058.5	94225 at	0.106	3422	1418236 s at	0.355	184	3004.875	2598.095	FALSE	autophagy-related 5 (yeast)	210639 s at	-0.172	8148	3.588E-03	FALSE
100751 at	0.254	330	1450104 at	-0.117	3110	100751 at	-0.167	2939	1450104 at	0.071	5642	3005.25	2169.8521	FALSE	a disintegrin and metallopeptidase domain 10	214895 s at	-0.110	22575	2.874E-01	FALSE
93093 at	0.132	4795	1416881 at	-0.177	804.5	93093 at	0.165	2565	1456381 x at	0.198	3859	3005.875	1729.0858	FALSE	myeloid cell leukemia sequence 1	200797 s at	0.474	3932	8.090E-05	FALSE
93942 at	0.138	1617	1418045 at	0.079	4167	93942 at	0.074	4347	1418045 at	0.305	1895	3006.5	1450.2693	TRUE	inositol polyphosphate-1-phosphatase	202794 at	0.222	11341	1.979E-02	TRUE
100401 at	-0.036	6831	1420951 a at	-0.126	1950	100401 at	0.189	2038	1455634 at	0.269	1209	3007	2576.3016	FALSE	Son cell proliferation protein	226465 s at	0.308	1915	3.317E-06	FALSE
104588 at	0.141	2505	1419197 x at	0.166	1375	104588 at	0.075	5443	1419197 x at	0.145	2713	3009	1725.876	TRUE	hepcidin antimicrobial peptide 1	NA	NA	NA	NA	
98570 at	0.239	1086	1416669 s at	0.372	906	98570 at	0.051	5617	1416669 s at	0.101	4428	3009.25	2375.9744	TRUE	nascent polypeptide-associated complex alpha polypeptide	222018 at	0.171	9756	8.870E-03	TRUE
161231 r at	-0.051	6317	1449465 at	-0.177	3025	161231 r at	0.112	1825	1449465 at	-0.487	875	3010.5	2373.3888	FALSE	reelin	205923 at	0.037	37497	8.050E-01	FALSE
102379 at	0.067	4462	1448855 at	0.093	3196.5	102379 at	0.194	1302	1457788 at	0.231	3091	3012.875	1299.5997	FALSE	Ras association (RalGDS/AF-6) domain family 1	NA	NA	NA	NA	
99138 at	0.167	1352	1416962 at	0.057	4984	99138 at	-0.083	3882	1416962 at	-0.199	1838	3014	1710.7059	FALSE	regulator of chromosome condensation 1	206499 s at	0.035	33934	6.961E-01	FALSE
97964 at	0.036	7092	1425839 at	0.112	1769.5	97964 at	0.197	661	1425938 a at	-0.175	2537	3014.875	2825.0663	FALSE	FK506 binding protein 11	219117 s at	-0.665	267	3.146E-08	FALSE
96065 at	-0.483	147	1416503 at	-0.122	4261	96065 at	-0.174	2916	1416503 at	-0.106	4738	3015.5	2062.0757	TRUE	latexin	218729 at	-0.038	30459	5.740E-01	FALSE
101715 at	0.111	3436	1450615 at	0.147	2269	101715 at	0.107	2302	1450615 at	0.140	4058	3016.25	881.28103	TRUE	eosinophil-associated, ribonuclease A family, member 4	206111 at	0.138	17040	1.154E-01	FALSE
100516 at	-0.164	1264	1450264 a at	-0.157	2050.5	100516 at	-0.005	8249.5	1453582 at	0.472	505	3017.25	3544.777	FALSE	choline kinase alpha	204266 s at	0.224	4895	2.433E-04	FALSE
98614 at	0.124	1636	1448523 at	0.193	722	98614 at	0.031	7077	1448523 at	0.181	2636	3017.75	2816.7916	TRUE	nephronophthisis 1 (juvenile) homolog (human)	206285 at	-0.059	22318	2.789E-01	FALSE
95050 at	0.238	353	1460645 at	-0.012	8240.5	160330 at	-0.296	894	1435574 at	-0.204	2585	3018.125	3609.044	FALSE	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	218566 s at	0.213	21795	2.612E-01	FALSE
94365 at	0.047	5875	1425196 a at	0.178	999.5	94365 at	0.211	458	1425196 a at	-0.124	4742	3018.625	2693.3601	FALSE	histidine triad nucleotide binding protein 2	224415 s at	0.059	24510	3.544E-01	FALSE
95618 at	-0.141	2201	1427405 s at	-0.093	4734	95618 at	0.261	664	1434314 s at	0.176	4478	3019.25	1939.5064	FALSE	RAB11 family interacting protein 5 (class I)	210879 s at	-0.204	5053	2.804E-04	FALSE
103723 at	0.159	2775	1454783 at	0.107	3278	103723 at	0.306	78	1451775 s at	0.104	5951	3020.5	2406.4298	TRUE	interleukin 13 receptor, alpha 1	201887 at	0.542	3685	5.835E-05	TRUE
94454 at	-0.209	2247	1415796 at	-0.178	861	94454 at	-0.058	6415	1415796 at	-0.154	2560	3020.75	2380.2264	TRUE	DAZ associated protein 2	214334 x at	0.285	2400	8.162E-06	FALSE
101105 at	-0.074	5299	1421082 s at	0.131	2056	101105 at	-0.080	4008	1421083 x at	0.282	721	3021	2031.8036	FALSE	barrier to autointegration factor 1	210125 s at	0.212	9487	7.740E-03	FALSE
100622 at	-0.423	189	1423223 a at	-0.233	632.5	100622 at	-0.026	7602	1423223 a at	-0.121	3661	3021.125	3421.5161	TRUE	peroxiredoxin 6	200845 s at	0.683	981	4.283E-07	FALSE
97345 at	0.220	633	1420592 a at	-0.110	3078.5	97345 at	-0.309	722	1447680 at	0.038	7653	3021.625	3288.7016	FALSE	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	208103 s at	0.155	7512	2.325E-03	FALSE
92546 r at	0.180	2780	1423860 at	-0.311	1232	92546 r at	0.225	3954	1423859 a at	-0.186	4128	3023.5	1335.9784	FALSE	prostaglandin D2 synthase (brain)	212187 x at	0.209	8710	4.952E-03	FALSE
100136 at	0.178	2529	1428094 at	-0.093	5923	100136 at	0.294	317	1434503 s at	-0.173	3332	3025.25	2314.5866	FALSE	lysosomal membrane glycoprotein 2	200821 at	0.538	2897	1.830E-05	FALSE
104412 at	0.170	3354	1427510 at	-0.073	4863	97195 at	-0.255	3308	1427510 at	0.314	576	3025.25	1785.5134	FALSE	guanine nucleotide binding protein, alpha inhibiting 1	227692 at	0.276	13428	4.294E-02	FALSE
95177 at	-0.109	2455	1420230 at	0.100	4914.5	95177 at	0.155	1205	1449785 at	0.116	3527	3025.375	1576.8654	FALSE	expressed sequence AA414993	NA	NA	NA	NA	
101423 at	0.156	1185	1424569 at	0.079	3655.5	101423 at	-0.127	2868	1424570 at	0.152	4397	3026.375	1377.2141	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	228039 at	0.037	29583	5.416E-01	FALSE
96835 at	0.122	2256	1418464 at	-0.184	2358.5	96835 at	0.111	2412	1418464 at	-0.176	5082	3027.125	1371.4449	FALSE	matrilin 4	207123 s at	0.003	43668	9.763E-01	FALSE
160145 at	0.174	1364	1434137 x at	0.225	851.5	160145 at	0.046	6403	1434137 x at	0.192	3491	3027.375	2523.9546	TRUE	RIKEN cDNA 1810010M01 gene	214142 at	-0.017	38910	8.483E-01	FALSE
160604 at	-0.087	4216	1419486 at	0.103	3605.5	160604 at	0.128	1692	1419486 at	-0.186	2598	3027.875	1112.7513	FALSE	forkhead box C1	NA	NA	NA	NA	
96343 at	-0.512	232	1423449 a at	-0.025	7321	96343 at	-0.176	2522	1444258 at	-0.271	2038	3028.25	3026.7475	TRUE	actinin alpha 4	200601 at	0.234	3921	7.991E-05	FALSE
100093 at	-0.240	787	1415956 a at	-0.172	1117	100093 at	-0.052	6018	1443296 at	0.215	4192	3028.5	2514.5574	FALSE	PCTAIRE-motif protein kinase 1	207239 s at	-0.270	2029	4.040E-06	FALSE
161105 at	0.123	2922	1440221 at	0.105	2287	161105 at	-0.085	3377	1440221 at	-0.150	3529	3028.75	557.70863	FALSE	expressed sequence AA408650	NA	NA	NA	NA	
104035 at	-0.070	4249	1431070 a at	-0.133	2355	104035 at	-0.062	5398	1456492 at	1.004	123	3031.25	2309.376	FALSE	RIKEN cDNA 9130404D08 gene	212505 s at	0.146	6955	1.530E-03	FALSE
98958 at	0.076	5052	1460392 a at	0.183	2322	98958 at	-0.228	3011	1460392 a at	-0.194	1740	3031.25	1443.8609	FALSE	enhancer of yellow 2 homolog (Drosophila)	226776 at	-0.173	10706	1.475E-02	FALSE
94522 at	-0.334	1131	1416247 at	-0.206	2295.5	94522 at	-0.184	1232	1416247 at	0.034	7468	3031.625	3004.1265	FALSE	dynactin 3	204246 s at	-0.398	2188	5.386E-06	FALSE
96261 at	-0.131	3383	1455126 x at	0.303	899.5	96261 at	0.046	5720	1436001 at	-0.186	2127	3032.375	2058.7315	FALSE	RIKEN cDNA 2310028O11 gene	224867 at	-0.188	9495	7.768E-03	FALSE
93597 at	0.066	5233	1417648 s at	0.098	2423	93598 at	0.177	2716	1417646 a at	-0.182	1759	3032.75	1520.4895	FALSE	sorting nexin 5	217792 at	0.205	4719	2.002E-04	FALSE
160670 at	-0.121	3620	1415921 a at	-0.222	551	160670 at	0.045	6046	1415921 a at	-0.210	1916	3033.25	2368.5967	FALSE	tumor necrosis factor receptor superfamily, member 19	227812 at	0.200	12820	3.506E-02	FALSE
103650 at	-0.083	4163	1455644 at	0.159	2209	103650 at	-0.086	4955	1455644 at	0.341	810	3034.25	1878.9787	FALSE	vacuolar protein sorting 53 (yeast)	235710 at	-0.048	19255	1.763E-01	FALSE
96075 at	-0.070	6008	1437591 a at	-0.269	133.5	96075 at	0.151	2865	1423054 at	0.211	3136	3035.625	2401.1477	FALSE	WD repeat domain 1	200609 s at	0.341	4325	1.248E-04	FALSE
99955 at	-0.394	186	1416891 at	-0.018	7796.5	161912 r at	0.138	1971	1457175 at	0.212	2193	3036.625	3297.9657	FALSE	numb gene homolog (Drosophila)	236930 at	0.173	6890	1.454E-03	FALSE
97196 at	-0.065	4447	1427727 x at	0.118	2178.5	97196 at	0.139	1217.5	1421418 a at	-0.094	4306	3037.25	1596.461	FALSE	pregnancy specific glycoprotein 19	NA	NA	NA	NA	
162205 f at	0.183	1741	1454267 a at	0.141	1867	162205 f at	0.086	3782	1454267 a at	-0.140	4765	3038.75	1482.0608	FALSE	protease, serine, 32	NA	NA	NA	NA	
98599 at	-0.211	774	1416597 at	0.084	3926	98599 at	-0.068	5713	1438912 at	-0.194	1743	3039	2217.1217	FALSE	hepatoma-derived growth factor, related protein 2	207730 x at	0.285	5154	3.199E-04	FALSE
95606 at	-0.173	1756	1422769 at	-0.155	2423	95606 at	-0.087	4156	1422768 at	-0.142	3822	3039.25	1138.1744	TRUE	synaptotagmin binding, cytoplasmic RNA interacting protein	217832 at	0.474	2081	4.403E-06	FALSE
160962 at	0.232	441	1423948 at	0.048	5965	162270 r at	0.090	3450	1423948 at	0.267	2303	3039.75	2310.9662	TRUE	Bcl2-associated athanogene 2	209406 at	0.081	17174	1.192E-01	FALSE
104622 at	-0.076	4757	1418107 at	0.116	4334	104622 at	0.134	1254	1418107 at	0.292	1815	3040	1761.9067	FALSE	transcription elongation factor A (SII), 2	203919 at	-0.355	5194	3.352E-04	FALSE
100380 at	0.167	1830	1423263 at	0.110	4823	100380 at	0.156	3739	1442087 at	0.372	1773	3041.25	1498.563	TRUE	H3 histone, family 3A	208755 x at	0.238	2218	5.676E-06	TRUE
101207 at	0.061	4917	1417451 a at	0.194	1992	101207 at	0.105	2158	1417451 a at	0.124	3099	3041.5	1341.9922	TRUE	peptidylprolyl isomerase A	217346 at	-0.036	24838	3.669E-01	FALSE
94791 s at	0.063	4557	1460300 a at	0.106	3300.5	94791 s at	0.082	2801	1460300 a at	0.329	1508	3041.625	1261.386	TRUE	leukocyte tyrosine kinase	207106 s at	-0.122	16615	1.041E-01	FALSE
104136 at	-0.111	4222	1426465 at	-0.287	1130	104136 at	-0.173	2319	1455548 at	-0.148	4496	3041.75	1600.5196	TRUE	discs, large homolog-associated protein 4 (Drosophila)	202572 s at	-0.539	396	6.025E-08	TRUE
100006 at	-0.104	4474	1450757 at	-0.247	2383	100006 at	-0.421	7	1450757 at	-0.134	5303	3041.75	2367.0129	TRUE	cadherin 11	239769 at	-0.181	5550	4.637E-04	TRUE
94367 at	-0.154	1591	1417137 at	0.052	6249	94367 at	0.107	4302	1441858 at	0.714	27	3042.25	2772.9692	FALSE	uridine-cytidine kinase 2	209825 s at	-0.126	7769	2.808E-03	FALSE
96264 at	0.078	4790	1416281 at	0.094	2932.5	96264 at	-0.095	2966	1441257 x at	-0.203	1481	3042.375	1355.2356	FALSE	Wdr45 like	209076 s at	0.165	10292	1.191E-02	FALSE
93686 s at	-0.203	3424	1426028 a at	-0.323	587	93686 s at	-0.077	3718	1426028 a at	-0.337	4441	3042.5	1691.8555	TRUE	citron	212801 at	-0.629	542	1.166E-07	TRUE
93468 at	-0.093	3458	1418135 at	0.077	4220.5	93468 at	-0.092	3022	1444937 at	0.204	1470	3042.625	1159.5259	FALSE	AF4/FMR2 family, member 1	201924 at	0.726	794	2.719E-07	FALSE
93195 at	-0.323	424	1429005 at	-0.088	4451.5	93195 at	0.032	6921	1436897 at	0.297	378	3043.625	3213.7279	FALSE	malignant fibrous histiocytoma amplified sequence 1	213457 at	0.228	14178	5.575E-02	FALSE
93309 at	0.361	1160	1416467 at	-0.030	7643	101542 f at	-0.297	591	1416467 at	0.172	2781	3043.75	3203.4687	FALSE	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	201210 at	0.307	8276	3.873E-03	FALSE
102389 s at	-0.069	6187	1423537 at	0.149	3647.5	102389 s at	0.353	1622	1423537 at	0.287	723	3044.875	2425.6809	FALSE	growth associated protein 43	216963 s at	-0.531	3192	2.977E-05	FALSE
104135 at	-0.453	496	1450706 a at	0.049	6776	104135 at	-0.299	1832	1450706 a at	-0.157	3076	3045	2701.24	FALSE	ADP-ribosylation factor-like 3	213433 at	-0.146	6404	9.828E-04	FALSE
161952 r at	-0.129	1785	1419916 at	0.103	4091	104749 at	0.109	4891	1419916 at	0.216	1416	3045.75	1707.1488	FALSE	Ring finger protein 20	213386 at	-0.494	2605	1.121E-05	FALSE
100955 at	0.016	7653	1422462 at	0.129	2145	100955 at	0.226	358	1422462 at	0.279	2031	3046.75	3177.6205	TRUE	ubiquitin-conjugating enzyme E2T (putative)	223229 at	-0.382	1423	1.188E-06	FALSE
92341 at	-0.245	814	1437644 at	0.066	4966.5	92341 at	0.088	5259	1437644 at	0.257	1148	3046.875	2392.3429	FALSE	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	217452 s at	-0.141	4706	1.980E-04	FALSE
162103 i at	0.271	364	1460693 a at	-0.082	5264	102070 at	0.164	487	1460693 a at	-0.223	6074	3047.25	3045.757	FALSE	procollagen, type IX, alpha 3	204724 s at	0.037	38876	8.471E-01	FALSE
95791 s at	0.051	6268	1452439 s at	-0.170	1764.5	94017 s at	0.171	2053	1452439 s at	0.303	2106	3047.875	2151.9883	FALSE	splicing factor, arginine/serine-rich 2 (SC-35)	200753 x at	-0.193	18213	1.462E-01	FALSE
100363 at	0.115	2578	1423258 at	-0.283	983.5	100363 at	-0.058	4980	1423258 at	-0.505	3655	3049.125	1691.5602	FALSE	synaptotagmin IX	232445 at	0.086	13981	5.201E-02	FALSE
104391 s at	0.161	1302	1425821 at	0.092	4353	104392 at	-0.146	1193	1425821 at	-0.094	5349	3049.25	2120.3114	FALSE	chloride channel 7	38069 at	0.133	3612	5.340E-05	FALSE
160733 at	0.209	1509	1451030 at	0.144	3050	160733 at	0.245	656	1451030 at	0.097	6984	3049.75	2803.7043	TRUE	aldo-keto reductase family 1, member C21	216594 x at	0.382	2702	1.378E-05	TRUE
93713 at	0.149	1203	1422853 at	0.102	3782.5	104350 at	0.161	1371	1422854 at	0.061	5850	3051.625	2206.5807	TRUE	src homology 2 domain-containing transforming protein C1	214853 s at	0.450	5400	3.990E-04	TRUE
94044 at	-0.091	4394	1427253 s at	-0.097	3998	103746 at	-0.332	1646	1452364 at	0.227	2172	3052.5	1347.481	FALSE	suppressor of zeste 12 homolog (Drosophila)	212287 at	0.137	14360	5.913E-02	FALSE
104187 at	-0.061	4502	1418375 at	-0.057	6114	104187 at	0.131	1083	1418375 at	-0.433	518	3054.25	2694.2185	FALSE	methyl-CpG binding domain protein 6	227833 s at	0.304	1193	7.127E-07	FALSE

94042 f at	-0.199	1849	1436946 s at	0.303	648.5	94042 f at	0.135	2839	1423985 at	-0.061	6884	3055.125	2705.154	FALSE	guanine nucleotide binding protein (G protein), gamma 5 subunit	207157 s at	0.016	39935	8.757E-01	FALSE
102957 at	-0.235	310	1418642 at	0.110	3158	102957 at	-0.011	7936	1418641 at	-0.292	819	3055.75	3481.8333	FALSE	lymphocyte cytosolic protein 2	205269 at	0.075	17575	1.286E-01	FALSE
103319 at	0.188	1354	1436559 a at	0.101	5552	103319 at	0.190	522	1436559 a at	0.147	4802	3057.5	2489.7445	TRUE	proteosome (prosome, macropain) 26S subunit, non-ATPase, 10	219485 s at	-0.150	15496	7.964E-02	FALSE
94492 at	-0.149	3671	1417124 at	-0.097	5744.5	94492 at	0.331	989	1417124 at	0.455	1826	3057.625	2112.7893	FALSE	destrin	201021 s at	-0.390	9710	8.700E-03	FALSE
104296 at	0.117	4754	1415765 at	-0.174	903.5	104609 at	-0.263	1186	1434551 at	-0.079	5388	3057.875	2341.7636	FALSE	heterogeneous nuclear ribonucleoprotein U-like 2	208906 at	-0.444	4092	9.523E-05	FALSE
97108 at	-0.095	3364	1421235 s at	0.045	6191	97108 at	-0.098	2315	1421235 s at	-0.316	362	3058	2431.0348	FALSE	RecQ protein-like 5	211468 s at	0.080	16894	1.115E-01	FALSE
95018 r at	0.118	1883	1454814 s at	0.179	2784	104039 at	0.131	2775	1433903 at	-0.097	4792	3058.5	1230.5209	FALSE	expressed sequence AU021838	NA	NA	NA	NA	
100078 at	0.150	1851	1417761 at	0.127	2444	100078 at	-0.079	5096	1417761 at	0.152	2846	3059.25	1418.0064	FALSE	apolipoprotein A-IV	206894 at	0.015	39534	8.652E-01	FALSE
103522 at	0.205	2377	1450805 at	0.105	2568	103522 at	0.134	1767	1444822 at	-0.076	5528	3060	1680.4192	FALSE	sarcoglycan, delta (dystrophin-associated glycoprotein)	228602 at	0.137	8357	4.065E-03	FALSE
100724 at	0.199	1151	1427587 at	0.070	5010	100724 at	0.094	3455	1439504 s at	0.176	2627	3060.75	1611.4479	TRUE	zinc finger protein 28	240034 at	-0.037	22524	2.858E-01	FALSE
161713 f at	0.183	2045	1420349 at	0.124	3441	97769 at	0.161	1141	1449828 at	0.076	5617	3061	1949.0333	TRUE	prostaglandin F receptor	207177 at	0.036	19522	1.854E-01	FALSE
102324 at	0.181	627	1417934 at	0.120	2337	102324 at	0.065	4127	1417934 at	0.093	5159	3062.5	1998.8733	TRUE	DnaJ (Hsp40) homolog, subfamily C, member 4	213919 at	0.025	32366	6.436E-01	FALSE
98946 at	0.354	830	1425241 a at	0.151	2738.5	98946 at	0.097	5172	1425241 a at	-0.147	3511	3062.875	1801.867	FALSE	WD repeat and SOCS box-containing 1	201294 s at	0.527	2657	1.275E-05	FALSE
94351 r at	0.254	286	1423627 at	-0.067	5681.5	94351 r at	0.123	2386	1423627 at	0.187	3898	3062.875	2289.3831	FALSE	NAD(P)H dehydrogenase, quinone 1	201467 s at	-0.227	7194	1.857E-03	FALSE
104208 at	-0.396	224	1435003 at	-0.180	1335	104208 at	-0.184	3286	1435003 at	0.038	7407	3063	3160.4836	FALSE	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	207081 s at	-0.779	1151	6.522E-07	FALSE
103913 at	0.196	2072	1449944 a at	0.163	1396.5	103913 at	-0.007	8188	1420644 a at	0.267	598	3063.625	3468.9649	FALSE	Sec61, alpha subunit 2 (S. cerevisiae)	219499 at	-0.280	6645	1.176E-03	FALSE
93650 i at	0.141	3117	1450837 at	0.152	1077	93650 i at	0.020	7426	1450837 at	0.298	635	3063.75	3102.5829	TRUE	proline rich protein HaeIII subfamily 1	NA	NA	NA	NA	
103507 at	-0.157	2392	1451161 a at	0.082	4734	103507 at	0.086	2614	1451161 a at	-0.163	2516	3064	1117.033	FALSE	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	207111 at	0.003	43388	9.692E-01	FALSE
161837 r at	-0.146	1501	1451625 a at	0.166	639.5	104726 at	0.113	1637	1451625 a at	0.002	8483	3065.125	3638.821	FALSE	RIKEN cDNA 1700013L23 gene	210324 at	-0.010	38776	8.436E-01	FALSE
103331 at	0.066	5339	1451085 at	0.235	269.5	103331 at	0.129	1656	1453450 at	-0.088	4999	3065.875	2497.434	FALSE	RIKEN cDNA C030006K11 gene	226710 at	0.006	42279	9.415E-01	FALSE
96539 at	0.215	2373	1437280 s at	-0.077	7095.5	96539 at	-0.156	2052	1418565 at	-0.281	744	3066.125	2777.1088	FALSE	Serpine1 mRNA binding protein 1	209669 s at	0.379	4602	1.729E-04	FALSE
98919 at	0.129	3793	1439234 a at	0.129	2887.5	98920 g at	-0.101	3705	1439454 x at	0.219	1882	3066.875	888.92542	FALSE	TM2 domain containing 2	224413 s at	-0.051	31500	6.126E-01	FALSE
100754 at	0.106	3606	1423011 at	0.100	2899	99391 at	0.147	1601	1438325 at	-0.138	4162	3067	1105.5807	FALSE	ecotropic viral integration site 1	221884 at	0.278	8178	3.656E-03	FALSE
96055 at	-0.699	90	1419473 a at	-0.305	2970.5	96055 at	-0.009	8471	1419473 a at	0.708	741	3068.125	3807.2443	FALSE	cholecystokinin	205827 at	-0.036	40783	9.014E-01	FALSE
103364 f at	-0.169	2614	1428189 at	0.142	1627.5	103364 f at	0.125	4237	1428189 at	0.121	3798	3069.125	1180.4818	FALSE	RIKEN cDNA 5730494M16 gene	213616 at	-0.372	3326	3.602E-05	FALSE
95940 f at	-0.367	1280	1435375 at	-0.081	5523	95940 f at	-0.590	481	1435375 at	-0.148	4993	3069.25	2557.4829	TRUE	cDNA sequence BC052328	219694 at	-0.012	36496	7.773E-01	FALSE
102632 at	0.103	2773	1422814 at	0.147	2132	102632 at	-0.041	5992	1458873 at	-0.256	1382	3069.75	2029.4072	FALSE	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	239002 at	-0.116	10688	1.465E-02	FALSE
92452 at	-0.096	4164	1460326 at	-0.109	5157	92452 at	-0.168	469	1440054 at	0.152	2490	3070	2053.7775	FALSE	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	215212 at	0.036	19325	1.787E-01	FALSE
99424 at	0.077	4010	1435747 at	-0.206	2300	99424 at	-0.105	5510	1435747 at	-0.418	461	3070.25	2178.4536	FALSE	fibroblast growth factor 14	221310 at	-1.042	42	3.454E-09	FALSE
96319 at	0.141	1937	1439377 x at	0.092	4810	96319 at	0.088	3580	1439377 x at	0.308	1954	3070.25	1392.4612	TRUE	cell division cycle 20 homolog (S. cerevisiae)	202870 s at	0.076	17184	1.195E-01	FALSE
98381 at	0.121	2372	1428453 at	0.093	5118	104404 at	-0.306	39	1428453 at	-0.101	4757	3071.5	2360.3975	FALSE	N-acetyltransferase 12	225679 at	-0.300	7223	1.900E-03	FALSE
97844 at	-0.547	273	1419248 at	-0.369	2811.5	97844 at	-0.066	7332	1419248 at	-0.226	1874	3072.625	3026.828	TRUE	regulator of G-protein signaling 2	202388 at	-0.547	6282	8.999E-04	TRUE
100290 f at	0.095	2844	1455488 at	0.062	5836.5	99777 s at	0.091	3405	1429665 at	-0.505	205	3072.625	2311.2061	FALSE	RIKEN cDNA 6230416J20 gene	218602 s at	0.050	13161	3.930E-02	FALSE
160061 at	0.115	2348	1451327 a at	0.096	3029	162484 r at	-0.072	3677	1451327 a at	-0.168	3237	3072.75	553.556	FALSE	transmembrane emp24 domain containing 1	203679 at	0.133	8744	5.025E-03	FALSE
103789 at	-0.269	1910	1451870 a at	0.060	5254	104352 at	0.151	2950	1424922 a at	0.511	2178	3073	1519.3731	FALSE	bromodomain containing 4	202103 at	0.154	6658	1.190E-03	FALSE
100933 at	-0.637	16	1437390 x at	0.210	587	100933 at	0.010	8239	1437390 x at	0.494	3450	3073	3757.4428	FALSE	syntaxin 1A (brain)	204729 s at	-0.136	9565	8.029E-03	FALSE
95447 at	0.110	3768	1428337 at	0.117	2102	95447 at	-0.097	3563	1450067 a at	0.231	2862	3073.75	755.09045	FALSE	RIKEN cDNA 1810034K20 gene	228763 at	-0.029	36390	7.741E-01	FALSE
97892 at	0.153	3809	1452350 at	0.140	2029.5	97892 at	0.048	5548	1452350 at	0.468	909	3073.875	2036.2634	TRUE	bromodomain containing 8	242265 at	0.174	6259	8.816E-04	TRUE
97172 s at	0.114	2767	1420408 a at	-0.021	7679.5	97172 s at	-0.190	557	1435752 s at	-0.255	1295	3074.625	3204.4244	FALSE	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	208561 at	0.126	11569	2.163E-02	FALSE
102967 at	0.020	7852	1423329 at	-0.203	1003	102967 at	0.242	2273	1423329 at	0.429	1172	3075	3234.0648	FALSE	ganglioside-induced differentiation-associated-protein 1	226269 at	-0.653	1863	3.055E-06	FALSE
162424 f at	-0.109	3047	1439037 at	-0.182	2226.5	162424 f at	0.304	2569	1439037 at	0.165	4459	3075.375	981.87367	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	208718 at	0.240	3316	3.552E-05	FALSE
103599 at	-0.042	6279	1451053 a at	-0.116	2428.5	103599 at	0.267	600	1451053 a at	-0.168	2995	3075.625	2367.5305	FALSE	transformed mouse 3T3 cell double minute 1	213761 at	0.340	8253	3.813E-03	FALSE
97937 at	-0.169	1723	1451739 at	0.116	3081	97937 at	-0.110	4578	1451021 a at	-0.322	2924	3076.5	1170.4331	FALSE	Kruppel-like factor 5	209212 s at	-0.289	5660	5.076E-04	FALSE
100474 at	0.072	5314	1420377 at	-0.252	339	100474 at	-0.039	6580	1420377 at	-0.890	73	3076.5	3356.3789	FALSE	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	221285 at	-0.094	18556	1.567E-01	FALSE
96940 at	0.275	909	1448519 at	0.165	1381.5	96940 at	0.076	3596	1448519 at	0.070	6427	3078.375	2521.0314	TRUE	TEA domain family member 2	226408 at	0.101	14684	6.488E-02	FALSE
162248 f at	-0.131	1893	1424242 at	0.103	3220	161769 r at	0.072	3804	1430531 at	0.135	3398	3078.75	827.41822	FALSE	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	205750 at	0.017	37652	8.104E-01	FALSE
104704 at	0.114	6394	1415986 at	0.164	1656	99672 at	-0.199	3185	1415986 at	0.214	1086	3080.25	2380.2964	FALSE	Chloride channel 4-2	205149 s at	-0.368	6050	7.275E-04	FALSE
104193 at	0.131	3791	1426986 at	-0.118	1903.5	104193 at	0.219	2579	1426985 s at	0.106	4050	3080.875	1013.504	FALSE	RIKEN cDNA 2810485I05 gene	NA	NA	NA	NA	
100683 r at	0.171	994	1425500 x at	0.099	3375	93928 f at	0.126	1593	1427443 at	-0.104	6362	3081	2409.7794	FALSE	Hypothetical protein LOC625794	NA	NA	NA	NA	
101776 at	0.111	4030	1434606 at	-0.165	1129	96771 at	-0.106	2822	1434606 at	-0.191	4355	3084	1460.7106	FALSE	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	226213 at	0.409	7342	2.055E-03	FALSE
162166 f at	-0.312	152	1418588 at	-0.090	5305.5	162166 f at	0.148	991	1418588 at	0.068	5891	3084.875	2932.0972	FALSE	vesicular membrane protein p24	239293 at	-0.691	1259	8.188E-07	FALSE
96846 at	0.116	4173	1417909 at	0.077	5205.5	96846 at	-0.210	253	1417909 at	-0.200	2708	3084.875	2148.0702	FALSE	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	210049 at	0.039	30043	5.584E-01	FALSE
95049 at	-0.252	1816	1452680 at	0.254	1448	95049 at	0.193	2844	1452680 at	0.072	6232	3085	2179.5886	FALSE	small nuclear ribonucleoprotein D2	200826 at	-0.237	6716	1.246E-03	FALSE
92945 at	-0.289	920	1421970 a at	0.040	7186	92946 f at	-0.358	64	1434146 at	-0.186	4171	3085.25	3256.3406	FALSE	glutamate receptor, ionotropic, AMPA2 (alpha 2)	236538 at	-0.995	1962	3.567E-06	FALSE
95735 at	0.002	8406	1428869 at	-0.161	1695	95735 at	-0.166	1144	1428869 at	-0.254	1097	3085.5	3557.3757	FALSE	nucleolar and coiled-body phosphoprotein 1	211949 s at	-0.110	13429	4.294E-02	FALSE
95118 r at	-0.121	2092	1423813 at	0.186	2365	95118 r at	-0.086	3668	1451128 s at	-0.134	4218	3085.75	1021.1145	FALSE	kinesin family member 22	216969 s at	-0.118	14479	6.096E-02	FALSE
104495 f at	0.137	3127	1419010 x at	0.345	209	104495 f at	0.105	3789	1449313 at	-0.099	5220	3086.25	2107.6824	FALSE	kallikrein 1-related peptidase b5	216699 s at	-0.089	19467	1.839E-01	FALSE
99100 at	-0.056	5169	1424272 at	0.102	3217	99100 at	0.086	2931	1460700 at	-0.217	1029	3086.5	1694.2376	FALSE	signal transducer and activator of transcription 3	225289 at	0.216	3206	3.041E-05	FALSE
95775 f at	0.105	3939	1420701 at	0.231	254	95775 f at	0.163	1017	1420701 at	-0.048	7137	3086.75	3132.5811	FALSE	kallikrein 1-related peptidase b1	210339 s at	0.020	34589	7.180E-01	FALSE
160085 at	-0.237	935	1448609 at	-0.127	2825	160085 at	-0.137	2034	1448609 at	-0.076	6564	3089.5	2442.5438	TRUE	thiosulfate sulfurtransferase, mitochondrial	209605 at	0.614	512	1.080E-07	FALSE
98504 at	-0.217	2075	1451041 at	-0.145	2249.5	98504 at	-0.486	506	1423592 at	-0.071	7528	3089.625	3061.0219	TRUE	Rho-associated coiled-coil forming kinase 2	202762 at	-0.548	524	1.122E-07	TRUE
97919 at	-0.245	3337	1428674 at	0.126	1924.5	97919 at	-0.121	5826	1456506 at	0.645	1273	3090.125	2017.1419	FALSE	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	230270 at	0.284	5098	2.996E-04	FALSE
161119 at	0.139	3907	1420557 at	0.086	3845.5	98376 at	0.083	4375	1437920 at	0.663	235	3090.625	1918.3776	TRUE	Eph receptor A5	231239 at	-0.048	21155	2.384E-01	FALSE
101626 at	0.159	1572	1420742 at	0.215	471.5	101626 at	0.073	4204	1420742 at	0.122	6119	3091.625	2554.5184	TRUE	a disintegrin and metallopeptidase domain 7	211238 at	0.043	23059	3.031E-01	FALSE
96295 at	0.277	2211	1454607 s at	0.200	2437	96295 at	0.280	1596	1454607 s at	0.103	6123	3091.75	2051.8417	TRUE	phosphoserine aminotransferase 1	223062 s at	0.422	4180	1.062E-04	TRUE
97705 at	0.047	5677	1428761 a at	0.131	1767	97705 at	0.148	2153	1428760 at	0.205	2772	3092.25	1772.1899	TRUE	small nuclear RNA activating complex, polypeptide 3	210465 s at	-0.188	9887	9.496E-03	FALSE
160608 at	0.136	1833	1438097 at	-0.038	6910	160608 at	0.092	2251	1438097 at	-0.221	1378	3093	2569.5186	FALSE	RAB20, member RAS oncogene family	237373 at	0.100	11785	2.372E-02	FALSE
97317 at	0.395	2603	1448136 at	-0.416	3083	161350 f at	0.110	1864	1443224 at	-0.104	4824	3093.5	1257.9084	FALSE	ectonucleotide pyrophosphatase/phosphodiesterase 2	209392 at	0.111	32215	6.390E-01	FALSE
99433 at	0.173	1801	1421410 a at	-0.115	2425	99433 at	-0.079	3531	1455405 at	0.144	4618	3093.75	1242.706	FALSE	proline-serine-threonine phosphatase-interacting protein 2	219938 s at	0.042	20470	2.151E-01	FALSE
96145 at	0.120	1887	1428740 a at	-0.113	3731	96145 at	-0.125	1800	1437594 x at	-0.171	4960	3094.5	1529.5979	FALSE	phosphatidylinositol glycan, class T	217770 at	-0.015	40186	8.824E-01	FALSE
93543 f at	-0.301	251	1416416 x at	-0.256	190.5	93543 f at	0.030	6501	1416416 x at	-0.118	5436	3094.625	3346.9176	FALSE	glutathione S-transferase, mu 1	205752 s at	0.382	10276	1.183E-02	FALSE
95085 r at	0.208	618	1417772 at	0.149	1061	95084 f at	0.217	2860	1417772 at	0.041	7843	3095.5	3310.1567	TRUE	Glyoxylate reductase/hydroxypyruvate reductase	214864 s at	0.141	14584	6.276E-02	FALSE
102936 at	0.128	3369	1435758 at	0.121	3841.5	102936 at	0.119	3466	1460329 at	0.233	1706	3095.625	948.56008	TRUE	similar to Beta-1,4-galactosyltransferase 6 (Beta-1,4-GalTase 6) (Beta4Gal-T6) (b4Gal-T6) (UDP-galactose:beta-N-ace	NA	NA	NA	NA	
104250 at	-0.142	1575	1434694 at	-0.164	1689.5	104250 at	0.119	2642	1434694 at	-0.105	6478	3096.125	2304.7576	FALSE	leucine rich repeat containing 8A	233487 s at	0.358	2377	7.747E-06	FALSE
160666 at	0.238	2787	1428502 at	0.241	1411.5	160666 at	0.253	1645	1428502 at	-0.079	6542	3096.375	2374.4008	FALSE	ARP6 actin-related protein 6 homolog (yeast)	241794 at	0.026	29130	5.255E-01	FALSE
92625 at	-0.074	5358	1448808 a at	0.242	2348.5	92625 at	0.257	2031	1448808 a at	0.190	2648	3096.375	1528.6518	FALSE	expressed in non-metastatic cells 2, protein	NA	NA	NA	NA	
94309 g at	0.134	2341	1422540 at	-0.226	754	94309 g at	-0.064	3968	1451119 a at	-0.115	5327	3097.5	1982.6518	FALSE	fibulin 1	202994 s at	0.227	9915	9.656E-03	FALSE
95568 at	0.077	5386	1451640 a at	0.106	4717.5	95568 at	0.244	598	1443559 at	-0.229	1690	3097.875	2315.9007	FALSE	RIKEN cDNA 1500011J06 gene	202301 s at	0.130	14024	5.270E-02	FALSE
94322 at	-0.148	2509	1415993 at	-0.200	1750	94322 at	-0.074	4631	1415993 at	0.159	3503	3098.25	1248.7512	FALSE	squalene epoxidase	213577 at	0.130	10365	1.234E-02	FALSE
95086 at	0.088	5147	1428201 at	0.104	2455	95086 at	0.198	2064	1428201 at	0.134	2734	3100	1392.0591	TRUE	RIKEN cDNA 2310036O22 gene	230213 at	0.055	16370	9.911E-02	FALSE
98507 at	-0.107	2855	1426464 at	-0.097	4789	98507 at	0.304	2401	1426464 at	-0.252	2360	3101.25	1147.3071	FALSE	nuclear receptor subfamily 1, group D, member 1	31637 s at	0.066	25252	3.814E-01	FALSE
93120 f at	-0.462	3736	1437367 at	0.130	2802.5	93120 f at	0.231	1344	1425336 x at	-0.522	4525	3101.875	1367.1319	FALSE	histocompatibility 2, K1, K region	216526 x at	0.369	7156	1.801E-03	FALSE
102698 at	0.126	2321	1449888 at	-0.213	2553	102698 at	-0.043	7127	1435436 at	-0.303	409	3102.5	2849.8091	FALSE	endothelial PAS domain protein 1	242868 at	0.181	12860	3.542E-02	FALSE
94110 f at	0.430	322	1427518 at	0.078	5249	94110 f at	-0.337	813	1427518 at	0.100	6029	3103.25	2952.1096	FALSE	cDNA sequence D10627	NA	NA	NA	NA	
103456 at	-0.132	3250	1455741 a at	-0.184	692	103456 at	-0.003	8311	1434177 at	0.914	164	3104.25	3723.5963	FALSE	endothelin converting enzyme 1	201749 at	0.288	1835	2.862E-06	FALSE
94197 at	0.074	4414	1421268 at	-0.149	2011	94197 at	-0.464	283	1439863 at	0.141	5716	3106	2428.3958	FALSE	UDP-glucose ceramide glucosyltransferase	224967 at	-0.364	8935	5.578E-03	FALSE
160944 at	0.176	1337	1418831 at	0.052	6325	160944 at	0.097	2917	1418831 at	-0.244	1845	3106	2244.7839	FALSE	plakophilin 3	209873 s at	0.055	21414	2.474E-01	FALSE
103094 at	-0.012	7984	1449509 at	0.225	207	103094 at	0.089	2997	1452502 at	-0.276	1237	3106.25	3449.837	FALSE	small EDRK-rich factor 1	NA	NA	NA	NA	
95453 f at	-0.209	3124	1417421 at	0.119	3583.5	95453 f at	0.370	769	1419814 s at	-0.162	4949	3106.375	1740.3589	FALSE	S100 calcium binding protein A1	205334 at	0.247	9882	9.474E-03	FALSE
101913 at	0.159	1290	1450787 at	0.154	1920	161451 r at	0.119	2423	1420295 x at	0.101	6795	3107	2501.9764	TRUE	chloride channel 5	232128 s at	0.072	16010	9.091E-02	FALSE
97551 at	-0.217	874	1425551 at	-0.189	1057	97551 at	0.077	4299	1425551 at	0.163	6202	3108	2594.1392	FALSE	huntingtin interacting protein 1 related	38340 at	0.409	569	1.268E-07	FALSE
99653 at	-0.054	5187	1438626 x at	0.234	1062	99653 at	0.118	3191	1422128 at	-0.255	2994	3108.5	1686.0448	FALSE	ribosomal protein L14	200074 s at	-0.290	6587	1.118E-03	FALSE
97834 g at	-0.202	3616	1430634 a at	-0.514	115	97833 at	-0.205	3855	1416069 at	0.122	4848	3108.5	2065.73	FALSE	phosphofructokinase, platelet	201037 at	0.167	21748	2.597E-01	FALSE
96017 at	-0.113	3052	1416628 at	0.163	1912.5	96017 at	0.085	3581	1416628 at	0.122	3890	3108.875	869.40711	FALSE	RIKEN cDNA 0610006I08 gene	238981 at	-0.093	11939	2.527E-02	FALSE
102613 at	0.122	2415	1426071 at	0.083	4319	102613 at	0.100	3309	1426071 at	0.181	2396	3109.75	911.79361	TRUE	TGF-beta1-induced anti-apoptotic factor 2	NA	NA	NA	NA	
94908 r at	0.093	4943	1416367 at	0.259	1278	94908 r at	0.336	168	1416367 at	0.084	6051	3110	2829.6618	TRUE	RIKEN cDNA 1110001J03 gene	226780 s at	0.165	9373	7.204E-03	TRUE
160196 at	-0.186	2623	1432029 a at	-0.155	2461	160196 at	0.106	5698	1423956 at	0.219	1659	3110.25	1775.9049	FALSE	stromal membrane-associated protein 1	218137 s at	-0.106	25016	3.731E-01	FALSE
99340 at	-0.145	3665	1455168 a at	0.026	7714	99340 at	0.333	314	1440120 at	-0.242	752	3111.25	3409.9176	FALSE	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	200651 at	0.136	13639	4.595E-02	FALSE
96276 r at	0.096	3180	1448375 at	-0.140	2165	162226 r at	0.114	3322	1448375 at	0.139	3779	3111.5	680.789	FALSE	transmembrane 9 superfamily member 3	239626 x at	-0.088	13225	4.005E-02	FALSE
94051 at	0.081	3590	1425622 at	-0.295	918	94051 at	0.027	6499	1425622 at	0.222	1440	3111.75	2537.024	FALSE	EGF-like repeats and discoidin I-like domains 3	233668 at	0.272	3613	5.368E-05	FALSE
99828 at	-0.282	573	1456430 at	0.130	4295	99828 at	0.263	2655	1429780 at	-0.092	4924	3111.75	1944.0681	FALSE	coiled-coil domain containing 39	241863 x at	0.055	21740	2.595E-01	FALSE
97818 at	0.123	3887	1460182 at	0.121	3041.5	97818 at	0.255	1580	1460182 at	0.116	3939	3111.875	1100.9917	TRUE	sorting nexin 4	205329 s at	-0.033	32656	6.525E-01	FALSE
160774 at	-0.023	7576	1423326 at	-0.121	2066.5	160774 at	-0.109	2281	1423326 at	-0.485	529	3113.125	3075.8636	TRUE	ectonucleoside triphosphate diphosphohydrolase 1	239418 x at	0.093	8116	3.529E-03	FALSE
103629 g at	0.089	3591	1421299 a at	-0.180	1428.5	103629 g at	0.090	3650	1421299 a at	0.221	3785	3113.625	1126.3474	FALSE	lymphoid enhancer binding factor 1	221558 s at	0.515	1166	6.642E-07	FALSE
100990 g at	-0.304	1437	1422157 a at	-0.135	5801.5	100989 at	0.135	3032	1445697 at	0.348	2188	3114.625	1906.0591	FALSE	integrin beta 1 binding protein 1	203336 s at	-0.667	3063	2.500E-05	FALSE
101059 at	0.212	1987	1437853 x at	0.261	480	101059 at	0.067	5627	1438978 x at	0.134	4365	3114.75	2315.7614	TRUE	necdin	209550 at	-0.338	9306	6.983E-03	FALSE
93653 r at	0.063	4598	1421862 a at	-0.363	374.5	93652 i at	-0.183	1174	1421863 at	-0.268	6313	3114.875	2810.9497	FALSE	vesicle-associated membrane protein 1	207101 at	-0.049	23987	3.377E-01	FALSE
96888 at	0.070	6060	1430123 a at	0.225	1077	96888 at	0.122	3785	1430123 a at	0.245	1543	3116.25	2291.0366	TRUE	aldo-keto reductase family 1, member A4 (aldehyde reductase)	201900 s at	-0.189	6664	1.197E-03	FALSE
93757 at	0.100	3567	1423670 a at	-0.071	5142	103680 at	-0.197	2165	1423670 a at	-0.236	1593	3116.75	1584.5088	FALSE	signal recognition particle receptor ('docking protein')	200917 s at	-0.213	8054	3.377E-03	FALSE
93325 at	-0.195	3253	1451093 at	0.118	3174	93325 at	-0.377	608	1451093 at	0.148	5433	3117	1973.2108	FALSE	polymerase (RNA) II (DNA directed) polypeptide E	213887 s at	-0.334	5866	6.154E-04	FALSE
94378 at	-0.066	4551	1426037 a at	-0.365	1102.5	161609 at	0.270	1096	1451452 a at	0.147	5720	3117.375	2378.6982	FALSE	regulator of G-protein signaling 16	209324 s at	-0.003	43701	9.772E-01	FALSE
100116 at	0.056	5313	1419153 at	-0.080	4877	100116 at	0.138	1560	1419153 at	0.429	720	3117.5	2315.878	FALSE	RIKEN cDNA 2810417H13 gene	211713 x at	0.175	11967	2.557E-02	FALSE
100542 at	0.123	3175	1450719 at	-0.077	4200.5	100542 at	0.164	702	1450719 at	-0.120	4393	3117.625	1696.8339	FALSE	meprin 1 alpha	206000 at	-0.007	41795	9.288E-01	FALSE
100370 at	0.071	4113	1451674 at	-0.226	1029.5	100370 at	-0.266	1013	1445933 at	-0.084	6318	3118.375	2583.4655	FALSE	solute carrier family 12, member 5	210040 at	-1.050	1311	9.002E-07	FALSE
97456 at	-0.195	3065	1428082 at	0.099	2846.5	97456 at	0.067	6222	1428082 at	0.415	340	3118.375	2410.2988	FALSE	acyl-CoA synthetase long-chain family member 5	218322 s at	0.154	15542	8.070E-02	FALSE
96733 at	-0.234	956	1425266 a at	-0.201	1991	96733 at	-0.107	5887	1459768 x at	0.157	3642	3119	2151.4573	FALSE	RAP1, GTP-GDP dissociation stimulator 1	209444 at	-0.396	5214	3.403E-04	FALSE
99039 g at	-0.253	1175	1460726 at	-0.094	4655.5	99039 g at	-0.490	752	1460726 at	-0.068	5895	3119.375	2546.1626	TRUE	adenylosuccinate synthetase, non muscle	227310 at	-0.055	22415	2.823E-01	FALSE
93646 at	0.156	1200	1420875 at	0.080	4969	93646 at	-0.311	983	1420875 at	0.111	5330	3120.5	2349.1892	FALSE	protein tyrosine kinase 9	201745 at	0.365	5914	6.428E-04	FALSE
95150 at	-0.276	187	1417128 at	-0.062	5269.5	95152 g at	-0.094	3831	1417128 at	0.180	3199	3121.625	2139.6721	FALSE	pleckstrin homology domain containing, family O member 1	218223 s at	-0.068	27046	4.449E-01	FALSE
162331 f at	0.143	3176	1418752 at	0.085	3523.5	99548 at	-0.075	3385	1418752 at	0.167	2405	3122.375	499.12446	FALSE	aldehyde dehydrogenase family 3, subfamily A1	205623 at	0.048	29437	5.366E-01	FALSE
102247 at	0.199	549	1420971 at	-0.025	7539.5	102247 at	-0.184	822	1450066 at	0.123	3579	3122.375	3247.2288	FALSE	ubiquitin protein ligase E3 component n-recognin 1	238528 at	-0.028	29678	5.454E-01	FALSE
161939 f at	0.061	6561	1416059 at	0.129	2797.5	161939 f at	-0.198	699	1416059 at	0.209	2440	3124.375	2467.6609	FALSE	SEC23B (S. cerevisiae)	201583 s at	-0.133	17177	1.192E-01	FALSE
100691 at	-0.152	2244	1421705 at	-0.118	2915	100691 at	0.130	1826	1439204 at	-0.140	5513	3124.5	1654.308	FALSE	sodium channel, voltage-gated, type III, alpha	210432 s at	-1.023	2169	5.185E-06	FALSE
99834 at	0.150	2026	1421017 at	0.087	2919	99834 at	-0.028	7263	1442950 at	0.829	294	3125.5	2965.7962	FALSE	neuregulin 3	234505 at	0.163	6750	1.278E-03	FALSE
160824 at	-0.012	8182	1428657 at	-0.165	2553	160824 at	-0.485	103	1428657 at	-0.449	1664	3125.5	3519.8218	TRUE	ras responsive element binding protein 1	215032 at	0.111	13242	4.038E-02	FALSE
160257 at	-0.117	4494	1416036 at	-0.232	509.5	160257 at	-0.195	1662	1448184 at	-0.078	5838	3125.875	2464.125	TRUE	FK506 binding protein 1a	214119 s at	-0.837	238	2.608E-08	TRUE
95513 at	0.074	4497	1438179 s at	0.119	2928.5	95513 at	0.243	2505	1438179 s at	0.173	2586	3129.125	930.20592	TRUE	signal transducer and activator of transcription interacting protein 1	231713 s at	0.097	14978	7.068E-02	FALSE
99970 at	0.000	8509	1419054 a at	0.143	1870	99970 at	0.148	972	1419055 a at	0.237	1169	3130	3606.6478	TRUE	protein tyrosine phosphatase, non-receptor type 21	226380 at	0.312	5339	3.765E-04	TRUE

101470 at	0.095	3487	1434793 at	-0.040	7233.5	101470 at	-0.180	428	1434793 at	-0.290	1379	3131.875	3018.4407	FALSE	WD repeat domain 78	229816 at	0.450	9844	9.247E-03	FALSE
98855 r at	-0.096	3689	1435169 at	-0.124	1773	98855 r at	-0.056	6181	1435169 at	-0.248	885	3132	2345.3884	TRUE	RIKEN cDNA A930001N09 gene	225957 at	0.389	3036	2.381E-05	FALSE
160263 r at	-0.035	6913	1452066 a at	-0.155	3007	160263 r at	-0.555	485	1452066 a at	-0.198	2124	3132.25	2728.5075	TRUE	Nedd4 family interacting protein 2	224802 at	-0.464	2864	1.770E-05	TRUE
102409 at	-0.228	1790	1448703 at	0.425	462.5	102409 at	0.065	6333	1448703 at	0.119	3946	3132.875	2571.3931	FALSE	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	219119 at	0.017	38777	8.436E-01	FALSE
93906 s at	-0.091	4073	1432826 a at	0.208	557.5	93905 at	-0.092	2913	1427717 at	0.098	4988	3132.875	1915.396	FALSE	CD80 antigen	207176 s at	-0.010	41270	9.144E-01	FALSE
92890 at	0.234	1634	1421053 at	-0.235	2970.5	92890 at	-0.431	1869	1450108 at	0.318	6060	3133.375	2036.2082	FALSE	kinesin family member 1A	203850 s at	-0.058	12055	2.651E-02	FALSE
99545 at	0.178	2523	1432075 a at	0.109	3260	99545 at	0.265	138	1432075 a at	-0.095	6617	3134.5	2676.8452	FALSE	tektin 1	239216 at	0.404	8739	5.016E-03	FALSE
102984 g at	0.088	5738	1448208 at	0.119	3586.5	102983 at	0.484	299	1416081 at	0.321	2919	3135.625	2241.2059	TRUE	MAD homolog 1 (Drosophila)	227798 at	0.452	3317	3.552E-05	TRUE
97963 at	-0.139	1350	1416206 at	0.032	6917.5	162007 i at	0.099	2850.5	1416206 at	-0.251	1427	3136.25	2613.5371	FALSE	signal-induced proliferation associated gene 1	204164 at	0.182	5226	3.434E-04	FALSE
103248 at	0.016	7682	1449429 at	0.262	431	103248 at	0.091	4330	1449429 at	0.628	106	3137.25	3586.5336	TRUE	FK506 binding protein 1b	209931 s at	-0.524	446	8.445E-08	FALSE
103892 r at	-0.133	3575	1450744 at	-0.205	3004	103892 r at	0.188	2139	1450744 at	0.215	3832	3137.5	750.23574	FALSE	elongation factor RNA polymerase II 2	235592 at	0.704	2299	6.733E-06	FALSE
98545 at	-0.202	1700	1438938 x at	0.077	4056.5	98545 at	-0.185	3408	1438938 x at	0.163	3390	3138.625	1007.9498	FALSE	prohibitin 2	201600 at	-0.045	25384	3.861E-01	FALSE
160519 at	0.093	5244	1419089 at	-0.428	29	160519 at	0.056	7144	1419088 at	-0.473	143	3140	3611.0553	FALSE	tissue inhibitor of metalloproteinase 3	201150 s at	0.288	9360	7.175E-03	FALSE
160149 at	0.296	1557	1453095 at	-0.170	1393	101933 at	-0.256	1783	1453095 at	-0.035	7828	3140.25	3129.2539	FALSE	RAB10, member RAS oncogene family	222980 at	0.208	9755	8.859E-03	FALSE
102980 at	-0.140	1890	1418082 at	-0.087	5680	102980 at	-0.200	2101	1415683 at	0.157	2897	3142	1746.6782	FALSE	N-myristoyltransferase 1	201157 s at	0.450	4449	1.450E-04	FALSE
95082 at	-0.110	3021	1423062 at	0.063	5757.5	95082 at	0.137	1345	1458268 s at	-0.145	2448	3142.875	1876.7279	FALSE	insulin-like growth factor binding protein 3	210095 s at	0.395	8761	5.061E-03	FALSE
100946 at	-0.341	227	1452318 a at	-0.101	3470	100946 at	-0.181	4352	1452318 a at	0.436	4523	3143	1998.0045	FALSE	heat shock protein 1B	202581 at	0.841	8757	5.057E-03	FALSE
160936 at	0.188	543	1423732 at	-0.080	6634.5	98956 at	0.127	2076	1444506 at	0.175	3319	3143.125	2589.7257	FALSE	translocating chain-associating membrane protein 1	201398 s at	0.463	2236	5.936E-06	FALSE
100335 at	0.140	2508	1450283 at	0.104	2553	100335 at	0.087	4365	1450283 at	0.165	3150	3144	864.99595	TRUE	ATPase, Cu++ transporting, beta polypeptide	233796 at	-0.068	21529	2.509E-01	FALSE
160692 at	-0.042	6322	1418340 at	0.144	2538.5	162181 f at	0.180	2081	1418340 at	-0.518	1637	3144.625	2149.9869	FALSE	Fc receptor, IgE, high affinity I, gamma polypeptide	204232 at	0.162	20538	2.177E-01	FALSE
92763 at	0.121	2544	1435006 s at	0.076	4069	92763 at	-0.249	1883	1419931 at	-0.138	4083	3144.75	1108.6726	FALSE	ATP-binding cassette, sub-family B (MDR/TAP), member 7	NA	NA	NA	NA	
98073 at	-0.161	906	1451435 at	-0.075	4523.5	98073 at	0.029	6483	1451435 at	-0.277	667	3144.875	2839.9596	FALSE	cut-like 1 (Drosophila)	214743 at	0.318	1399	1.131E-06	FALSE
94036 at	-0.068	4159	1436801 x at	-0.097	3798	94036 at	0.100	2731	1436801 x at	-0.191	1892	3145	1032.1515	FALSE	CDC42 effector protein (Rho GTPase binding) 4	218062 x at	0.421	1916	3.317E-06	FALSE
98118 at	0.224	999	1422241 a at	0.302	768	98118 at	0.340	2729	1422241 a at	-0.015	8084	3145	3406.9645	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	202298 at	-0.260	6357	9.518E-04	FALSE
94201 at	-0.180	3437	1450120 at	-0.166	3004	162255 s at	0.185	6074	1450120 at	0.582	69	3146	2459.4009	FALSE	sodium channel, voltage-gated, type I, alpha	210383 at	-0.409	4213	1.102E-04	FALSE
93372 at	-0.245	4016	1434555 at	0.109	1970.5	93372 at	-0.417	5158	1421918 at	0.272	1444	3147.125	1740.0808	FALSE	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	235954 at	0.184	8589	4.606E-03	FALSE
94103 at	0.176	1220	1427636 at	0.177	699	94103 at	0.057	5689	1427636 at	-0.086	4981	3147.25	2551.5585	FALSE	testis specific protein-Y encoded, pseudogene	NA	NA	NA	NA	
92357 at	-0.045	5672	1423378 at	-0.108	2677.5	92357 at	-0.101	3246	1423378 at	-0.364	994	3147.375	1935.7397	TRUE	a disintegrin and metallopeptidase domain 23	244463 at	-0.891	438	8.131E-08	TRUE
92851 at	0.052	6202	1417496 at	0.160	911	92851 at	0.060	4520	1417497 at	-0.316	968	3150.25	2643.5991	FALSE	ceruloplasmin	227253 at	0.886	5031	2.768E-04	FALSE
160520 at	-0.199	539	1416487 a at	-0.027	7659	160520 at	0.132	1854	1448363 at	-0.175	2551	3150.75	3119.1247	FALSE	ves-associated protein 1	224894 at	0.913	1112	6.045E-07	FALSE
99070 at	0.199	1852	1451383 a at	0.295	772.5	99070 at	0.123	5527	1428210 s at	-0.132	4452	3150.875	2212.2869	FALSE	conserved helix-loop-helix ubiquitous kinase	209666 s at	0.032	34938	7.281E-01	FALSE
160667 at	-0.222	1871	1450106 a at	0.030	7226	161808 f at	0.160	1575	1445957 at	0.290	1935	3151.75	2720.6895	FALSE	Ena-vasodilator stimulated phosphoprotein	217838 s at	-0.516	954	3.909E-07	FALSE
94030 at	0.018	7940	1433594 at	0.237	912	94030 at	0.266	604	1442321 at	0.250	3152	3152	3387.9614	TRUE	COMM domain containing 2	223491 at	0.091	18668	1.600E-01	FALSE
103205 at	0.155	3298	1420635 a at	0.104	2520	103205 at	-0.062	4087	1420635 a at	-0.201	2709	3153.5	705.03073	FALSE	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	204158 s at	0.126	11008	1.722E-02	FALSE
161021 at	0.117	3771	1417923 at	0.112	2724.5	161021 at	0.051	5796	1417924 at	0.574	323	3153.625	2277.4169	TRUE	p21 (CDKN1A)-activated kinase 3	236277 at	-0.564	3219	3.102E-05	FALSE
100540 at	-0.138	5210	1453528 at	0.173	2102	100540 at	-0.143	3290	1426807 at	0.233	2019	3155.25	1487.7897	FALSE	leukotriene A4 hydrolase	208771 s at	-0.020	36726	7.838E-01	FALSE
101221 at	0.089	3730	1419991 at	0.249	1082	101221 at	-0.031	6747	1456442 at	-0.251	1063	3155.5	2702.2756	FALSE	RAB3A interacting protein (rabin3)-like 1	219579 at	0.026	34914	7.278E-01	FALSE
160265 at	0.060	6508	1415723 at	-0.124	2706	160265 at	0.170	3148	1454664 a at	0.457	262	3156	2569.9354	FALSE	eukaryotic translation initiation factor 5	208290 s at	-0.302	13886	5.036E-02	FALSE
102561 at	-0.161	2200	1450640 x at	0.293	518	102561 at	0.134	3122	1422525 at	0.051	6789	3157.25	2650.3345	FALSE	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	207335 x at	0.096	18789	1.634E-01	FALSE
103252 at	0.113	2360	1450875 at	-0.406	539.5	103252 at	0.097	3359	1450875 at	-0.112	6371	3157.375	2439.7483	FALSE	G protein-coupled receptor 37	214586 at	0.147	21980	2.675E-01	FALSE
162278 r at	0.229	803	1416016 at	0.100	2870	162278 r at	0.038	5623	1448177 at	-0.137	3335	3157.75	1977.9217	FALSE	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	202307 s at	0.214	12009	2.601E-02	FALSE
95075 at	0.240	636	1426447 at	-0.120	3854.5	95075 at	-0.024	7437	1426447 at	-0.249	705	3158.125	3223.4891	FALSE	nucleoporin 35	225470 at	-0.176	12954	3.647E-02	FALSE
100971 at	0.076	5525	1420593 a at	0.119	2384	100971 at	0.099	3564	1420593 a at	-0.255	1160	3158.25	1858.1895	FALSE	TEA domain family member 3	209454 s at	0.047	24283	3.464E-01	FALSE
93014 at	-0.219	2086	1448203 at	0.309	2527	93014 at	0.151	1036	1448203 at	0.056	6986	3158.75	2627.0269	FALSE	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	NA	NA	NA	NA	
100502 at	0.044	5852	1426036 a at	0.121	2268	100502 at	-0.064	4337	1440374 at	-0.539	183	3160	2469.169	FALSE	phosphodiesterase 1C	239218 at	0.314	10828	1.584E-02	FALSE
102033 at	-0.134	3769	1450662 at	-0.143	2855	102033 at	-0.094	3293	1450662 at	-0.239	2723	3160	473.48495	TRUE	testis specific protein kinase 1	204106 at	-0.121	15150	7.363E-02	FALSE
100694 at	-0.140	2354	1416277 a at	0.193	1924.5	100694 at	0.091	2986.5	1416277 a at	-0.086	5378	3160.75	1541.1814	FALSE	ribosomal protein, large, P1	200763 s at	0.075	20389	2.129E-01	FALSE
93810 at	-0.203	1041	1448118 a at	-0.129	2109	93810 at	0.046	5897	1448118 a at	-0.210	3600	3161.75	2103.9264	FALSE	cathepsin D	200766 at	0.159	11526	2.123E-02	FALSE
161924 f at	0.146	2307	1417950 a at	0.135	2724.5	99648 at	0.144	3050	1417950 a at	-0.112	4569	3162.625	985.66774	FALSE	apolipoprotein A-II	219465 at	0.026	29330	5.326E-01	FALSE
161304 r at	0.087	3722	1418647 at	-0.216	665.5	98403 at	0.046	5391	1418647 at	-0.136	2872	3162.625	1966.2699	FALSE	guanine nucleotide binding protein, related sequence 1	NA	NA	NA	NA	
101943 at	0.178	1173	1434117 at	0.060	5432	101943 at	0.114	2496	1434117 at	0.136	3555	3164	1798.7968	TRUE	transcription elongation factor B (SIII), polypeptide 3	202818 s at	0.060	27475	4.605E-01	FALSE
162417 at	0.149	3027	1428684 at	0.135	2606	160723 at	0.306	141	1428684 at	0.067	6883	3164.25	2786.8514	TRUE	RIKEN cDNA 1500001M20 gene	234697 x at	0.189	4670	1.897E-04	TRUE
95041 at	-0.083	3709	1449046 a at	-0.145	1540	95041 at	-0.051	4849	1449046 a at	-0.219	2559	3164.25	1430.5769	TRUE	Josephin domain containing 2	227096 at	0.099	10775	1.537E-02	FALSE
92528 at	-0.504	35	1455363 at	-0.211	921	92528 at	-0.010	8145	1455363 at	-0.237	3558	3164.75	3641.7617	TRUE	brain-specific angiogenesis inhibitor 1	206083 at	-0.098	15958	9.013E-02	FALSE
102819 at	0.361	423	1418046 at	0.151	3226	102819 at	0.103	5584	1418046 at	0.129	3427	3165	2116.7971	TRUE	nucleosome assembly protein 1-like 2	219368 at	-0.695	3102	2.625E-05	FALSE
104336 at	-0.002	8423	1424840 at	0.135	2274.5	104336 at	0.169	1417	1424841 s at	-0.436	550	3166.125	3574.5992	FALSE	ribokinase	57540 at	0.032	31128	6.011E-01	FALSE
97703 at	-0.058	5198	1450423 s at	0.201	1605	160585 at	0.236	1668	1425884 at	0.143	4197	3167	1814.0843	FALSE	brix domain containing 1	225866 at	-0.089	21718	2.592E-01	FALSE
92690 at	0.061	6293	1419020 at	0.113	2804.5	92690 at	0.107	2369	1419020 at	0.235	1204	3167.625	2190.3922	TRUE	gastric intrinsic factor	207033 at	0.031	30627	5.795E-01	FALSE
162127 r at	0.126	3913	1435372 a at	0.226	308	100125 at	-0.112	4678	1435372 a at	-0.144	3772	3167.75	1947.6089	FALSE	proliferation-associated 2G4	214794 at	-0.139	13832	4.949E-02	FALSE
100435 at	0.125	3002	1426110 a at	-0.335	155.5	100435 at	0.024	7554	1426110 a at	0.366	1962	3168.375	3151.4094	FALSE	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	204037 at	0.574	4593	1.712E-04	FALSE
104712 at	0.066	4739	1424942 a at	-0.090	4180.5	104712 at	0.158	1374	1424942 a at	-0.177	2387	3170.125	1562.2181	FALSE	myelocytomatosis oncogene	202431 s at	0.052	26424	4.218E-01	FALSE
161489 r at	0.120	4603	1437008 x at	-0.146	2593.5	160378 at	-0.072	4200	1456057 x at	-0.309	1287	3170.875	1526.6987	FALSE	transmembrane protein 109	201361 at	0.172	3409	4.079E-05	FALSE
92638 at	-0.146	3311	1456390 at	-0.150	2829	92638 at	0.085	6359	1444875 at	0.419	185	3171	2530.8828	FALSE	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	208652 at	-0.329	4790	2.149E-04	FALSE
92271 at	0.172	893	1456342 at	0.099	4116	92271 at	-0.100	3813	1456342 at	0.125	3867	3172.25	1525.2194	FALSE	paired box gene 6	205646 s at	0.642	1154	6.543E-07	FALSE
95643 at	0.444	417	1415770 at	-0.126	5910	95643 at	0.189	1073	1455940 x at	0.246	5290	3172.5	2827.1536	FALSE	WD repeat domain 6	217734 s at	0.349	3045	2.422E-05	FALSE
104031 at	0.126	2506	1428853 at	-0.421	450	104031 at	-0.007	8123	1439663 at	-0.254	1614	3173.25	3405.5151	FALSE	patched homolog 1	209815 at	0.444	2913	1.881E-05	FALSE
93921 at	0.226	514	1433890 a at	-0.129	3866	93912 at	-0.294	1631	1433890 a at	-0.079	6687	3174.5	2724.9759	FALSE	HLA-B-associated transcript 3	210208 x at	-0.147	10140	1.086E-02	FALSE
98874 at	0.113	3628	1435350 at	-0.061	5647	104190 at	0.179	755	1435350 at	0.196	2668	3174.5	2035.4722	FALSE	Tnf receptor-associated factor 6	205558 at	0.066	20699	2.233E-01	FALSE
162021 r at	0.179	972	1416434 at	0.075	5535.5	162021 r at	-0.106	3263	1416434 at	-0.167	2929	3174.875	1870.2432	FALSE	Bcl2-like 10	236491 at	-0.140	6340	9.387E-04	FALSE
100596 at	0.095	2522	1417580 s at	0.036	6958.5	100596 at	0.117	2392	1450699 at	-0.502	829	3175.375	2636.7964	FALSE	selenium binding protein 1	214433 s at	0.525	3769	6.454E-05	FALSE
102991 s at	-0.186	1095	1454987 a at	-0.027	7061.5	102992 at	-0.128	2877	1454987 a at	-0.205	1669	3175.625	2694.941	TRUE	H2-K region expressed gene 6	213540 at	0.090	20359	2.119E-01	FALSE
161567 r at	-0.180	887	1423176 at	-0.194	3190	161567 r at	0.049	6765	1440844 at	0.166	1863	3176.25	2571.9387	FALSE	transducer of ErbB-2.1	202704 at	0.590	4766	2.099E-04	FALSE
98106 at	-0.061	5185	1448801 a at	0.089	3698.5	98106 at	-0.213	387	1439371 x at	-0.121	3435	3176.375	2012.8494	FALSE	translocase of inner mitochondrial membrane 44	203093 s at	0.033	30311	5.677E-01	FALSE
101327 at	0.135	2705	1415983 at	0.061	6536	101327 at	-0.135	1884	1415983 at	-0.463	1582	3176.75	2289.2167	FALSE	lymphocyte cytosolic protein 1	208885 at	0.077	21090	2.366E-01	FALSE
99068 at	0.131	1783	1417570 at	0.058	5403	99068 at	-0.060	4929	1444271 at	0.317	600	3178.75	2352.9225	FALSE	anaphase promoting complex subunit 1	229267 at	-0.324	1457	1.283E-06	FALSE
97525 at	0.007	8157	1422704 at	0.110	3121	97525 at	0.189	819	1422703 at	0.279	619	3179	3507.4705	TRUE	glycerol kinase	214681 at	-0.027	24553	3.563E-01	FALSE
96516 at	0.164	1488	1427967 at	-0.071	5027.5	96516 at	0.160	1916	1434407 at	0.106	4287	3179.625	1741.5764	FALSE	SLIT-ROBO Rho GTPase activating protein 2	213329 at	0.166	7958	3.198E-03	FALSE
103082 at	0.261	397	1460450 at	0.097	2996	103082 at	0.052	6257	1437521 s at	0.149	3069	3179.75	2398.5548	TRUE	RIKEN cDNA E230022H04 gene	223297 at	0.167	6795	1.326E-03	TRUE
95406 at	-0.119	3384	1424365 at	0.203	1505.5	95406 at	0.314	210	1424365 at	-0.033	7620	3179.875	3234.1957	FALSE	RIKEN cDNA 1810037I17 gene	NA	NA	NA	NA	
95649 at	-0.141	1677	1424170 at	0.123	1976	95649 at	0.098	3124	1424170 at	0.083	5959	3184	1952.3096	FALSE	PHD finger protein 5A	225309 at	0.109	13529	4.444E-02	FALSE
162196 f at	0.097	4099	1417413 at	0.163	1106.5	162196 f at	-0.062	5126	1417413 at	0.160	2406	3184.375	1782.3092	FALSE	CUB and zona pellucida-like domains 1	220275 at	-0.016	40062	8.788E-01	FALSE
95101 at	0.262	1814	1437513 a at	-0.326	503.5	95101 at	0.003	8289	1454811 a at	0.161	2133	3184.875	3475.0349	FALSE	serine incorporator 1	208671 at	-0.300	11420	2.032E-02	FALSE
104589 at	-0.329	1057	1419273 at	0.063	6061.5	161431 i at	-0.152	2447	1458125 at	0.206	3176	3185.375	2109.2938	FALSE	expressed sequence C80913	222266 at	0.525	1538	1.520E-06	FALSE
95078 at	0.228	922	1428196 a at	0.121	2615.5	95078 at	0.063	4592	1428196 a at	0.114	4614	3185.875	1776.4371	TRUE	RIKEN cDNA 1200015F23 gene	218126 at	0.078	13435	4.301E-02	TRUE
101900 at	0.180	1106	1449152 at	0.074	4641.5	101900 at	0.195	1064	1449152 at	0.096	5934	3186.375	2483.2283	TRUE	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	236313 at	0.207	11151	1.836E-02	TRUE
103807 at	0.004	8289	1418202 a at	0.191	1544	103807 at	0.122	2021	1434280 at	-0.637	896	3187.5	3432.1077	FALSE	widely-interspaced zinc finger motifs	221783 at	-0.113	15988	9.062E-02	FALSE
160600 at	-0.012	8014	1426803 at	0.141	1370	160600 at	-0.216	1373	1442038 at	0.234	1993	3187.5	3230.9776	FALSE	RIKEN cDNA 1700009P03 gene	218422 s at	0.107	19680	1.898E-01	FALSE
99455 s at	0.295	1124	1422874 at	0.119	3932	99456 at	0.045	6494	1422874 at	-0.412	1200	3187.5	2562.2523	FALSE	proacrosin binding protein	223717 s at	0.045	22844	2.963E-01	FALSE
102920 at	-0.213	746	1452009 at	-0.082	4643	102920 at	-0.091	5314	1452008 at	0.223	2047	3187.5	2152.684	FALSE	RIKEN cDNA 9130422G05 gene	NA	NA	NA	NA	
97925 at	-0.301	1834	1417175 at	-0.057	6136	97925 at	-0.395	95	1417175 at	0.123	4687	3188	2728.7158	FALSE	casein kinase 1, epsilon	225756 at	0.190	6330	9.339E-04	FALSE
160777 at	-0.282	298	1456029 a at	-0.153	2066.5	160777 at	-0.094	5718	1445066 at	0.150	4674	3189.125	2464.3426	FALSE	tetratricopeptide repeat domain 7B	226152 at	-0.436	1894	3.209E-06	FALSE
96195 at	0.138	1654	1438114 x at	0.094	3311.5	96195 at	0.036	5800	1438114 x at	-0.334	1991	3189.125	1881.8215	FALSE	embryonal Fyn-associated substrate	204400 at	0.483	6308	9.214E-04	FALSE
94343 at	-0.147	4296	1433887 at	-0.244	2573.5	102414 i at	-0.130	3112	1419162 s at	-0.152	2776	3189.375	770.45153	TRUE	DnaJ (Hsp40) homolog, subfamily C, member 3	233351 at	-0.084	9149	6.360E-03	TRUE
160428 at	0.066	4548	1427441 a at	-0.045	5806	160428 at	-0.111	1711	1435841 s at	-0.254	694	3189.75	2387.8217	FALSE	succinate-Coenzyme A ligase, GDP-forming, beta subunit	214835 s at	0.320	5276	3.603E-04	FALSE
162307 at	0.248	628	1419501 at	0.101	4603	162307 at	0.059	4500	1449483 at	0.135	3029	3190	1853.1445	TRUE	polymerase (DNA directed), kappa	223260 s at	-0.161	9510	7.795E-03	FALSE
100385 at	0.081	4299	1422277 at	0.069	5507	100385 at	-0.118	1630	1422277 at	-0.243	1324	3190	2042.3782	FALSE	glycine receptor, alpha 1 subunit	207972 at	-0.008	40881	9.039E-01	FALSE
161540 r at	-0.111	3262	1424782 at	-0.051	7083.5	96688 at	0.222	896	1445545 at	-0.256	1524	3191.375	2781.0376	FALSE	transmembrane protein 77	236883 at	0.121	8399	4.142E-03	FALSE
100046 at	0.061	5200	1419254 at	0.234	1340.5	100046 at	-0.098	2957	1419253 at	-0.147	3268	3191.375	1583.3631	FALSE	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydr	201761 at	0.466	12721	3.396E-02	FALSE
94991 at	-0.008	8216	1434089 at	0.129	2565.5	94991 at	0.180	1090	1434089 at	-0.268	897	3192.125	3431.1566	FALSE	synaptopodin	235128 at	-0.482	895	3.459E-07	FALSE
97254 at	-0.006	8350	1418119 at	0.225	1875	97254 at	0.370	827	1418119 at	0.216	1721	3193.25	3468.742	FALSE	RNA binding motif protein 8a	217856 at	-0.142	14761	6.635E-02	FALSE
102383 at	0.049	5513	1433639 at	-0.049	6717	102383 at	-0.191	521	1433639 at	-0.725	25	3194	3414.517	FALSE	RIKEN cDNA 5730593F17 gene	221249 s at	-0.275	3383	3.887E-05	FALSE
161387 i at	-0.321	471	1424452 at	0.030	6860.5	161387 i at	-0.094	4210	1429624 at	0.394	1236	3194.375	2928.2515	FALSE	SAFB-like, transcription modulator	217828 at	0.290	8815	5.235E-03	FALSE
101950 at	-0.138	2014	1417178 at	0.027	7520	101950 at	-0.105	3073	1417178 at	-0.586	171	3194.5	3123.0244	FALSE	GIPC PDZ domain containing family, member 2	219970 at	0.033	21556	2.519E-01	FALSE
100386 at	0.183	1938	1426517 at	-0.094	4860	100386 at	-0.186	2864	1426517 at	0.175	3117	3194.75	1220.3714	FALSE	guanine nucleotide binding protein, alpha z subunit	204993 at	0.007	42192	9.392E-01	FALSE
100016 at	0.139	2130	1417234 at	0.048	6253	100016 at	0.104	1732	1417234 at	-0.200	2672	3196.75	2073.6019	FALSE	matrix metallopeptidase 11	203878 s at	0.053	23624	3.245E-01	FALSE
161934 f at	-0.120	1797	1435113 x at	0.133	3788.5	160170 at	0.178	3627	1460181 at	0.136	3578	3197.625	938.07101	FALSE	Stathmin-like 3	218207 s at	-0.282	1490	1.369E-06	FALSE
161678 at	0.188	2643	1418110 a at	0.051	6056	102884 at	-0.079	3231.5	1418110 a at	-0.296	860	3197.625	2155.8877	FALSE	inositol polyphosphate-5-phosphatase D	203332 s at	0.154	12463	3.099E-02	FALSE
160379 at	-0.271	1353	1424092 at	0.071	5752	160379 at	-0.057	4540	1444150 at	0.632	1147	3198	2304.6696	FALSE	erythrocyte protein band 4.1	225051 at	-0.374	832	2.946E-07	FALSE
94068 at	-0.271	962	1449243 a at	0.305	1849.5	94068 at	0.083	3402	1449243 a at	-0.060	6581	3198.625	2470.1182	FALSE	ribosomal protein S19	202649 x at	0.096	19429	1.821E-01	FALSE
93214 at	0.059	5780	1427763 a at	-0.093	4541	93214 at	0.144	2291	1427763 a at	0.723	186	3199.5	2474.2108	FALSE	calcium/calmodulin-dependent protein kinase II, delta	240593 x at	0.141	4910	2.465E-04	FALSE
97163 g at	0.075	4205	1437909 at	-0.048	6301	99825 at	-0.119	1722	1441653 at	0.637	570	3199.5	2564.3459	FALSE	RIKEN cDNA D030022P06 gene	38766 at	0.087	9232	6.642E-03	FALSE
160865 at	0.067	5057	1451156 s at	-0.083	3946	160865 at	-0.077	3554	1438258 at	0.663	243	3200	2071.5638	FALSE	very low density lipoprotein receptor	209822 s at	-0.556	2764	1.533E-05	FALSE
97310 at	-0.082	5228	1416851 at	-0.073	5750	97309 at	-0.203	1313	1416851 at	0.369	509	3200	2671.924	FALSE	suppression of tumorigenicity 13	208667 s at	0.368	3935	8.123E-05	FALSE
92646 at	-0.197	1497	1416948 at	0.350	355	92646 at	0.080	5289	1416948 at	0.086	5660	3200.25	2671.4387	FALSE	mitochondrial ribosomal protein L23	213897 s at	-0.157	11026	1.739E-02	FALSE
102378 at	-0.001	8491	1417644 at	-0.156	2095.5	102378 at	0.229	1238	1417644 at	-0.480	977	3200.375	3559.2965	FALSE	sarcospan	204964 s at	0.900	1276	8.413E-07	FALSE
160229 at	0.093	2952	1423383 a at	-0.050	6845.5	99416 at	0.151	1548	1438614 x at	0.289	1458	3200.875	2524.2054	FALSE	oxysterol binding protein-like 9	236472 at	0.419	1632	1.891E-06	FALSE
162253 i at	0.198	2665	1421841 at	-0.284	288.5	160919 r at	-0.044	5873	1421841 at	-0.134	3978	3201.125	2346.1504	FALSE	fibroblast growth factor receptor 3	204379 s at	0.482	2069	4.358E-06	FALSE
102058 at	-0.081	6025	1430976 a at	-0.140	1159	102058 at	-0.109	4547	1437749 s at	-0.365	1078	3202.25	2480.8318	TRUE	mitochondrial ribosomal protein L9	209609 s at	-0.024	37611	8.087E-01	FALSE
96177 at	-0.123	1757	1417967 at	0.094	3764.5	96177 at	-0.098	3496	1458646 at	0.130	3792	3202.375	972.79095	FALSE	MMS19 (MET18 S. cerevisiae)-like	229226 at	0.011	39688	8.698E-01	FALSE
101480 at	0.093	3559	1416870 at	0.158	1226.5	101480 at	-0.088	3661	1416870 at	-0.110	4364	3202.625	1365.1584	FALSE	dynein, axonemal, light chain 4	204008 at	-0.240	1808	2.685E-06	FALSE
96547 at	0.027	7338	1422754 at	-0.449	457	96547 at	0.100	4270	1422754 at	-0.571	747	3203	3256.2333	FALSE	Tropomodulin 1	203661 s at	-0.577	1328	9.417E-07	FALSE
95287 at	0.273	440	1436766 at	-0.120	4566.5	95287 at	-0.028	6856	1423251 at	-0.228	952	3203.625	3049.8475	FALSE	LUC7-like 2 (S. cerevisiae)	217842 at	0.209	5727	5.406E-04	FALSE
103471 at	0.175	3629	1416062 at	-0.055	6410	103471 at	-0.650	89	1416061 at	0.139	2687	3203.75	2609.5705	FALSE	TBC1 domain family, member 15	218268 at	0.237	5813	5.931E-04	FALSE
94486 at	-0.128	3222	1416235 at	-0.276	222	94486 at	-0.099	3224	1416235 at	0.197	6151	3204.75	2420.596	FALSE	leucine rich repeat containing 59	222231 s at	-0.180	8084	3.460E-03	FALSE
161920 r at	0.145	2939	1452276 at	0.003	8446	161920 r at	0.260	367	1452276 at	0.218	1068	3205	3658.7726	TRUE	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containin	223197 s at	-0.038	29345	5.333E-01	FALSE
98019 at	-0.038	6431	1418136 at	0.165	1797	98019 at	-0.107	3042	1418136 at	0.216	1553	3205.75	2246.8653	FALSE	transforming growth factor beta 1 induced transcript 1	209651 at	0.314	5457	4.288E-04	FALSE
99610 at	0.074	5423	1419361 at	-0.097	3581.5	99610 at	0.151	3340	1436257 at	0.343	481	3206.375	2041.2145	FALSE	synovial sarcoma translocation, Chromosome 18	202817 s at	0.170	18590	1.578E-01	FALSE
160995 at	0.085	4130	1425535 at	-0.125	2970.5	162273 at	0.092	4940	1434044 at	-0.278	790	3207.625	1803.0565	FALSE	replication initiator 1	219041 s at	0.140	10928	1.654E-02	FALSE

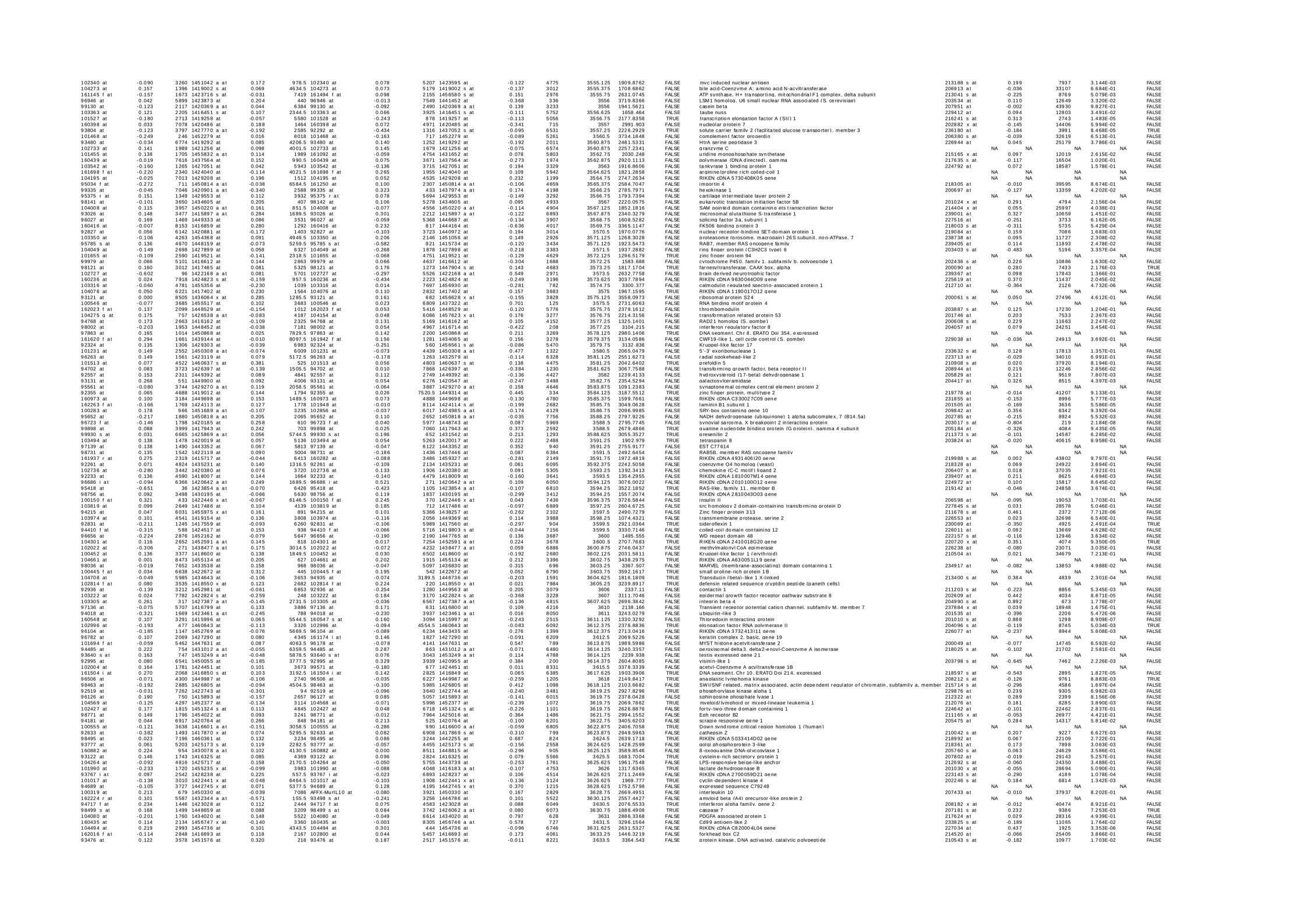
96072 at	-0.245	923	1419737 a at	0.122	3139	96072 at	-0.048	6462	1419737 a at	0.179	2308	3208	2354.0392	FALSE	lactate dehydrogenase A	200650 s at	-0.516	3742	6.210E-05	FALSE
92940 s at	0.164	2167	1417121 at	0.124	2403	92939 at	0.144	1989	1417121 at	-0.205	6277	3209	2052.3502	FALSE	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6	207182 at	-0.054	22476	2.842E-01	FALSE
104186 at	-0.089	3503	1429108 at	-0.139	1297	104186 at	-0.112	3674	1429108 at	-0.170	4363	3209.25	1327.9208	TRUE	male-specific lethal 2-like 1 (Drosophila)	218733 at	0.344	183	1.780E-08	FALSE
100567 at	0.054	6047	1417023 a at	0.160	1552	100567 at	0.142	1678	1424155 at	0.149	3560	3209.25	2102.9388	TRUE	fatty acid binding protein 4, adipocyte	235978 at	-0.058	17296	1.218E-01	FALSE
102719 f at	0.174	741	1422260 x at	0.084	4627	161968 f at	0.228	1188	1422259 a at	-0.086	6285	3210.25	2686.2588	FALSE	chemokine (C-C motif) receptor 5	206991 s at	-0.041	30635	5.798E-01	FALSE
103254 at	-0.140	1836	1428346 at	0.140	2672	161576 f at	-0.093	3600	1428346 at	-0.123	4735	3210.75	1245.6648	FALSE	TRAF type zinc finger domain containing 1	35254 at	0.138	2622	1.157E-05	FALSE
93667 at	-0.616	88	1451558 at	-0.057	6074	93667 at	-0.128	2867	1424986 s at	0.245	3815	3211	2478.7799	FALSE	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	222729 at	-0.174	8196	3.692E-03	FALSE
93730 at	0.044	7314	1453467 s at	0.319	2950	93730 at	0.330	507	1457726 at	0.223	2075	3211.5	2915.7527	TRUE	ribosomal protein S15a	NA	NA	NA	NA	
103225 at	0.099	3268	1429173 at	0.071	5868.5	103225 at	0.166	807	1429173 at	-0.200	2906	3212.375	2076.6791	FALSE	deoxyribonuclease 1-like 1	203912 s at	0.014	38212	8.279E-01	FALSE
96216 at	0.039	6693	1451219 at	0.201	2016.5	96216 at	0.110	2258	1451219 at	0.279	1885	3213.125	2325.0535	TRUE	ORM1-like 1 (S. cerevisiae)	228801 at	-0.121	8337	4.040E-03	FALSE
161735 r at	0.136	3821	1452716 at	-0.220	2145	161735 r at	0.051	5560	1435496 at	0.197	1330	3214	1876.5555	FALSE	RIKEN cDNA 5730469M10 gene	228155 at	-0.200	11920	2.500E-02	FALSE
94484 at	0.058	5840	1453604 a at	-0.125	1832	94484 at	0.103	4240	1440050 at	-0.442	946	3214.5	2236.2393	FALSE	Hbs1-like (S. cerevisiae)	240602 at	0.038	25415	3.870E-01	FALSE
161807 i at	0.119	2941	1451107 at	0.098	3168	97184 at	-0.220	841	1451107 at	0.077	5910	3215	2079.7585	FALSE	TBC1 domain family, member 22a	240238 at	0.118	8876	5.398E-03	FALSE
101370 at	0.308	1813	1449504 at	-0.252	506.5	101370 at	-0.095	3339	1449504 at	-0.080	7202	3215.125	2899.0298	FALSE	karyopherin (importin) alpha 1	202058 s at	-0.165	11809	2.394E-02	FALSE
160143 r at	-0.110	2464	1449534 at	0.065	5041.5	160143 r at	0.067	4217	1449534 at	-0.338	1138	3215.125	1752.9058	FALSE	synaptonemal complex protein 3	241861 at	0.077	23468	3.193E-01	FALSE
103460 at	-0.001	8501	1428306 at	-0.341	399	103460 at	0.247	2591	1428306 at	-0.402	1370	3215.25	3636.1634	FALSE	DNA-damage-inducible transcript 4	202887 s at	0.809	6430	9.973E-04	FALSE
94922 i at	0.148	3032	1434469 at	-0.062	5893	160728 r at	-0.179	1957	1434469 at	-0.185	1980	3215.5	1854.0911	FALSE	OTU domain containing 4	238848 at	-0.135	8424	4.173E-03	FALSE
100012 at	-0.093	3977	1426025 s at	0.108	2221	100012 at	0.050	5095	1426025 s at	-0.252	1576	3217.25	1611.3535	FALSE	lysosomal-associated protein transmembrane 5	201721 s at	0.437	8454	4.232E-03	FALSE
102337 s at	-0.120	4019	1435477 s at	0.179	2184.5	102337 s at	0.040	6075	1435477 s at	-0.762	594	3218.125	2363.4402	FALSE	Fc receptor, IgG, low affinity IIb	210889 s at	0.031	34915	7.278E-01	FALSE
97580 at	0.085	3943	1422048 at	-0.112	4610.5	97580 at	-0.094	2958	1422048 at	0.395	1366	3219.375	1409.7491	FALSE	transient receptor potential cation channel, subfamily C, member 5	220552 at	0.017	31580	6.157E-01	FALSE
101560 at	0.342	323	1415856 at	0.154	4682	101560 at	0.130	2663	1415857 at	0.204	5210	3219.5	2221.1409	TRUE	embigin	236921 at	-0.020	31635	6.179E-01	FALSE
97777 at	0.088	3731	1449566 at	0.164	1404.5	97777 at	0.124	1654	1449566 at	0.075	6090	3219.875	2179.1755	TRUE	NK2 transcription factor related, locus 5 (Drosophila)	206578 at	0.062	21547	2.516E-01	FALSE
101383 at	0.162	1944	1419606 a at	-0.553	77.5	101383 at	0.101	2584	1419606 a at	-0.057	8278	3220.875	3535.1256	FALSE	troponin T1, skeletal, slow	213201 s at	-0.113	17618	1.298E-01	FALSE
160183 f at	0.284	1684	1419918 at	0.109	4587.5	160183 f at	0.239	2968	1427315 at	0.139	3649	3222.125	1221.5945	TRUE	transmembrane emp24 protein transport domain containing 7	NA	NA	NA	NA	
96704 at	0.160	1752	1448612 at	0.063	6329	96704 at	-0.111	3161	1448612 at	-0.198	1648	3222.5	2182.9296	FALSE	stratifin	33322 i at	0.193	12100	2.691E-02	FALSE
96609 at	0.189	2467	1427269 at	0.204	1603	96609 at	-0.005	8429	1439095 at	0.420	392	3222.75	3573.6505	FALSE	splicing factor, arginine/serine-rich 11	236948 x at	-0.258	6350	9.428E-04	FALSE
92804 at	0.138	1638	1424473 at	0.140	2617	92804 at	0.088	3673	1424473 at	0.122	4965	3223.25	1427.8801	TRUE	polymerase (RNA) II (DNA directed) polypeptide H	209302 at	0.246	3309	3.543E-05	TRUE
100758 at	-0.265	1627	1451101 a at	0.241	2741	100758 at	0.269	496	1451101 a at	-0.017	8033	3224.25	3334.2747	FALSE	ribosomal protein S28	208904 s at	0.104	14063	5.366E-02	FALSE
97538 at	-0.088	4696	1448124 at	-0.121	2211	97538 at	0.064	3970	1448124 at	-0.236	2023	3225	1315.5311	FALSE	glucuronidase, beta	202605 at	0.290	3297	3.465E-05	FALSE
92232 at	-0.042	6486	1416576 at	0.234	315	92232 at	0.138	2312	1455899 x at	-0.167	3787	3225	2598.181	FALSE	suppressor of cytokine signaling 3	227697 at	0.402	20661	2.220E-01	FALSE
101409 at	-0.157	1276	1455797 x at	0.190	1303	101409 at	0.019	7380	1437720 at	0.158	2945	3226	2877.2154	FALSE	ligatin	218253 s at	0.156	3761	6.409E-05	FALSE
94885 at	-0.305	379	1426666 a at	0.176	372	94885 at	0.010	8178	1426667 a at	0.152	3979	3227	3712.1438	FALSE	unc-84 homolog A (C. elegans)	206487 at	0.061	14669	6.458E-02	FALSE
160448 at	0.035	6379	1426845 at	0.219	430	160448 at	0.050	5436	1426844 a at	0.272	666	3227.75	3119.6534	TRUE	programmed cell death 2-like	224467 s at	-0.189	4419	1.394E-04	FALSE
102026 s at	-0.104	2958	1448448 a at	0.079	4895	102026 s at	0.166	801	1448448 a at	0.147	4257	3227.75	1807.4806	FALSE	choline kinase beta	210069 at	0.093	18797	1.635E-01	FALSE
97768 at	0.153	1464	1421156 a at	0.116	2531.5	103506 f at	0.084	3884	1426911 at	-0.104	5033	3228.125	1558.3291	FALSE	desmocollin 2	204750 s at	0.041	21011	2.338E-01	FALSE
92899 at	-0.193	3522	1421978 at	-0.242	1746.5	92899 at	-0.919	803	1421978 at	-0.063	6842	3228.375	2659.7555	TRUE	glutamic acid decarboxylase 2	206780 at	-0.876	1210	7.418E-07	TRUE
102553 at	0.217	713	1426200 at	0.111	2672	97171 f at	0.074	4475	1452463 x at	-0.255	5057	3229.25	1960.8336	FALSE	Immunoglobulin kappa chain complex	NA	NA	NA	NA	
94532 at	-0.143	2189	1420038 at	0.192	1170	94532 at	-0.003	8377	1449712 s at	0.205	1183	3229.75	3464.5394	FALSE	VATPase, H+ transporting, lysosomal V1 subunit E1	208678 at	-0.419	3452	4.284E-05	FALSE
94556 at	0.096	5755	1431055 a at	0.169	1627.5	94556 at	0.155	4103	1459764 x at	0.435	1434	3229.875	2076.1644	TRUE	sorting nexin 10	218404 at	-0.515	3031	2.349E-05	FALSE
93057 at	0.006	8339	1449643 s at	0.360	613	93057 at	0.313	1663	1449643 s at	0.209	2307	3230.5	3476.4919	TRUE	basic transcription factor 3	208517 x at	-0.131	17983	1.403E-01	FALSE
98995 at	-0.030	6904	1460207 s at	0.122	2559	98995 at	-0.172	1216	1417444 at	-0.205	2245	3231	2514.9509	FALSE	E2F transcription factor 5	221586 s at	-0.040	21907	2.654E-01	FALSE
98011 at	0.070	6807	1422051 a at	-0.313	587	98011 at	-0.109	3414	1437188 at	0.188	2118	3231.5	2648.9475	FALSE	gamma-aminobutyric acid (GABA-B) receptor, 1	203146 s at	-0.637	472	9.201E-08	FALSE
94335 r at	-0.439	808	1448992 at	-0.153	1723	94335 r at	-0.130	4234	1448991 a at	-0.096	6167	3233	2433.864	TRUE	internexin neuronal intermediate filament protein, alpha	204465 s at	-0.884	1249	8.087E-07	TRUE
100457 at	0.139	3803	1417087 at	-0.147	3614	94364 at	-0.156	3508	1448580 at	0.196	2008	3233.25	825.89562	FALSE	golgi apparatus protein 1	207966 s at	0.300	5296	3.636E-04	FALSE
95022 at	0.206	1111	1419706 a at	-0.134	3380.5	95022 at	0.095	2815	1458235 at	-0.221	5627	3233.375	1864.6358	FALSE	A kinase (PRKA) anchor protein (gravin) 12	210517 s at	-0.494	2600	1.109E-05	FALSE
161816 r at	0.138	2870	1419027 s at	-0.126	2104	104524 at	0.108	3029	1419027 s at	-0.091	4938	3235.25	1204.8556	FALSE	glycolipid transfer protein	226177 at	0.268	9214	6.596E-03	FALSE
104700 at	0.124	2119	1425178 s at	0.098	3602.5	104700 at	0.072	4920	1425177 at	0.205	2301	3235.625	1302.8292	TRUE	serine hydroxymethyl transferase 1 (soluble)	224954 at	0.108	8830	5.276E-03	TRUE
96206 at	0.073	5264	1424468 s at	-0.214	1606.5	96206 at	0.093	4787	1424468 s at	-0.294	1286	3235.875	2079.756	FALSE	pleckstrin homology-like domain, family B, member 1	212134 at	0.296	3247	3.220E-05	FALSE
101929 at	0.209	2161	1418371 at	-0.337	403.5	161960 f at	0.100	3370	1418371 at	0.085	7016	3237.625	2797.9175	FALSE	dynein light chain LC8-type 2	229106 at	-0.218	7966	3.217E-03	FALSE
98791 at	0.131	2124	1453200 at	-0.168	2262.5	98791 at	-0.015	7830	1420454 at	0.536	735	3237.875	3138.156	FALSE	retinoic acid induced 1	226143 at	-0.160	11914	2.495E-02	FALSE
160168 at	0.161	1389	1423491 at	0.172	2759.5	162451 r at	0.060	4344	1423490 at	0.094	4465	3239.375	1457.9118	TRUE	F-box only protein 3	218432 at	-0.570	3137	2.776E-05	FALSE
104153 at	0.114	2241	1449001 at	0.133	2137	104153 at	-0.123	2980	1418238 at	-0.143	5600	3239.5	1617.7978	FALSE	isovaleryl coenzyme A dehydrogenase	203681 at	-0.027	30624	5.794E-01	FALSE
100880 at	-0.289	2305	1434380 at	-0.072	5317	100880 at	0.164	986	1434380 at	-0.441	4350	3239.5	1957.9555	FALSE	RIKEN cDNA 9830147J24 gene	NA	NA	NA	NA	
95511 at	0.093	4309	1422444 at	-0.117	2887.5	95511 at	0.092	3018	1422445 at	-0.350	2744	3239.625	721.6455	FALSE	integrin alpha 6	201656 at	0.553	1212	7.423E-07	FALSE
160942 at	-0.374	256	1424407 s at	-0.253	1085.5	162138 s at	0.060	6711	1429290 at	-0.151	4907	3239.875	3075.3242	FALSE	chromobox homolog 6	NA	NA	NA	NA	
101860 at	0.104	4426	1431687 at	0.135	3417	101860 at	-0.184	1846	1448570 at	-0.120	3275	3241	1061.8195	FALSE	glia maturation factor, beta	202544 at	0.196	5981	6.841E-04	FALSE
98151 s at	0.178	2670	1422450 at	-0.048	6136	98151 s at	-0.249	929	1445830 at	0.149	3238	3243.25	2164.2858	FALSE	catenin (cadherin associated protein), delta 1	238884 at	0.321	2782	1.561E-05	FALSE
98424 at	0.060	5080	1452127 a at	0.140	2123.5	98424 at	-0.076	4173	1452127 a at	-0.294	1601	3244.375	1652.1608	FALSE	protein tyrosine phosphatase, non-receptor type 13	243792 x at	0.526	1819	2.772E-06	FALSE
99574 at	0.131	2287	1434016 at	-0.079	4381	104418 at	0.138	2991	1455291 s at	-0.240	3321	3245	871.50292	FALSE	zinc and ring finger 2	226261 at	0.054	14748	6.602E-02	FALSE
103487 at	0.164	1317	1422625 at	0.242	2543	103487 at	0.139	2990	1422625 at	-0.167	6132	3245.5	2050.1854	FALSE	lymphocyte antigen 6 complex, locus H	206773 at	-0.385	11543	2.135E-02	FALSE
101122 at	0.109	2831	1421527 at	0.039	7083.5	101122 at	-0.288	505	1421527 at	0.165	2563	3245.625	2761.5334	FALSE	Eph receptor A6	NA	NA	NA	NA	
103636 at	-0.141	2277	1418746 at	-0.227	995.5	103636 at	-0.131	3306	1451399 at	0.075	6407	3246.375	2309.3456	FALSE	paroxysmal nonkinesiogenic dyskinesia	233177 s at	-0.669	140	1.290E-08	FALSE
93432 at	0.199	1577	1418313 at	-0.229	1261.5	93432 at	-0.039	6091	1444934 at	-0.132	4059	3247.125	2271.4746	FALSE	zinc finger protein (C2H2 type) 276	231922 at	0.064	17224	1.203E-01	FALSE
97406 at	-0.242	780	1434757 at	-0.062	4940	98371 at	-0.098	3539	1444403 at	0.148	3730	3247.25	1757.924	FALSE	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 homolog (human)	238549 at	0.300	5494	4.416E-04	FALSE
92195 at	0.034	7279	1425262 at	-0.095	2354	92195 at	-0.337	438	1451639 at	0.140	2920	3247.75	2889.7451	FALSE	CCAAT/enhancer binding protein (C/EBP), gamma	225527 at	0.140	16036	9.176E-02	FALSE
101970 at	0.102	3116	1434210 s at	-0.252	471.5	101970 at	0.014	7649	1434210 s at	-0.342	1756	3248.125	3126.2993	FALSE	leucine-rich repeats and immunoglobulin-like domains 1	211596 s at	0.595	4796	2.164E-04	FALSE
160277 at	0.312	1216	1448936 at	0.120	3339.5	160277 at	0.052	6250	1448936 at	0.174	2187	3248.125	2181.3697	TRUE	syntaxin 12	212112 s at	-0.037	33894	6.952E-01	FALSE
104393 at	0.094	2744	1418389 at	0.056	5398	104393 at	-0.173	808	1418389 at	-0.138	4051	3250.25	1955.7526	FALSE	RIKEN cDNA 2810453I06 gene	NA	NA	NA	NA	
99668 at	-0.225	725	1425532 a at	-0.079	4858	92220 s at	-0.281	946	1444120 at	0.078	6473	3250.5	2866.905	FALSE	bridging integrator 1	214643 x at	0.260	6009	6.974E-04	FALSE
99596 f at	0.115	4543	1419449 a at	-0.163	3837	99596 f at	0.163	2654	1435652 a at	-0.190	1968	3250.5	1156.8862	FALSE	guanine nucleotide binding protein, alpha inhibiting 2	201040 at	0.104	12306	2.928E-02	FALSE
161349 f at	-0.089	3952	1415675 at	0.120	1837.5	161349 f at	0.155	1773	1415675 at	0.083	5444	3251.625	1777.9309	FALSE	Dolichol-phosphate (beta-D) mannosyltransferase 2	209391 at	-0.077	12364	2.991E-02	FALSE
104410 at	-0.206	572	1449188 at	-0.221	548	104410 at	0.095	4465	1449188 at	0.046	7424	3252.25	3335.2146	FALSE	midnolin	225954 s at	0.290	8344	4.052E-03	FALSE
102951 at	0.160	1609	1427505 a at	-0.054	5823	102951 at	0.099	2089	1443430 at	-0.133	3490	3252.75	1890.2117	FALSE	CASP2 and RIPK1 domain containing adaptor with death domain	209833 at	-0.056	23927	3.357E-01	FALSE
101561 at	-0.467	143	1428942 at	0.044	7730.5	101561 at	-0.175	4810	1428942 at	-0.580	328	3252.875	3683.2947	FALSE	metallothionein 2	212185 x at	0.621	4469	1.489E-04	FALSE
100050 at	-0.153	3208	1425895 a at	-0.189	954	100050 at	-0.026	6764	1425895 a at	-0.237	2086	3253	2515.0504	TRUE	inhibitor of DNA binding 1	208937 s at	0.680	5513	4.515E-04	FALSE
103367 at	-0.364	660	1418655 at	-0.152	2352.5	103367 at	-0.265	2440	1418655 at	-0.059	7561	3253.375	2986.3234	TRUE	beta-1,4-N-acetyl-galactosaminyl transferase 1	206435 at	-0.257	2767	1.536E-05	TRUE
98336 s at	0.165	2292	1418342 at	0.050	5499	98336 s at	-0.193	1102	1451920 a at	0.186	4125	3254.5	1945.5259	FALSE	replication factor C 1	208021 s at	0.117	13502	4.401E-02	FALSE
102333 at	-0.076	4287	1427226 at	-0.160	1790.5	102333 at	-0.051	5865	1440175 at	0.222	1077	3254.875	2218.5257	FALSE	epsin 2	203464 s at	0.148	13554	4.472E-02	FALSE
160430 at	0.172	2046	1430533 a at	-0.320	385	160430 at	0.062	6278	1430533 a at	0.138	4311	3255	2578.9045	FALSE	catenin (cadherin associated protein), beta 1	242558 at	0.370	2503	9.589E-06	FALSE
95355 at	0.095	4034	1422965 at	0.094	3705	95355 at	0.089	3586	1460596 at	-0.212	1697	3255.5	1056.1353	FALSE	angiotensin II, type I receptor-associated protein	225059 at	0.350	4130	1.009E-04	FALSE
162462 r at	0.279	1093	1425615 a at	-0.057	6018	97398 at	0.040	5523	1452620 at	0.313	391	3256.25	2924.3077	FALSE	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	202847 at	0.159	7845	2.950E-03	FALSE
103219 at	0.093	4361	1419832 s at	0.153	1122	103219 at	-0.084	5335	1453943 a at	0.179	2209	3256.75	1931.6167	FALSE	acid phosphatase, prostate	237077 at	0.078	17215	1.202E-01	FALSE
104583 at	-0.047	6712	1438463 x at	0.102	2411	104583 at	-0.131	3149	1441763 at	-0.546	756	3257	2511.2683	FALSE	zinc finger, DHHC domain containing 6	218249 at	0.030	32648	6.523E-01	FALSE
96595 at	0.071	5570	1449359 at	0.198	1059.5	96595 at	0.075	3886	1449359 at	0.225	2514	3257.375	1925.8474	TRUE	paired box gene 1	214401 at	0.073	14758	6.630E-02	FALSE
97543 at	-0.162	3146	1423473 at	0.075	4266.5	97543 at	0.168	3749	1423473 at	-0.236	1870	3257.875	1032.3503	FALSE	septin 2	200015 s at	0.326	3780	6.555E-05	FALSE
101094 at	-0.057	6623	1416480 a at	0.326	1085.5	101094 at	0.197	1082	1416480 a at	0.111	4242	3258.125	2692.348	FALSE	HIG1 domain family, member 1A	221896 s at	-0.189	13407	4.264E-02	FALSE
103691 at	0.122	1960	1417888 at	0.127	3339.5	103691 at	0.092	3038	1417888 at	0.105	4698	3258.875	1127.4519	TRUE	tripartite motif protein 13	229943 at	0.365	3887	7.571E-05	TRUE
102820 at	0.094	3473	1449479 at	0.108	3446	102820 at	0.119	1911	1449479 at	-0.134	4207	3259.25	965.50035	FALSE	cytochrome P450, family 2, subfamily b, polypeptide 13	NA	NA	NA	NA	
97890 at	-0.239	3613	1416041 at	-0.505	841.5	97890 at	-0.118	6285	1416041 at	-0.214	2299	3259.625	2312.8551	TRUE	serum/glucocorticoid regulated kinase	201739 at	0.540	5294	3.634E-04	FALSE
101732 at	0.780	879	1422320 x at	0.097	6807.5	101732 at	-0.098	4091	1422320 x at	-0.214	1262	3259.875	2765.0487	FALSE	per-hexamer repeat gene 5	NA	NA	NA	NA	
94423 at	0.077	4281	1425108 a at	0.109	1849.5	94423 at	0.115	3411	1425108 a at	-0.120	3500	3260.375	1018.5532	FALSE	cDNA sequence BC004728	209679 s at	-0.066	24048	3.396E-01	FALSE
162246 r at	0.247	809	1448273 at	0.051	6640.5	162246 r at	0.148	1269	1448273 at	0.159	4326	3261.125	2740.7793	TRUE	glutathione synthetase	211630 s at	-0.132	7707	2.683E-03	FALSE
103039 at	0.034	6950	1423267 s at	-0.146	3348.5	103039 at	-0.108	2435	1423267 s at	-0.427	317	3262.625	2766.814	FALSE	integrin alpha 5 (fibronectin receptor alpha)	201389 at	0.024	36336	7.725E-01	FALSE
101462 r at	0.149	2368	1451792 a at	-0.325	77.5	101461 f at	0.022	7895	1426449 a at	0.179	2711	3262.875	3301.9471	FALSE	praja1, RING-H2 motif containing	218667 at	-0.556	614	1.458E-07	FALSE
160913 at	0.109	2808	1421253 at	0.096	4292.5	160913 at	-0.097	3199	1421253 at	-0.195	2753	3263.125	714.39746	FALSE	nebulin-related anchoring protein	207089 at	-0.080	18131	1.437E-01	FALSE
104423 at	-0.062	5271	1434695 at	0.155	2004	104423 at	0.045	5602	1434695 at	0.800	176	3263.25	2621.5539	FALSE	denticleless homolog (Drosophila)	222680 s at	-0.059	22964	3.001E-01	FALSE
103813 at	-0.017	7537	1449579 at	0.150	1994.5	103813 at	-0.092	3363	1449579 at	0.553	160	3263.625	3136.5998	FALSE	Sh3 domain YSC-like 1	NA	NA	NA	NA	
102791 at	-0.609	2186	1422962 a at	0.054	5791	102791 at	0.159	533	1422962 a at	-0.438	4545	3263.75	2355.6411	FALSE	proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	209040 s at	0.365	4669	1.896E-04	FALSE
93118 at	0.213	3324	1433829 a at	-0.109	5393	93117 at	-0.174	3806	1433830 at	-0.283	532	3263.75	2024.3376	FALSE	heterogeneous nuclear ribonucleoprotein A2/B1	225932 s at	0.392	4780	2.132E-04	FALSE
161520 at	0.021	7294	1417921 at	0.207	686.5	161520 at	0.232	296	1417921 at	0.174	4779	3263.875	3365.9399	TRUE	RIKEN cDNA 2610029G23 gene	223294 at	0.013	40596	8.949E-01	FALSE
102306 at	-0.085	3838	1422739 at	-0.133	2707	102306 at	-0.102	4230	1440905 at	-0.270	2282	3264.25	919.63847	TRUE	heparan sulfate 2-O-sulfotransferase 1	203284 s at	-0.292	9742	8.805E-03	TRUE
160064 at	0.168	2291	1418436 at	0.036	7154.5	160064 at	0.113	2856	1418436 at	0.235	757	3264.625	2740.6952	TRUE	syntaxin 7	212632 at	0.196	12853	3.532E-02	TRUE
162145 r at	-0.034	6444	1455229 x at	-0.143	3046	162145 r at	0.141	1210	1454045 a at	0.184	2359	3264.75	2250.7675	FALSE	phosphatidylglycerophosphate synthase 1	NA	NA	NA	NA	
160293 at	-0.010	8027	1448102 a at	0.260	1456.5	160293 at	0.111	2204	1459985 at	0.303	1377	3266.125	3195.7042	FALSE	WD repeat domain 61	221531 at	-0.144	19163	1.737E-01	FALSE
103504 at	-0.160	3178	1451542 at	-0.225	1186.5	103504 at	-0.079	7252	1451542 at	0.244	1448	3266.125	2800.3205	FALSE	single-stranded DNA binding protein 2	203787 at	0.073	24156	3.430E-01	FALSE
103960 at	-0.240	307	1449246 at	-0.123	1946	103960 at	0.005	8273	1436674 at	0.173	2539	3266.25	3468.749	FALSE	Rap2 interacting protein	213439 x at	-0.380	689	1.838E-07	FALSE
95000 g at	0.121	3240	1426990 at	0.165	738	95000 g at	0.095	4051	1452270 s at	0.083	5042	3267.75	1840.4573	TRUE	cubilin (intrinsic factor-cobalamin receptor)	206775 at	0.033	31014	5.955E-01	FALSE
161162 at	0.136	3618	1419977 s at	0.128	3515.5	161162 at	0.122	2766	1419977 s at	-0.143	3173	3268.125	385.0477	FALSE	RNA binding motif protein 35b	225139 at	0.287	1770	2.505E-06	FALSE
104014 at	0.045	6174	1422645 at	0.169	1417.5	104014 at	0.078	3184	1450702 at	-0.320	2297	3268.125	2067.1303	FALSE	hemochromatosis	211327 x at	0.125	8075	3.435E-03	FALSE
161832 r at	0.096	3192	1423593 a at	-0.026	7363	161832 r at	-0.213	838	1419873 s at	-0.286	1681	3268.5	2898.1758	FALSE	colony stimulating factor 1 receptor	203104 at	0.358	9082	6.119E-03	FALSE
97088 at	0.111	2592	1460188 at	-0.013	7991	97088 at	-0.166	1960	1460188 at	-0.510	531	3268.5	3264.2374	FALSE	Protein tyrosine phosphatase, non-receptor type 6	206687 s at	0.146	10935	1.660E-02	FALSE
92566 at	0.079	4647	1423446 at	-0.137	2572	92566 at	0.081	3567	1423446 at	-0.204	2293	3269.75	1068.655	FALSE	death-associated kinase 3	203891 s at	0.042	32081	6.342E-01	FALSE
93648 at	-0.105	2911	1421446 at	-0.433	1052.5	93648 at	-0.551	858	1421446 at	-0.017	8258	3269.875	3451.7665	TRUE	protein kinase C, gamma	NA	NA	NA	NA	
104192 at	0.075	4617	1426948 at	0.050	5257	95007 at	0.184	2536	1456112 at	0.848	670	3270	2086.5709	TRUE	translocated promoter region	201730 s at	0.275	8088	3.463E-03	TRUE
93043 at	-0.111	5038	1415821 at	-0.254	1361.5	93043 at	-0.502	471	1415821 at	-0.083	6210	3270.125	2783.6545	TRUE	neuroplastin	NA	NA	NA	NA	
161163 at	0.086	3165	1426720 at	0.083	3332.5	160903 at	-0.175	3233	1440135 at	-0.130	3351	3270.375	87.293924	FALSE	amyloid beta (A4) precursor protein-binding, family B, member 2	216750 at	0.062	20683	2.226E-01	FALSE
96187 at	-0.146	4264	1438677 at	-0.445	151	96187 at	0.018	8025	1438677 at	0.378	646	3271.5	3661.1287	FALSE	plakophilin 4	201928 at	0.402	5835	6.024E-04	FALSE
100907 at	0.124	2088	1416640 at	-0.033	7051	100907 at	-0.130	3130	1416640 at	-0.475	817	3271.5	2691.337	FALSE	potassium voltage-gated channel, Isk-related family, member 1-like	220010 at	0.012	40841	9.029E-01	FALSE
94235 at	0.107	4161	1423899 at	0.126	2301	94235 at	-0.044	5891	1440314 at	0.829	738	3272.75	2237.0722	FALSE	thyroid hormone receptor interactor 12	242688 at	0.355	2282	6.510E-06	FALSE
101210 at	-0.157	913	1435360 at	-0.060	5489	101210 at	-0.066	3967	1439542 at	-0.218	2722	3272.75	1937.8246	TRUE	zinc finger protein 651	NA	NA	NA	NA	
100321 f at	0.009	8077	1449910 at	0.104	3746	100321 f at	0.353	256	1449910 at	-0.255	1014	3273.25	3535.8881	FALSE	RIKEN cDNA 2210418O10 gene	NA	NA	NA	NA	
99923 at	0.200	1213	1427159 at	0.166	1471	99923 at	0.075	5422	1427160 at	-0.107	4989	3273.75	2240.0639	FALSE	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	203378 at	0.238	5554	4.639E-04	FALSE
102670 at	0.077	4476	1449095 at	0.152	1355	102670 at	0.097	2689	1449095 at	0.127	4577	3274.25	1545.682	TRUE	vacuolar protein sorting 54 (yeast)	222627 at	0.248	3262	3.279E-05	TRUE
160718 at	0.147	3294	1423098 at	0.110	3236.5	160718 at	0.079	4615	1423096 at	0.197	1952	3274.375	1087.4696	TRUE	calpain 7	239778 x at	0.253	7574	2.439E-03	TRUE
162287 r at	0.097	5936	1416306 at	0.094	3873	100623 at	0.279	415	1416306 at	0.184	2878	3275.5	2293.1589	TRUE	chloride channel calcium activated 3	210107 at	-0.032	33454	6.804E-01	FALSE
160594 at	0.140	1351	1418799 a at	0.162	1646	160594 at	0.019	7750	1418799 a at	-0.201	2356	3275.75	3012.5073	FALSE	procollagen, type XVII, alpha 1	204636 at	-0.092	14528	6.184E-02	FALSE
97519 at	-0.130	2704	1449254 at	-0.247	4194	97519 at	0.414	346.5	1449254 at	-0.560	5860	3276.125	2340.152	FALSE	secreted phosphoprotein 1	209875 s at	0.229	22740	2.928E-01	FALSE
97509 f at	-0.091	5706	1425911 a at	-0.274	429	97509 f at	-0.061	6417	1436551 at	-0.293	556	3277	3228.7555	TRUE	fibroblast growth factor receptor 1	211535 s at	0.466	1364	1.034E-06	FALSE

103519 at	0.196	1711	1449486 at	0.093	4018.5	103519 at	0.116	2573	1449486 at	-0.092	4809	3277.875	1395.805	FALSE	carboxylesterase 1	NA	NA	NA	NA	
160076 at	-0.031	7336	1430500 s at	0.254	949	160076 at	0.210	768	1430500 s at	0.102	4065	3279.5	3098.9818	FALSE	metaxin 2	203517 at	-0.282	5551	4.638E-04	FALSE
101862 at	0.163	2027	1419590 at	0.122	2491.5	101862 at	0.157	1847	1419590 at	0.060	6754	3279.875	2331.9453	TRUE	cytochrome P450, family 2, subfamily b, polypeptide 9	NA	NA	NA	NA	
161201 r at	0.061	5954	1417397 at	-0.264	300	99922 at	-0.082	4316	1417397 at	-0.166	2550	3280	2424.6561	FALSE	solute carrier family 9 (sodium/hydrogen exchanger), member 1	209453 at	-0.276	2598	1.103E-05	FALSE
161059 at	-0.063	5715	1452142 at	-0.211	1460	161059 at	0.076	5558	1457183 at	1.110	389	3280.5	2756.1319	FALSE	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	205152 at	-0.097	22521	2.857E-01	FALSE
162367 f at	-0.067	5241	1424201 a at	0.096	2893.5	160758 at	-0.138	3501	1424202 at	-0.317	1493	3282.125	1553.179	FALSE	SEH1-like (S. cerevisiae	223225 s at	-0.152	4919	2.484E-04	FALSE
104369 at	0.158	1921	1427700 x at	0.132	2651.5	104369 at	0.100	2336	1422784 at	0.063	6222	3282.625	1982.2854	TRUE	keratin complex 2, basic, gene 6a	214580 x at	-0.107	15917	8.895E-02	FALSE
162364 f at	-0.158	1267	1416209 at	-0.165	1706.5	162364 f at	-0.076	5333	1416209 at	-0.111	4825	3282.875	2092.0383	TRUE	glutamate dehydrogenase 1	200947 s at	0.135	17951	1.393E-01	FALSE
92379 f at	-0.171	4176	1427019 at	-0.105	3742.5	92378 at	-0.101	3880	1418690 at	-0.291	1334	3283.125	1311.945	TRUE	protein tyrosine phosphatase, receptor type Z, polypeptide 1	204469 at	0.354	7382	2.108E-03	FALSE
92368 at	0.127	2512	1420401 a at	-0.384	709	92368 at	0.129	2138	1420401 a at	-0.195	7780	3284.75	3095.908	FALSE	receptor (calcitonin) activity modifying protein 3	205326 at	0.256	8832	5.276E-03	FALSE
161229 at	0.231	1590	1448105 at	0.142	3581.5	161229 at	-0.149	1182	1448105 at	-0.050	6787	3285.125	2559.1372	FALSE	Protamine 2	210122 at	-0.010	41176	9.123E-01	FALSE
92698 at	-0.122	2747	1422869 at	-0.099	5190.5	92698 at	-0.233	163	1422869 at	-0.088	5041	3285.375	2362.9638	TRUE	c-mer proto-oncogene tyrosine kinase	211913 s at	-0.110	18880	1.658E-01	FALSE
94798 at	0.145	1379	1418872 at	0.141	3626.5	94798 at	0.066	3990	1449594 at	0.118	4146	3285.375	1289.419	TRUE	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	NA	NA	NA	NA	
101212 at	-0.155	2708	1435593 x at	0.272	1969	101212 at	0.189	919	1435593 x at	0.035	7546	3285.5	2933.6474	FALSE	ribosomal protein S7	NA	NA	NA	NA	
99161 at	-0.071	5716	1417423 at	-0.108	3486	99160 s at	-0.568	230	1436297 a at	-0.140	3714	3286.5	2270.6254	TRUE	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	212090 at	-0.185	7692	2.662E-03	TRUE
104161 at	-0.241	476	1420937 at	0.022	7781.5	104161 at	-0.107	3374	1420937 at	0.370	1523	3288.625	3226.0143	FALSE	cleavage and polyadenylation specific factor 2	225986 x at	0.150	12928	3.615E-02	FALSE
98984 f at	-0.026	7917	1417434 at	0.216	330	98984 f at	0.229	4511	1417434 at	0.365	398	3289	3652.6351	FALSE	glycerol phosphate dehydrogenase 2, mitochondrial	243598 at	0.291	2648	1.240E-05	FALSE
104006 at	0.088	4787	1419251 at	-0.118	4467	104006 at	-0.229	1308	1440729 at	0.335	2596	3289.5	1636.6935	FALSE	epidermal growth factor receptor pathway substrate 15	237586 at	0.178	11031	1.743E-02	FALSE
94063 at	-0.186	1023	1448110 at	-0.152	1963	161530 r at	0.109	3273	1448110 at	0.101	6899	3289.5	2577.1681	FALSE	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic dc	219259 at	-0.111	14486	6.116E-02	FALSE
100026 at	0.184	1051	1430111 a at	-0.122	2112	100026 at	0.034	6449.5	1430111 a at	0.311	3548	3290.125	2341.6383	FALSE	branched chain aminotransferase 1, cytosolic	226517 at	-0.404	8864	5.367E-03	FALSE
161771 r at	0.124	3285	1418611 at	-0.054	5679	103931 at	0.130	2981	1418611 at	0.228	1216	3290.25	1835.2387	FALSE	G protein-coupled receptor 162	205056 s at	-0.120	13579	4.509E-02	FALSE
93046 at	0.139	4085	1422719 s at	-0.115	3775.5	93046 at	0.223	1440	1450722 at	0.153	3862	3290.625	1240.6205	FALSE	nucleoporin 50	222583 s at	-0.162	5612	4.855E-04	FALSE
99063 at	-0.097	2490	1418089 at	0.137	2621.5	99063 at	-0.056	5452	1418089 at	0.187	2599	3290.625	1442.0605	FALSE	syntaxin 8	204690 at	0.149	12813	3.503E-02	FALSE
97548 at	-0.058	6391	1428171 at	0.140	2469.5	161795 r at	-0.085	2884	1428172 at	-0.283	1419	3290.875	2156.7642	FALSE	PRP39 pre-mRNA processing factor 39 homolog (yeast)	220553 s at	0.029	32259	6.403E-01	FALSE
93613 at	0.173	2807	1450472 s at	-0.235	304	93613 at	-0.039	7298	1450472 s at	-0.273	2759	3292	2915.2183	FALSE	MAD homolog 3 (Drosophila)	218284 at	-0.248	3942	8.193E-05	FALSE
92360 at	0.165	2785	1416862 at	0.125	3249	92360 at	0.069	5839	1457828 at	-0.223	1296	3292.25	1891.2185	FALSE	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	203544 s at	-0.073	32270	6.406E-01	FALSE
162490 f at	-0.186	904	1416027 at	-0.062	6577	162490 f at	0.157	1920	1416027 at	-0.144	3769	3292.5	2490.2263	FALSE	Programmed cell death 6	81811 at	0.211	4545	1.625E-04	FALSE
98380 at	-0.285	341	1418414 at	-0.088	4391.5	98380 at	-0.165	1713	1446763 at	-0.065	6726	3292.875	2840.3577	TRUE	potassium voltage-gated channel, subfamily H (eag-related), member 1	207635 s at	-0.008	40965	9.062E-01	FALSE
97061 g at	0.153	2362	1420828 s at	-0.179	2322	97061 g at	0.120	2954	1420828 s at	0.084	5538	3294	1523.6518	FALSE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	212426 s at	0.133	22027	2.692E-01	FALSE
102939 s at	0.114	3891	1419769 at	0.116	2970.5	102939 s at	0.179	904	1419769 at	-0.125	5411	3294.125	1884.5734	FALSE	CD22 antigen	204581 at	0.341	5354	3.833E-04	FALSE
162185 i at	0.181	2821	1437837 x at	0.122	3119	162185 i at	-0.027	7124	1440022 at	0.429	114	3294.5	2888.809	FALSE	polymerase (DNA-directed), delta interacting protein 3	212100 s at	0.209	4488	1.539E-04	FALSE
96508 at	0.125	3543	1450458 at	-0.105	3128	96508 at	-0.124	3658	1446827 at	0.209	2852	3295.25	373.01061	FALSE	nuclear receptor coactivator 2	242369 x at	0.329	2355	7.482E-06	FALSE
100412 g at	0.189	1878	1450637 a at	0.075	5534	100412 g at	-0.074	4809	1422514 at	-0.343	964	3296.25	2217.1123	FALSE	AE binding protein 1	201792 at	1.036	85	5.954E-09	FALSE
162259 f at	0.171	3070	1421709 a at	0.022	7392	160088 at	-0.102	1914	1440899 at	-0.296	814	3297.5	2880.8871	FALSE	flavin containing monooxygenase 5	240422 at	0.028	29680	5.455E-01	FALSE
103823 at	-0.057	5276	1438387 x at	0.104	3854.5	103823 at	-0.104	1849	1448173 a at	-0.157	2211	3297.625	1581.4915	FALSE	topoisomerase (DNA) III beta	213660 s at	-0.071	18022	1.413E-01	FALSE
97839 at	0.111	3554	1425148 a at	0.125	3570	97839 at	0.126	4275	1425148 a at	0.275	1793	3298	1058.1547	TRUE	sorting nexin 6	217789 at	0.478	956	3.941E-07	TRUE
97211 at	0.311	768	1456739 x at	0.091	6249	97211 at	0.222	1948	1415780 a at	0.106	4228	3298.25	2435.6177	TRUE	armadillo repeat containing, X-linked 2	203404 at	-0.444	2488	9.495E-06	FALSE
102374 at	0.167	2304	1450450 at	-0.081	5070.5	102374 at	0.356	426	1450450 at	0.113	5393	3298.375	2364.1207	FALSE	Down syndrome critical region gene 1-like 2	219864 s at	-0.001	43550	9.738E-01	FALSE
97187 at	0.100	3863	1447462 at	0.121	3674	97187 at	0.140	883	1447462 at	-0.112	4774	3298.5	1680.4167	FALSE	DNA segment, Chr 7, Wayne State University 130, expressed	NA	NA	NA	NA	
104463 at	0.067	4307	1452252 at	0.183	1123	104463 at	0.062	4876	1459028 at	0.176	2892	3299.5	1673.6803	TRUE	UTP20, small subunit (SSU) processome component, homolog (yeast)	209725 at	0.046	27654	4.676E-01	FALSE
96517 at	0.092	4013	1443696 s at	0.079	5111.5	96517 at	0.161	1321	1443696 s at	-0.201	2758	3300.875	1633.0037	FALSE	hyaluronic acid binding protein 2	206010 at	0.055	27240	4.517E-01	FALSE
96110 at	0.013	8092	1460196 at	0.205	807	96110 at	0.260	1179	1460196 at	0.185	3126	3301	3351.9758	TRUE	carbonyl reductase 1	209213 at	0.123	25142	3.774E-01	FALSE
94432 at	-0.084	3893	1420927 at	0.062	5535.5	94432 at	0.096	3566	1446739 at	0.501	213	3301.875	2232.2948	FALSE	beta galactoside alpha 2,6 sialyltransferase 1	201998 at	0.204	16356	9.869E-02	FALSE
102659 at	0.034	6567	1417551 at	0.176	622.5	102659 at	0.089	3023	1417551 at	-0.190	2996	3302.125	2450.2668	FALSE	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	209275 s at	0.064	16855	1.102E-01	FALSE
93089 at	0.233	1411	1450934 at	0.105	4243.5	93089 at	0.088	3261	1450934 at	0.101	4300	3303.875	1349.0706	TRUE	eukaryotic translation initiation factor 4A2	200912 s at	-0.345	1426	1.215E-06	FALSE
104611 at	0.276	401	1423962 at	-0.053	5580	104612 g at	-0.131	1787	1423963 at	0.090	5448	3304	2614.4222	FALSE	WD repeat domain 26	224905 at	-0.101	16027	9.145E-02	FALSE
98925 at	0.186	2875	1420833 at	-0.435	3165.5	98925 at	-0.756	932	1420834 at	-0.153	6244	3304.125	2196.4522	FALSE	vesicle-associated membrane protein 2	214792 x at	-0.409	3992	8.470E-05	FALSE
96717 at	-0.292	800	1423752 at	0.152	1285.5	96717 at	-0.023	7389	1438380 at	-0.137	3745	3304.875	3012.5328	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	220890 s at	0.119	13494	4.389E-02	FALSE
101646 at	-0.059	5015	1415946 at	-0.120	3468	100594 at	-0.194	1861	1415946 at	-0.129	2876	3305	1319.0711	TRUE	phosphatidylinositol glycan, class O	204144 s at	0.043	26465	4.233E-01	FALSE
100603 at	-0.187	1438	1415841 at	0.179	1849.5	100603 at	-0.113	5203	1415841 at	0.088	4732	3305.625	1935.8806	FALSE	dynein cytoplasmic 1 intermediate chain 2	211684 s at	0.094	23484	3.198E-01	FALSE
95672 at	0.120	3379	1416291 at	0.113	2274.5	95672 at	0.064	5404	1416291 at	0.170	2165	3305.625	1502.5318	TRUE	proteasome (prosome, macropain) 26S subunit, ATPase, 4	201252 at	0.019	37709	8.115E-01	FALSE
160432 at	-0.259	1146	1434305 at	0.085	4218	160432 at	-0.310	212	1434305 at	-0.031	7648	3306	3362.6946	FALSE	U2 small nuclear RNA auxiliary factor 1-like 4	NA	NA	NA	NA	
97424 at	-0.136	3935	1417225 at	0.102	4143.5	97424 at	-0.255	2283	1440360 at	-0.167	2868	3307.375	882.30998	FALSE	ADP-ribosylation factor-like 6 interacting protein 5	200760 s at	-0.195	18854	1.651E-01	FALSE
95870 at	0.158	1082	1442974 at	0.173	1536	95870 at	0.133	2284	1442974 at	0.008	8329	3307.75	3383.9857	TRUE	DNA segment, Chr 6, ERATO Doi 160, expressed	NA	NA	NA	NA	
100294 at	0.094	3740	1437051 at	0.078	4420	100294 at	-0.094	3998	1437051 at	-0.227	1074	3308	1515.4784	FALSE	DNA fragmentation factor, beta subunit	206752 s at	-0.042	32787	6.574E-01	FALSE
95472 f at	0.164	2812	1455997 a at	0.488	41.5	95472 f at	0.107	4265	1416337 at	-0.075	6114	3308.125	2562.91	FALSE	ubiquinol-cytochrome c reductase binding protein	NA	NA	NA	NA	
99541 at	0.098	3622	1452314 at	0.113	4597.5	99541 at	0.180	974	1452314 at	0.176	4042	3308.875	1607.0382	TRUE	kinesin family member 11	204444 at	-0.033	24304	3.469E-01	FALSE
103736 at	0.140	3847	1448005 at	-0.225	604	103736 at	-0.140	4947	1432055 at	0.132	3842	3310	1877.3739	FALSE	SAM and SH3 domain containing 1	41644 at	0.414	819	2.861E-07	FALSE
100611 at	-0.327	3721	1423547 at	0.076	5524	100611 at	0.145	2343	1423547 at	-0.755	1653	3310.25	1707.9671	FALSE	lysozyme	213975 s at	0.199	14954	7.015E-02	FALSE
99453 at	-0.140	1381	1449298 a at	0.012	8210	99453 at	-0.169	2678	1449298 a at	0.681	972	3310.25	3346.4762	FALSE	phosphodiesterase 1A, calmodulin-dependent	242789 at	-0.068	26886	4.388E-01	FALSE
101866 at	0.086	3037	1451735 at	0.009	8165	101866 at	-0.233	1035	1425508 s at	-0.285	1009	3311.5	3372.2283	FALSE	ADP-ribosylation factor related protein 1	203174 s at	-0.093	17471	1.259E-01	FALSE
103312 f at	0.094	5300	1434942 at	0.140	3277	103312 f at	0.303	3732	1453727 at	0.446	938	3311.75	1804.2214	TRUE	RIKEN cDNA 2610101J03 gene	218859 s at	0.185	10841	1.596E-02	TRUE
94928 at	0.021	7433	1418099 at	0.202	371	94928 at	0.074	4052	1418099 at	-0.270	1394	3312.5	3154.8082	FALSE	tumor necrosis factor receptor superfamily, member 1b	203508 at	0.225	6101	7.621E-04	FALSE
101581 at	0.090	5395	1416681 at	0.093	6241.5	101581 at	0.269	1466	1416682 at	0.758	150	3313.125	2962.3647	TRUE	ubiquitin protein ligase E3A	211575 s at	-0.092	14734	6.565E-02	FALSE
162216 i at	-0.109	2710	1416930 at	0.171	1370	162216 i at	0.103	2983	1416930 at	0.076	6191	3313.5	2043.7417	FALSE	lymphocyte antigen 6 complex, locus D	206276 at	0.002	44019	9.849E-01	FALSE
93712 at	0.123	2339	1419313 at	0.084	3896	93712 at	-0.135	3662	1456477 at	0.142	3358	3313.75	686.14594	FALSE	cyclin T1	206967 at	0.166	9807	9.099E-03	FALSE
104140 s at	-0.027	6883	1451169 at	-0.325	166.5	104140 s at	-0.034	5851	1451170 s at	-0.336	357	3314.375	3550.809	TRUE	nodal modulator 1	221853 s at	-0.484	2300	6.738E-06	TRUE
160838 at	0.104	3133	1418225 at	0.128	3797	160838 at	0.119	3617	1418227 at	0.214	2717	3316	487.93852	TRUE	origin recognition complex, subunit 2-like (S. cerevisiae)	204853 at	0.041	31736	6.221E-01	FALSE
101305 at	-0.115	4349	1422331 at	-0.279	2241	101305 at	-0.129	5277	1435197 at	-0.227	1398	3316.25	1802.4945	TRUE	POU domain, class 3, transcription factor 3	208563 x at	-0.089	16289	9.711E-02	FALSE
96290 f at	-0.105	4192	1455767 x at	0.217	3403	96290 f at	0.206	588	1423070 at	-0.168	5083	3316.5	1944.1551	FALSE	ribosomal protein L21	216479 at	0.001	44125	9.873E-01	FALSE
92572 at	0.311	674	1417865 at	0.080	5257	93215 at	-0.277	1049	1417866 at	0.103	6289	3317.25	2870.8684	FALSE	tumor necrosis factor, alpha-induced protein 1 (endothelial)	201207 at	0.056	20724	2.244E-01	FALSE
98835 at	0.087	3318	1420416 at	0.074	5032.5	98835 at	-0.204	393	1420417 at	-0.124	4526	3317.375	2078.0117	FALSE	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	244163 at	-0.116	5907	6.353E-04	FALSE
103930 at	-0.098	5037	1418154 at	-0.034	6572	103930 at	-0.231	1487	1446957 s at	0.520	174	3317.5	2987.7959	FALSE	cDNA sequence BC004022	32069 at	0.148	9051	5.984E-03	FALSE
104584 f at	0.234	1931	1455115 a at	0.168	2021.5	104584 f at	-0.040	6615	1455115 a at	0.203	2704	3317.875	2225.0008	FALSE	crumbs homolog 3 (Drosophila)	232609 at	0.019	33898	6.954E-01	FALSE
100133 at	0.000	8520	1448765 at	-0.219	410	100133 at	0.251	2432	1417558 at	0.172	1913	3318.75	3571.941	FALSE	Fyn proto-oncogene	210105 s at	0.334	2893	1.820E-05	FALSE
103085 at	-0.235	470	1418172 at	-0.021	7938	103085 at	-0.326	454	1418172 at	-0.237	4414	3319	3599.0375	TRUE	heme binding protein 1	235373 at	-0.059	19695	1.903E-01	FALSE
102216 at	-0.084	4768	1418266 at	0.127	1665	102216 at	-0.164	2938	1418266 at	0.155	3906	3319.25	1332.2971	FALSE	arachidonate 12-lipoxygenase, 12R type	207381 at	-0.068	20931	2.313E-01	FALSE
161383 r at	0.085	4083	1423434 at	0.099	4460.5	161383 r at	0.165	1228	1456717 at	-0.178	3508	3319.875	1448.53	FALSE	TEA domain family member 1	224955 at	0.698	358	5.089E-08	FALSE
93560 at	-0.334	886	1421022 x at	0.207	2350.5	93560 at	0.119	3946	1450095 a at	0.104	6100	3320.625	2234.9169	FALSE	acylphosphatase 1, erythrocyte (common) type	205260 s at	-0.092	21588	2.534E-01	FALSE
101764 at	0.017	7566	1422290 at	-0.198	744	101764 at	-0.087	3108	1422290 at	-0.275	1865	3320.75	2990.3321	FALSE	5-hydroxytryptamine (serotonin) receptor 1D	207368 at	-0.162	10002	1.012E-02	FALSE
103826 at	-0.139	3361	1450093 s at	-0.205	2060	103826 at	-0.131	1523	1437255 at	0.087	6340	3321	2155.5267	FALSE	zinc finger and BTB domain containing 7a	219186 at	-0.295	5246	3.469E-04	FALSE
96358 at	-0.170	2031	1460175 at	0.286	1102.5	96358 at	0.095	2746	1460175 at	0.033	7411	3322.625	2807.4043	FALSE	ribosomal protein S23	227722 at	-0.254	10396	1.250E-02	FALSE
96900 at	-0.221	1228	1433720 s at	-0.153	2516	96900 at	0.038	6141	1433720 s at	-0.118	3406	3322.75	2080.728	FALSE	Nur77 downstream gene 2	224932 at	-0.342	2374	7.722E-06	FALSE
93900 at	0.148	3611	1422799 at	-0.147	2123.5	93900 at	-0.266	1258	1442802 x at	0.067	6300	3323.125	2209.7133	FALSE	HLA-B associated transcript 2	208132 x at	-0.052	23606	3.241E-01	FALSE
100126 at	-0.058	6052	1422505 at	0.109	3536	100126 at	0.315	874	1459859 x at	0.225	2833	3323.75	2139.3542	FALSE	chromatin accessibility complex 1	231764 at	0.134	8937	5.580E-03	FALSE
93045 at	0.224	3149	1416679 at	-0.069	5580	93045 at	-0.515	1307	1416679 at	-0.146	3260	3324	1750.4805	FALSE	ATP-binding cassette, sub-family D (ALD), member 3	202850 at	0.317	4503	1.585E-04	FALSE
94014 at	-0.081	5403	1416979 at	0.236	878	94014 at	0.167	1030	1416979 at	0.067	5988	3324.75	2748.6049	FALSE	RIKEN cDNA 2510048O06 gene	217769 s at	-0.179	6191	8.246E-04	FALSE
160266 r at	0.091	3683	1423841 at	0.105	3616.5	161746 i at	0.103	3067	1423841 at	-0.240	2933	3324.875	380.07201	FALSE	brix domain containing 2	219177 at	-0.040	18385	1.516E-01	FALSE
100892 at	0.219	1585	1423711 at	0.079	5822	161507 f at	0.181	1214	1423711 at	0.161	4680	3325.25	2277.0562	TRUE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	204125 at	-0.188	12086	2.680E-02	FALSE
104348 at	-0.084	4122	1426313 at	-0.124	2861	104348 at	-0.169	995	1446758 at	-0.123	5324	3325.5	1850.712	TRUE	brain and reproductive organ-expressed protein	205550 s at	-0.155	5429	4.123E-04	TRUE
160719 at	0.050	5913	1455894 at	0.118	2657	160719 at	0.109	2845	1451845 a at	0.228	1891	3326.5	1773.012	TRUE	peptidyl-tRNA hydrolase 2	218732 at	-0.045	28913	5.177E-01	FALSE
162162 f at	-0.039	6596	1432431 s at	0.144	2350.5	162162 f at	0.120	2181	1443058 at	-0.226	2179	3326.625	2181.0649	FALSE	RIKEN cDNA 2900006F19 gene	NA	NA	NA	NA	
103811 at	-0.053	5693	1419308 at	0.146	2642.5	103811 at	0.118	2173	1460491 at	-0.133	2800	3327.125	1599.5772	FALSE	inversin	210114 at	0.088	13815	4.917E-02	FALSE
96345 at	0.090	4372	1456745 x at	0.176	1486	96345 at	0.101	3062	1423548 s at	0.131	4391	3327.75	1376.4235	TRUE	ERGIC and golgi 3	216032 s at	-0.066	22949	2.995E-01	FALSE
100317 at	0.149	2220	1422159 at	0.070	6072	100317 at	-0.155	796	1422159 at	0.123	4224	3328	2307.3101	FALSE	protein phosphatase, EF hand calcium-binding domain 2	208411 x at	0.000	44348	9.930E-01	FALSE
160105 r at	0.259	587	1428488 at	0.119	2625	160105 r at	0.007	8396	1428488 at	0.223	1707	3328.75	3479.4421	TRUE	phosphatidylinositol glycan, class K	227639 at	-0.139	15419	7.822E-02	FALSE
103362 at	-0.085	3851	1424208 at	0.113	3515.5	103362 at	0.092	2755	1424208 at	0.192	3198	3329.875	466.86907	FALSE	prostaglandin E receptor 4 (subtype EP4)	204897 at	0.065	15977	9.044E-02	FALSE
101980 at	0.259	2793	1422693 a at	0.268	1832	101980 at	-0.044	6788	1422692 at	0.163	1907	3330	2346.2783	FALSE	SUB1 homolog (S. cerevisia	224587 at	-0.648	2535	1.011E-05	FALSE
94969 at	0.075	3848	1448963 at	0.141	1127.5	94969 at	-0.218	1387	1448963 at	0.046	6959	3330.375	2711.9624	FALSE	nuclear transcription factor-Y gamma	202216 x at	-0.208	2853	1.731E-05	FALSE
161223 r at	0.267	2073	1426750 at	-0.068	5468	95637 at	-0.073	4319	1445534 at	0.883	1466	3331.5	1880.0444	FALSE	filamin, beta	208614 s at	0.181	9429	7.453E-03	FALSE
101937 s at	0.152	4710	1422886 a at	0.083	3545	101937 s at	-0.466	1081	1422886 a at	-0.173	3992	3332	1575.5268	FALSE	CDC like kinase 4	228751 at	0.105	22087	2.711E-01	FALSE
161791 r at	0.257	692	1448587 at	0.088	2990	96131 at	-0.189	1127	1448587 at	0.000	8521	3332.5	3599.7365	FALSE	TBC1 domain family, member 10a	226133 s at	-0.110	8752	5.049E-03	FALSE
160357 at	0.171	3177	1419542 at	0.102	2997	160357 at	-0.072	4239	1419542 at	-0.345	2918	3332.75	613.81125	FALSE	deleted in azoospermia-like	NA	NA	NA	NA	
93826 at	-0.357	484	1423911 at	-0.094	4460.5	93826 at	-0.075	4643	1423911 at	-0.136	3748	3333.875	1938.7607	TRUE	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	202187 s at	0.131	8772	5.094E-03	FALSE
93454 at	0.104	3243	1419589 at	-0.117	2917	93454 at	0.051	5662	1456046 at	-0.274	1515	3334.25	1723.4186	FALSE	CD93 antigen	202878 s at	0.252	18567	1.572E-01	FALSE
100367 g at	0.126	2561	1437537 at	0.268	1790.5	103711 at	0.127	2687	1437537 at	0.073	6301	3334.875	2016.7314	TRUE	caspase 9	210775 x at	0.072	23046	3.028E-01	FALSE
160626 at	0.151	2113	1425349 a at	-0.155	5114	160626 at	0.051	5915	1425349 a at	0.608	199	3335.25	2655.1221	FALSE	myelin basic protein expression factor 2, repressor	229464 at	-0.118	9564	8.022E-03	FALSE
103923 at	0.090	3502	1449670 x at	-0.082	3757.5	103923 at	0.067	5468	1443208 at	0.477	622	3337.375	2009.6791	FALSE	G protein-coupled receptor 137B	230278 at	-0.083	19984	2.001E-01	FALSE
103716 at	0.140	2166	1455072 at	0.211	963	103716 at	-0.037	7327	1431102 at	0.143	2895	3337.75	2776.2432	FALSE	centrosomal protein 350	204373 s at	0.583	1638	1.926E-06	FALSE
93833 s at	-0.249	1601	1418072 at	-0.270	2705	93833 s at	0.017	8010	1418072 at	-0.404	1035	3337.75	3191.0944	FALSE	histone 1, H2bc	208527 x at	0.030	30824	5.877E-01	FALSE
101503 at	0.117	2994	1454613 at	0.099	4049.5	101503 at	0.060	5360	1415877 at	0.476	957	3340.125	1860.3042	TRUE	dihydropyrimidinase-like 3	201431 s at	0.693	639	1.600E-07	TRUE
102227 g at	0.306	309	1460248 at	0.072	4596	102226 at	0.205	957	1419000 at	-0.034	7506	3342	3356.5223	FALSE	carboxypeptidase X 2 (M14 family)	236144 at	0.062	17820	1.358E-01	FALSE
97107 at	-0.236	786	1455700 at	0.155	1706.5	97107 at	-0.015	8083	1455700 at	-0.133	2794	3342.375	3265.2402	FALSE	MTERF domain containing 3	225341 at	-0.091	17167	1.188E-01	FALSE
94061 at	-0.167	1934	1416326 at	0.060	6245.5	94061 at	0.147	1792	1416326 at	-0.161	3403	3343.625	2067.1225	FALSE	cysteine-rich protein 1 (intestinal)	205081 at	0.291	11106	1.803E-02	FALSE
161467 f at	-0.057	4949	1418453 a at	-0.267	755	161467 f at	-0.037	6695	1455949 at	-0.242	979	3344.5	2949.6537	TRUE	ATPase, Na+/K+ transporting, beta 1 polypeptide	201243 s at	-0.237	10859	1.608E-02	TRUE
161686 i at	-0.104	2921	1451968 at	0.135	2243.5	96063 at	0.261	151	1451968 at	0.020	8066	3345.375	3360.6822	FALSE	X-ray repair complementing defective repair in Chinese hamster cells 5	233007 at	0.154	8229	3.769E-03	FALSE
97778 at	-0.095	3751	1421915 a at	-0.106	2703	97778 at	-0.207	1292	1450406 a at	-0.080	5641	3346.75	1831.5215	TRUE	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	225905 s at	-0.124	6428	9.960E-04	TRUE
102261 f at	0.092	3944	1422866 at	0.106	2858	102261 f at	-0.104	4158	1422866 at	-0.145	2427	3346.75	836.59045	FALSE	procollagen, type XIII, alpha 1	211809 x at	0.045	23740	3.287E-01	FALSE
92747 at	0.110	5040	1421112 at	-0.208	2019	92747 at	0.390	153	1421112 at	-0.137	6176	3347	2758.9074	FALSE	NK2 transcription factor related, locus 2 (Drosophila)	206915 at	0.377	9780	8.965E-03	FALSE
161602 at	0.078	4375	1415843 at	-0.112	3937	161602 at	0.297	276	1415842 at	-0.126	4801	3347.25	2077.6622	FALSE	G protein beta subunit-like	220587 s at	-0.038	30664	5.809E-01	FALSE
161645 r at	-0.064	5298	1449363 at	0.131	3025	104155 f at	0.102	2039	1449363 at	-0.155	3030	3348	1380.9941	FALSE	activating transcription factor 3	202672 s at	0.375	13658	4.616E-02	FALSE
160825 at	-0.224	598	1434529 x at	0.039	7415	160825 at	0.166	450	1434529 x at	-0.151	4929	3348	3415.6968	FALSE	checkpoint with forkhead and ring finger domains	218803 at	0.067	20021	2.009E-01	FALSE
161373 r at	0.216	734	1437324 x at	0.088	3668	99152 at	-0.036	5667	1415939 at	0.175	3323	3348	2025.9798	FALSE	fibromodulin	202709 at	-0.019	38119	8.255E-01	FALSE
94893 at	0.077	4822	1429451 at	0.134	2603	94893 at	0.126	2237	1456448 at	0.167	3731	3348.25	1170.2864	TRUE	RIKEN cDNA 2610301B20 gene	244569 at	0.056	26967	4.420E-01	FALSE
160177 at	0.078	4554	1432043 at	0.087	4980.5	160177 at	0.206	2230	1432043 at	-0.229	1630	3348.625	1665.4267	FALSE	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	239788 at	0.204	4958	2.562E-04	FALSE
103639 at	-0.002	8477	1418293 at	0.140	1957	103639 at	0.214	615	1418293 at	-0.511	2349	3349.5	3498.0377	FALSE	interferon-induced protein with tetratricopeptide repeats 2	226757 at	0.337	10589	1.389E-02	FALSE
92413 at	0.106	3810	1428354 at	-0.182	759.5	92413 at	0.160	2263	1428354 at	0.076	6568	3350.125	2480.5499	FALSE	forkhead box K2	242938 s at	-0.085	14615	6.327E-02	FALSE
93588 at	-0.221	1055	1452896 at	-0.086	6480	93588 at	-0.158	1872	1452896 at	-0.135	3998	3351.25	2426.8159	TRUE	gene trap locus 3	217957 at	-0.328	6788	1.318E-03	TRUE

96269 at	-0.340	447	1451122 at	-0.276	1348	96269 at	0.032	6811	1451122 at	0.116	4803	3352.25	2973.5009	FALSE	isopentenyl-diphosphate delta isomerase	233014 at	0.191	8067	3.414E-03	FALSE
104528 at	0.107	2278	1416651 at	0.179	459	104528 at	0.074	3487	1416651 at	0.042	7187	3352.75	2843.025	TRUE	zinc finger, HIT domain containing 2	222814 s at	-0.047	27885	4.760E-01	FALSE
100676 at	0.038	6536	1427685 a at	-0.091	4315	100676 at	0.129	2004	1427685 a at	0.284	565	3355	2623.5893	FALSE	synaptojanin 2	210612 s at	0.487	6194	8.271E-04	FALSE
93358 at	0.202	1378	1449576 at	0.091	4356	93358 at	0.031	6456	1449576 at	0.211	1231	3355.25	2519.1339	TRUE	eukaryotic translation initiation factor 1A, Y-linked	201018 at	-0.286	5539	4.596E-04	FALSE
96852 at	0.163	2674	1425550 a at	-0.257	622.5	96852 at	-0.006	8214	1425550 a at	0.194	1912	3355.625	3347.7577	FALSE	protein kinase, cAMP dependent regulatory, type I, alpha	242482 at	0.201	9819	9.133E-03	FALSE
92200 at	0.100	2628	1423427 at	0.015	8077	92200 at	0.187	566	1423427 at	0.354	2153	3356	3268.4927	TRUE	adenylate cyclase activating polypeptide 1	206281 at	0.005	42462	9.460E-01	FALSE
99077 at	-0.146	2474	1454675 at	-0.082	3988.5	99077 at	-0.080	4148	1443952 at	-0.212	2814	3356.125	836.46243	TRUE	thyroid hormone receptor alpha	35846 at	-0.122	14905	6.900E-02	FALSE
103574 at	-0.186	1044	1454708 at	0.040	6903	103574 at	0.220	1063	1442376 at	0.128	4415	3356.25	2846.3944	FALSE	actin-binding LIM protein 1	200965 s at	0.357	4665	1.887E-04	FALSE
94352 at	-0.091	5835	1448641 at	-0.082	5309	94542 at	-0.242	854	1441526 at	0.321	1429	3356.75	2577.6592	FALSE	mbt domain containing 1	207115 x at	0.149	3719	6.098E-05	FALSE
162475 f at	0.124	2778	1449184 at	-0.041	7366	162475 f at	-0.155	1605	1449184 at	-0.356	1679	3357	2725.9561	FALSE	peptidoglycan recognition protein 1	207384 at	0.068	18582	1.577E-01	FALSE
96812 at	0.075	4254	1427049 s at	0.128	2750	96812 at	0.041	5683	1427049 s at	-0.449	742	3357.25	2115.1484	FALSE	smoothened homolog (Drosophila)	218629 at	0.116	12511	3.143E-02	FALSE
97138 at	-0.062	5163	1426880 at	-0.298	1214.5	97138 at	0.045	5601	1432901 at	-0.218	1451	3357.375	2346.6511	FALSE	cDNA sequence BC026657	231807 at	-0.268	5160	3.214E-04	FALSE
93316 at	-0.330	1020	1460192 at	-0.134	4115	93317 at	0.036	6592	1416823 a at	0.229	1703	3357.5	2532.2633	FALSE	oxysterol binding protein-like 1A	209485 s at	0.435	6148	7.903E-04	FALSE
92912 at	0.121	3724	1421597 a at	0.157	1519.5	92912 at	0.116	1785	1421597 a at	-0.077	6404	3358.125	2255.843	FALSE	homeo box, msh-like 3		NA	NA	NA	NA
92462 at	0.035	6822	1431973 at	0.077	3679	92462 at	-0.208	1537	1420877 at	0.318	1396	3358.5	2534.2863	FALSE	septin 6	212414 s at	0.205	4336	1.261E-04	FALSE
160533 r at	0.199	1331	1415924 at	0.137	1182	161216 at	0.046	5918	1415924 at	-0.108	5003	3358.5	2456.5103	FALSE	transition protein 1	206568 at	-0.045	30325	5.681E-01	FALSE
97300 at	0.098	3357	1426677 at	-0.067	5345	97300 at	0.098	3865	1426677 at	-0.313	874	3360.25	1859.7002	FALSE	filamin, alpha		NA	NA	NA	NA
160155 at	0.096	3804	1454618 at	0.118	3640	160155 at	0.319	164	1433483 s at	-0.081	5833	3360.25	2352.7063	FALSE	expressed sequence C86187		NA	NA	NA	NA
99018 at	0.119	2182	1428845 at	0.088	6057	99018 at	-0.276	2074	1428845 at	-0.152	3130	3360.75	1859.0487	FALSE	BCL2-associated transcription factor 1	239504 at	0.240	3024	2.282E-05	FALSE
160247 at	0.140	4043	1417984 at	-0.220	891	160247 at	0.131	2356	1417984 at	-0.067	6156	3361.5	2264.8085	FALSE	ubiquitin-conjugating enzyme E2 variant 2	209096 at	-0.258	9984	1.008E-02	FALSE
161599 i at	-0.090	5166	1423264 at	-0.138	1696	160878 at	-0.273	242	1430491 at	-0.136	6346	3362.5	2867.5557	TRUE	block of proliferation 1	212563 at	-0.203	7312	2.012E-03	TRUE
93342 at	0.130	2429	1424001 at	0.198	1858.5	93342 at	0.130	1455	1424001 at	0.025	7712	3363.625	2926.3253	TRUE	Mki67 (FHA domain) interacting nucleolar phosphoprotein	224713 at	-0.140	10208	1.132E-02	FALSE
97729 at	0.006	8264	1420964 at	-0.294	462.5	97729 at	-0.424	1287	1450061 at	0.269	3442	3363.875	3499.9388	FALSE	ectodermal-neural cortex 1	201341 at	-0.918	370	5.493E-08	FALSE
160445 at	0.009	8070	1437097 at	0.174	1058	160445 at	-0.109	2542	1453848 s at	-0.255	1787	3364.25	3195.1361	FALSE	zinc finger, BED domain containing 3	228402 at	0.223	4619	1.765E-04	FALSE
99153 at	-0.277	665	1451178 at	0.072	5899	99153 at	0.095	3670	1451178 at	0.152	3223	3364.25	2146.6519	FALSE	mitochondrial ribosomal protein L53	225523 at	0.100	20150	2.052E-01	FALSE
103632 at	-0.065	5020	1429349 at	0.164	944	103632 at	0.087	3889	1429349 at	-0.125	3607	3365	1725.6309	FALSE	high-mobility group box 4	230473 s at	0.026	30785	5.860E-01	FALSE
93643 at	0.133	2298	1419324 at	-0.102	4937.5	93643 at	0.113	2703	1441313 x at	-0.310	3523	3365.375	1165.3973	FALSE	LIM homeobox protein 9		NA	NA	NA	NA
96629 at	-0.018	7747	1432332 a at	0.144	1255	96629 at	0.353	1674	1432332 a at	0.150	2787	3365.75	2991.5206	FALSE	nudix (nucleoside diphosphate linked moiety X)-type motif 19		NA	NA	NA	NA
101137 at	-0.155	3343	1435151 a at	0.170	1549	101137 at	0.195	885	1447563 at	-0.038	7687	3366	3062.0483	FALSE	ribosomal protein S3	208692 at	0.058	29823	5.506E-01	FALSE
160369 at	-0.193	706	1418129 at	-0.269	1431.5	160369 at	0.034	6810	1418129 at	0.372	4518	3366.375	2828.7883	FALSE	24-dehydrocholesterol reductase	200862 at	-0.133	26637	4.292E-01	FALSE
93605 r at	0.082	5751	1417376 a at	-0.118	3486	93604 f at	0.225	1038	1417377 at	0.275	3191	3366.5	1928.1107	FALSE	immunoglobulin superfamily, member 4A	244345 at	0.442	3065	2.500E-05	FALSE
104481 at	0.089	3523	1449013 at	0.053	6065	104481 at	-0.116	3475	1439860 at	0.399	405	3367	2315.7899	FALSE	eukaryotic elongation factor-2 kinase	225546 at	0.101	17367	1.235E-01	FALSE
99841 at	0.187	818	1422003 at	0.181	1483	99841 at	-0.065	6504	1422003 at	-0.110	4663	3367	2681.2461	FALSE	Burkitt lymphoma receptor 1	206126 at	-0.048	30977	5.939E-01	FALSE
95081 at	0.061	5812	1449738 s at	0.208	1790.5	95081 at	0.155	637	1428291 at	0.113	5232	3367.875	2542.6036	TRUE	exosome component 8	215136 s at	0.211	9834	9.215E-03	TRUE
101208 at	0.092	3398	1421533 at	0.063	6707	101208 at	-0.119	2923	1454992 at	0.293	444	3368	2575.3719	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	212295 s at	0.310	3128	2.714E-05	FALSE
103513 at	0.121	3696	1439373 x at	0.043	5937	103513 at	0.112	2563	1439373 x at	-0.240	1277	3368.25	1977.174	FALSE	wingless-related MMTV integration site 5B	221029 s at	-0.158	8136	3.566E-03	FALSE
99107 at	0.057	6725	1417962 s at	0.143	1487.5	99108 s at	-0.079	3646	1417962 s at	-0.247	1617	3368.875	2446.0179	FALSE	growth hormone receptor	241584 at	-0.022	35995	7.619E-01	FALSE
102010 at	0.213	603	1423863 at	0.094	3597.5	102010 at	0.071	4614	1423863 at	0.124	4662	3369.125	1908.3014	TRUE	ATP-binding cassette, sub-family F (GCN20), member 2	209246 at	0.061	26652	4.300E-01	FALSE
94321 at	-0.393	1096	1452166 a at	0.002	8488	94321 at	-0.355	3027	1452166 a at	-0.354	869	3370	3546.7191	FALSE	keratin complex 1, acidic, gene 10	213287 s at	-0.109	16484	1.014E-01	FALSE
101465 at	-0.328	4924	1420915 at	0.177	539.5	101465 at	-0.052	4710	1450034 at	-0.658	3307	3370.125	2018.7633	FALSE	signal transducer and activator of transcription 1	209969 s at	0.062	21523	2.507E-01	FALSE
103518 at	0.115	2701	1452352 at	-0.070	5237.5	103518 at	-0.173	410	1452352 at	-0.178	5135	3370.875	2295.7888	FALSE	cytotoxic T lymphocyte-associated protein 2 beta		NA	NA	NA	NA
94501 at	0.104	4717	1450015 x at	-0.119	2399	94501 at	0.110	3129	1420821 at	-0.219	3242	3371.75	971.54563	FALSE	sphingosine-1-phosphate phosphatase 1	221268 s at	-0.234	13678	4.642E-02	FALSE
101393 at	-0.153	2436	1460330 at	0.074	6041	101393 at	-0.146	2257	1460330 at	-0.458	2754	3372	1791.1641	FALSE	annexin A3	209369 at	0.253	8309	3.966E-03	FALSE
104413 at	-0.196	1292	1433595 at	-0.059	5829	104413 at	-0.086	4268	1445629 at	-0.191	2099	3372	2064.5091	TRUE	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), membe	209712 at	0.132	10794	1.553E-02	FALSE
103330 at	0.066	5503	1452061 s at	0.136	3182	103330 at	0.245	1547	1444001 at	0.309	3257	3372.25	1624.9216	TRUE	spermatid perinuclear RNA binding protein	223245 at	-0.216	2837	1.684E-05	FALSE
103933 at	-0.087	3151	1416538 at	-0.024	7601	103933 at	-0.302	96	1416539 at	-0.179	2643	3372.75	3119.6633	TRUE	sialic acid acetylesterase	223744 s at	-0.025	36028	7.634E-01	FALSE
103386 at	0.139	2034	1417449 at	0.116	1953	103386 at	-0.072	4481	1417449 at	0.142	5024	3373	1608.6004	FALSE	acyl-CoA thioesterase 8	204212 at	-0.100	14988	7.089E-02	FALSE
95738 at	0.120	3732	1437620 x at	0.146	1261.5	161391 r at	0.107	2785	1437620 x at	0.087	5714	3373.125	1863.0922	TRUE	aldehyde dehydrogenase 18 family, member A1	222416 at	-0.078	16075	9.247E-02	FALSE
102646 at	0.188	3603	1434393 at	-0.035	7194	102647 g at	0.138	2269	1460126 at	0.668	427	3373.25	2860.6918	FALSE	ubiquitin specific peptidase 34		NA	NA	NA	NA
98102 at	0.288	1995	1449137 at	-0.116	2794	98102 at	0.064	5397	1418560 at	0.124	3311	3374.25	1453.1046	FALSE	pyruvate dehydrogenase E1 alpha 1	200980 s at	-0.193	9531	7.877E-03	FALSE
103545 at	0.054	6656	1419798 at	0.147	1500	103545 at	0.416	249	1419798 at	0.097	5092	3374.25	3000.0305	TRUE	RIKEN cDNA 2610019E17 gene		NA	NA	NA	NA
97355 at	-0.110	3148	1437728 at	-0.106	3557.5	97355 at	0.047	6239	1437728 at	0.372	555	3374.875	2326.6379	FALSE	alkB, alkylation repair homolog 5 (E. coli)	234302 s at	-0.087	18283	1.484E-01	FALSE
99445 at	-0.171	1210	1438559 x at	-0.178	4076.5	99445 at	0.049	6688	1428065 at	-0.200	1527	3375.375	2554.1078	FALSE	solute carrier family 44, member 2	225175 s at	0.442	801	2.755E-07	FALSE
99880 at	0.116	2383	1422109 at	-0.103	5192	99880 at	-0.160	2959	1436059 at	-0.335	2968	3375.5	1241.539	FALSE	regulatory factor X, 1 (influences HLA class II expression)	226786 at	0.080	13947	5.145E-02	FALSE
99329 at	0.121	2289	1452233 at	0.185	934	99329 at	-0.151	4062	1459270 at	-0.088	6218	3375.75	2287.101	FALSE	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	202804 at	0.112	8803	5.209E-03	FALSE
97487 at	-0.239	2283	1416666 at	-0.155	2559	97487 at	-0.165	4697	1416666 at	-0.132	3969	3377	1148.7419	TRUE	serine (or cysteine) peptidase inhibitor, clade E, member 2	236599 at	0.153	7865	3.001E-03	FALSE
162399 f at	-0.133	5928	1419866 s at	-0.215	1447	93535 at	-0.081	5813	1443516 at	0.423	322	3377.5	2915.4543	FALSE	ataxin 2	238589 s at	0.165	3275	3.357E-05	FALSE
98440 at	0.003	8373	1417777 at	0.178	458	98440 at	0.186	403	1417777 at	-0.115	4276	3377.5	3791.8093	FALSE	leukotriene B4 12-hydroxydehydrogenase	231897 at	-0.237	15313	7.676E-02	FALSE
103502 at	0.058	6764	1436399 s at	0.149	2839.5	93919 at	0.165	1618	1450079 at	-0.182	2289	3377.625	2312.1778	FALSE	Nik related kinase	232771 at	0.034	29340	5.331E-01	FALSE
101176 at	0.157	1975	1422304 at	0.171	1954	101176 at	-0.031	7164	1422304 at	-0.152	2419	3378	2533.0918	FALSE	lipocalin 4		NA	NA	NA	NA
103048 at	-0.223	378	1425922 a at	0.084	4684	103048 at	-0.159	795	1417155 at	-0.056	7659	3379	3449.8542	FALSE	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	209756 s at	0.044	23873	3.339E-01	FALSE
160341 at	0.036	6343	1424151 at	0.130	1346	160341 at	-0.085	3005	1451262 a at	0.161	2822	3379	2110.9642	FALSE	JTV1 gene	202138 x at	-0.043	32074	6.341E-01	FALSE
95971 at	0.134	3833	1459925 at	0.055	6467	95971 at	0.128	2084	1459925 at	-0.223	1133	3379.25	2342.6054	FALSE	expressed sequence C78282		NA	NA	NA	NA
104277 at	0.220	1784	1433144 at	0.077	5218	104277 at	-0.209	2608	1433144 at	0.157	3908	3379.5	1505.5704	FALSE	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)	225621 at	0.119	17409	1.244E-01	FALSE
161989 f at	0.066	4788	1448544 at	0.063	5064	103646 at	-0.141	998	1441919 x at	0.222	2669	3379.75	1914.6597	FALSE	carnitine acetyltransferase	209522 s at	0.200	4470	1.489E-04	FALSE
104556 at	0.211	608	1429982 at	0.130	4072.5	104556 at	0.006	8174	1429981 a at	-0.383	665	3379.875	3583.1644	FALSE	RIKEN cDNA 4933426K21 gene	229344 x at	0.211	5212	3.391E-04	FALSE
101977 at	-0.312	613	1451575 a at	-0.050	6572	101977 at	-0.068	4686	1451575 a at	-0.210	1649	3380	2741.4807	TRUE	nudix (nucleotide diphosphate linked moiety X)-type motif 3	221579 s at	-0.014	39718	8.703E-01	FALSE
97868 at	-0.036	6761	1432066 at	0.152	951.5	97868 at	0.076	4457	1432066 at	-0.196	1356	3381.375	2743.7973	FALSE	DnaJ (Hsp40) homolog, subfamily A, member 3	205963 s at	-0.074	15445	7.871E-02	FALSE
161335 r at	0.017	7733	1419260 a at	0.170	1041.5	160555 r at	0.091	2986.5	1437193 s at	0.226	1768	3382.25	3009.4605	TRUE	small nuclear ribonucleoprotein B	213175 s at	-0.060	25893	4.003E-01	FALSE
161088 r at	0.160	3125	1450983 at	0.080	5377.5	161088 r at	0.194	1535	1433669 at	-0.122	3492	3382.375	1578.14	FALSE	A kinase (PRKA) anchor protein 8	203847 s at	-0.142	12921	3.605E-02	FALSE
160371 at	0.062	6523	1423818 a at	0.152	2764.5	160371 at	0.091	2549	1451131 at	0.242	1696	3383.125	2143.4915	TRUE	ADP-ribosylation factor-like 6 interacting protein 1	211935 at	-0.014	40507	8.929E-01	FALSE
97322 at	0.102	2346	1418826 at	0.137	3061	97322 at	0.021	7088	1418826 at	-0.659	1045	3385	2605.9103	FALSE	membrane-spanning 4-domains, subfamily A, member 6B	219666 at	0.263	7231	1.905E-03	FALSE
92876 at	-0.073	4807	1438166 x at	0.287	1144	92876 at	-0.061	5542	1418117 at	-0.206	2054	3386.75	2118.8332	FALSE	NADH dehydrogenase (ubiquinone) Fe-S protein 4	209303 at	-0.350	7730	2.726E-03	FALSE
96541 at	-0.284	352	1434964 at	0.056	6100.5	96541 at	-0.096	2774	1434964 at	-0.104	4322	3387.125	2437.5056	FALSE	expressed sequence AA408420		NA	NA	NA	NA
101875 at	-0.053	5372	1450560 a at	-0.163	751	101875 at	-0.030	6798	1450560 a at	-0.385	631	3388	3168.5525	TRUE	protein phosphatase 2, regulatory subunit B (B56), delta isoform	202513 s at	-0.267	2117	4.632E-06	TRUE
98433 at	0.021	7474	1417045 at	0.167	2241	98433 at	0.105	2724	1448560 at	0.358	1113	3388	2806.3931	TRUE	BH3 interacting domain death agonist	211725 s at	-0.225	4709	1.990E-04	FALSE
92903 at	0.081	4277	1423340 at	0.122	3586.5	92903 at	0.120	2465	1435670 at	-0.134	3224	3388.125	754.66288	FALSE	transcription factor AP-2 beta	215686 x at	-0.026	31690	6.204E-01	FALSE
160207 at	-0.172	3544	1425326 at	-0.506	89.5	160207 at	-0.237	4263	1451666 at	-0.081	5657	3388.375	2367.7291	TRUE	ATP citrate lyase	210337 s at	-0.415	4265	1.167E-04	TRUE
96726 at	-0.284	612	1460389 at	-0.082	4637	96726 at	-0.073	5834	1460389 at	-0.151	2472	3388.75	2315.7538	TRUE	cyclin-dependent kinase 8	204831 at	-0.006	42025	9.354E-01	FALSE
97238 at	0.051	5645	1455834 x at	0.084	5036	97238 at	0.238	636	1436872 at	0.192	2239	3389	2359.6366	TRUE	transforming, acidic coiled-coil containing protein 3	218308 at	0.006	42412	9.443E-01	FALSE
92427 at	0.023	7161	1420894 at	-0.081	4660.5	92427 at	-0.227	788	1420894 at	-0.253	947	3389.125	3086.166	FALSE	transforming growth factor, beta receptor I	236561 at	0.389	4303	1.214E-04	FALSE
98473 at	-0.061	6946	1418847 at	-0.105	4384	161246 at	0.143	2127	1418847 at	-1.012	100	3389.25	2946.8876	FALSE	arginase type II	203946 s at	-0.474	3168	2.906E-05	FALSE
97960 at	0.282	2616	1456043 at	-0.171	2255	97960 at	-0.504	1012	1437151 at	0.026	7679	3390.5	2940.3914	FALSE	ubiquitin specific peptidase 22	220862 s at	0.059	19560	1.866E-01	FALSE
161606 f at	0.142	2913	1449646 s at	0.146	1870	161606 f at	0.043	6165	1460743 at	0.170	2614	3390.5	1900.9409	TRUE	tigger transposable element derived 5	229758 at	-0.018	37158	7.957E-01	FALSE
99647 at	0.128	1895	1416705 at	0.103	2439.5	99647 at	0.086	4552	1416705 at	-0.099	4677	3390.875	1431.2099	FALSE	ribulose-5-phosphate-3-epimerase	221770 at	-0.238	1845	2.938E-06	FALSE
92356 at	-0.073	4854	1417995 at	0.122	4034	161848 r at	0.104	2734	1417995 at	-0.199	1942	3391	1301.9304	FALSE	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	236539 at	-0.046	15933	8.934E-02	FALSE
95992 at	0.096	3157	1443416 at	0.142	2562	95992 at	-0.132	1572	1443416 at	-0.079	6280	3392.75	2032.8196	FALSE	expressed sequence C79741		NA	NA	NA	NA
98028 at	0.232	463	1418733 at	-0.009	8163	98028 at	0.106	3403	1418733 at	0.205	1545	3393.5	3403.5767	FALSE	twist gene homolog 1 (Drosophila)	213943 at	0.095	9244	6.711E-03	FALSE
161003 at	0.069	4343	1450074 at	-0.109	2509	161003 at	-0.174	2335	1450074 at	0.184	4395	3395.5	1126.5432	FALSE	kinesin family member 3B	225205 at	-0.236	6019	7.030E-04	FALSE
102794 at	0.054	5282	1448710 at	0.127	1882	102794 at	-0.188	2168	1448710 at	-0.141	4252	3396	1642.1441	FALSE	chemokine (C-X-C motif) receptor 4	217028 at	0.680	4985	2.660E-04	FALSE
94957 at	0.060	6010	1452034 at	-0.403	153	94957 at	0.075	6351	1426346 at	0.272	1071	3396.25	3239.7374	FALSE	prolyl endopeptidase-like	212215 at	-0.561	2719	1.401E-05	FALSE
99661 r at	-0.116	3134	1459885 s at	0.200	899.5	99660 f at	0.101	2316	1448112 at	0.043	7237	3396.625	2721.5704	FALSE	cytochrome c oxidase, subunit VIIc	213846 at	-0.357	3586	5.168E-05	FALSE
104510 at	-0.119	3551	1449999 a at	-0.021	8059	104510 at	-0.228	1933	1441608 at	0.900	49	3398	3421.0308	FALSE	calcium channel, voltage-dependent, alpha2/delta subunit 1	207050 at	-0.099	11453	2.068E-02	FALSE
97140 at	-0.052	5514	1447984 at	0.055	5895	97140 at	-0.151	780	1447984 at	0.361	1404	3398.25	2679.703	FALSE	DNA segment, Chr 1, ERATO Doi 75, expressed		NA	NA	NA	NA
93196 at	0.122	3945	1419176 at	-0.133	3664	93196 at	0.226	2199	1419176 at	0.181	3797	3401.25	809.67581	FALSE	Vacuolar protein sorting 37A (yeast)	225378 at	-0.142	15091	7.254E-02	FALSE
101858 at	-0.204	697	1421160 a at	-0.120	4734	101858 at	-0.066	5112	1460704 at	-0.129	3065	3402	2010.7145	TRUE	radical fringe gene homolog (Drosophila)	212968 at	0.062	18652	1.596E-01	FALSE
97553 at	-0.111	2755	1426756 at	0.115	4818	97553 at	-0.056	4784	1425610 s at	0.290	1253	3402.5	1727.4055	FALSE	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	239930 at	0.220	4411	1.380E-04	FALSE
103610 at	0.085	3342	1422474 at	-0.231	851.5	103610 at	-0.013	7963	1442700 at	-0.327	1454	3402.625	3220.0452	FALSE	phosphodiesterase 4B, cAMP specific	211302 s at	-0.306	12902	3.584E-02	FALSE
103939 at	0.020	7553	1451512 s at	0.138	2444	103939 at	0.141	1271	1451512 s at	-0.168	2343	3402.75	2817.2803	FALSE	3-hydroxyisobutyryl-Coenzyme A hydrolase	213374 x at	0.432	2059	4.322E-06	FALSE
95915 at	0.101	3173	1452498 at	0.107	3380.5	95915 at	-0.090	4629	1458566 at	0.188	2430	3403.125	913.45702	FALSE	G patch domain containing 2	236026 at	0.097	17231	1.204E-01	FALSE
93013 at	-0.612	78	1435176 a at	-0.278	2677.5	93013 at	-0.025	7801	1435176 a at	0.133	3058	3403.625	3216.7998	FALSE	inhibitor of DNA binding 2	201565 s at	0.696	3816	6.803E-05	FALSE
103301 i at	0.398	210	1435192 at	0.072	5868.5	103301 i at	0.124	2364	1450485 at	0.103	5173	3403.875	2613.1945	TRUE	SRY-box containing gene 3	214633 at	0.210	1196	7.175E-07	TRUE
99527 at	0.007	8199	1417520 at	0.166	1139.5	99527 at	0.242	237	1454240 at	-0.150	4044	3404.875	3585.13	FALSE	nuclear factor, erythroid derived 2, like 3	236471 at	-0.049	17498	1.267E-01	FALSE
96563 at	0.130	1545	1448013 at	-0.100	3969.5	96563 at	-0.139	3310	1448013 at	-0.146	4797	3405.375	1381.4182	FALSE	ubiquitin specific peptidase 24		NA	NA	NA	NA
161004 at	0.140	2001	1455692 x at	0.053	6346	161004 at	0.113	2784	1436419 a at	-0.159	2492	3405.75	1986.6139	FALSE	RIKEN cDNA 1700097N02 gene		NA	NA	NA	NA
101510 at	0.141	4878	1417056 at	0.288	450	101510 at	0.419	133	1417056 at	0.029	8164	3406.25	3840.8251	TRUE	proteasome (prosome, macropain) 28 subunit, alpha	200814 at	0.080	17321	1.224E-01	FALSE
96301 at	0.037	6462	1415716 a at	0.491	757	96300 f at	0.228	1160	1460699 at	0.093	5251	3407.5	2875.4634	TRUE	ribosomal protein S27	200741 s at	-0.230	4162	1.041E-04	FALSE
95395 at	-0.028	7658	1426842 at	-0.093	3986.5	95395 at	-0.248	1485	1445235 at	0.424	501	3407.625	3190.911	FALSE	YTH domain family 3	221749 at	-0.041	33544	6.841E-01	FALSE
104252 at	-0.114	5658	1433935 at	0.184	1178	104252 at	0.171	947	1433935 at	-0.191	5851	3408.5	2711.7134	FALSE	expressed sequence AU020206		NA	NA	NA	NA
101349 at	0.138	1740	1448191 at	0.041	7302.5	93099 f at	-0.117	2390	1459616 at	0.262	2203	3408.875	2610.0894	FALSE	polo-like kinase 1 (Drosophila)	201429 s at	-0.011	39080	8.529E-01	FALSE
94472 at	0.016	7568	1448258 a at	0.163	3087	94472 at	0.147	1928	1427500 at	-0.271	1054	3409.25	2894.8432	FALSE	signal peptidase complex subunit 1 homolog (S. cerevisiae)	217927 at	-0.118	25020	3.733E-01	FALSE
96069 at	0.062	4719	1417294 at	0.109	2984	96069 at	-0.172	1222	1458300 at	0.141	4713	3409.5	1671.3377	FALSE	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	214259 s at	0.434	1440	1.257E-06	FALSE
95318 at	0.195	1217	1460252 s at	0.072	4517	95318 at	0.151	779	1460252 s at	-0.071	7125	3409.5	2986.5299	FALSE	zinc finger protein 105	206096 at	0.056	21115	2.370E-01	FALSE
102253 at	0.222	1201	1425160 at	0.086	5170	102253 at	0.085	4646	1425160 at	0.237	2622	3409.75	1837.2008	TRUE	cDNA sequence AF067063		NA	NA	NA	NA
93435 at	0.049	5940	1418866 at	0.134	2546.5	93435 at	0.099	2961	1418867 at	0.210	2196	3410.875	1714.83	TRUE	cytochrome P450, family 24, subfamily a, polypeptide 1	206504 at	-0.003	42341	9.430E-01	FALSE
99878 at	0.301	202	1428563 at	0.131	4099	99878 at	0.038	6766	1452838 at	0.162	2577	3411	2752.1268	TRUE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	204977 at	-0.160	7415	2.160E-03	FALSE
98869 g at	0.077	3970	1422938 at	-0.022	7575	98869 g at	-0.165	2011	1443837 x at	-0.631	89	3411.25	3196.1988	FALSE	B-cell leukemia/lymphoma 2	203685 at	0.656	897	3.460E-07	FALSE
97213 at	0.147	1346	1453560 at	0.122	4054.5	97213 at	-0.195	373	1437063 at	-0.021	7875	3412.125	3358.3256	FALSE	feminization 1 homolog a (C. elegans)	223175 s at	-0.068	18058	1.421E-01	FALSE
101666 at	0.246	2237	1418315 at	0.098	3649	100700 s at	-0.092	2624	1418315 at	0.100	5142	3413	1297.5148	FALSE	nuclear receptor subfamily 5, group A, member 1	210333 at	0.047	28935	5.186E-01	FALSE
93558 at	-0.072	4514	1422827 x at	-0.087	3896	93558 at	0.176	1456	1432533 a at	-0.116	3788	3413.5	1343.6223	FALSE	solute carrier family 35 (UDP-galactose transporter), member 2	207440 at	0.089	12092	2.686E-02	FALSE
103037 at	0.135	2762	1449093 at	0.133	2746.5	103037 at	0.075	4746	1449093 at	0.138	3401	3413.875	938.98051	TRUE	cardiotrophin 1	206813 at	0.049	28985	5.201E-01	FALSE
101381 at	0.131	4261	1426023 a at	-0.181	1742	101381 at	-0.109	1985	1443856 at	0.089	5672	3415	1884.4623	FALSE	rabaptin, RAB GTPase binding effector protein 1	231002 s at	0.100	12043	2.639E-02	FALSE
92533 at	0.152	3840	1427355 at	0.308	386	92533 at	0.021	7197	1452004 at	-0.249	2238	3415.25	2889.309	FALSE	calcitonin/calcitonin-related polypeptide, alpha	210728 s at	0.015	35057	7.321E-01	FALSE
92579 at	-0.304	1534	1453928 a at	0.258	1229.5	92579 at	-0.038	7960	1416423 x at	-0.157	2940	3415.875	3119.6804	FALSE	Sjogren syndrome antigen B	201139 s at	-0.034	33694	6.884E-01	FALSE
94236 at	-0.067	6154	1451338 at	0.205	315	94236 at	-0.053	6545	1430151 at	0.701	650	3416	3393.8298	FALSE	nischarin		NA	NA	NA	NA
99428 at	0.185	2366	1420177 at	0.138	2203	99428 at	-0.115	3436	1420177 at	-0.085	5664	3417.25	1594.5498	FALSE	immunoglobulin lambda-like polypeptide 1		NA	NA	NA	NA
92866 at	-0.888	2084	1435290 x at	0.071	5347.5	92866 at	0.059	5066	1435290 x at	-1.404	1174	3417.875	2101.9012	FALSE	histocompatibility 2, class II antigen A, alpha	212671 s at	0.243	19006	1.694E-01	FALSE
93458 at	0.036	6388	1419961 s at	0.116	2285.5	93458 at	0.154	1275	1419960 at	0.142	3725	3418.375	2220.3719	TRUE	RIKEN cDNA C330003B14 gene		NA	NA	NA	NA

102660 at	0.216	1068	1422870 at	0.011	8139	102660 at	0.099	2747	1422870 at	0.263	1724	3419.5	3221.2942	TRUE	homeo box C4	206194 at	0.068	15473	7.920E-02	FALSE
162420 r at	0.143	2015	1423225 at	0.180	2722	160403 at	0.183	2360	1447909 s at	0.063	6582	3419.75	2127.8371	TRUE	selenoprotein K	223070 at	0.167	11107	1.803E-02	TRUE
96610 at	-0.136	4302	1415826 at	0.138	4610.5	96610 at	0.139	2708	1457639 at	0.360	2064	3421.125	1230.2966	FALSE	ATPase. H+ transporting. lysosomal V1 subunit H	221504 s at	-0.724	1450	1.271E-06	FALSE
162146 r at	-0.083	5048	1455326 at	-0.076	5833	103999 at	0.239	851	1455326 at	-0.261	1953	3421.25	2396.1634	FALSE	RIKEN cDNA 4932416N17 gene	244100 at	0.133	6721	1.254E-03	FALSE
102824 g at	-0.418	2858	1424631 a at	0.117	2260	102823 at	0.266	1257	1426174 s at	0.043	7312	3421.75	2676.295	FALSE	Immunoglobulin heavy chain (gamma polypeptide)	NA	NA	NA	NA	
160708 at	-0.258	2144	1423025 a at	0.171	2327	160708 at	-0.035	7395	1423025 a at	0.314	1825	3422.75	2656.2784	FALSE	schwannomin interacting protein 1	204030 s at	0.192	13147	3.911E-02	FALSE
160961 at	-0.130	3416	1434261 at	-0.162	1278	160961 at	0.153	3741	1434261 at	-0.141	5259	3423.5	1640.4362	FALSE	signal-induced proliferation-associated 1 like 2	225056 at	0.347	6323	9.273E-04	FALSE
103061 at	-0.179	1923	1416562 at	-0.560	16.5	103061 at	-0.081	5984	1416562 at	-0.119	5771	3423.625	2939.7316	TRUE	glutamic acid decarboxylase 1	206670 s at	-0.671	3020	2.277E-05	TRUE
103852 at	0.139	2927	1423958 a at	0.068	6450.5	103852 at	0.203	2075	1423958 a at	0.184	2243	3423.875	2051.1195	TRUE	RIKEN cDNA 2900001O04 gene	219421 at	-0.277	6613	1.145E-03	FALSE
103238 at	-0.130	2012	1450782 at	-0.130	2728	103238 at	0.032	6751	1450782 at	0.234	2206	3424.25	2238.3486	FALSE	wingless-related MMTV integration site 4	208606 s at	-0.006	41911	9.325E-01	FALSE
100925 at	-0.139	3670	1460464 at	-0.069	6213	100925 at	-0.533	155	1453208 at	-0.156	3659	3424.25	2488.6826	TRUE	RIKEN cDNA 2700089E24 gene	NA	NA	NA	NA	
161337 f at	0.070	4483	1415694 at	-0.258	2340	98606 s at	-0.347	1046	1437832 x at	0.094	5831	3425	2140.488	FALSE	tryptophanyl-tRNA synthetase	200628 s at	-0.113	28653	5.076E-01	FALSE
99436 at	0.141	2089	1422133 at	0.064	6552	99436 at	0.113	3330	1422133 at	0.177	1732	3425.75	2193.8016	TRUE	sialophorin	206056 x at	0.250	5038	2.777E-04	TRUE
161772 i at	0.172	2199	1418343 at	0.123	2609.5	161772 i at	-0.052	5450	1418343 at	0.172	3445	3425.875	1445.5839	FALSE	GTF2I repeat domain containing 2	NA	NA	NA	NA	
93312 at	-0.290	929	1415688 at	-0.231	437.5	93312 at	-0.122	4844	1415688 at	-0.028	7494	3426.125	3352.8838	TRUE	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog. C. elegans)	209142 s at	-0.349	8520	4.416E-03	TRUE
93478 at	-0.192	1271	1460711 at	0.113	4172.5	93478 at	-0.021	7347	1457281 at	0.234	914	3426.125	2993.6417	FALSE	RIKEN cDNA 4930461P20 gene	230893 at	0.116	13462	4.344E-02	FALSE
92398 at	-0.148	1936	1424380 at	0.071	4427	92398 at	-0.064	3863	1424380 at	-0.254	3479	3426.25	1067.0643	FALSE	vacuolar protein sorting 37B (yeast)	221704 s at	0.232	5585	4.755E-04	FALSE
92571 at	-0.194	2173	1416146 at	-0.054	7125	100353 g at	-0.301	511	1416147 at	0.187	3896	3426.25	2826.7021	FALSE	heat shock protein 4	208815 x at	0.148	15687	8.376E-02	FALSE
95025 at	-0.326	180	1448900 at	0.000	8516	95025 at	0.125	1468	1446626 at	0.142	3541	3426.25	3664.7694	FALSE	DNA segment. Chr 16. human D22S680E. expressed	235396 at	0.068	22579	2.874E-01	FALSE
93622 at	0.160	2980	1451802 at	0.124	2657	93622 at	-0.069	3912	1451802 at	0.116	4158	3426.75	721.64043	FALSE	mast cell protease 6	207741 x at	0.065	21398	2.468E-01	FALSE
161471 f at	0.062	5411	1434336 s at	-0.177	1097.5	104558 at	-0.074	5596	1437545 at	0.331	1603	3426.875	2407.9288	FALSE	REST corepressor 1	212612 at	0.079	23561	3.223E-01	FALSE
94833 at	0.095	5304	1448259 at	-0.197	692	94833 at	-0.066	5430	1416221 at	-0.227	2285	3427.75	2332.3468	FALSE	follistatin-like 1	208782 at	0.519	3122	2.676E-05	FALSE
104256 at	-0.048	6403	1451206 s at	0.099	3640	104257 g at	0.115	2026	1451206 s at	-0.172	1644	3428.25	2163.6257	FALSE	pleckstrin homology. Sec7 and coiled-coil domains. binding protein	209606 at	0.021	33442	6.798E-01	FALSE
160856 at	0.110	3706	1424539 at	-0.093	5154	160856 at	-0.237	800	1424538 at	0.141	4054	3428.5	1857.832	FALSE	ubiquitin-like 4	221746 at	-0.086	17372	1.237E-01	FALSE
101949 at	0.143	1457	1431938 a at	0.087	3350	101949 at	0.029	6936	1439953 at	0.205	1971	3428.5	2471.1561	TRUE	phosphomannomutase 2	203201 at	-0.055	23246	3.102E-01	FALSE
94040 at	0.024	7714	1430536 a at	0.185	2315.5	94040 at	0.207	1853	1430536 a at	0.201	1834	3429.125	2865.2462	TRUE	enhancer of rudimentary homolog (Drosophila)	200043 at	0.026	34697	7.222E-01	FALSE
93722 at	0.056	6673	1423330 at	0.207	1037	93722 at	-0.120	4507	1428620 at	0.246	1502	3429.75	2653.3382	FALSE	endosulfine alpha	202596 at	-0.426	2112	4.610E-06	FALSE
103653 at	-0.204	829	1449590 a at	-0.100	4880	103653 at	-0.088	3845	1449590 a at	-0.172	4165	3429.75	1787.0041	TRUE	muscle and microspikes RAS	225185 at	0.269	9514	7.802E-03	FALSE
102403 at	0.117	2313	1416575 at	0.190	1361.5	102403 at	0.056	5186	1457838 at	0.095	4863	3430.875	1885.3296	TRUE	cell division cycle 45 homolog (S. cerevisiae)-like	204126 s at	-0.052	25905	4.008E-01	FALSE
98320 at	0.122	2964	1419430 at	0.061	5589	98320 at	-0.096	2709	1419430 at	-0.207	2462	3431	1453.1917	FALSE	cytochrome P450. family 26. subfamily a. polypeptide 1	206424 at	0.001	44229	9.897E-01	FALSE
98168 at	-0.100	5068	1422613 a at	0.124	2420.5	98168 at	0.191	777	1422613 a at	0.081	5460	3431.375	2225.716	FALSE	ribosomal protein L7a	234873 x at	-0.090	16087	9.263E-02	FALSE
93725 at	0.145	2160	1427321 s at	-0.093	3394.5	93725 at	0.053	5730	1453282 at	-0.202	2441	3431.375	1620.9332	FALSE	coxsackievirus and adenovirus receptor	226374 at	-0.135	18602	1.580E-01	FALSE
160820 at	-0.166	823	1460675 at	-0.036	7179	160820 at	-0.212	753	1460675 at	-0.111	4971	3431.5	3182.8944	TRUE	immunoglobulin superfamily. member 8	225025 at	-0.183	15602	8.215E-02	FALSE
99536 at	0.140	1676	1422852 at	0.032	7475	99536 at	0.237	721	1422852 at	0.290	3860	3433	2997.8929	TRUE	calcium and integrin binding family member 2	214065 s at	0.070	15845	8.696E-02	FALSE
99606 at	0.117	1657	1452060 a at	0.069	5683	99606 at	0.067	4022	1418581 a at	0.179	2376	3434.5	1796.3701	TRUE	LIM motif-containing protein kinase 2	202193 at	0.552	4239	1.126E-04	TRUE
104547 at	0.118	1864	1419172 at	0.064	5489	104547 at	0.157	1053	1430750 at	0.091	5334	3435	2307.0242	TRUE	dihydrofolate reductase	202532 s at	0.168	7160	1.804E-03	TRUE
100043 f at	0.033	7188	1429457 at	0.148	942.5	100043 f at	-0.059	4071	1440186 s at	0.210	1539	3435.125	2845.867	FALSE	RIKEN cDNA 2310020A21 gene	NA	NA	NA	NA	
96753 at	0.212	575	1449523 at	0.089	4838	96753 at	0.084	3267	1443898 at	0.097	5061	3435.25	2067.213	TRUE	B-cell CLL/lymphoma 7C	219072 at	0.062	23857	3.333E-01	FALSE
101716 at	0.150	1045	1450616 at	0.046	6510	101716 at	-0.079	3373	1450616 at	0.178	2813	3435.25	2277.3122	FALSE	eosinophil-associated. ribonuclease A family. member 5	NA	NA	NA	NA	
100086 at	-0.075	4539	1426697 a at	0.131	1381.5	161988 f at	0.128	1698	1426696 at	-0.093	6124	3435.625	2286.4504	FALSE	low density lipoprotein receptor-related protein associated protein 1	201186 at	-0.774	14	2.182E-09	FALSE
94100 s at	0.076	5085	1451033 a at	0.096	5471.5	94100 s at	-0.184	2527	1423579 a at	0.317	659	3435.625	2265.7207	FALSE	transient receptor potential cation channel. subfamily C. member 4	224219 s at	-0.058	21034	2.345E-01	FALSE
93559 at	-0.007	8319	1416135 at	0.243	339	93559 at	0.112	3743	1416135 at	0.202	1342	3435.75	3555.0051	FALSE	apurinic/apyrimidinic endonuclease 1	210027 s at	-0.107	17724	1.329E-01	FALSE
160640 at	-0.088	4446	1424748 at	-0.004	8412.5	160640 at	0.171	857	1424748 at	0.577	30	3436.375	3831.35	FALSE	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	219013 at	-0.194	13481	4.363E-02	FALSE
96234 at	-0.118	2176	1437852 x at	0.095	3499	96234 at	-0.038	7409	1422855 at	-0.279	663	3436.75	2890.5492	FALSE	cleavage and polyadenylation specificity factor 3	225082 at	0.068	22883	2.973E-01	FALSE
94300 f at	-0.201	1300	1424461 at	0.059	5950	94299 at	-0.127	4430	1424461 at	0.158	2068	3437	2140.2607	FALSE	dynactin 2	200932 s at	-0.138	8378	4.100E-03	FALSE
103763 at	-0.140	3287	1450071 at	-0.155	1698	103763 at	-0.022	7888	1420985 at	0.331	878	3437.75	3130.8412	FALSE	ash1 (absent. small. or homeotic)-like (Drosophila)	218554 s at	-0.100	14121	5.471E-02	FALSE
94837 at	-0.111	4063	1456083 x at	0.121	1935	94837 at	-0.105	5230	1415859 at	0.319	2524	3438	1494.0207	FALSE	eukaryotic translation initiation factor 3. subunit 8	210949 s at	-0.308	10873	1.619E-02	FALSE
101498 at	0.027	7155	1423127 at	0.175	1400	101498 at	0.150	3109	1430495 at	0.234	2089	3438.25	2575.3689	TRUE	inositol (myo)-1(or 4)-monophosphatase 1	203011 at	0.149	22330	2.795E-01	FALSE
103718 at	0.128	2110	1420645 at	0.187	614	96961 at	-0.089	3684	1420645 at	-0.056	7346	3438.5	2890.8787	FALSE	polycomb group ring finger 2	214239 x at	0.177	4932	2.506E-04	FALSE
160081 at	-0.069	6130	1416807 at	0.419	454.5	160081 at	0.356	554	1416807 at	-0.051	6622	3440.125	3396.2445	FALSE	ribosomal protein L36a	201406 at	-0.141	12796	3.476E-02	FALSE
102637 at	0.039	6447	1425620 at	-0.049	6599.5	102637 at	-0.210	209	1447314 at	-0.338	506	3440.375	3562.4058	FALSE	transforming growth factor. beta receptor III	204731 at	0.504	2253	6.094E-06	FALSE
103443 at	0.035	7346	1426942 at	0.160	2289	103443 at	0.159	818	1426942 at	-0.151	3312	3441.25	2797.1949	FALSE	absent in melanoma 1	212543 at	0.079	20333	2.110E-01	FALSE
104671 at	-0.096	3599	1422573 at	-0.194	1092	104671 at	0.000	8520	1422573 at	-0.346	557	3442	3635.7694	FALSE	AMP deaminase 3	207992 s at	0.229	13595	4.542E-02	FALSE
98927 at	-0.245	801	1448305 at	0.102	4504.5	98927 at	0.203	4198	1448304 a at	0.244	4269	3443.125	1766.2811	FALSE	RAB6. member RAS oncogene family	201047 x at	-0.364	2852	1.731E-05	FALSE
102222 at	-0.364	719	1427672 a at	0.072	4958	102222 at	-0.091	5941	1446278 at	-0.256	2163	3445.25	2421.6926	FALSE	ubiquitously transcribed tetratricopeptide repeat gene. X chromosome	203991 s at	0.231	4877	2.392E-04	FALSE
101019 at	-0.241	3373	1416382 at	-0.035	7287	101020 at	0.160	510	1437939 s at	-0.148	2616	3446.5	2832.408	FALSE	cathepsin C	201487 at	0.191	12250	2.864E-02	FALSE
96593 at	0.095	3674	1421896 at	0.068	4610.5	96593 at	-0.199	1551	1421896 at	0.115	3951	3446.625	1323.3912	FALSE	ELK1. member of ETS oncogene family	210376 x at	-0.328	4181	1.068E-04	FALSE
103051 at	-0.065	4457	1417160 s at	0.108	3253	103051 at	-0.047	5247	1417160 s at	0.546	832	3447.25	1926.6517	FALSE	extracellular proteinase inhibitor	NA	NA	NA	NA	
104174 at	0.076	4741	1459546 s at	0.119	2999.5	104174 at	0.039	5766	1459546 s at	0.393	284	3447.625	2398.4037	TRUE	ectonucleotide pyrophosphatase/phosphodiesterase 1	205066 s at	0.079	23044	3.027E-01	FALSE
94495 at	0.129	1919	1416909 at	0.113	2489	94495 at	-0.117	3900	1416909 at	0.104	5487	3448.75	1593.6692	FALSE	RIKEN cDNA 1810008A14 gene	NA	NA	NA	NA	
161684 r at	0.106	4104	1427747 a at	0.087	5155	160564 at	0.119	2705	1427747 a at	-0.352	1835	3449.75	1471.7326	FALSE	lipocalin 2	212531 at	-0.019	39500	8.642E-01	FALSE
102771 at	0.198	736	1458215 at	0.186	1261.5	102771 at	-0.032	6609	1458215 at	-0.118	5196	3450.625	2897.3047	FALSE	SET domain. bifurcated 1	203155 at	0.129	7172	1.824E-03	FALSE
95554 at	0.105	2530	1452831 s at	0.077	5230	95553 at	0.115	2842	1428543 at	-0.186	3202	3451	1217.3693	FALSE	phosphoribosyl pyrophosphate amidotransferase	209433 s at	0.291	10660	1.452E-02	FALSE
103227 at	0.026	7619	1427960 at	0.118	3812.5	103227 at	0.242	457	1427961 s at	0.161	1919	3451.875	3099.1377	TRUE	UDP glucuronosyltransferase 2 family. polypeptide B34	NA	NA	NA	NA	
100613 at	-0.164	1138	1416113 at	0.015	7924	100613 at	-0.113	1727	1416113 at	-0.166	3019	3452	3083.0988	FALSE	FK506 binding protein 8	208255 s at	-0.259	3651	5.672E-05	FALSE
160309 at	-0.074	6121	1423462 at	-0.192	1798	160309 at	0.241	2152	1451003 at	0.112	3737	3452	1968.9677	FALSE	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	212184 s at	0.217	9705	8.676E-03	FALSE
92506 at	-0.076	3903	1426294 at	-0.044	5992	92506 at	-0.134	3629	1421633 a at	-0.541	285	3452.25	2360.5239	TRUE	hyaluronan and proteoglycan link protein 1	205523 at	-0.085	17919	1.386E-01	FALSE
97148 at	0.151	1369	1456136 at	0.041	5974.5	98471 f at	-0.152	1301	1449877 s at	0.091	5171	3453.875	2468.7138	FALSE	Kinesin family member C1	209680 s at	0.029	32602	6.506E-01	FALSE
99503 at	-0.331	984	1455958 s at	-0.069	5647	99503 at	0.074	6674	1455958 s at	-0.398	517	3455.5	3157.2408	FALSE	PTC7 protein phosphatase homolog (S. cerevisiae)	225213 at	-0.307	7590	2.461E-03	FALSE
95027 at	-0.007	8209	1454034 a at	-0.157	867	95027 at	-0.207	534	1454034 a at	-0.133	4217	3456.75	3578.2273	TRUE	ubiquitin specific peptidase 21	232219 x at	0.173	7096	1.694E-03	FALSE
98884 r at	-0.295	664	1422568 at	-0.065	5901.5	98884 r at	-0.110	5734	1424893 at	0.371	1532	3457.875	2748.744	FALSE	nuclear distribution gene E-like homolog 1 (A. nidulans)	208093 s at	-0.512	534	1.158E-07	FALSE
93933 at	-0.023	7185	1425631 at	-0.340	360.5	93933 at	-0.261	1131	1433691 at	-0.097	5160	3459.125	3255.5984	TRUE	protein phosphatase 1. regulatory (inhibitor) subunit 3C	204284 at	0.098	30319	5.679E-01	FALSE
99076 at	0.178	4068	1416959 at	-0.146	2489	99076 at	-0.262	823	1416958 at	-0.061	6457	3459.25	2397.7963	FALSE	nuclear receptor subfamily 1. group D. member 2	209750 at	0.304	8087	3.463E-03	FALSE
93717 at	-0.140	3647	1419282 at	0.097	3192.5	93717 at	-0.089	3669	1419282 at	-0.819	3331	3459.875	235.82987	FALSE	chemokine (C-C motif) ligand 12	216598 s at	0.452	12754	3.430E-02	FALSE
95629 at	-0.097	4978	1436019 a at	0.188	1647.5	95629 at	0.085	4567	1436019 a at	0.213	2649	3460.375	1578.2532	FALSE	trafficking protein particle complex 1	225294 s at	-0.183	8488	4.327E-03	FALSE
94305 at	0.140	2689	1423669 at	-0.115	4063.5	103709 at	0.062	5385	1455494 at	-0.215	1704	3460.375	1607.0484	FALSE	procollagen. type I. alpha 1	202310 s at	0.130	17676	1.317E-01	FALSE
94543 at	0.160	2488	1424087 at	0.129	2243.5	94543 at	0.021	7289	1424087 at	0.211	1824	3461.125	2566.6053	TRUE	RIKEN cDNA 1810042K04 gene	223363 at	0.033	33013	6.659E-01	FALSE
101435 at	0.056	5649	1449168 a at	-0.283	639.5	101435 at	-0.087	4618	1449168 a at	0.465	2939	3461.375	2187.7948	FALSE	A kinase (PRKA) anchor protein 2	226694 at	0.485	2815	1.638E-05	FALSE
97200 f at	-0.134	4529	1451294 s at	0.502	675	97200 f at	0.388	1331	1451294 s at	-0.034	7313	3462	3070.1368	FALSE	small nuclear ribonucleoprotein E	231112 at	0.051	21584	2.530E-01	FALSE
103558 at	0.219	1625	1421589 at	0.129	3173	103558 at	0.036	6835	1421589 at	0.162	2218	3462.75	2336.8606	TRUE	keratin complex 1. acidic. gene 1	206677 at	-0.028	29992	5.567E-01	FALSE
100901 at	0.065	5225	1450439 at	-0.156	1458	100900 at	0.139	3452	1421972 s at	-0.136	3722	3464.25	1548.3179	FALSE	host cell factor C1	231177 at	0.030	31207	6.030E-01	FALSE
104480 at	0.148	1742	1425619 s at	0.087	4506	98319 at	0.041	5859	1449740 s at	0.319	1751	3464.5	2059.2427	TRUE	desmoglein 2	217901 at	0.016	37543	8.066E-01	FALSE
94206 at	-0.111	3652	1416522 a at	0.186	3051.5	94206 at	0.078	4089	1429782 at	-0.144	3067	3464.875	501.24219	FALSE	gene rich cluster. C10 gene	224719 s at	-0.059	31617	6.171E-01	FALSE
92759 at	0.120	3121	1417812 a at	0.196	1463	161188 f at	0.119	2429	1417812 a at	-0.082	6847	3465	2354.9636	FALSE	laminin. beta 3	209270 at	-0.057	21177	2.389E-01	FALSE
97102 at	0.228	449	1423361 at	0.113	4597.5	97102 at	0.074	4791	1423361 at	0.154	4027	3466.125	2037.3943	TRUE	YME1-like 1 (S. cerevisiae)	232216 at	0.159	11440	2.048E-02	TRUE
96557 at	-0.107	2760	1422655 at	-0.080	4045	96557 at	-0.108	3464	1422655 at	-0.209	3599	3467	532.71819	TRUE	patched homolog 2	221292 at	-0.052	19907	1.977E-01	FALSE
101829 at	-0.083	4576	1450833 at	-0.086	5218	101829 at	-0.508	175	1439611 at	-0.283	3900	3467.25	2259.8403	TRUE	cholinergic receptor. muscarinic 1. CNS	231783 at	-0.924	1103	5.941E-07	TRUE
100331 g at	0.049	7019	1418506 a at	0.230	1801.5	100331 g at	0.107	2286	1418506 a at	0.212	2770	3469.125	2399.3851	TRUE	peroxiredoxin 2	215067 x at	0.242	4416	1.391E-04	TRUE
98784 at	0.037	6516	1449472 at	-0.202	926	98784 at	-0.031	6210	1457702 at	-0.795	227	3469.75	3355.3291	FALSE	G-protein coupled receptor 12	214558 at	-0.257	6186	8.177E-04	FALSE
97758 at	0.148	4876	1434731 x at	0.201	1858.5	97055 s at	0.300	258	1434731 x at	-0.066	6888	3470.125	2976.2077	FALSE	peroxiredoxin 1	208680 at	0.272	5772	5.710E-04	FALSE
102566 at	0.118	2404	1422162 at	0.078	5608.5	102566 at	0.150	2141	1443278 at	-0.291	3727	3470.125	1585.5418	FALSE	deleted in colorectal carcinoma	206939 at	-0.194	10268	1.180E-02	FALSE
95117 at	-0.100	3426	1424112 at	0.100	3231	95117 at	-0.049	6582	1424112 at	0.275	645	3471	2430.653	FALSE	insulin-like growth factor 2 receptor	201392 s at	0.332	902	3.560E-07	FALSE
94217 f at	0.072	5837	1448001 x at	0.174	1914	94217 f at	0.164	2042	1448001 x at	0.113	4093	3471.5	1866.4698	TRUE	cell division cycle associated 3	221436 s at	-0.026	35398	7.433E-01	FALSE
93070 at	-0.187	2501	1426945 at	-0.029	7127	161757 f at	0.135	1748	1426945 at	0.169	2511	3471.75	2462.8955	FALSE	RAN binding protein 5	211952 at	-0.139	11322	1.965E-02	FALSE
98111 at	-0.169	4062	1423566 a at	-0.375	111.5	98111 at	-0.285	1565	1425993 a at	-0.016	8151	3472.375	3519.9787	TRUE	heat shock protein 110	208744 x at	-0.603	2216	5.636E-06	TRUE
100978 at	0.007	8201	1417253 at	0.339	2238	100978 at	0.103	2598	1417253 at	0.280	858	3473.75	3239.4988	TRUE	FSHD region gene 1	204145 at	-0.098	16798	1.090E-01	FALSE
102255 at	0.121	4607	1418675 at	0.075	4297	102255 at	0.155	2049	1418674 at	-0.419	2942	3473.75	1193.6871	FALSE	oncostatin M receptor	205729 at	0.079	25758	3.954E-01	FALSE
99562 at	-0.119	4053	1436781 at	0.084	5394	162150 r at	0.130	3505	1416340 a at	-0.217	945	3474.25	1863.5488	FALSE	mannosidase 2. alpha B1	209166 s at	0.217	4246	1.143E-04	FALSE
162124 r at	-0.133	2468	1438017 at	-0.142	1840	162124 r at	-0.042	5812	1437991 x at	0.128	3778	3474.5	1755.0547	FALSE	RUN and SH3 domain containing 1	206949 s at	-0.215	4335	1.258E-04	FALSE
102353 at	-0.092	4048	1450678 at	-0.054	5408.5	102353 at	-0.108	2030	1450678 at	-0.510	2412	3474.625	1558.2837	TRUE	integrin beta 2	229041 s at	0.136	12187	2.781E-02	FALSE
160328 at	-0.068	5427	1428365 a at	0.065	5023.5	160328 at	-0.117	2083	1428365 a at	-0.227	1365	3474.625	2049.221	FALSE	protease. serine. 15	209017 s at	-0.017	38430	8.348E-01	FALSE
160350 at	-0.016	8083	1427552 a at	0.110	3043	160350 at	0.235	1709	1458134 at	0.357	1064	3474.75	3180.7737	FALSE	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	242617 at	-0.135	15050	7.187E-02	FALSE
93926 at	0.239	896	1421382 at	0.142	4666	95030 at	0.124	2700	1421382 at	-0.092	5638	3475	2109.4167	FALSE	prolactin receptor	227629 at	-0.325	10522	1.339E-02	FALSE
98509 at	-0.228	1837	1426234 s at	-0.161	1361.5	98509 at	0.067	6211	1426234 s at	-0.141	4491	3475.125	2285.3066	FALSE	cDNA sequence BC002199	219023 at	-0.399	2073	4.371E-06	FALSE
160787 at	0.141	1169	1437713 x at	0.062	4403	160787 at	0.039	6381	1423656 x at	0.163	1950	3475.75	2376.9223	TRUE	RIKEN cDNA 1500010J02 gene	240875 at	-0.005	41252	9.143E-01	FALSE
160540 at	-0.284	1110	1416394 at	-0.027	7124	160540 at	0.285	1187	1416394 at	0.147	4486	3476.75	2896.2895	FALSE	Bcl2-associated athanogene 1	211475 s at	-0.154	10019	1.019E-02	FALSE
102993 at	0.125	3229	1418483 a at	0.140	1390	102993 at	-0.002	8463	1418483 a at	-0.422	825	3476.75	3479.0024	FALSE	glycoprotein galactosyltransferase alpha 1. 3	NA	NA	NA	NA	
95955 at	0.069	4650	1443949 at	0.019	7753.5	95955 at	0.142	1170	1428463 a at	0.356	335	3477.125	3408.7532	TRUE	Protein phosphatase 2. regulatory subunit B (B56). epsilon isoform	203338 at	-0.046	31601	6.166E-01	FALSE
160353 i at	0.140	2155	1426648 at	-0.106	2811.5	160353 i at	0.159	861	1426648 at	-0.017	8083	3477.625	3175.3879	FALSE	MAP kinase-activated protein kinase 2	201460 at	0.337	1223	7.580E-07	FALSE
103271 at	-0.115	2179	1451022 at	-0.099	3655.5	103271 at	0.021	7107	1451022 at	0.335	970	3477.875	2656.979	FALSE	low density lipoprotein receptor-related protein 6	225745 at	0.322	5007	2.711E-04	FALSE
94640 at	0.018	7527	1427618 at	-0.188	2216.5	94640 at	-0.189	479	1427618 at	-0.267	3690	3478.125	3001.3735	FALSE	cadherin 9	207729 at	-0.121	11226	1.888E-02	FALSE
103845 at	-0.176	1793	1455285 at	0.027	7539.5	103845 at	0.091	2243	1433750 at	-0.361	2340	3478.875	2717.5524	FALSE	solute carrier family 31. member 1	203971 at	0.052	17917	1.386E-01	FALSE
161042 at	-0.122	2058	1427912 at	-0.040	7499.5	161042 at	0.077	3883	1427912 at	-0.298	476	3479.125	3020.2034	FALSE	carbonyl reductase 3	205379 at	-0.137	19635	1.885E-01	FALSE
93911 at	0.007	8164	1450400 at	0.156	957.5	93911 at	-0.077	4647	1450401 at	0.826	149	3479.375	3686.0236	FALSE	nuclear receptor coactivator 6 interacting protein	236371 s at	-0.101	12533	3.171E-02	FALSE
92882 at	0.117	3898	1416082 at	0.078	5424.5	92882 at	-0.170	1774	1416082 at	0.132	2823	3479.875	1559.689	FALSE	RAB1. member RAS oncogene family	207791 s at	-0.222	16048	9.208E-02	FALSE
92180 at	-0.232	1017	1436517 at	0.043	6333.5	92180 at	-0.199	1522	1436517 at	-0.133	5052	3481.125	2614.9426	FALSE	H1 histone family. member X	231004 s at	-0.064	23104	3.050E-01	FALSE
160783 at	-0.166	1215	1426780 at	0.027	7554	160783 at	-0.134	3201	1426780 at	-0.265	1956	3481.5	2835.966	FALSE	DNA segment. Chr 14. ERATO Doi 436. expressed	204568 at	0.206	11582	2.171E-02	FALSE
102846 at	0.105	3055	1449489 at	0.210	839	102846 at	0.031	6315	1449489 at	0.133	3718	3481.75	2254.5778	TRUE	testis-specific serine kinase 2	214371 at	-0.038	27425	4.588E-01	FALSE
102622 r at	0.142	3189	1427591 at	0.176	2037	102622 r at	0.083	3963	1448082 at	0.100	4740	3482.25	1152.9381	TRUE	chloride channel 1	208437 at	0.015	40534	8.936E-01	FALSE
102676 at	-0.044	5741	1421071 at	-0.156	2045.5	102676 at	-0.100	2773	1434708 at	-0.129	3373	3483.125	1600.1219	TRUE	von Hippel-Lindau syndrome homolog	203844 at	0.013	32093	6.348E-01	FALSE
102362 i at	-0.248	816	1415899 at	-0.059	6647.5	102362 i at	-0.063	5260	1415899 at	-0.525	1210	3483.375	2912.6853	TRUE	Jun-B oncogene	201473 at	0.134	26909	4.397E-01	FALSE
103657 i at	0.176	3479	1418515 at	0.165	1888.5	161470 r at	0.109	2407	1418514 at	0.155	6170	3486.125	1907.8917	TRUE	metal response element binding transcription factor 2	203347 s at	-0.077	11857	2.437E-02	FALSE
98348 at	-0.038	6601	1420087 at	0.159	1414.5	98348 at	-0.065	5039	1438101 at	0.355	893	3486.875	2776.6762	FALSE	frizzled homolog 3 (Drosophila)	219683 at	-0.197	19562	1.866E-01	FALSE
104431 at	0.313	473	1426044 a at	0.038	6967	161853 f at	0.360	63	1426044 a at	0.108	6447	3487.5	3727.3749	TRUE	protein kinase C. theta	210038 at	0.151	12076	2.668E-02	TRUE
160114 at	0.187	3459	1431645 a at	-0.255	998	94642 at	-0.066	5493	1435898 x at	-0.115	4004	3488.5	1869.6899	FALSE	guanosine diphosphate (GDP) dissociation inhibitor 2	200008 s at	-0.306	9133	6.300E-03	FALSE
100535 at	0.065	6165	1428363 at	0.100	2919	100535 at	0.356	1022	1428363 at	0.171	3849	3488.75	2137.0981	TRUE	RIKEN cDNA E130105L11 gene	NA	NA	NA	NA	
97835 at	-0.065	4918	1428538 s at	0.171	1882	97835 at	0.115	4536	1437902 s at	-0.324	2620	3489	1469.2243	FALSE	retinoic acid receptor responder (tazarotene induced) 2	209496 at	0.505	3683	5.834E-05	FALSE
92841 f at	-0.549	64	1415885 at	-0.359	2981	92841 f at	-0.339	2476	1415885 at	0.006	8436	3489.25	3534.9525	FALSE	chromogranin B	204260 at	-0.784	3388	3.898E-05	FALSE

93087 r at	0.223	1191	1448939 at	-0.179	2753	93087 r at	0.017	7817	1445861 at	0.170	2199	3490	2956.2465	FALSE	ubiquitin specific peptidase 25	220419 s at	-0.497	113	9.781E-09	FALSE
93188 at	-0.429	319	1417312 at	-0.095	5436	93188 at	-0.755	842	1417312 at	0.129	7363	3490	3457.0792	FALSE	dickkopf homolog 3 (Xenopus laevis)	214247 s at	-0.569	1315	9.098E-07	FALSE
99584 at	0.274	240	1416401 at	-0.075	5549	99584 at	0.101	2664	1441759 at	-0.120	5508	3490.25	2553.2059	FALSE	CD82 antigen	203904 x at	0.068	22470	2.840E-01	FALSE
100575 at	-0.055	6794	1417118 a at	0.143	1608	161589 at	0.146	2712	1417118 a at	0.157	2849	3490.75	2271.16	FALSE	N-acetyltransferase ARD1 homolog (S. cerevisiae)	203025 at	0.095	13770	4.806E-02	FALSE
92647 at	-0.039	7409	1434892 x at	0.205	1306.5	92647 at	0.128	5228	1454791 a at	0.655	20	3490.875	3424.8004	FALSE	retinoblastoma binding protein 4	244872 at	0.345	4514	1.596E-04	FALSE
95110 at	0.136	3238	1452920 a at	-0.031	7003.5	95110 at	-0.266	464	1452920 a at	0.166	3261	3491.625	2684.3555	FALSE	peptidylprolyl isomerase (cyclophilin)-like 2	217407 x at	0.105	8025	3.316E-03	FALSE
93218 at	0.298	625	1423543 at	-0.041	6222	93218 at	-0.171	774	1423543 at	-0.093	6347	3492	3225.4787	FALSE	SWA-70 protein	209307 at	0.502	3455	4.319E-05	FALSE
99460 at	0.159	1825	1448415 a at	0.165	1029.5	99460 at	0.094	4313	1431795 a at	-0.065	6806	3493.375	2614.0278	FALSE	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	203071 at	0.363	8039	3.343E-03	FALSE
93910 at	0.196	2030	1422711 a at	0.148	3992.5	93910 at	-0.247	811	1422711 a at	-0.084	7140	3493.375	2761.8594	FALSE	pregnancy upregulated non-ubiquitously expressed CaM kinase	NA	NA	NA	NA	
161314 r at	0.443	1387	1454668 at	-0.077	4518	104041 at	-0.191	1819	1454668 at	-0.057	6254	3494.5	2302.9871	FALSE	zinc finger, UBR1 type 1	NA	NA	NA	NA	
96032 at	0.050	6182	1416020 a at	0.235	269.5	96032 at	0.077	4815	1416020 a at	0.219	2727	3498.375	2579.147	TRUE	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	208972 s at	-0.276	3760	6.391E-05	FALSE
103416 at	-0.165	2235	1419169 at	-0.169	1081	103416 at	0.065	6683	1459146 at	0.147	3995	3498.5	2437.7784	FALSE	mitogen-activated protein kinase 6	207121 s at	-0.289	5512	4.509E-04	FALSE
92926 at	0.146	1826	1421461 at	0.107	2907	92926 at	0.018	7158	1451919 a at	0.200	2107	3499.5	2481.6216	TRUE	myeloproliferative leukemia virus oncogene	207550 at	0.093	15351	7.728E-02	FALSE
161123 i at	-0.147	1583	1453612 at	-0.004	8424	161123 i at	0.159	1425	1453612 at	0.157	2568	3500	3321.391	FALSE	NIMA (never in mitosis gene a)-related expressed kinase 1	213328 at	0.230	7684	2.636E-03	FALSE
94540 at	0.128	3627	1448683 at	0.046	6496	94540 at	0.124	2005	1459077 at	0.207	1873	3500.25	2150.527	TRUE	cytochrome P450, family 2, subfamily d, polypeptide 26	NA	NA	NA	NA	
160107 at	0.205	2630	1448736 a at	0.135	2341.5	160107 at	0.360	6678	1448736 a at	0.160	2352	3500.375	2122.6249	TRUE	hypoxanthine guanine phosphoribosyl transferase 1	202854 at	-0.975	1606	1.776E-06	FALSE
160072 at	0.097	2967	1423700 at	0.116	3963	160072 at	0.078	3406	1423700 at	0.219	3669	3501.25	422.63016	TRUE	replication factor C (activator 1) 3	204128 s at	-0.059	16769	1.079E-01	FALSE
95673 s at	-0.028	7048	1428572 at	0.091	3785.5	95673 s at	0.330	2787	1428572 at	0.410	385	3501.375	2761.7266	FALSE	brain abundant, membrane attached signal protein 1	202391 at	-0.584	2403	8.187E-06	FALSE
93599 at	-0.093	5855	1423408 a at	-0.131	3843	93599 at	-0.224	3419	1423408 a at	-0.250	889	3501.5	2040.2244	TRUE	RIKEN cDNA 2500003M10 gene	NA	NA	NA	NA	
97993 at	0.091	2991	1423482 at	0.116	2766.5	97993 at	-0.030	6286.5	1440535 at	0.196	1963	3501.75	1908.2315	FALSE	uroporphyrinogen III synthase	203031 s at	-0.569	2204	5.460E-06	FALSE
102284 at	0.138	1218	1419677 at	0.159	2546.5	102284 at	0.027	6993	1425985 s at	0.172	3251	3502.125	2475.1915	TRUE	mannan-binding lectin serine peptidase 1	232224 at	0.336	7451	2.198E-03	TRUE
96435 at	0.183	1194	1420754 at	0.076	4359.5	96435 at	-0.026	6730	1420754 at	-0.210	1725	3502.125	2558.6379	FALSE	transcription termination factor 1	204771 s at	0.246	8171	3.645E-03	FALSE
94708 at	-0.117	3668	1425724 at	-0.086	5719	94708 at	-0.422	353	1459726 at	-0.120	4270	3502.5	2269.2634	TRUE	protein tyrosine phosphatase, receptor type, N polypeptide 2	211534 x at	-0.394	759	2.377E-07	TRUE
103769 at	0.036	6253	1421843 at	0.085	4316	103769 at	-0.106	2979	1442614 at	0.683	462	3502.5	2432.127	FALSE	interleukin 1 receptor accessory protein	210233 at	-0.008	38698	8.419E-01	FALSE
92873 f at	0.080	3972	1435507 x at	0.131	2076	92873 f at	0.060	4343	1433573 x at	0.169	3619	3502.5	995.88236	TRUE	protease, serine, 2	NA	NA	NA	NA	
96019 at	0.134	4553	1422879 at	-0.234	379.5	96019 at	0.082	6038	1435082 at	0.391	3041	3502.875	2415.1205	FALSE	synaptophysin-like protein	201260 s at	0.380	6135	7.826E-04	FALSE
101396 at	0.221	558	1421224 a at	0.106	2851	101396 at	0.067	4096	1441484 at	0.076	6510	3503.75	2482.7287	TRUE	transcription factor 2	205313 at	-0.032	34131	7.031E-01	FALSE
96605 at	-0.142	1532	1423909 at	-0.144	4734	96605 at	0.063	4925	1425603 at	-0.304	2831	3505.5	1620.0664	FALSE	RIKEN cDNA 0610011I04 gene	218345 at	0.348	2788	1.573E-05	FALSE
160383 at	-0.249	860	1432263 a at	0.144	2903	160383 at	0.229	2605	1432263 a at	-0.030	7656	3506	2909.7094	FALSE	cytochrome c oxidase subunit VIIa polypeptide 2-like	201256 at	-0.374	1441	1.257E-06	FALSE
104012 at	-0.095	2919	1427694 at	0.102	2403	104012 at	0.078	5321	1421665 a at	0.132	3384	3506.75	1274.1382	FALSE	gonadotropin releasing hormone receptor	211522 s at	-0.065	16063	9.237E-02	FALSE
97084 at	0.080	4905	1457475 at	0.128	1865.5	97084 at	-0.126	3449	1457475 at	-0.131	3809	3507.125	1257.4437	FALSE	expressed sequence C80993	NA	NA	NA	NA	
95471 at	0.357	733	1417649 at	0.015	8015.5	95471 at	0.321	543	1417649 at	0.331	4741	3508.125	3574.4321	TRUE	cyclin-dependent kinase inhibitor 1C (P57)	213348 at	0.662	2664	1.305E-05	TRUE
160712 r at	-0.296	123	1426980 s at	-0.267	1769.5	160712 r at	-0.068	6005	1426980 s at	0.276	6135	3508.125	3034.0702	FALSE	RIKEN cDNA E130012A19 gene	228066 at	-0.046	29256	5.298E-01	FALSE
100912 at	-0.150	1451	1439049 at	-0.134	4130.5	100912 at	0.115	2088	1439049 at	-0.225	6365	3508.625	2220.9309	FALSE	DPH5 homolog (S. cerevisiae)	222360 at	-0.162	4707	1.984E-04	FALSE
96993 at	0.101	3086	1459916 at	-0.082	4251	102578 at	-0.065	4530	1421765 at	0.217	2168	3508.75	1090.904	FALSE	paired box gene 5	244223 at	-0.049	25891	4.003E-01	FALSE
101203 r at	0.090	3358	1427902 at	0.146	3536	101203 r at	0.027	6944	1437638 at	0.613	198	3509	2755.9315	TRUE	serine/arginine repetitive matrix 2	207435 s at	0.215	2061	4.358E-06	TRUE
93871 at	0.050	5556	1451798 at	0.226	1159	93871 at	0.179	966	1451798 at	0.072	6355	3509	2844.8359	TRUE	interleukin 1 receptor antagonist	216244 at	-0.034	26143	4.094E-01	FALSE
96026 at	0.190	763	1417125 at	0.023	7917.5	96025 g at	0.204	1259	1417125 at	0.132	4097	3509.125	3285.5051	TRUE	S-adenosylhomocysteine hydrolase	200903 s at	-0.171	11617	2.210E-02	FALSE
160202 at	0.252	1456	1423662 at	0.125	4234	160202 at	0.143	4761	1439456 x at	0.125	3593	3511	1450.8593	TRUE	ATPase, H+ transporting, lysosomal accessory protein 2	201444 s at	-0.468	6939	1.512E-03	FALSE
160108 at	-0.229	361	1419666 x at	0.143	2439.5	160108 at	-0.003	8402	1419665 a at	-0.381	2842	3511.125	3437.0556	FALSE	nuclear protein 1	209230 s at	0.627	4576	1.659E-04	FALSE
104194 at	-0.034	6850	1448696 at	0.085	3187.5	104194 at	0.144	1237	1448696 at	-0.309	2771	3511.375	2378.5324	FALSE	hephaestin	203903 s at	0.628	2071	4.365E-06	FALSE
100733 at	0.082	6441	1448206 at	0.274	1175	100733 at	0.268	965	1448206 at	0.110	5466	3511.75	2848.7386	TRUE	proteasome (prosome, macropain) subunit, alpha type 2	201317 s at	-0.207	15970	9.034E-02	FALSE
161184 f at	-0.224	500	1416238 at	-0.062	6114	161184 f at	-0.142	2294	1416238 at	-0.151	5141	3512.25	2580.679	TRUE	tyrosine kinase receptor 1	204468 s at	0.341	7057	1.651E-03	FALSE
101495 at	-0.078	6043	1416330 at	-0.226	1498.5	101495 at	0.132	1397	1416330 at	-0.134	5112	3512.625	2414.7717	FALSE	CD 81 antigen	200675 at	0.369	1764	2.499E-06	FALSE
161420 r at	-0.140	2230	1448549 a at	0.153	1449	161420 r at	0.089	2918	1448549 a at	-0.044	7454	3512.75	2695.1618	FALSE	Dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-	209509 s at	0.041	27965	4.792E-01	FALSE
162372 f at	0.074	5250	1417856 at	0.121	1555	103091 at	0.115	1793	1417856 at	-0.126	5453	3512.75	2127.0428	FALSE	avian reticuloendotheliosis viral (v-rel) oncogene related B	205205 at	0.014	39393	8.614E-01	FALSE
101525 at	-0.181	3466	1428322 a at	0.156	2816	101525 at	-0.219	776	1428322 a at	-0.060	6999	3514.25	2590.4553	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	223112 s at	-0.362	3773	6.493E-05	FALSE
101651 at	0.153	1606	1419429 at	-0.146	1045	101651 at	-0.018	7848	1431663 a at	0.193	3563	3515.5	3083.4166	FALSE	ciliary neurotrophic factor receptor	205723 at	-0.017	40345	8.882E-01	FALSE
162102 r at	0.093	4637	1415945 at	0.117	2589	100156 at	0.089	2473	1415945 at	0.112	4366	3516.25	1144.0161	TRUE	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	216237 s at	0.330	5620	4.880E-04	TRUE
160710 at	-0.116	5653	1426709 a at	-0.150	4162.5	160710 at	-0.291	1808	1426709 a at	-0.196	2445	3517.125	1736.7624	TRUE	ubiquitin specific peptidase 33	244733 at	0.072	19468	1.839E-01	FALSE
93815 at	-0.058	5834	1431241 at	0.149	804.5	93815 at	0.067	4653	1437599 at	-0.184	2793	3521.125	2201.5713	FALSE	coiled-coil-helix-coiled-coil-helix domain containing 3	217972 at	-0.176	9391	7.283E-03	FALSE
100468 g at	-0.393	151	1419120 at	-0.049	6355	100467 at	0.187	1600	1419120 at	-0.120	5981	3521.75	3116.1031	FALSE	lymphoblastomic leukemia	210044 s at	0.088	19404	1.813E-01	FALSE
100697 at	0.147	1998	1420389 at	0.061	5742	100697 at	0.203	792	1441743 at	0.084	5556	3522	2506.0615	TRUE	paired box gene 3	231490 at	-0.070	15210	7.461E-02	FALSE
160884 at	0.228	850	1429574 at	0.034	7061.5	160884 at	0.083	5586	1429574 at	0.258	593	3522.625	3291.7462	TRUE	chloride intracellular channel 3	219529 at	0.021	33453	6.804E-01	FALSE
95621 at	0.064	6538	1426284 at	0.229	759.5	95621 at	-0.133	1212	1426284 at	-0.088	5583	3523.125	2961.5018	FALSE	RIKEN cDNA 9030623C06 gene	213953 at	-0.019	32499	6.471E-01	FALSE
93348 at	0.020	7446	1448517 at	0.231	285	93348 at	-0.051	5951	1448517 at	0.340	411	3523.25	3717.2705	FALSE	translocase of inner mitochondrial membrane 22 homolog (yeast)	222841 s at	-0.120	8612	4.672E-03	FALSE
98021 at	0.208	369	1435057 x at	0.111	3723	98021 at	0.147	3092	1419058 at	-0.075	6911	3523.75	2686.5107	FALSE	polymerase (RNA) I polypeptide E	218997 at	0.099	14078	5.391E-02	FALSE
98006 at	0.133	1945	1425794 at	0.112	3099	161739 r at	-0.027	7238	1448369 at	0.242	1813	3523.75	2542.6484	FALSE	polymerase (DNA directed), alpha 2	204441 s at	0.102	14942	6.983E-02	FALSE
94494 at	0.209	1571	1423708 a at	0.112	3477	94494 at	0.048	6638	1430986 at	0.204	2410	3524	2217.6872	TRUE	phenylalanine-tRNA synthetase-like, beta subunit	223035 s at	-0.214	6763	1.294E-03	FALSE
97888 at	-0.073	5356	1424614 at	0.105	3879	97888 at	0.218	578	1424614 at	0.117	4283	3524	2060.5215	FALSE	FGF receptor activating protein 1	41858 at	0.068	17797	1.351E-01	FALSE
160948 at	-0.074	4513	1430025 at	0.180	1410	160948 at	0.163	3989	1430025 at	0.124	4189	3525.25	1426.5998	FALSE	protein phosphatase 3, catalytic subunit, gamma isoform	32541 at	0.109	6392	9.728E-04	FALSE
100762 at	0.231	632	1421414 a at	0.055	6545	100762 at	-0.088	4229	1425903 at	-0.200	2697	3525.75	2494.7309	FALSE	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	225660 at	0.603	1293	8.615E-07	FALSE
100910 at	-0.060	6083	1433609 s at	0.135	1894.5	100910 at	0.110	3428	1453117 at	0.147	2705	3527.625	1815.0919	FALSE	surfeit gene 2	205224 at	-0.008	41309	9.155E-01	FALSE
161422 f at	0.255	992	1418197 at	0.107	2956	161422 f at	0.053	5285	1418197 at	0.121	4881	3528.5	1972.8268	TRUE	uncoupling protein 1 (mitochondrial, proton carrier)	221384 at	-0.007	41306	9.154E-01	FALSE
161871 f at	0.105	3519	1425171 at	0.136	2312.5	96567 at	-0.072	4402	1451618 at	0.171	3882	3528.875	888.20234	FALSE	rhodopsin	206454 s at	-0.066	22614	2.885E-01	FALSE
103569 at	0.075	3820	1418012 at	-0.141	3549	98945 at	0.170	1500	1418010 a at	0.099	4235	3529.75	1545.2897	FALSE	SH3-domain GRB2-like B1 (endophilin)	210101 x at	0.045	32749	6.558E-01	FALSE
92216 at	-0.182	2597	1423389 at	-0.246	251.5	92216 at	-0.058	6057	1423389 at	-0.156	5215	3530.125	2635.9062	TRUE	MAD homolog 7 (Drosophila)	204790 at	0.056	30829	5.879E-01	FALSE
160102 at	0.330	797	1415785 a at	0.074	6375	160102 at	0.181	2715	1415785 a at	-0.076	5250	3530.5	2361.1129	TRUE	chaperonin subunit 8 (theta)	200873 s at	-0.130	20812	2.271E-01	FALSE
96657 at	-0.086	6048	1420502 at	0.276	1453	96657 at	0.350	160	1420502 at	-0.135	6462	3530.75	3194.1496	FALSE	spermidine/spermine N1-acetyl transferase 1	203455 s at	0.258	12794	3.475E-02	FALSE
104351 at	0.217	1288	1439030 at	0.087	3992.5	104351 at	0.005	8153	1439030 at	0.270	692	3531.375	3399.3546	TRUE	GDP-mannose pyrophosphorylase B	219920 s at	0.062	20558	2.181E-01	FALSE
99592 f at	0.029	6731	1449209 a at	-0.099	3196.5	99592 f at	0.075	3878	1418760 at	0.448	321	3531.625	2631.628	FALSE	retinol dehydrogenase 11	217775 s at	0.108	11631	2.220E-02	FALSE
93696 at	0.123	2756	1425723 at	0.133	2570	93696 at	0.119	2466	1425723 at	-0.065	6335	3531.75	1872.6794	FALSE	nuclear receptor subfamily 1, group I, member 2	240035 at	-0.067	23620	3.244E-01	FALSE
98131 at	0.116	2799	1438610 a at	0.165	1756.5	98131 at	0.113	1621	1451848 a at	-0.024	7951	3531.875	2992.7229	FALSE	crystallin, zeta	202950 at	0.206	12917	3.604E-02	FALSE
103376 s at	-0.076	5632	1438974 x at	0.068	4709	103376 s at	0.272	442	1438854 x at	0.130	3347	3532.5	2264.0416	FALSE	phosphatidylinositol membrane-associated 1	203826 s at	-0.195	5543	4.625E-04	FALSE
162406 f at	0.135	3051	1416252 at	0.025	7767	94460 at	0.149	2761	1439938 at	0.534	553	3533	3035.0982	TRUE	serine/threonine kinase 38	202951 at	0.344	1609	1.788E-06	TRUE
162439 at	0.133	2570	1416957 at	0.098	5156	162439 at	-0.070	3999	1416957 at	-0.215	2409	3533.5	1296.409	FALSE	POU domain, class 2, associating factor 1	205267 at	0.159	3873	7.408E-05	FALSE
160683 at	0.184	1326	1419657 a at	0.131	3753.5	160683 at	0.105	4989	1419657 a at	0.164	4067	3533.875	1562.5362	TRUE	solute carrier family 25, member 36	201918 at	0.361	3767	6.440E-05	TRUE
96042 at	-0.118	5004	1448610 a at	0.223	1546	96042 at	0.058	4856	1448610 a at	0.190	2730	3534	1683.958	FALSE	superoxide dismutase 2, mitochondrial	215078 at	0.290	14158	5.545E-02	FALSE
98032 at	0.053	5414	1417778 at	0.164	1166	98032 at	0.061	5200	1445906 at	-0.181	2357	3534.25	2105.7626	FALSE	zinc finger protein 35	NA	NA	NA	NA	
99390 at	0.261	170	1436791 at	-0.065	5688	99390 at	0.035	6974	1456976 at	0.310	1306	3534.5	3304.2294	FALSE	wingless-related MMTV integration site 5A	213425 at	0.088	7317	2.020E-03	FALSE
102817 at	-0.011	8111	1449354 at	0.115	2970.5	102817 at	0.150	922	1449354 at	0.157	2137	3535.125	3164.4172	FALSE	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 1	NA	NA	NA	NA	
103525 at	0.093	5365	1427144 at	0.107	6151	103525 at	-0.222	1418	1459670 at	-0.382	1207	3535.25	2588.0256	FALSE	heterogeneous nuclear ribonucleoprotein L-like	225385 s at	-0.092	17642	1.307E-01	FALSE
162213 i at	0.090	6440	1417162 at	-0.178	1645	162213 i at	0.081	3538	1417162 at	-0.184	2519	3535.5	2085.137	FALSE	transmembrane BAX inhibitor motif containing 1	217730 at	0.431	4661	1.878E-04	FALSE
98323 at	0.145	3608	1421920 a at	0.063	5616	98323 at	0.191	323	1421919 a at	-0.110	4596	3535.75	2293.3638	FALSE	chemokine (C-C motif) receptor 9	207445 s at	0.074	14228	5.676E-02	FALSE
94706 s at	0.255	940	1421727 at	0.053	6391	94706 s at	0.080	5171	1421727 at	0.346	1642	3536	2655.2277	TRUE	eyes absent 1 homolog (Drosophila)	214608 s at	-0.820	260	2.983E-08	FALSE
99630 at	-0.099	3079	1448699 at	0.096	4072.5	99630 at	0.052	5597	1456788 at	0.195	1397	3536.375	1762.5477	FALSE	mitochondrial ribosomal protein L54	225797 at	-0.095	21527	2.509E-01	FALSE
161586 f at	-0.043	6374	1439040 at	0.121	1799.5	161586 f at	0.136	2895	1439040 at	0.132	3080	3537.125	1973.87	FALSE	centromere protein E	205046 at	-0.078	22713	2.922E-01	FALSE
101029 f at	-0.149	1985	1415927 at	0.157	1554	101029 f at	-0.070	4509	1415927 at	0.080	6101	3537.25	2149.4087	FALSE	actin, alpha, cardiac	205132 at	0.016	30927	5.915E-01	FALSE
160086 at	0.223	1202	1418393 a at	0.019	7664	161497 f at	-0.118	1868	1418393 a at	-0.133	3416	3537.5	2903.1337	FALSE	integrin alpha 7	216331 at	0.413	509	1.080E-07	FALSE
102955 at	0.060	5032	1418932 at	-0.017	7856	102955 at	0.199	684	1418932 at	0.351	578	3537.5	3548.9001	FALSE	nuclear factor, interleukin 3, regulated	203574 at	0.019	42567	9.490E-01	FALSE
97876 at	-0.023	7592	1417660 s at	0.227	1077	97876 at	0.180	1629	1455302 at	-0.128	3853	3537.75	2957.1914	FALSE	vacuolar protein sorting 29 (S. pombe)	223026 s at	-0.355	6842	1.377E-03	FALSE
160664 at	0.000	8523	1432848 a at	-0.198	671	160664 at	-0.083	3012	1432848 a at	-0.230	1946	3538	3458.3741	TRUE	RIKEN cDNA 1200004M23 gene	227964 at	0.212	6220	8.511E-04	FALSE
92302 at	0.198	1956	1452281 at	-0.040	7140.5	92302 at	0.302	2205	1452281 at	0.167	2851	3538.125	2431.0209	FALSE	Son of sevenless homolog 2 (Drosophila)	217576 x at	-0.097	11362	1.992E-02	FALSE
94835 f at	0.040	6820	1427838 at	0.171	3640	161614 r at	0.172	1858	1427838 at	0.290	1837	3538.75	2345.0463	TRUE	tubulin, beta 2a	204141 at	-0.473	6515	1.060E-03	FALSE
94123 at	0.025	7373	1418054 at	0.150	1942.5	94123 at	0.105	2546	1418054 at	-0.199	2295	3539.125	2567.8755	FALSE	neurogenic differentiation 4	221318 at	-0.032	34544	7.157E-01	FALSE
162463 at	0.260	1209	1419494 a at	-0.095	3986.5	160249 at	0.179	4464	1419493 a at	0.107	4500	3539.875	1571.443	FALSE	tumor protein D52	228818 at	0.248	3141	2.789E-05	FALSE
92629 f at	-0.110	4301	1415888 at	-0.138	2403	92630 r at	0.064	3932	1415888 at	0.139	3525	3540.25	821.7418	FALSE	hepatoma-derived growth factor	200896 x at	0.122	10695	1.468E-02	FALSE
98365 at	0.059	4983	1438483 at	-0.293	577	98365 at	-0.060	5620	1438483 at	-0.239	2990	3542.5	2272.3331	FALSE	nitric oxide synthase 1, neuronal	240911 at	-0.338	2769	1.538E-05	FALSE
162264 s at	-0.089	3761	1438571 at	0.100	3096	104097 at	0.081	3036	1438571 at	0.118	4277	3542.5	589.67138	FALSE	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	215509 s at	-0.103	19636	1.885E-01	FALSE
97521 at	0.001	8460	1416239 at	-0.197	1641	97521 at	-0.133	2915	1416239 at	-0.431	1155	3542.75	3361.1219	FALSE	argininosuccinate synthetase 1	207076 s at	-0.063	26404	4.213E-01	FALSE
160796 at	0.022	7180	1423186 at	-0.182	3084	160796 at	-0.090	3100	1423186 at	-0.543	808	3543	2652.981	FALSE	T-cell lymphoma invasion and metastasis 2	222942 s at	-0.384	2034	4.049E-06	FALSE
160096 at	-0.029	7003	1416525 at	-0.258	1672	160096 at	0.095	2928	1455510 at	-0.210	2571	3543.5	2366.0973	FALSE	speckle-type POZ protein	204640 s at	0.284	1982	3.715E-06	FALSE
100289 at	0.011	8120	1431170 at	-0.189	1071.5	100289 at	-0.144	2637	1455344 at	-0.164	2351	3544.875	3125.1094	FALSE	ephrin A3	210132 at	-0.297	3235	3.167E-05	FALSE
93467 at	0.249	283	1436031 at	-0.107	3179	93467 at	-0.030	7132	1436030 at	-0.281	3586	3545	2807.303	FALSE	cache domain containing 1	225627 s at	-0.184	10996	1.713E-02	FALSE
98564 f at	-0.277	1731	1415876 a at	0.256	3020.5	98564 f at	0.188	2589	1415876 a at	-0.047	6841	3545.375	2261.5074	FALSE	ribosomal protein S26	217753 s at	0.013	43362	9.684E-01	FALSE
95523 at	0.326	1225	1428333 at	0.042	7624	95523 at	0.436	194	1428333 at	0.093	5144	3546.75	3454.7856	TRUE	RIKEN cDNA 2900062L11 gene	NA	NA	NA	NA	
161715 f at	-0.071	4197	1452686 s at	0.030	7416	161715 f at	0.214	185	1452686 s at	-0.186	2390	3547	3056.8695	FALSE	DNA segment, Chr 4, ERATO Doi 196, expressed	52078 at	0.079	9456	7.560E-03	FALSE
99111 at	0.092	4453	1454168 a at	-0.065	5841.5	162000 r at	0.098	2048	1443550 at	-0.248	1847	3547.375	1934.1291	FALSE	ClpB caseinolytic peptidase B homolog (E. coli)	224510 s at	-0.061	18119	1.434E-01	FALSE
94130 at	0.202	553	1420706 at	-0.048	6811	94130 at	-0.103	2859	1420706 at	0.114	3967	3547.5	2599.197	FALSE	P140 gene	232547 at	0.098	19820	1.950E-01	FALSE
93913 at	0.060	5811	1452751 at	0.110	2635.5	104492 at	0.089	3964	1428349 s at	-0.251	1780	3547.625	1756.199	FALSE	early B-cell factor 3	227243 s at	-0.054	23439	3.182E-01	FALSE
98053 at	0.046	5687	1436783 x at	-0.247	1964	98053 at	0.057	4205	1436783 x at	0.313	2335	3547.75	1730.8374	FALSE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	217718 s at	-0.341	3512	4.715E-05	FALSE
94255 g at	-0.145	5284	1423392 at	-0.386	4.5	94254 at	0.107	3442	1438606 a at	-0.161	5461	3547.875	2532.5148	FALSE	chloride intracellular channel 4 (mitochondrial)	201560 at	0.486	5845	6.074E-04	FALSE
94325 at	-0.487	30	1433446 at	-0.414	257	94325 at	0.007	8320	1441536 at	-0.107	5585	3548	4087.7197	FALSE	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	205822 s at	-0.069	25212	3.801E-01	FALSE
95946 at	0.034	7258	1452291 at	-0.099	2880.5	95946 at	-0.118	3847	1436895 at	1.038	207	3548.125	2913.265	FALSE	Centaurin, delta 1	213618 at	0.173	10693	1.468E-02	FALSE
92948 at	0.094	2929	1427429 at	0.174	2032	92948 at	0.044	5515	1427429 at	-0.152	3720	3549	1481.0003	FALSE	colony stimulating factor 2 (granulocyte-macrophage)	210229 s at	0.046	24678	3.606E-01	FALSE
162143 f at	0.171	2671	1426482 at	-0.082	4670	162143 f at	0.130	2019	1426482 at	-0.088	4836	3549	1417.1326	FALSE	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 rep	209323 at	0.044	25076	3.754E-01	FALSE
93639 r at	0.125	5093	1430523 s at	0.272	286.5	93638 s at	-0.078	4701	1430523 s at	0.147	4116	3549.125	2211.8194	FALSE	immunoglobulin lambda chain, variable 1	NA	NA	NA	NA	
103761 at	0.046	5849	1418091 at	0.184	835	103761 at	0.106	1829	1418091 at	-0.180	5687	3550	2593.9183	FALSE	transcription factor CP2-like 1	227642 at	0.217	6599	1.128E-03	FALSE
104047 at	-0.233	596	1420931 at	0.078	5512	104047 at	-0.039	6172	1437045 at	0.173	1924	3551	2713.8113	FALSE	mitogen activated protein kinase 8	210477 x at	-0.099	17547	1.278E-01	FALSE
98349 at	0.102	2563	1460295 s at	-0.142	2184.5	98349 at	-0.082	5792	1452843 at	-0.116	3667	3551.625	1620.5968	FALSE	interleukin 6 signal transducer	204863 s at	0.401	3777	6.528E-05	FALSE
95345 at	-0.220	585	1423312 at	0.114	2206	95345 at	-0.194	4983	1423312 at	0.123	6438	3553	2645.2195	FALSE	trophoblast glycoprotein	203476 at	-1.228	6	1.536E-09	FALSE
93986 at	-0.062	6499	1428213 at	0.182	931	93986 at	0.253	327	1428213 at	0.060	6456	3553.25	3385.67	FALSE	RIKEN cDNA 2410003A14 gene	211376 s at	-0.190	6696	1.233E-03	FALSE
93592 at	0.357	1123	1416371 at	0.101	5928.5	93592 at	0.306	3187	1444749 at	0.296	3975	3553.375	1988.294	TRUE	apolipoprotein D	201525 at	0.282	8581	4.579E-03	TRUE
102265 at	0.073	5383	1419150 at	0.106	3463	102265 at	-0.178	2040	1419150 at	0.137	3330	3554	1377.9083	FALSE	myogenic factor 6	206372 at	-0.026	32473	6.463E-01	FALSE
102874 at	0.010	7946	1427699 a at	-0.207	899.5	102874 at	-0.279	2574	1451225 at	-0.154	2797	3554.125	3047.9219	FALSE	protein tyrosine phosphatase, non-receptor type 11	205867 at	-0.128	8133	3.562E-03	FALSE
162457 f at	-0.487	27	1452757 s at	-0.181	3818	162457 f at	-0.144	4147	1417714 x at	-0.281	6225	3554.25	2581.6864	TRUE	hemoglobin alpha, adult chain 1	204018 x at	-0.021	43099	9.624E-01	FALSE
161192 at	0.053	6878	1447858 x at	0.154	1337.5	161192 at	0.093	2847	1423996 a at	0.200	3155	3554.375	2353.784	TRUE	Interleukin 4 receptor, alpha	203233 at	0.216	10155	1.095E-02	TRUE
102942 at	-0.105	4628	1428794 at	-0.206	942.5	102942 at	0.081	5153	1458440 at	-0.145	3496	3554.875	1873.817	FALSE	spectrin domain with coiled-coils 1	240765 at	0.232	2970	2.098E-05	FALSE



161328 i at	0.158	2471	1417206 at	0.146	1588.5	94275 at	-0.047	5075	1417206 at	0.101	5531	3666.375	1932.8336	FALSE	uroporphyrinogen decarboxylase	208971 at	-0.111	13071	3.790E-02	FALSE
97194 at	0.211	2135	1448075 at	0.171	3187.5	97194 at	0.147	2800	1448075 at	-0.052	6543	3666.375	1966.3848	FALSE	expressed sequence AA408251	NA	NA	NA	NA	
101956 at	0.050	5456	1452181 at	0.088	4021.5	101956 at	0.114	2300	1426755 at	0.147	2890	3666.875	1390.2769	TRUE	cytoskeleton-associated protein 4	200999 s at	0.532	393	5.982E-08	TRUE
102393 at	0.080	4243	1452486 a at	0.099	4988	102393 at	0.166	1333	1452486 a at	-0.119	4104	3667	1603.6772	FALSE	crystallin, alpha A	210199 at	-0.018	38011	8.220E-01	FALSE
101625 at	-0.087	4974	1421342 at	-0.044	7023	101625 at	-0.419	176	1457325 at	-0.190	2497	3667.5	2973.6042	TRUE	K+ voltage-gated channel, subfamily S, 2	232401 at	-0.270	2586	1.095E-05	TRUE
161840 f at	0.106	3204	1427380 at	0.061	5020	94714 at	-0.081	3814	1427380 at	0.159	2632	3667.5	1022.7106	FALSE	kallikrein 1-related peptidase b3	NA	NA	NA	NA	
98039 at	-0.089	4778	1427909 at	0.173	1588.5	98039 at	0.280	1342	1427909 at	0.069	6967	3668.875	2698.771	FALSE	RIKEN cDNA 2410015M20 gene	225823 at	-0.183	10394	1.247E-02	FALSE
92405 at	0.275	376	1418590 at	0.112	4599.5	160624 at	0.078	3914	1426796 at	0.074	5787	3669.125	2327.7763	TRUE	karyopherin (importin) alpha 6	212102 s at	-0.075	13472	4.356E-02	FALSE
102326 at	-0.121	1695	1448561 at	0.067	4910	102326 at	0.051	4796	1448561 at	-0.228	3276	3669.25	1512.3199	FALSE	neutrophil cytosolic factor 2	209949 at	-0.009	41170	9.121E-01	FALSE
100614 at	0.036	6677	1422420 at	0.183	1217.5	100614 at	0.130	2962	1451203 at	0.191	3821	3669.375	2278.9521	TRUE	myoglobin	204179 at	-0.031	34351	7.094E-01	FALSE
95317 at	0.120	2483	1450467 at	-0.239	1068	95317 at	-0.022	7803	1450467 at	-0.282	3325	3669.75	2908.6129	FALSE	bassoon	204586 at	-0.764	733	2.176E-07	FALSE
104739 at	0.102	3196	1420124 s at	0.075	5474	104739 at	0.094	2672	1420123 at	0.146	3341	3670.75	1236.0333	TRUE	T-cell leukemia translocation altered gene	203054 s at	0.025	33685	6.882E-01	FALSE
160617 at	-0.029	7944	1432543 a at	-0.413	198.5	160617 at	-0.330	1112	1456030 at	0.100	5432	3671.625	3649.9491	FALSE	Kruppel-like factor 13	225390 s at	0.225	9829	9.188E-03	FALSE
93362 at	-0.072	5152	1450894 a at	-0.094	4832.5	93362 at	-0.085	3353	1457122 at	0.417	1353	3672.625	1733.6552	FALSE	adaptor protein complex AP-2, mu1	200613 at	-0.298	8777	5.110E-03	FALSE
95426 at	-0.102	4488	1452341 at	-0.057	5961.5	95426 at	0.265	376	1452341 at	0.181	3865	3672.625	2367.0326	FALSE	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	201135 at	0.070	21961	2.673E-01	FALSE
160464 s at	0.214	2061	1420760 s at	-0.348	335	160464 s at	-0.047	6620	1420760 s at	-0.122	5677	3673.25	2968.8164	FALSE	N-myc downstream regulated-like	NA	NA	NA	NA	
92868 at	-0.272	146	1416086 at	-0.035	7157	92868 at	0.047	6065	1416086 at	-0.243	1329	3674.25	3454.1752	FALSE	protein-tyrosine sulfotransferase 2	204079 at	0.417	2482	9.278E-06	FALSE
103308 at	0.113	3200	1434767 at	0.053	6647.5	103308 at	0.088	2866	1434767 at	-0.199	1984	3674.375	2047.3838	FALSE	expressed sequence C79407	226630 at	-0.092	17945	1.393E-01	FALSE
97745 at	0.156	2510	1427354 at	0.057	6098.5	97746 f at	0.118	2618	1420226 x at	-0.143	3476	3675.625	1672.0672	FALSE	homeo box A4	206289 at	-0.003	42769	9.538E-01	FALSE
97535 at	-0.103	4317	1416004 at	-0.095	3460	97535 at	-0.117	5733	1416004 at	0.213	1194	3676	1901.6756	FALSE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	201020 at	-0.833	1342	9.846E-07	FALSE
97216 at	0.105	4620	1417246 at	0.200	978.5	97216 at	0.099	3209	1417246 at	0.067	5899	3676.625	2107.7206	TRUE	pregnancy zone protein	NA	NA	NA	NA	
160933 at	-0.556	2613	1417141 at	0.034	7196	160933 at	0.123	1586	1417141 at	-0.718	3317	3678	2450.6689	FALSE	interferon gamma induced GTPase	NA	NA	NA	NA	
104044 at	-0.083	3914	1430293 a at	0.161	884	104044 at	0.032	6228	1430293 a at	0.118	3689	3678.75	2188.2071	FALSE	RIKEN cDNA B230118G17 gene	226451 at	-0.148	8028	3.323E-03	FALSE
98943 at	-0.080	6022	1416433 at	0.195	840	98943 at	0.147	1781	1454011 a at	0.080	6086	3682.25	2765.597	FALSE	replication protein A2	201756 at	-0.128	18829	1.645E-01	FALSE
93782 at	-0.087	4939	1451072 a at	-0.216	835	93782 at	-0.075	5607	1445749 at	0.118	3350	3682.75	2121.4229	FALSE	ring finger protein 4	212696 s at	-0.079	23196	3.085E-01	FALSE
92513 at	0.329	263	1421849 at	0.049	6517	104595 at	0.313	948	1421849 at	0.041	7004	3683	3570.1177	TRUE	stromal antigen 2	209023 s at	0.672	610	1.426E-07	TRUE
94186 at	0.065	5042	1423602 at	0.230	294	94186 at	-0.076	4789	1423602 at	-0.119	4608	3683.25	2266.4997	FALSE	Tnf receptor-associated factor 1	235116 at	0.222	3051	2.447E-05	FALSE
95948 at	0.171	2334	1431878 at	0.143	2587	95948 at	-0.017	7309	1429086 at	0.159	2503	3683.25	2419.4554	FALSE	Grainyhead-like 2 (Drosophila)	219388 at	-0.040	27669	4.680E-01	FALSE
103488 at	-0.084	4189	1449127 at	-0.067	5925	103488 at	-0.120	2771	1449127 at	-0.262	1850	3683.75	1777.0979	TRUE	selectin, platelet (p-selectin) ligand	209879 at	0.163	16361	9.883E-02	FALSE
161045 at	0.134	2539	1416053 at	-0.164	2523.5	161959 f at	-0.037	6344	1432715 at	-0.173	3336	3685.625	1812.409	FALSE	leucine rich repeat protein 1, neuronal	226884 at	-0.705	3181	2.940E-05	FALSE
96801 at	-0.231	843	1423988 at	0.052	5754.5	96801 at	0.116	4045	1423988 at	-0.140	4106	3687.125	2054.8007	FALSE	adenylate kinase 1	202587 s at	0.665	4785	2.143E-04	FALSE
100507 at	-0.031	7286	1426852 x at	0.561	440	100507 at	-0.191	6317	1426851 a at	1.134	706	3687.25	3619.3494	FALSE	nephroblastoma overexpressed gene	204501 at	-0.084	18660	1.598E-01	FALSE
104531 at	0.072	4059	1422847 a at	-0.495	2040	160698 s at	0.297	1867	1422847 a at	-0.526	6784	3687.5	2291.637	FALSE	protein kinase C, delta	202545 at	-0.462	1042	5.113E-07	FALSE
102256 at	0.208	837	1418755 at	0.097	5091	100355 g at	0.100	2493	1418755 at	0.063	6329	3687.5	2483.2449	TRUE	T-box 15	230438 at	-0.029	31788	6.242E-01	FALSE
100393 at	-0.169	1372	1428664 at	0.002	8459	100393 at	0.068	4197	1428664 at	1.029	722	3687.5	3520.5366	FALSE	vasoactive intestinal polypeptide	206577 at	0.011	35450	7.446E-01	FALSE
102300 at	0.035	6780	1449331 a at	0.091	4902.5	102300 at	-0.083	2674	1449331 a at	-0.361	394	3687.625	2763.6996	FALSE	receptor-associated protein of the synapse	211570 s at	0.018	33337	6.768E-01	FALSE
100581 at	-0.083	4700	1422507 at	0.167	2006	100581 at	0.239	953	1422507 at	0.050	7092	3687.75	2764.0977	FALSE	cystatin B	236449 at	0.067	17424	1.249E-01	FALSE
94939 at	-0.118	5703	1448617 at	0.087	4160.5	94939 at	0.133	1346	1448617 at	-0.311	3543	3688.125	1806.421	FALSE	CD53 antigen	203416 at	0.135	23887	3.343E-01	FALSE
160481 at	0.045	5719	1455209 at	0.128	1175	160481 at	-0.067	4086	1455209 at	-0.121	3774	3688.5	1880.2419	FALSE	phosphoenolpyruvate carboxykinase 1, cytosolic	208383 s at	0.060	19947	1.987E-01	FALSE
96958 at	0.055	5568	1448564 at	0.102	2731.5	96957 at	0.205	318	1425856 at	0.130	6137	3688.625	2695.91	TRUE	calcium and integrin binding 1 (calmyrin)	201953 at	0.468	873	3.281E-07	TRUE
97489 at	-0.086	4168	1433504 at	-0.156	2061	97489 at	-0.280	994	1433504 at	0.034	7534	3689.25	2882.5264	FALSE	brain glycogen phosphorylase	201481 s at	0.193	4520	1.604E-04	FALSE
96018 r at	0.082	4748	1426311 s at	0.075	4704.5	96018 r at	0.246	2837	1426310 at	0.161	2468	3689.375	1206.8507	TRUE	zinc finger, DHHC domain containing 5	224868 at	-0.114	12977	3.668E-02	FALSE
97296 at	-0.112	4841	1437391 x at	0.138	2376	97296 at	-0.223	926	1426651 at	-0.050	6616	3689.75	2533.283	FALSE	mitochondrial ribosomal protein L44	222555 s at	-0.209	10911	1.642E-02	FALSE
94438 at	-0.214	888	1416780 at	-0.102	3540.5	94438 at	-0.154	2483	1416780 at	0.022	7849	3690.125	2979.244	FALSE	phosphofructokinase, muscle	210976 s at	-0.300	4173	1.054E-04	FALSE
99553 f at	-0.287	576	1453060 at	-0.201	602	99553 f at	-0.006	8313	1453060 at	-0.104	5270	3690.25	3790.3944	TRUE	regulator of G-protein signaling 8	244675 at	-1.008	495	9.893E-08	TRUE
95097 at	0.050	6892	1417157 at	0.094	4463	95097 at	0.303	2065	1417157 at	0.227	1343	3690.75	2516.5694	TRUE	ARP10 actin-related protein 10 homolog (S. cerevisiae)	222230 s at	-0.430	3918	7.960E-05	FALSE
92207 at	0.108	4144	1420854 at	0.061	5563	92836 at	-0.068	3867	1446221 at	0.221	1189	3690.75	1825.7941	FALSE	elastin	216269 s at	0.192	6223	8.535E-04	FALSE
99985 at	-0.211	1089	1424486 a at	-0.147	1441	99985 at	-0.050	6779	1421529 a at	0.139	5455	3691	2856.5914	FALSE	thioredoxin reductase 1	201266 at	0.103	25321	3.834E-01	FALSE
92906 at	-0.116	3615	1452380 at	0.104	4844	92906 at	-0.366	1037	1443485 at	0.150	5275	3692.75	1905.0761	FALSE	Eph receptor A7	238533 at	-0.660	724	2.147E-07	FALSE
94024 at	0.033	7123	1424143 a at	0.145	2036	161787 f at	-0.079	3583	1455791 at	-0.182	2030	3693	2400.5706	FALSE	chromatin licensing and DNA replication factor 1	228868 x at	-0.083	19352	1.795E-01	FALSE
97253 at	-0.102	3708	1436828 a at	0.251	494	97253 at	0.012	7662	1436828 a at	0.149	2910	3693.5	2977.6879	FALSE	tumor protein D52-like 2	201379 s at	0.242	3565	5.010E-05	FALSE
104144 at	-0.148	1412	1416691 at	-0.142	3513	104144 at	-0.054	6301	1416690 at	-0.131	3551	3694.25	2004.7596	TRUE	GTP binding protein 2	231115 at	0.021	32003	6.316E-01	FALSE
96338 at	-0.249	450	1416533 at	-0.106	2418.5	96338 at	0.097	4060	1416533 at	-0.021	7853	3695.375	3140.1521	FALSE	EGL nine homolog 2 (C. elegans)	223083 s at	-0.086	11239	1.902E-02	FALSE
100571 at	0.130	3219	1436915 x at	-0.098	5476	100571 at	0.176	3469	1438365 x at	0.213	2618	3695.5	1239.5619	FALSE	lysosomal-associated protein transmembrane 4B	214039 s at	0.288	9134	6.308E-03	FALSE
92344 at	0.170	1380	1425996 a at	0.099	3128	92343 at	-0.109	3058	1450889 at	-0.042	7216	3695.5	2482.1982	FALSE	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member	202983 at	0.006	43280	9.669E-01	FALSE
103229 at	-0.025	7343	1418594 a at	-0.174	2619	103229 at	-0.205	1157	1459277 at	0.132	3664	3695.75	2639.9547	FALSE	nuclear receptor coactivator 1	243826 at	0.264	4316	1.229E-04	FALSE
161907 s at	0.253	1038	1450798 at	-0.054	5748	102916 s at	-0.127	2272	1450798 at	-0.097	5725	3695.75	2409.7223	FALSE	tenascin XB	206093 x at	0.166	6069	7.375E-04	FALSE
99431 at	0.174	1233	1460722 at	0.106	2880.5	97132 at	-0.109	2722	1460722 at	-0.019	7948	3695.875	2930.2781	FALSE	sterol O-acyltransferase 2	210677 at	-0.007	41668	9.254E-01	FALSE
100699 at	0.169	1913	1451781 at	0.227	1125	96561 at	0.008	7940	1434836 at	0.110	3808	3696.5	3044.8431	TRUE	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	217527 s at	0.146	9937	9.786E-03	TRUE
160497 at	0.071	4709	1449842 at	0.164	1550	160497 at	0.035	5900.5	1436963 x at	-0.164	2629	3697.125	1968.9074	FALSE	RIKEN cDNA 1810059G22 gene	228089 x at	0.117	6910	1.475E-03	FALSE
100957 at	0.062	6573	1427965 at	0.262	1271.5	100957 at	0.209	3211	1452616 s at	0.113	3734	3697.375	2190.2809	TRUE	single-stranded DNA binding protein 1	202591 s at	-0.264	15079	7.240E-02	FALSE
101135 at	0.120	3101	1418688 at	0.010	8142	101135 at	0.176	1427	1418688 at	-0.335	2123	3698.25	3041.0311	FALSE	calcitonin receptor	207887 s at	0.055	25187	3.791E-01	FALSE
100633 at	-0.110	4434	1416766 at	0.167	1336	100633 at	0.270	1343	1416766 at	0.031	7682	3698.75	3029.7975	FALSE	MOCO sulphurase C-terminal domain containing 2	227417 at	0.269	8307	3.959E-03	FALSE
102028 at	-0.152	1597	1422638 s at	-0.077	5754.5	102028 at	0.095	4013	1422638 s at	0.195	3433	3699.375	1713.9463	FALSE	Ras association (RalGDS/AF-6) domain family 5	223322 at	0.016	37200	7.967E-01	FALSE
101215 at	0.138	3231	1421738 at	-0.170	5701	101215 at	-0.096	5632	1421738 at	0.403	241	3701.25	2576.9013	FALSE	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	207014 at	-0.330	11547	2.138E-02	FALSE
96584 f at	0.100	3917	1451852 at	0.178	1627.5	96584 f at	0.127	1477	1451852 at	0.024	7784	3701.375	2941.8318	TRUE	2-cell-stage, variable group, member 3	NA	NA	NA	NA	
92229 at	-0.416	84	1418790 at	0.050	5370	92229 at	-0.058	7103	1418790 at	0.730	2256	3703.25	3137.4012	FALSE	zinc finger protein 312	233897 at	0.036	25810	3.970E-01	FALSE
103209 at	0.151	1619	1448870 at	0.032	7336	103209 at	0.082	3792	1446232 at	-0.175	2071	3704.5	2595.7068	FALSE	latent transforming growth factor beta binding protein 1	202729 s at	0.429	1591	1.749E-06	FALSE
97415 at	0.051	5930	1449259 at	0.139	1703.5	97415 at	0.117	2362	1449259 at	-0.103	4823	3704.625	2000.8498	FALSE	RAB3D, member RAS oncogene family	225001 at	-0.072	19556	1.865E-01	FALSE
97753 at	-0.194	2662	1419392 at	0.069	5288.5	97753 at	0.081	6777	1452423 at	0.521	93	3705.125	2948.3922	FALSE	piccolo (presynaptic cytomatrix protein)	213558 at	-0.968	1671	2.048E-06	FALSE
94127 at	-0.005	8276	1427564 at	-0.192	2291	94127 at	-0.167	1123	1444745 at	-0.148	3134	3706	3156.2741	TRUE	diaphanous homolog 2 (Drosophila)	205726 at	-0.860	195	1.922E-08	TRUE
92998 at	0.137	2175	1421272 at	0.050	5974.5	92998 at	0.083	3379	1435244 at	-0.168	3296	3706.125	1608.8383	FALSE	Vav2 oncogene	226063 at	0.039	28617	5.061E-01	FALSE

104071 at	-0.147	2633	1425592 at	-0.182	3796	104071 at	-0.083	5215	1425592 at	0.379	3181	3706.25	1112.375	FALSE	transportin 2 (importin 3, karyopherin beta 2b)	210585 s at	-0.239	3150	2.810E-05	FALSE
160359 at	-0.251	835	1438511 a at	0.051	6566	160359 at	-0.106	3849	1418003 at	-0.219	3575	3706.25	2342.3529	FALSE	RIKEN cDNA 1190002H23 gene	218723 s at	0.343	7511	2.325E-03	FALSE
93969 at	0.179	1991	1451994 s at	0.070	4767	93969 at	0.032	6579	1451994 s at	0.183	1489	3706.5	2396.9538	TRUE	RIKEN cDNA 3930401K13 gene	212414 s at	0.205	4336	1.261E-04	TRUE
160769 at	0.103	2998	1448438 at	-0.067	6408	160769 at	-0.346	123	1435101 at	-0.080	5297	3706.5	2779.1628	FALSE	Der1-like domain family, member 2	218333 at	0.159	9388	7.268E-03	FALSE
96775 at	-0.118	3725	1450797 a at	0.099	2807.5	160797 r at	-0.069	3507	1450797 a at	-0.088	4787	3706.625	819.72021	FALSE	chromobox homolog 1 (Drosophila HP1 beta)	201518 at	0.074	25184	3.790E-01	FALSE
93542 at	0.032	6551	1453578 at	0.127	1714	93542 at	0.073	3903	1453578 at	0.147	2661	3707.25	2097.0548	TRUE	phosphotriesterase related	222798 at	0.163	5577	4.713E-04	TRUE
95714 at	0.063	6600	1436681 x at	0.319	402	95714 at	0.272	2596.5	1417054 a at	0.144	5234	3708.125	2760.2783	TRUE	RIKEN cDNA 0610009D07 gene	223416 at	0.051	31522	6.138E-01	FALSE
101524 at	0.212	2928	1452712 at	-0.095	3241	101524 at	-0.212	1070	1452712 at	-0.028	7594	3708.25	2762.036	FALSE	heterogeneous nuclear ribonucleoprotein A3	211930 at	0.222	8058	3.391E-03	FALSE
104747 at	-0.031	7788	1460386 a at	-0.200	2646.5	104747 at	-0.476	224	1448299 at	-0.139	4179	3709.375	3169.2939	TRUE	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), membe	213664 at	-0.646	2255	6.096E-06	TRUE
96648 at	-0.299	415	1455269 a at	0.196	2496	96648 at	-0.029	7543	1416246 a at	0.124	4385	3709.75	3026.4575	FALSE	coronin, actin binding protein 1A	209083 at	-0.190	12505	3.135E-02	FALSE
160736 at	0.112	4070	1428625 a at	0.054	5364	160736 at	0.177	867	1428625 a at	0.108	4542	3710.75	1969.7874	TRUE	RIKEN cDNA 4932432N11 gene	218979 at	0.255	2033	4.048E-06	TRUE
99322 at	0.066	5805	1449464 at	0.060	5180	161796 r at	-0.127	2744	1442029 at	0.447	1114	3710.75	2177.3298	FALSE	potassium voltage-gated channel, subfamily Q, member 1	237249 at	0.111	10718	1.486E-02	FALSE
99939 at	0.152	2707	1417257 at	0.061	6075	99939 at	-0.065	5009	1417257 at	0.344	1052	3710.75	2262.1227	FALSE	carboxyl ester lipase	205910 s at	-0.020	34126	7.031E-01	FALSE
100917 at	0.012	7936	1426496 at	0.206	899.5	100917 at	0.166	1166	1426496 at	0.141	4842	3710.875	3342.222	TRUE	WD repeat domain 55	219809 at	-0.038	27935	4.779E-01	FALSE
160499 at	0.082	6397	1438040 a at	-0.436	264	160499 at	0.047	6034	1415889 a at	-0.193	2154	3712.25	2995.384	FALSE	heat shock protein 90kDa beta (Grp94), member 1	216450 x at	-0.070	21298	2.434E-01	FALSE
94242 at	0.041	6193	1423035 s at	0.184	1037	94242 at	0.209	802	1423034 at	-0.059	6819	3712.75	3236.8983	FALSE	thioredoxin-like 5	228743 at	-0.101	14610	6.320E-02	FALSE
104318 at	-0.052	5588	1422063 a at	-0.103	4039	104318 at	-0.095	2878	1426770 at	0.179	2346	3712.75	1436.1772	FALSE	peroxisome biogenesis factor 5	203244 at	0.138	14878	6.833E-02	FALSE
94668 at	0.126	3505	1446856 at	0.108	3390	94668 at	0.139	2350	1446856 at	-0.087	5607	3713	1365.3569	FALSE	DNA segment, Chr 3, Wayne State University 167, expressed		NA	NA	NA	NA
93243 at	0.075	4928	1418910 at	0.074	5127	93243 at	-0.085	4190	1432410 a at	-0.283	608	3713.25	2109.042	FALSE	bone morphogenetic protein 7	209590 at	0.427	1790	2.614E-06	FALSE
103568 at	0.178	2438	1451939 a at	-0.047	6857	162156 f at	0.117	2329	1451939 a at	-0.161	3230	3713.5	2133.7842	FALSE	sushi-repeat-containing protein	204955 at	1.033	1158	6.587E-07	FALSE
162283 r at	-0.021	7316	1437948 x at	0.121	2328	162283 r at	0.213	1777	1437948 x at	0.157	3437	3714.5	2498.2725	FALSE	eukaryotic translation initiation factor 3, subunit 6 interacting protein	217719 at	-0.272	1226	7.591E-07	FALSE
97500 g at	0.192	629	1417872 at	0.044	7433	97500 g at	-0.320	741	1459003 at	0.072	6055	3714.5	3543.4068	FALSE	four and a half LIM domains 1	210298 x at	-0.301	16446	1.005E-01	FALSE
103264 at	0.030	6864	1421880 at	0.080	4700	103264 at	-0.198	1272	1421879 at	0.172	2025	3715.25	2563.2515	FALSE	myotubularin related protein 1	214975 s at	-0.224	11052	1.759E-02	FALSE
96510 at	0.087	4982	1421441 at	0.097	3854.5	96510 at	0.120	2551	1457381 at	-0.168	3475	3715.625	1006.1881	FALSE	angiopoietin 1	205608 s at	0.397	1602	1.767E-06	FALSE
99097 at	0.092	3890	1450909 at	0.036	6987.5	99097 at	-0.123	2635	1459371 at	0.410	1357	3717.375	2412.9113	FALSE	eukaryotic translation initiation factor 4E	201435 s at	-0.196	17328	1.225E-01	FALSE
100732 at	-0.089	5494	1455319 x at	0.292	983.5	100732 at	0.258	931	1436760 a at	-0.030	7463	3717.875	3287.5553	FALSE	ribosomal protein S8	200858 s at	0.074	22846	2.963E-01	FALSE
161950 at	0.100	3399	1435799 at	0.042	6990.5	101942 at	-0.129	2077	1435799 at	0.183	2407	3718.375	2252.5999	FALSE	splicing factor, arginine/serine-rich 14	214092 x at	-0.195	5670	5.120E-04	FALSE
103797 at	0.073	4742	1426021 a at	0.080	3854.5	103797 at	-0.159	2568	1426021 a at	0.142	3709	3718.375	892.5224	FALSE	cell division cycle 7 (S. cerevisiae)	204510 at	-0.147	14269	5.738E-02	FALSE
99949 at	0.144	2550	1424429 s at	0.123	3116.5	99949 at	-0.110	2214	1451347 at	-0.089	6996	3719.125	2216.1018	FALSE	coiled-coil domain containing 95	227286 at	0.122	9927	9.728E-03	FALSE
160327 at	-0.131	3492	1448368 at	0.118	3241	160327 at	-0.173	2735	1416499 a at	0.108	5409	3719.25	1169.6679	FALSE	dynactin 6	203261 at	-0.193	15341	7.719E-02	FALSE
93615 at	-0.193	4149	1421193 a at	0.005	8429	93616 g at	-0.481	573	1442270 at	-0.309	1734	3721.25	3474.0236	FALSE	pre B-cell leukemia transcription factor 3	204082 at	-0.465	762	2.403E-07	FALSE
99330 at	0.189	861	1420703 at	0.194	3206	99330 at	-0.049	5478	1420703 at	-0.163	5342	3721.75	2172.5187	FALSE	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	211287 x at	-0.042	23436	3.181E-01	FALSE
94771 at	-0.057	4885	1428392 at	-0.085	4878	94771 at	-0.063	4852	1428392 at	-0.574	273	3722	2299.3772	TRUE	Ras association (RalGDS/AF-6) domain family 2	203185 at	0.273	11596	2.183E-02	FALSE
103393 at	0.047	6874	1423193 at	0.142	1911	103393 at	-0.152	5867	1457723 at	0.680	236	3722	3160.5931	FALSE	paraspeckle protein 1		NA	NA	NA	NA
93033 at	0.080	4091	1448671 at	-0.074	4502	93033 at	0.032	6105	1448671 at	-0.403	192	3722.5	2508.9273	FALSE	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	232528 at	0.332	1145	6.452E-07	FALSE
98905 at	-0.143	4187	1437995 x at	-0.164	2325	98905 at	-0.061	5714	1438911 at	-0.150	2666	3723	1554.6736	TRUE	septin 7	213151 s at	0.237	5475	4.355E-04	FALSE
101466 at	0.028	6833	1448896 at	0.196	1233	101466 at	0.131	1251	1448896 at	0.071	5575	3723	2910.4918	TRUE	phosphatidylinositol glycan, class F	237951 at	0.201	6928	1.504E-03	TRUE
96614 at	-0.088	4501	1454606 at	-0.079	3405.5	96614 at	-0.288	1850	1456808 at	-0.092	5137	3723.375	1439.1681	TRUE	RIKEN cDNA 4933426M11 gene	202181 at	0.303	8584	4.593E-03	FALSE
96122 at	0.066	5521	1451322 at	0.112	4006	96122 at	0.233	1319	1451322 at	0.265	4052	3724.5	1751.2225	TRUE	RIKEN cDNA 2310016A09 gene	234981 x at	0.285	1348	9.941E-07	TRUE
99646 at	0.150	2594	1422467 at	0.167	1870	99646 at	-0.038	6103	1420016 at	0.118	4333	3725	1892.5057	FALSE	palmitoyl-protein thioesterase 1	200975 at	-0.074	20357	2.119E-01	FALSE
92289 at	0.140	2356	1427486 at	0.007	8309	92289 at	-0.166	3260	1436367 at	-0.302	975	3725	3197.1832	FALSE	protein tyrosine phosphatase, receptor type, B	230250 at	0.144	21086	2.365E-01	FALSE
92865 at	0.053	6302	1424592 a at	0.264	399	160452 at	0.170	1117	1424592 a at	0.067	7083	3725.25	3453.5505	TRUE	deoxyribonuclease I	243127 x at	0.068	13030	3.729E-02	TRUE
92273 at	-0.112	2183	1419125 at	0.062	5288.5	92273 at	-0.058	4176	1419125 at	-0.288	3254	3725.375	1322.5654	FALSE	protein tyrosine phosphatase, non-receptor type 18	213521 at	0.067	19943	1.987E-01	FALSE
92375 at	0.073	4485	1460703 at	0.054	5636	92375 at	-0.117	2855	1438539 at	-0.253	1927	3725.75	1655.2163	FALSE	activating signal cointegrator 1 complex subunit 1	219336 s at	0.259	5987	6.853E-04	FALSE
96778 at	0.095	4791	1416998 at	-0.087	4998.5	96778 at	0.081	5087	1416998 at	0.674	29	3726.375	2468.0364	FALSE	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	209567 at	-0.080	19535	1.859E-01	FALSE
160859 s at	-0.186	3153	1438244 at	-0.111	3882	160859 s at	-0.083	7140	1434101 at	0.766	737	3728	2642.1056	FALSE	nuclear factor I/B	209290 s at	0.576	309	4.061E-08	FALSE
94452 g at	-0.286	600	1423850 at	-0.041	7018	94451 at	-0.121	2354	1453759 at	0.128	4941	3728.25	2826.5249	FALSE	NOL1/NOP2/Sun domain family 2	223076 s at	0.254	7245	1.919E-03	FALSE
101031 at	0.017	7717	1450561 a at	0.216	244	101031 at	0.198	1651	1450561 a at	0.098	5301	3728.25	3407.7673	TRUE	surfeit gene 1	217646 at	0.135	8118	3.537E-03	TRUE
92938 at	0.148	5082	1421280 at	-0.323	480	92938 at	-0.069	6987	1421281 at	0.244	2371	3730	2877.8078	FALSE	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	206678 at	-0.810	2501	9.577E-06	FALSE
99984 at	0.060	4845	1448797 at	-0.081	5364	99984 at	0.124	3098	1442986 at	0.223	1613	3730	1712.1423	FALSE	ELK3, member of ETS oncogene family	221773 at	0.326	9781	8.965E-03	FALSE
161302 r at	-0.161	4840	1416139 at	0.098	2500	161302 r at	0.190	5332	1416139 at	0.170	2252	3731	1580.7049	FALSE	regenerating islet-derived 2	205886 at	-0.034	33138	6.695E-01	FALSE
101169 at	0.249	868	1420511 at	-0.070	5740	101169 at	0.099	5201	1420511 at	0.149	3116	3731.25	2219.0069	FALSE	retinal degeneration, slow (retinitis pigmentosa 7)	206625 at	-0.028	32916	6.617E-01	FALSE
98979 at	0.100	3784	1432177 a at	0.078	4486.5	98979 at	0.118	2613	1432177 a at	0.134	4043	3731.625	800.17825	TRUE	menage a trois 1	203565 s at	-0.089	13825	4.940E-02	FALSE
100512 at	0.072	5792	1419453 at	0.059	6161.5	100512 at	0.167	1935	1419452 at	0.380	1040	3732.125	2621.8405	TRUE	ubiquitin carboxyl-terminal esterase L5	219960 s at	-0.169	12795	3.475E-02	FALSE
97783 at	0.048	6140	1419413 at	0.083	4792	97783 at	0.212	629	1419413 at	0.193	3371	3733	2358.0352	TRUE	chemokine (C-C motif) ligand 17	207900 at	0.034	29376	5.346E-01	FALSE
102252 at	-0.278	939	1421950 at	0.136	2394	102252 at	0.122	3699	1421950 at	0.027	7903	3733.75	2999.4117	FALSE	prefoldin 2	218336 at	-0.171	12618	3.283E-02	FALSE
103848 at	0.192	601	1425604 at	-0.035	7070.5	103848 at	0.069	5539	1421954 at	0.230	1727	3734.375	3067.7894	FALSE	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	212180 at	0.223	9464	7.604E-03	FALSE
103584 at	-0.151	3412	1453015 at	-0.140	1960.5	103584 at	0.044	7430	1453015 at	0.220	2136	3734.625	2547.0901	FALSE	RIKEN cDNA 5830471E12 gene		NA	NA	NA	NA
93441 at	0.038	6236	1427141 at	0.082	3573.5	93441 at	0.091	3074	1445682 at	0.170	2056	3734.875	1782.9793	TRUE	RIKEN cDNA 2700099C18 gene		NA	NA	NA	NA
102151 at	0.092	3462	1423420 at	-0.042	6420.5	102151 at	-0.168	978	1423420 at	0.195	4084	3736.125	2236.7599	FALSE	adrenergic receptor, beta 1	208214 at	-0.100	10579	1.381E-02	FALSE
96934 at	-0.108	3878	1434823 x at	0.391	403.5	96934 at	0.100	4128	1433516 a at	0.083	6535	3736.125	2524.1358	FALSE	myeloma overexpressed 2	226845 s at	0.079	24824	3.663E-01	FALSE
92589 at	-0.122	1693	1415673 at	0.150	2942.5	92589 at	0.043	5189	1415673 at	-0.117	5121	3736.375	1715.8987	FALSE	phosphoserine phosphatase	205194 at	0.125	8279	3.879E-03	FALSE
102331 at	0.083	4172	1428372 at	0.087	4738	102331 at	0.055	4931	1428372 at	-0.260	1108	3737.25	1782.1806	FALSE	suppression of tumorigenicity 5	202440 s at	0.391	2067	4.358E-06	FALSE
161210 f at	0.161	1803	1422181 at	0.152	1949	101181 at	-0.051	5374	1422181 at	-0.079	5824	3737.5	2158.1348	FALSE	cyclic nucleotide gated channel alpha 2		NA	NA	NA	NA
102140 at	0.027	7144	1447287 at	0.244	352	102140 at	0.083	3922	1447287 at	0.130	3532	3737.5	2777.4162	TRUE	expressed sequence C77137		NA	NA	NA	NA
94692 at	0.153	1904	1420698 at	0.088	4571	94692 at	0.126	3221	1420698 at	-0.097	5258	3738.5	1487.1822	FALSE	glutathione peroxidase 5	208028 s at	0.058	20083	2.031E-01	FALSE
95014 at	0.060	5318	1417501 at	0.215	279	162050 at	-0.011	7782	1417501 at	0.203	1581	3740	3438.3935	FALSE	F-box only protein 6b	231769 at	-0.132	14685	6.488E-02	FALSE
104607 at	-0.290	560	1419056 at	-0.044	6680	104607 at	-0.162	2198	1419056 at	0.116	5523	3740.25	2846.8025	FALSE	reticulon 2 (Z-band associated protein)	204217 s at	-0.704	12	2.043E-09	FALSE
103721 at	-0.144	1701	1452106 at	-0.179	1269.5	103721 at	-0.027	7126	1421429 a at	0.107	4865	3740.375	2768.3636	FALSE	Nephronectin	244747 at	-0.069	17399	1.241E-01	FALSE
98981 s at	0.099	5294	1421908 a at	-0.166	1246	98981 s at	0.167	3417	1444620 at	0.137	5005	3740.5	1856.4756	FALSE	transcription factor 12	208986 at	0.535	1994	3.820E-06	FALSE
101342 at	0.052	6234	1451889 at	0.132	2315.5	104188 at	-0.106	3116	1455556 at	-0.228	3297	3740.625	1716.0866	FALSE	Notch gene homolog 2 (Drosophila)	212377 s at	0.692	1066	5.523E-07	FALSE
96351 at	0.208	2196	1451222 at	-0.174	1547.5	96351 at	-0.029	6617	1451222 at	-0.111	4602	3740.625	2324.5906	FALSE	basic transcription factor 3-like 4	225976 at	-0.191	9339	7.098E-03	FALSE
95717 at	-0.097	3593	1437338 x at	0.153	1411.5	95717 at	-0.016	7705	1437338 x at	0.161	2258	3741.875	2790.523	FALSE	elongation protein 3 homolog (S. cerevisiae)	221094 s at	-0.063	19986	2.003E-01	FALSE
104621 at	0.078	5180	1433834 at	0.070	5604.5	104621 at	0.202	3598	1445928 at	0.550	588	3742.625	2273.4116	TRUE	membrane-associated ring finger (C3HC4) 6	201737 s at	0.322	8560	4.516E-03	TRUE
96904 at	-0.107	2172	1453725 a at	0.110	2553	96904 at	0.184	1954	1453725 a at	0.010	8294	3743.25	3043.9154	FALSE	mitochondrial ribosomal protein S7	217932 at	-0.121	13786	4.842E-02	FALSE
101957 f at	-0.232	1102	1435368 a at	0.098	3413	101957 f at	-0.096	5060	1422503 s at	-0.092	5399	3743.5	1963.0423	FALSE	poly (ADP-ribose) polymerase family, member 1	208644 at	0.132	10267	1.180E-02	FALSE
102867 at	0.138	4875	1460683 at	0.163	1620.5	102868 g at	-0.106	3366	1460683 at	-0.108	5115	3744.125	1613.5817	FALSE	TEA domain family member 4	41037 at	0.096	14949	7.001E-02	FALSE
96617 at	-0.188	2424	1451676 at	0.193	908	96617 at	-0.071	4034	1451676 at	0.047	7611	3744.25	2876.519	FALSE	Dr1 associated protein 1 (negative cofactor 2 alpha)	203258 at	-0.292	3022	2.281E-05	FALSE
94174 at	0.068	4271	1420930 s at	0.129	2228	94174 at	0.016	7561	1420929 at	-0.269	917	3744.25	2894.6734	FALSE	catenin (cadherin associated protein), alpha-like 1	202468 s at	0.153	15350	7.727E-02	FALSE
103521 r at	0.306	762	1455179 at	0.016	8112	103521 r at	0.114	2609	1455179 at	-0.173	3497	3745	3126.2852	FALSE	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	238778 at	-0.384	2336	7.135E-06	FALSE
97732 at	0.168	1315	1450453 a at	0.151	2687.5	97732 at	0.072	4840	1425100 a at	0.063	6139	3745.375	2156.6538	TRUE	phosphodiesterase 6G, cGMP-specific, rod, gamma	210060 at	-0.017	36970	7.900E-01	FALSE
160834 at	-0.174	1371	1417406 at	0.077	5387	160834 at	0.101	2472	1417406 at	-0.118	5758	3747	2160.6112	FALSE	SERTA domain containing 1	223394 at	0.147	11191	1.863E-02	FALSE
162345 at	0.068	4707	1416841 at	0.291	447	162345 at	0.096	4478	1416841 at	0.117	5361	3748.25	2232.4091	TRUE	RIKEN cDNA 1110059E24 gene	239621 at	0.036	18147	1.441E-01	FALSE
160694 at	-0.046	6011	1423558 at	0.128	2140.5	160694 at	-0.054	6554	1423557 at	0.392	289	3748.625	3030.0462	FALSE	interferon gamma receptor 2	201642 at	-0.215	2950	1.995E-05	FALSE
99873 at	0.129	1818	1452018 at	0.138	3071	99873 at	-0.032	7014	1443817 x at	0.152	3093	3749	2256.768	FALSE	NK2 transcription factor related, locus 6 (Drosophila)		NA	NA	NA	NA
92828 at	0.045	6894	1449438 at	0.115	3365	92828 at	0.364	670	1419353 at	-0.116	4070	3749.75	2557.4571	FALSE	dolichol-phosphate (beta-D) mannosyltransferase 1	237213 at	-0.207	1337	9.778E-07	FALSE
99005 at	-0.180	894	1448414 at	0.155	2899	99005 at	0.001	8460	1448414 at	0.337	2749	3750.5	3269.4055	FALSE	RAD1 homolog (S. pombe)	204460 s at	-0.178	3385	3.891E-05	FALSE
100878 at	0.209	2333	1423536 at	0.084	3932	100878 at	0.090	5429	1457343 at	0.175	3308	3750.5	1298.129	TRUE	striatin, calmodulin binding protein 3		NA	NA	NA	NA
96056 at	-0.056	5401	1448605 at	-0.048	6181.5	162468 at	-0.107	2769	1448605 at	-0.350	653	3751.125	2529.2791	TRUE	ras homolog gene family, member C	200885 at	0.413	1795	2.644E-06	FALSE
94929 at	-0.194	3327	1438670 at	0.155	1894.5	94929 at	0.052	5888	1417068 a at	0.144	3899	3752.125	1654.7947	FALSE	protein tyrosine phosphatase, non-receptor type 1	202716 at	0.115	11653	2.238E-02	FALSE
102413 at	-0.019	7313	1418478 at	0.075	5416.5	102413 at	-0.265	1608	1418478 at	-0.360	673	3752.625	3137.3161	FALSE	LIM domain only 1	206718 at	0.014	38768	8.435E-01	FALSE
93398 at	0.060	5303	1421128 at	0.180	1318	93398 at	0.061	5638	1421128 at	0.178	2752	3752.75	2072.5951	TRUE	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 2	213876 x at	0.174	9043	5.957E-03	TRUE
94065 at	0.183	745	1436835 at	0.199	1965	94065 at	-0.016	7723	1425855 a at	0.135	4579	3753	3092.3661	FALSE	v-crk sarcoma virus CT10 oncogene homolog (avian)	202224 at	0.126	14194	5.591E-02	FALSE
101328 at	0.128	1553	1417814 at	0.145	2072	94665 at	0.076	3470.5	1417814 at	-0.027	7917	3753.125	2891.6237	FALSE	phospholipase A2, group V	215870 s at	0.105	20799	2.268E-01	FALSE
162414 f at	0.105	4490	1415951 at	0.026	7464	162414 f at	0.130	1983	1415951 at	-0.212	1076	3753.25	2864.3742	FALSE	FK506 binding protein 10	219249 s at	0.136	9662	8.509E-03	FALSE
100444 at	-0.124	3911	1450674 at	0.029	7120	100444 at	-0.178	821	1450674 at	0.160	3163	3753.75	2601.6901	FALSE	cyclin-dependent kinase 5	204247 s at	-0.747	211	2.100E-08	FALSE
161598 at	0.031	7245	1419080 at	-0.077	5341.5	92738 at	0.128	1710	1419080 at	-0.419	719	3753.875	3060.3049	FALSE	glial cell line derived neurotrophic factor	221359 at	0.038	24494	3.541E-01	FALSE
161026 s at	0.085	5803	1417336 a at	-0.041	7422	161026 s at	0.226	683	1417336 a at	-0.335	1109	3754.25	3370.4446	FALSE	synaptotagmin-like 4	227703 s at	0.899	3068	2.516E-05	FALSE
97518 at	-0.260	230	1448130 at	-0.196	1505.5	97518 at	-0.026	7615	1438322 x at	0.091	5671	3755.375	3466.8204	FALSE	farnesyl diphosphate farnesyl transferase 1	241954 at	0.691	2383	7.813E-06	FALSE
96219 at	-0.052	5991	1450675 at	-0.116	3990	96219 at	-0.147	1941	1450675 at	-0.292	3101	3755.75	1710.0907	TRUE	stromal membrane-associated protein 1-like	225282 at	-0.438	1757	2.452E-06	TRUE
93168 at	-0.158	945	1440201 at	-0.261	2724.5	93168 at	-0.070	5649	1420210 at	0.115	5711	3757.375	2336.0351	FALSE	expressed sequence AV344025		NA	NA	NA	NA
104759 at	0.085	3025	1449857 at	-0.079	6015.5	104759 at	0.125	2907	1454998 at	-0.124	3084	3757.875	1506.8811	FALSE	RIKEN cDNA 1200011I18 gene	229891 x at	-0.274	7850	2.972E-03	FALSE
102235 at	0.073	4072	1422088 at	-0.098	4394.5	102235 at	0.155	2270	1422087 at	-0.198	4296	3758.125	1001.2186	FALSE	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	214058 at	-0.097	10136	1.085E-02	FALSE
160792 at	-0.086	5028	1426578 s at	0.098	4641.5	160792 at	0.068	4661	1426578 s at	0.276	710	3760.125	2041.1735	FALSE	SNAP-associated protein	223066 at	0.131	9897	9.560E-03	FALSE
100764 at	0.118	3909	1448759 at	-0.103	3014.5	100764 at	-0.114	2481	1448759 at	0.123	5636	3760.125	1382.4119	FALSE	interleukin 2 receptor, beta chain	205291 at	-0.021	35806	7.552E-01	FALSE
97786 at	0.151	1495	1419621 at	0.124	3431	97786 at	-0.032	6702	1419621 at	0.116	3415	3760.75	2161.2383	FALSE	ankyrin repeat domain 2 (stretch responsive muscle)	221232 s at	-0.105	17157	1.184E-01	FALSE
104376 at	-0.194	1524	1415743 at	-0.294	168	104376 at	0.024	7253	1415743 at	-0.093	6104	3762.25	3444.6831	FALSE	histone deacetylase 5	202455 at	0.136	9905	9.602E-03	FALSE
93794 at	-0.062	6119	1423781 at	0.123	4557.5	93794 at	0.243	1295	1423781 at	0.138	3088	3764.875	2059.8221	FALSE	amyloid beta precursor protein binding protein 1	202268 s at	0.015	41484	9.201E-01	FALSE
94541 at	0.074	5420	1428076 s at	0.271	2329.5	94541 at	-0.084	3410	1432427 at	-0.164	3902	3765.375	1283.8067	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4		NA	NA	NA	NA
100113 s at	0.067	5528	1451783 a at	0.115	3014.5	161604 r at	0.031	6284	1417181 a at	0.539	237	3765.875	2736.3943	TRUE	kinesin-associated protein 3	203333 at	-0.443	3950	8.254E-05	FALSE
100729 at	-0.081	5749	1448109 a at	0.369	1248.5	100729 at	0.185	1526	1448109 a at	-0.055	6540	3765.875	2767.8374	FALSE	ribosomal protein L26	222229 x at	-0.119	11786	2.372E-02	FALSE
98051 at	0.017	7450	1438950 x at	0.098	3065.5	98051 at	-0.105	1823	1438949 at	0.188	2725	3765.875	2511.4064	FALSE	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	221647 s at	-0.008	39980	8.771E-01	FALSE
99185 at	-0.064	6432	1428588 a at	0.357	360.5	99185 at	0.160	3591	1428588 a at	0.140	4686	3767.375	2554.8649	FALSE	mitochondrial ribosomal protein L41	227186 s at	-0.176	7740	2.747E-03	FALSE
104110 at	0.079	4191	1451197 s at	-0.114	3149	93145 at	0.084	3189.5	1455505 at	-0.114	4540	3767.375	705.39225	FALSE	GATA zinc finger domain containing 2A	218131 s at	0.122	9121	6.220E-03	FALSE
93573 at	-0.562	104	1422557 s at	0.056	6724.5	93573 at	-0.027	7407	1451612 at	-0.304	834	3767.375	3830.4249	FALSE	metallothionein 1		NA	NA	NA	NA
95478 at	-0.124	3824	1427955 a at	0.210	3439	95478 at	0.436	325	1427955 a at	0.043	7486	3768.5	2931.9589	FALSE	differentially expressed in B16F10 1	218283 at	-0.168	7522	2.341E-03	FALSE
98957 at	0.064	5289	1423504 at	0.139	1246	98957 at	0.164	3218	1423503 at	0.103	5322	3768.75	1948.6182	TRUE	junction adhesion molecule 3	212813 at	0.197	14657	6.419E-02	FALSE
95622 at	0.123	3906	1460678 at	0.090	5098	95622 at	-0.063	4952	1435086 s at	0.366	1131	3771.75	1838.7961	FALSE	kelch domain containing 2	217906 at	-0.101	27234	4.515E-01	FALSE
96674 at	-0.091	5415	1453124 at	0.226	2672	96674 at	0.128	5842	1429369 at	0.383	1159	3772	2237.7159	FALSE	transportin 3	212317 at	0.097	12180	2.776E-02	FALSE
93673 at	0.081	3932	1449281 at	-0.104	3033	93673 at	-0.054	4431	1449281 at	-0.169	3696	3773	580.73918	FALSE	neurturin	210683 at	0.024	22316	2.789E-01	FALSE
100130 at	0.037	6608	1417409 at	-0.551	4.5	100130 at	-0.026	7464	1417409 at	0.287	1016	3773.125	3806.282	FALSE	Jun oncogene	201464 x at	0.401	9971	9.990E-03	FALSE
96548 at	0.182	2417	1421522 at	-0.026	7577.5	96548 at	0.119	1670	1439853 at	-0.136	3428	3773.125	2636.5754	FALSE	beta-1,4-N-acetyl-galactosaminyl transferase 2		NA	NA	NA	NA
160762 at	-0.292	637	1433477 at	-0.076	5439.5	160762 at	-0.250	1385	1433477 at	0.028	7632	3773.375	3326.9677	FALSE	active BCR-related gene	214671 s at	-0.179	16943	1.126E-01	FALSE
93849 at	0.086	3457	1425388 a at	0.096	4399	93849 at	0.082	3920	1425388 a at	0.199	3318	3773.5	490.02211	TRUE	thiamin pyrophosphokinase	221218 s at	0.044	24811	3.660E-01	FALSE
103430 at	-0.234	1641	1451734 a at	-0.329	1718	103430 at	-0.014	8092	1426024 a at	-0.177	3645	3774	3024.268	TRUE	drebrin 1	217025 s at	-0.319	1346	9.901E-07	TRUE
104294 at	0.067	4635	1454905 at	0.076	4215.5	104294 at	0.138	3771	1439285 at	0.163	2475	3774.125	935.17435	TRUE	inhibitor of Bruton agammaglobulinemia tyrosine kinase	215086 at	0.028	28227	4.900E-01	FALSE
160358 at	-0.161	957	1416072 at	0.130	3275.5	160358 at	0.055	6604	1416072 at	0.235	4261	3774.375	2340.2322	FALSE	CD34 antigen	209543 s at	0.124	18314	1.493E-01	FALSE
95036 at	0.146	3882	1451129 at	-0.188	5355	95036 at	0.257	308	1451129 at	-0.558	5560	3776.25	2429.9627	FALSE	calbindin 2	205428 s at	-0.075	30597	5.789E-01	FALSE

95733 at	-0.028	6872	1451782 a at	-0.221	288.5	161687 r at	0.254	1279	1451782 a at	-0.096	6671	3777.625	3481.5655	FALSE	solute carrier family 29 (nucleoside transporters), member 1	201801 s at	-0.201	8198	3.703E-03	FALSE
95546 g at	0.124	1976	1452014 a at	0.030	6888	95545 at	-0.074	3911	1452014 a at	0.247	2339	3778.5	2236.6428	FALSE	insulin-like growth factor 1	209541 at	-0.122	14730	6.563E-02	FALSE
103064 at	0.075	4834	1449708 s at	0.108	1624	103064 at	0.029	7307	1449708 s at	-0.248	1350	3778.75	2834.5414	FALSE	checkpoint kinase 1 homolog (S. pombe)	238075 at	-0.093	10716	1.483E-02	FALSE
99521 at	0.135	1467	1421830 at	0.056	6082	99521 at	-0.101	4466	1421829 at	0.228	3100	3778.75	1964.8717	FALSE	adenylate kinase 3 alpha-like 1	204348 s at	0.148	15304	7.662E-02	FALSE
102402 at	0.035	7130	1419484 a at	0.069	5685	102402 at	0.334	546	1444503 at	0.247	1755	3779	3131.0755	TRUE	glioblastoma amplified sequence	232285 at	0.045	25944	4.021E-01	FALSE
95688 at	0.075	6028	1423346 at	-0.108	4049.5	95688 at	0.356	1992	1423346 at	0.184	3047	3779.125	1718.5618	FALSE	degenerative spermatocyte homolog 1 (Drosophila)	207431 s at	-0.262	9414	7.390E-03	FALSE
97305 at	0.035	6557	1448480 at	0.107	4400.5	97305 at	0.176	1441	1448480 at	0.215	2731	3782.375	2211.1874	TRUE	nuclear import 7 homolog (S. cerevisiae)	223397 s at	0.067	14667	6.455E-02	FALSE
96297 at	-0.057	6219	1437512 x at	0.128	3870	96297 at	-0.052	4566	1457668 x at	-0.315	475	3782.5	2415.065	FALSE	EBNA1 binding protein 2	201323 at	-0.281	7489	2.284E-03	FALSE
92499 at	0.175	1689	1419633 at	0.052	7292	92499 at	0.312	1239	1419633 at	0.130	4913	3783.25	2854.6309	TRUE	Unc4.1 homeobox (C. elegans)	NA	NA	NA	NA	
101114 at	-0.008	8184	1425348 a at	0.181	648.5	101114 at	0.135	2626	1421012 at	-0.118	3675	3783.375	3190.8308	FALSE	signal recognition particle receptor, B subunit	227737 at	0.044	22718	2.924E-01	FALSE
101198 at	0.038	6877	1417747 at	-0.460	10	101198 at	-0.218	2209	1448832 a at	0.096	6042	3784.5	3234.6516	FALSE	complexin 1	223500 at	-1.227	922	3.676E-07	FALSE
96202 at	-0.307	131	1451627 a at	-0.085	5811.5	96202 at	-0.095	4277	1451627 a at	-0.126	4920	3784.875	2515.8635	TRUE	solute carrier family 1 (glial high affinity glutamate transporter), member 2	225491 at	-0.166	13887	5.039E-02	FALSE
92274 at	0.127	1966	1449830 at	0.106	4819.5	92274 at	-0.062	4836	1449830 at	0.125	3519	3785.125	1360.6749	FALSE	prolactin-like protein J	NA	NA	NA	NA	
95468 at	-0.093	4081	1451110 at	-0.182	1811	95468 at	-0.056	6297	1423785 at	-0.179	2952	3785.25	1913.8377	TRUE	EGL nine homolog 1 (C. elegans)	NA	NA	NA	NA	
103712 at	-0.720	71	1433871 at	-0.133	3565	103712 at	-0.137	4805	1444848 at	0.181	6703	3786	2792.6878	FALSE	R3H domain 1 (binds single-stranded nucleic acids)	202754 at	-0.384	2804	1.626E-05	FALSE
162334 r at	0.099	4493	1416621 at	-0.097	3323	162334 r at	0.152	2404	1416621 at	-0.115	4925	3786.25	1143.3085	FALSE	Lethal giant larvae homolog 1 (Drosophila)	236594 at	0.442	929	3.701E-07	FALSE
96650 at	-0.229	1506	1447952 at	0.062	5012	96650 at	-0.100	4274	1458436 at	-0.137	4353	3786.25	1555.7537	FALSE	AU RNA binding protein/enoyl-coenzyme A hydratase	205052 at	-0.370	5361	3.863E-04	FALSE
95736 at	-0.191	3257	1416510 at	-0.086	3183.5	95736 at	-0.233	1775	1416510 at	0.052	6930	3786.375	2203.9135	FALSE	mitochondrial ribosomal protein L4	223743 s at	-0.378	893	3.428E-07	FALSE
96790 f at	0.240	1056	1452583 s at	-0.043	6187.5	96790 f at	0.146	1282	1452583 s at	0.092	6621	3786.625	3029.1551	FALSE	galactose mutarotase	234974 at	0.178	5573	4.706E-04	FALSE
99362 at	0.100	2661	1419957 at	0.192	2019	99362 at	-0.031	6049	1419957 at	0.104	4419	3787	1817.4862	FALSE	expressed sequence C77144	NA	NA	NA	NA	
102271 at	-0.268	297	1460739 at	-0.187	667.5	102271 at	-0.001	8482	1460739 at	-0.121	5702	3787.125	3984.2034	TRUE	DNA segment, Chr 11, Brigham & Women's Genetics 0280e expressed	221525 at	-0.100	17942	1.392E-01	FALSE
100609 at	0.028	6920	1417314 at	0.103	3221	100609 at	0.095	2220	1417314 at	-0.172	2790	3787.75	2128.0304	FALSE	complement factor B	202357 s at	0.161	11184	1.858E-02	FALSE
104093 at	-0.105	4199	1417756 a at	0.115	2665	104093 at	0.148	942	1417756 a at	0.046	7347	3788.25	2720.0641	FALSE	lymphocyte specific 1	203523 at	-0.003	43586	9.747E-01	FALSE
160120 i at	0.116	2868	1433948 at	0.080	5086	160120 i at	-0.050	5221	1433949 x at	-0.173	1979	3788.5	1618.3503	FALSE	phospholipase A2, group IB, pancreas	206311 s at	-0.033	26485	4.245E-01	FALSE
160221 at	0.147	2559	1417079 s at	0.106	4079	160221 at	0.130	2680	1417078 at	-0.080	5839	3789.25	1530.7276	FALSE	lectin, galactose-binding, soluble 2	208450 at	-0.090	23357	3.149E-01	FALSE
104312 at	-0.199	833	1425699 a at	-0.058	5907	104312 at	-0.080	5302	1425699 a at	0.201	3118	3790	2306.7485	FALSE	abhydrolase domain containing 14A	210006 at	-0.234	3327	3.602E-05	FALSE
100306 at	0.268	358	1459902 at	-0.109	3170	100306 at	-0.070	6755	1459902 at	-0.174	4877	3790	2716.359	FALSE	RIKEN cDNA 2700007P21 gene	226383 at	-0.127	12513	3.144E-02	FALSE
101344 at	-0.027	7428	1454770 at	0.187	2480.5	101344 at	0.077	4246	1460663 at	0.783	1007	3790.375	2763.0212	FALSE	cholecystokinin B receptor	210381 s at	-0.230	6149	7.921E-04	FALSE
99427 at	0.068	5193	1450553 at	0.070	5224.5	99427 at	0.191	417	1450553 at	0.152	4329	3790.875	2287.1996	TRUE	homeo box D12	221411 at	-0.017	33864	6.946E-01	FALSE
103667 at	0.112	5865	1442145 at	-0.036	6333.5	95978 at	-0.188	906	1434513 at	-0.244	2061	3791.375	2713.0491	FALSE	ATPase type 13A3	219558 at	-0.145	8812	5.227E-03	FALSE
96333 g at	0.192	1019	1460224 at	0.056	6777	96331 at	0.137	3497	1460224 at	0.115	3874	3791.75	2358.9194	TRUE	sorting nexin 2	202113 s at	-0.149	26222	4.126E-01	FALSE
162061 f at	0.066	4844	1439383 x at	0.124	2212	93762 at	0.114	1816	1439383 x at	-0.068	6296	3792	2143.0271	FALSE	protein phosphatase 2A, regulatory subunit B (PR 53)	208874 x at	-0.128	9940	9.817E-03	FALSE
92485 at	0.080	5422	1450210 at	0.109	4059.5	92485 at	-0.103	2233	1420006 at	-0.123	3454	3792.125	1325.793	FALSE	bone morphogenetic protein 15	221332 at	-0.028	34629	7.196E-01	FALSE
103387 at	0.119	2109	1416542 at	0.137	1544	103387 at	0.010	8022	1416542 at	-0.138	3494	3792.25	2936.4205	FALSE	PHD finger protein 1	40446 at	0.110	9970	9.989E-03	FALSE
161058 f at	-0.105	3048	1418802 at	0.190	881	161058 f at	0.057	5453	1418802 at	-0.083	5790	3793	2293.3511	FALSE	expressed sequence R74862	NA	NA	NA	NA	
160737 at	0.120	2987	1420013 s at	0.059	4894	160737 at	-0.035	6241	1420014 at	0.268	1053	3793.75	2262.8992	FALSE	lanosterol synthase	202245 at	0.240	5373	3.894E-04	FALSE
100962 at	-0.362	176	1417930 at	-0.015	8120	100962 at	-0.276	527	1417930 at	-0.146	6354	3794.25	4042.7338	TRUE	Ngfi-A binding protein 2	216017 s at	-0.113	10612	1.404E-02	TRUE
98479 f at	0.034	7069	1454167 at	0.114	2484	98479 f at	0.065	5594	1425014 at	0.852	34	3795.25	3152.7405	TRUE	nuclear receptor subfamily 2, group C, member 2	206038 s at	-0.082	13616	4.562E-02	FALSE
97692 at	0.286	889	1450477 at	0.039	7446	97692 at	-0.109	4783	1450477 at	0.307	2065	3795.75	2929.373	FALSE	5-hydroxytryptamine (serotonin) receptor 2C	207307 at	-1.308	1648	1.958E-06	FALSE
161682 f at	0.118	3691	1455954 x at	0.127	1766	100911 at	-0.065	4321	1438152 at	0.110	5405	3795.75	1527.1357	FALSE	GPI anchor attachment protein 1	215690 x at	-0.175	10070	1.048E-02	FALSE
95031 at	0.154	3746	1460455 at	0.085	5868.5	95031 at	-0.132	3357	1429107 at	0.202	2216	3796.875	1526.0924	FALSE	RIKEN cDNA 1110059H15 gene	234982 at	-0.434	4758	2.090E-04	FALSE
101107 at	0.216	2063	1415870 at	-0.024	7539.5	161208 r at	0.178	1768	1441477 at	-0.154	3817	3796.875	2653.9469	FALSE	calumenin	200755 s at	-0.172	10121	1.070E-02	FALSE
160738 at	-0.100	3675	1437377 a at	0.129	3055	160738 at	-0.084	3445	1437377 a at	0.126	5016	3797.75	851.53014	FALSE	polymerase (RNA) mitochondrial (DNA directed)	203782 s at	-0.101	19483	1.846E-01	FALSE
160502 at	0.103	3061	1415947 at	-0.059	6397	160502 at	0.239	334	1415947 at	0.203	5400	3798	2699.6092	FALSE	cellular repressor of E1A-stimulated genes 1	201200 at	-0.186	15126	7.313E-02	FALSE
102352 at	0.144	1324	1418194 at	0.034	6871	102352 at	-0.079	3069	1418195 at	-0.226	3929	3798.25	2317.5135	FALSE	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10	212256 at	0.406	539	1.161E-07	FALSE
101534 at	0.098	4196	1422419 s at	0.155	3612	101534 at	0.073	4531	1422419 s at	-0.181	2854	3798.25	735.16999	FALSE	transition protein 2	217460 at	-0.027	27277	4.527E-01	FALSE
94861 at	0.102	3317	1423976 at	0.144	1732	94861 at	0.018	7712	1449719 at	-0.188	2433	3798.5	2688.3909	FALSE	RIKEN cDNA 4930453N24 gene	226524 at	-0.083	18677	1.603E-01	FALSE
97955 at	0.177	1189	1415862 at	0.114	3800	97954 at	0.081	4081	1415861 at	-0.079	6125	3798.75	2025.0021	FALSE	tyrosinase-related protein 1	205694 at	-0.003	43614	9.752E-01	FALSE
96952 at	0.059	6733	1437144 x at	0.289	607.5	96952 at	0.215	2331	1416506 at	0.100	5525	3799.125	2824.1889	TRUE	proteasome (prosome, macropain) subunit, alpha type 6	208805 at	-0.143	19891	1.975E-01	FALSE
99911 at	-0.135	1454	1448790 at	-0.012	8108.5	99911 at	-0.079	3137	1448790 at	-0.182	2499	3799.625	2955.1682	TRUE	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	223567 at	-0.599	2604	1.120E-05	TRUE
102002 at	0.135	3274	1420844 at	0.209	2857	102002 at	-0.248	4033	1420844 at	-0.121	5047	3802.75	961.8026	FALSE	ubiquilin 2	215884 s at	-0.366	6130	7.787E-04	FALSE
92529 s at	0.151	2431	1425064 at	-0.057	6281	92529 s at	-0.130	2371	1421721 a at	0.157	4130	3803.25	1842.1383	FALSE	aryl hydrocarbon receptor nuclear translocator	230619 at	0.244	3338	3.661E-05	FALSE
104210 at	0.184	702	1455158 at	-0.050	6455	104211 at	-0.081	3387	1421997 s at	-0.124	4669	3803.25	2420.2146	FALSE	integrin alpha 3	201474 s at	-0.042	29598	5.422E-01	FALSE
99081 at	0.076	5243	1416625 at	-0.172	3106	99081 at	-0.034	6511	1416625 at	-0.676	355	3803.75	2694.5238	FALSE	serine (or cysteine) peptidase inhibitor, clade G, member 1	200986 at	0.749	3425	4.185E-05	FALSE
104662 at	0.081	5207	1422303 a at	-0.060	5678	104662 at	-0.077	3821	1422303 a at	0.359	510	3804	2333.1674	FALSE	tumor necrosis factor receptor superfamily, member 18	223851 s at	0.049	22572	2.872E-01	FALSE
102025 at	-0.206	4146	1448859 at	0.202	1387	102025 at	0.125	2750	1417851 at	0.145	6935	3804.5	2371.5627	FALSE	chemokine (C-X-C motif) ligand 13	205242 at	-0.039	32085	6.343E-01	FALSE
101699 at	-0.105	2800	1422287 at	0.188	2221	101699 at	0.008	8040	1422287 at	-0.180	2159	3805	2838.0523	FALSE	per-hexamer repeat gene 2	NA	NA	NA	NA	
161194 r at	0.127	2596	1417291 at	-0.028	7167	161194 r at	0.163	848	1417291 at	-0.140	4610	3805.25	2717.6337	FALSE	tumor necrosis factor receptor superfamily, member 1a	207643 s at	0.397	4871	2.382E-04	FALSE
93823 at	-0.125	4029	1417948 s at	-0.038	7598.5	93823 at	-0.262	2178	1417948 s at	-0.277	1421	3806.625	2755.0797	TRUE	interleukin enhancer binding factor 2	200052 s at	-0.089	27849	4.747E-01	FALSE
102277 at	0.374	287	1427120 at	0.060	6006	102277 at	-0.275	1200	1427120 at	-0.028	7735	3807	3626.368	FALSE	zinc finger protein 26	214715 x at	0.429	1615	1.800E-06	FALSE
93695 at	0.168	1474	1421058 at	0.072	4172.5	93695 at	-0.046	6721	1450110 at	0.171	2861	3807.125	2233.2929	FALSE	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	210505 at	-0.003	43024	9.606E-01	FALSE
97370 at	0.183	1433	1452076 at	0.047	6443	97370 at	-0.065	4211	1452076 at	0.162	3145	3808	2096.4914	FALSE	SPRY domain containing 4	225616 at	-0.095	8955	5.631E-03	FALSE
98826 at	0.117	2607	1449729 at	0.105	3559	98826 at	-0.031	6583	1449729 at	0.160	2484	3808.25	1911.1953	FALSE	fibroblast growth factor 4	206783 at	0.001	44306	9.918E-01	FALSE
160581 at	-0.187	574	1428169 at	0.066	6236.5	160581 at	-0.119	2413	1441852 x at	0.073	6012	3808.875	2778.4892	FALSE	autophagy-related 16-like 1 (yeast)	232612 s at	-0.142	10170	1.108E-02	FALSE
96260 at	-0.081	5584	1437037 x at	0.113	1868	96260 at	-0.067	5413	1444538 at	0.404	2372	3809.25	1962.642	FALSE	expressed sequence AL033314	232525 at	0.130	8526	4.421E-03	FALSE
100557 g at	0.084	5051	1426379 at	-0.154	1882	100557 g at	-0.117	2506	1426380 at	-0.065	5801	3810	1908.0323	FALSE	eukaryotic translation initiation factor 4B	211938 at	-0.166	11338	1.976E-02	FALSE
98970 at	0.129	2111	1419805 s at	0.097	5313	98970 at	-0.112	2963	1419505 a at	0.100	4857	3811	1523.0697	FALSE	geranylgeranyl diphosphate synthase 1	202322 s at	-0.099	12110	2.701E-02	FALSE
160274 at	0.198	1706	1418742 at	0.029	7330	160274 at	0.133	1422	1418742 at	-0.106	4791	3812.25	2797.7432	FALSE	keratin complex 1, acidic, gene 4	206969 at	0.075	21590	2.536E-01	FALSE
93956 at	-0.011	8351	1449025 at	0.194	1436	93956 at	0.130	2097	1449025 at	-0.963	3366	3812.5	3129.8582	FALSE	interferon-induced protein with tetratricopeptide repeats 3	204747 at	0.088	22637	2.891E-01	FALSE
100554 at	-0.148	1419	1416554 at	0.044	6196	100554 at	-0.027	6541	1416554 at	0.269	1103	3814.75	2954.9956	FALSE	PDZ and LIM domain 1 (elfin)	208690 s at	0.388	4813	2.198E-04	FALSE
93534 at	0.247	3621	1449368 at	-0.060	6715	93534 at	0.116	1815	1441506 at	0.147	3111	3815.5	2077.1175	FALSE	decorin	209335 at	0.167	11121	1.816E-02	FALSE
97189 at	-0.004	8375	1426881 at	0.100	2593.5	97189 at	0.091	3866	1456992 at	0.485	430	3816.125	3353.9272	FALSE	Ubiquitin protein ligase E3C	201817 at	-0.144	12626	3.290E-02	FALSE
102806 g at	0.040	6801	1427711 a at	0.128	2123.5	102806 g at	-0.106	4339	1460681 at	-0.231	2004	3816.875	2260.6526	FALSE	CEA-related cell adhesion molecule 1	210610 at	0.077	19240	1.761E-01	FALSE
92577 f at	-0.152	2355	1453729 a at	0.256	1821	92577 f at	0.072	4253	1453729 a at	-0.048	6840	3817.25	2269.3674	FALSE	ribosomal protein L37	224763 at	-0.215	11990	2.584E-02	FALSE
104445 at	0.189	836	1429159 at	-0.089	4549	104445 at	0.260	2698	1429159 at	-0.088	7186	3817.25	2709.5207	FALSE	RIKEN cDNA 4631408O11 gene	NA	NA	NA	NA	
100584 at	-0.011	8012	1421223 a at	0.098	3579.5	100584 at	0.192	562	1443341 at	0.162	3119	3818.125	3094.9774	FALSE	annexin A4	201301 s at	0.287	6321	9.272E-04	FALSE
97991 at	0.071	5552	1426229 s at	-0.108	2790	97991 at	-0.085	4593	1451979 at	0.248	2338	3818.25	1511.5737	FALSE	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	214352 s at	0.193	10641	1.431E-02	FALSE
101173 at	0.135	2141	1420984 at	0.076	4773.5	101173 at	-0.062	5252	1420984 at	-0.200	3107	3818.375	1447.6631	FALSE	phosphatidylcholine transfer protein	218676 s at	0.130	12971	3.663E-02	FALSE
96695 at	-0.148	3532	1448772 at	0.079	5048.5	96695 at	-0.092	4755	1448772 at	0.177	1939	3818.625	1414.7479	FALSE	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	201898 s at	-0.135	16668	1.053E-01	FALSE
102133 at	0.245	390	1459929 at	0.087	2814.5	102133 at	0.048	5274	1459929 at	0.068	6799	3819.375	2814.5151	TRUE	zinc finger protein 568	NA	NA	NA	NA	
102912 at	-0.016	7910	1452772 at	-0.263	595	102912 at	-0.078	6438	1457468 at	-0.305	337	3820	3920.6266	TRUE	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	218228 s at	0.068	25034	3.740E-01	FALSE
104672 at	-0.090	4714	1448424 at	0.152	2962	104672 at	0.066	5466	1448424 at	0.642	2138	3820	1535.5607	FALSE	frizzled-related protein	203697 at	0.035	38442	8.352E-01	FALSE
104160 at	-0.071	4367	1450720 at	-0.144	1761	93219 at	-0.271	1185	1422716 a at	-0.030	7970	3820.75	3093.2406	TRUE	acid phosphatase 1, soluble	201629 s at	-0.322	3569	5.029E-05	TRUE
160271 at	0.099	3963	1428380 at	0.123	4860	160271 at	-0.086	4986	1428380 at	-0.318	1474	3820.75	1629.4497	FALSE	RIKEN cDNA 0610007C21 gene	219329 s at	0.281	6512	1.057E-03	FALSE
93038 f at	0.158	1418	1448213 at	0.077	5470	93038 f at	0.208	958	1448213 at	-0.060	7440	3821.5	3151.0601	FALSE	annexin A1	201012 at	0.850	9234	6.664E-03	FALSE
161532 f at	-0.065	4761	1452581 at	0.131	3742.5	92282 at	-0.079	5777	1452581 at	0.289	1011	3822.875	2050.3483	FALSE	RIKEN cDNA 2610304G08 gene	225024 at	0.155	8212	3.730E-03	FALSE
96051 at	-0.066	5472	1416905 at	0.030	7278	96051 at	0.216	1061	1416905 at	0.334	1483	3823.5	3041.9549	FALSE	guanylate cyclase activator 2a (guanylin)	207003 at	-0.007	42931	9.583E-01	FALSE
161545 r at	0.047	6178	1427026 at	0.034	6621	98488 at	0.170	987	1458368 at	0.220	1509	3823.75	2987.3243	TRUE	myosin, heavy polypeptide 4, skeletal muscle	208148 at	-0.009	37685	8.110E-01	FALSE
95884 at	0.033	6621	1449640 at	0.061	5223	95884 at	-0.123	2596.5	1422010 at	-0.408	855	3823.875	2588.5728	FALSE	toll-like receptor 7	220146 at	0.068	17482	1.263E-01	FALSE
94866 at	-0.061	4925	1448869 a at	0.199	858.5	94866 at	0.139	2397	1448869 a at	0.054	7118	3824.625	2762.4358	FALSE	mitochondrial ribosomal protein S16	218046 s at	0.116	9336	7.096E-03	FALSE
162155 f at	0.175	1539	1424166 at	0.090	4458	162155 f at	-0.031	7039	1422261 a at	-0.193	2265	3825.25	2475.8757	FALSE	mutS homolog 3 (E. coli)	210947 s at	-0.141	7073	1.665E-03	FALSE
161054 at	0.233	2723	1419672 at	-0.247	610	161054 at	-0.045	7346	1419672 at	0.417	4623	3825.5	2862.6836	FALSE	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	202363 at	-0.093	28540	5.032E-01	FALSE
93505 at	0.097	3472	1423610 at	0.124	3592	93505 at	0.016	7824	1457416 at	0.598	416	3826	3043.6916	TRUE	methionine aminopeptidase 2	244185 at	0.103	11979	2.571E-02	TRUE
96500 at	0.195	1423	1450125 at	0.193	1258	96500 at	-0.067	4932	1450125 at	0.028	7693	3826.5	3084.6911	FALSE	GATA binding protein 5	238095 at	-0.038	25068	3.752E-01	FALSE
104409 at	-0.351	556	1418784 at	-0.071	5255	104409 at	-0.148	3423	1418784 at	-0.148	6075	3827.25	2446.4495	TRUE	glutamate receptor, ionotropic, kainate 5 (gamma 2)	214966 at	-0.336	4352	1.282E-04	TRUE
102981 at	0.200	840	1450664 at	0.088	4432.5	102981 at	-0.159	2891	1450665 at	-0.058	7146	3827.375	2657.1072	FALSE	GA repeat binding protein, alpha	243498 at	0.067	19716	1.913E-01	FALSE
96365 at	-0.221	943	1459092 at	0.189	1404.5	96365 at	-0.063	6174	1429406 at	0.080	6788	3827.375	3080.1457	FALSE	solute carrier organic anion transporter family, member 6c1	NA	NA	NA	NA	
95457 at	0.123	5571	1437288 at	-0.163	3293	95457 at	0.314	1057	1437290 at	-0.092	5389	3827.5	2116.5566	FALSE	inositol monophosphatase domain containing 1	218516 s at	-0.078	12685	3.347E-02	FALSE
104145 at	-0.078	4721	1424643 at	0.109	2937	104145 at	-0.058	5106	1423600 a at	-0.169	2549	3828.25	1272.8518	FALSE	Treacher Collins Franceschetti syndrome 1, homolog	202384 s at	0.149	13703	4.688E-02	FALSE
98764 at	-0.009	7964	1432408 a at	0.084	3910	98764 at	-0.085	3320	1432408 a at	0.534	119	3828.25	3221.1781	FALSE	DNA segment, KIST 2	NA	NA	NA	NA	
94828 at	0.000	8504	1451956 a at	-0.267	414	94828 at	-0.078	3351	1416750 at	0.176	3046	3828.75	3384.2489	FALSE	opioid receptor, sigma 1	201692 at	-0.086	18226	1.467E-01	FALSE
101000 at	-0.021	7626	1426764 at	-0.212	1821	101000 at	-0.288	1968	1442735 at	0.153	3901	3829	2702.9477	FALSE	ornithine decarboxylase antizyme 2	201364 s at	-0.178	11683	2.264E-02	FALSE
161064 f at	-0.238	239	1449800 x at	-0.020	7542	161632 r at	0.093	3323	1449800 x at	-0.113	4213	3829.25	3004.328	FALSE	PHD finger protein 7	215622 x at	0.070	19508	1.851E-01	FALSE
98511 at	-0.520	355	1418573 a at	-0.080	6416.5	98511 at	-0.229	6131	1418573 a at	-0.283	2417	3829.875	2947.1329	TRUE	hnRNP-associated with lethal yellow	201271 s at	0.270	3010	2.244E-05	FALSE
102360 at	-0.108	4480	1450498 at	0.111	3944.5	102360 at	0.075	5857	1434087 at	-0.217	1038	3829.875	2028.1028	FALSE	5,10-methylenetetrahydrofolate reductase	206800 at	-0.046	28098	4.848E-01	FALSE
95968 at	0.113	3344	1443472 at	0.081	4902.5	95968 at	0.056	5487	1443472 at	0.178	1586	3829.875	1748.1073	TRUE	expressed sequence C77691	NA	NA	NA	NA	
160621 at	-0.047	6201	1416595 at	0.177	909	160621 at	0.158	2320	1443032 at	-0.100	5893	3830.75	2626.1473	FALSE	mitochondrial ribosomal protein S22	228059 x at	-0.138	5966	6.784E-04	FALSE
98929 at	-0.095	3147	1423242 at	0.100	3067	98929 at	0.083	3180	1423242 at	0.068	5930	3831	1400.1374	FALSE	mitochondrial ribosomal protein S36	224302 s at	-0.174	12897	3.578E-02	FALSE
97593 f at	0.051	6410	1439356 at	0.173	1436	97594 r at	0.083	3972	1448189 a at	-0.144	3507	3831.25	2042.231	FALSE	flightless I homolog (Drosophila)	212024 x at	0.099	9704	8.675E-03	FALSE
99344 at	0.035	6401	1456252 x at	0.163	1144	99344 at	0.091	3707	1452657 at	-0.125	4075	3831.75	2152.5008	FALSE	Adaptor-related protein complex 1, sigma 2 subunit	203299 s at	-0.082	14593	6.291E-02	FALSE
103957 at	0.123	3767	1422966 a at	-0.105	3158	AFFX-TransRecMu	-0.198	582	1422967 a at	-0.025	7825	3833	2998.0575	FALSE	transferrin receptor	208691 at	0.337	12013	2.608E-02	FALSE
103762 at	-0.055	5562	1417699 at	-0.064	5292	103762 at	0.171	1207	1417699 at	0.210	3272	3833.25	2027.2082	FALSE	general transcription factor IIF, polypeptide 1	202354 s at	-0.131	9297	6.957E-03	FALSE
103372 at	0.228	1820	1437969 s at	-0.046	5774	103372 at	0.164	2762	1437969 s at	0.100	4977	3833.25	1850.714	FALSE	RIKEN cDNA 0610007P22 gene	214067 at	-0.101	16536	1.025E-01	FALSE
93427 at	0.102	3405	1435463 s at	-0.180	1611	93427 at	0.020	7860	1447006 at	0.153	2458	3833.5	2782.554	FALSE	myosin ID	241210 at	0.107	11063	1.764E-02	FALSE
92962 at	0.128	2779	1460415 a at	0.116	3128	92962 at	0.046	5970.5	1439221 s at	-0.142	3460	3834.375	1450.9731	FALSE	CD40 antigen	35150 at	0.048	20532	2.174E-01	FALSE
94414 at	0.061	5590	1436615 a at	0.095	2800	94414 at	0.112	2328	1420525 a at	0.104	4620	3834.5	1531.7227	TRUE	ornithine transcarbamylase	207200 at	-0.070	25681	3.939E-01	FALSE
161658 at	-0.082	3880	1450669 at	-0.026	7690	161658 at	0.082	3205	1450669 at	-0.303	568	3835.75	2940.1381	FALSE	mitogen activated protein kinase kinase kinase 11	203652 at	0.215	4025	8.816E-05	FALSE
100148 at	-0.067	6195	1418330 at	0.066	5239.5	100148 at	-0.258	2176	1449042 at	0.268	1733	3835.875	2214.5656	FALSE	CCCTC-binding factor	202521 at	0.123	14959	7.027E-02	FALSE
102998 at	0.109	3586	1450715 at	0.032	7061.5	102998 at	-0.079	4109	1450715 at	0.289	590	3836.625	2650.6222	FALSE	cytochrome P450, family 1, subfamily a, polypeptide 2	207608 x at	0.057	23925	3.356E-01	FALSE
97517 at	0.044	6051	1437712 x at	0.152	1422	97517 at	-0.048	5587	1460679 at	-0.158	2287	3836.75	2323.7198	FALSE	exosome component 4	58696 at	-0.076	12124	2.716E-02	FALSE
102871 at	-0.310	194	1418051 at	-0.093	4690	102871 at	-0.231	2949	1418051 at	0.094	7515	3837	3072.2026	FALSE	Eph receptor B6	204718 at	-0.970	157	1.418E-08	FALSE
100608 at	0.069	4210	1422691 at	0.083	4427	100608 at	-0.048	6177	1422691 at	-0.354	534	3837	2371.5423	FALSE	serine palmitoyltransferase, long chain base subunit 1	202278 s at	-0.179	10092	1.057E-02	FALSE
95880 s at	0.118	3862	1426273 at	0.126	3200	95880 s at	-0.043	5906	1426272 at	0.165	2381	3837.25	1506.3301	FALSE	Limb region 1	224410 s at	-0.524	2474	9.153E-06	FALSE
161380 f at	0.061	4770	1431691 a at	-0.244	1163	161380 f at	0.091	4215	1431691 a at	-0.116	5204	3838	1828.6912	FALSE	RAB31, member RAS oncogene family	217763 s at	0.543	1205	7.315E-07	FALSE
94453 at	-0.222	1137	1449412 at	0.044	7053.5	94453 at	0.081	4423	1449412 at	0.173	2741	3838.625	2528.5354	FALSE	RIKEN cDNA 1810046J19 gene	224447 s at	-0.243	3549	4.941E-05	FALSE
160347 at	-0.046	6212	1423698 at	-0.093	4209	160347 at	-0.093	3082	1423698 at	0.165	1852	3838.75	1851.9581	FALSE	DNA segment, Chr 15, ERATO Doi 785, expressed	209718 at	0.070	21839	2.626E-01	FALSE
101998 at	0.022	7297	1419637 s at	0.179	2095.5	101998 at	-0.089	5532	1430220 at	0.474	435	3839.875	3133.2102	FALSE	RIKEN cDNA 4833420G17 gene	229886 at	-0.174	2125	4.732E-06	FALSE
98030 at	0.096	4681	1417961 a at	0.125	3690	98030 at	0.092	4489	1451860 a at	-0.764	2501	3840.25	990.60634	FALSE	tripartite motif protein 30	NA	NA	NA	NA	

97349 at	-0.413	31	1451264 at	-0.097	4086	97349 at	-0.082	4393	1457184 at	-0.137	6852	3840.5	2825.2993	TRUE	FERM domain containing 6	225481 at	0.758	919	3.654E-07	FALSE
100731 at	0.160	3770	1450373 at	0.138	2093	100731 at	0.103	4711	1450373 at	0.105	4789	3840.75	1253.814	TRUE	proline-rich protein 15	NA	NA	NA	NA	
94713 at	0.105	3312	1421385 a at	0.136	2464	94713 at	0.093	2416	1421385 a at	-0.100	7173	3841.25	2258.9687	FALSE	myosin VIIa	33197 at	0.079	16263	9.656E-02	FALSE
98069 s at	-0.221	964	1427897 s at	-0.062	6045	98069 s at	-0.067	6073	1427897 s at	0.168	2283	3841.25	2616.8641	FALSE	RIKEN cDNA 2400003N08 gene	224974 at	-0.103	20459	2.148E-01	FALSE
102907 at	0.143	1560	1454862 at	0.064	5839	102907 at	0.137	936	1454862 at	-0.057	7035	3842.5	3046.0694	FALSE	pleckstrin homology-like domain, family B, member 2	225688 s at	0.169	11866	2.445E-02	FALSE
92601 at	0.041	6034	1415777 at	0.135	3479	92601 at	0.149	1093	1415777 at	-0.087	4768	3843.5	2109.5893	FALSE	pancreatic lipase related protein 1	210722 at	0.012	39755	8.711E-01	FALSE
101424 at	0.175	1465	1425719 a at	0.188	886	101424 at	-0.016	7687	1425719 a at	-0.199	5337	3843.75	3235.5887	FALSE	N-myc (and STAT) interactor	203964 at	0.280	7719	2.701E-03	FALSE
160510 f at	0.175	2240	1422454 at	0.067	5387	100109 s at	0.125	1469	1422454 at	0.058	6281	3844.25	2347.5703	TRUE	keratin complex 1, acidic, gene 13	207935 s at	0.006	41488	9.203E-01	FALSE
100348 at	-0.082	4040	1456319 at	-0.130	3671.5	100348 at	0.046	6644	1456319 at	-0.761	1023	3844.625	2299.7255	FALSE	hypothetical protein LOC665081	NA	NA	NA	NA	
99392 at	-0.098	3545	1450829 at	0.079	5817	99392 at	-0.162	1215	1433699 at	0.118	4805	3845.5	1984.7152	FALSE	tumor necrosis factor, alpha-induced protein 3	202644 s at	0.273	7939	3.151E-03	FALSE
93548 at	-0.175	2174	1417083 at	0.128	6143	93548 at	0.151	1011	1417083 at	0.103	6054	3845.5	2644.7609	FALSE	Sec61 beta subunit	244700 at	-0.051	22828	2.959E-01	FALSE
99663 g at	-0.091	4185	1437520 a at	0.068	4650.5	99662 at	0.095	3245	1437520 a at	-0.186	3304	3846.125	687.29086	FALSE	nucleoporin 85	218014 at	0.124	20188	2.065E-01	FALSE
96493 at	0.131	2093	1424094 at	-0.060	6136	96493 at	-0.043	5665	1460744 at	0.206	1496	3847.5	2390.8409	FALSE	NIMA (never in mitosis gene a)-related expressed kinase 9	231316 at	0.262	2151	4.921E-06	FALSE
97740 at	0.079	4552	1418401 a at	0.021	7776	97740 at	0.403	58	1418401 a at	0.183	3007	3848.25	3214.3522	TRUE	dual specificity phosphatase 16	224832 at	0.213	6672	1.210E-03	TRUE
94506 at	-0.046	7300	1417681 at	0.178	1481	94506 at	0.243	603	1455966 s at	-0.547	6010	3848.5	3302.6889	FALSE	nudix (nucleoside diphosphate linked moiety X)-type motif 21	213461 at	-0.178	12308	2.931E-02	FALSE
160634 at	-0.133	1645	1428751 at	0.058	6469	160634 at	0.140	1728	1428751 at	0.143	5553	3848.75	2524.8282	FALSE	Park2 co-regulated	243122 at	0.202	8449	4.220E-03	FALSE
103835 f at	-0.090	3131	1448812 at	-0.151	2075	103835 f at	-0.075	3578	1448812 at	0.124	6614	3849.5	1947.7564	FALSE	hippocalcin-like 1	NA	NA	NA	NA	
99053 at	-0.023	7411	1448862 at	0.040	6912	99053 at	-0.165	981	1448862 at	-0.428	95	3849.75	3846.5461	FALSE	intercellular adhesion molecule 2	213620 s at	0.405	6036	7.153E-04	FALSE
96728 at	-0.107	3132	1424786 s at	0.122	1639.5	96728 at	-0.048	5907	1451754 a at	0.104	4722	3850.125	1861.3138	FALSE	WD repeat domain 45	215553 x at	0.224	5159	3.211E-04	FALSE
95048 at	0.100	3871	1420884 at	0.122	2578	95048 at	-0.075	6145	1420884 at	-0.674	2810	3851	1629.6263	FALSE	sarcolipin	NA	NA	NA	NA	
104360 at	0.040	6755	1460735 at	-0.119	2536	104360 at	-0.039	6027	1460694 s at	-0.414	88	3851.5	3112.2117	FALSE	supervillin	202565 s at	0.155	9645	8.401E-03	FALSE
161259 f at	0.155	1425	1418813 at	0.080	3955.5	101187 at	0.094	2365	1418813 at	-0.029	7661	3851.625	2745.948	FALSE	serine (or cysteine) peptidase inhibitor, clade A, member 5	209443 at	0.296	6749	1.278E-03	FALSE
95531 at	0.126	3901	1427584 at	0.092	3339.5	95531 at	-0.067	4409	1454890 at	-0.143	3761	3852.625	441.05392	FALSE	angiomotin	NA	NA	NA	NA	
93994 at	0.050	6844	1435446 a at	-0.233	891	93994 at	-0.202	1413	1435446 a at	-0.110	6268	3854	3136.0987	FALSE	choline phosphotransferase 1	221675 s at	0.246	9509	7.795E-03	FALSE
101610 at	0.153	1546	1449685 s at	0.062	5478	101610 at	-0.023	7249	1419973 at	-0.228	1143	3854	2991.086	FALSE	3-oxoacyl-ACP synthase, mitochondrial	219133 at	-0.073	17374	1.237E-01	FALSE
101225 at	0.133	3223	1448085 at	0.135	1781.5	101225 at	-0.109	2953	1448085 at	0.046	7460	3854.375	2483.8447	FALSE	DNA segment, Chr 5, ERATO Doi 102, expressed	NA	NA	NA	NA	
160994 at	-0.250	568	1433756 at	-0.043	7232	160994 at	-0.068	6562	1433756 at	-0.530	1060	3855.5	3528.3788	TRUE	S100P binding protein	218370 s at	-0.144	15407	7.805E-02	FALSE
161666 f at	-0.296	316	1449773 s at	0.097	3626.5	161666 f at	-0.078	5322	1420197 at	0.090	6161	3856.375	2584.9855	FALSE	growth arrest and DNA-damage-inducible 45 beta	207574 s at	0.315	21294	2.432E-01	FALSE
93446 at	0.120	2380	1422954 at	-0.039	6464.5	93446 at	-0.069	6072	1430187 at	0.352	514	3857.625	2890.3551	FALSE	zinc finger protein 60	NA	NA	NA	NA	
98072 r at	-0.123	2491	1428838 a at	-0.089	4234	98071 f at	0.096	3685	1428838 a at	0.109	5021	3857.75	1063.4163	FALSE	deoxycytidine kinase	203302 at	-0.367	3187	2.970E-05	FALSE
161313 at	0.088	3534	1422612 at	-0.023	7798	161313 at	-0.118	1680	1422612 at	-0.290	2421	3858.25	2734.79	FALSE	hexokinase 2	202934 at	0.140	17136	1.179E-01	FALSE
98464 at	-0.151	3974	1435322 at	-0.138	1567.5	98464 at	0.176	3177	1435322 at	-0.047	6715	3858.375	2151.4379	FALSE	RIKEN cDNA 1110011C06 gene	NA	NA	NA	NA	
92366 at	0.084	3680	1426285 at	0.050	5587	92366 at	0.172	1268	1426285 at	0.124	4901	3859	1898.8655	TRUE	laminin, alpha 2	213519 s at	0.318	448	8.445E-08	TRUE
102964 at	-0.025	7472	1424237 at	0.156	1951	102964 at	0.227	2267	1424237 at	0.132	3747	3859.25	2532.5376	FALSE	zinc finger protein 639	222623 s at	-0.089	23077	3.040E-01	FALSE
162134 r at	0.091	4135	1435089 at	0.068	5439.5	97933 at	-0.086	2686	1458947 at	-0.454	3177	3859.375	1213.1514	FALSE	RIKEN cDNA 2010111I01 gene	233599 at	0.444	3646	5.658E-05	FALSE
160458 at	-0.049	6160	1416357 a at	-0.139	4172.5	160458 at	0.078	3081	1416357 a at	-0.250	2029	3860.625	1765.1305	FALSE	melanoma cell adhesion molecule	211042 x at	0.186	6157	7.956E-04	FALSE
96184 at	-0.063	4720	1454753 at	-0.035	6438	96184 at	0.106	3345	1454753 at	-0.233	941	3861	2321.7426	FALSE	arginyl aminopeptidase (aminopeptidase B)-like 1	218301 at	-0.008	41962	9.343E-01	FALSE
104108 at	-0.087	5785	1424015 at	-0.193	1642.5	104108 at	0.109	3926	1424015 at	-0.120	4091	3861.125	1701.0431	FALSE	Rab6 interacting protein 1	212561 at	0.327	2362	7.567E-06	FALSE
93001 at	-0.097	3320	1427701 a at	0.081	5298	93000 g at	0.086	2840	1439753 x at	-0.123	3987	3861.25	1067.0781	FALSE	sine oculis-related homeobox 4 homolog (Drosophila)	229796 at	0.102	15963	9.025E-02	FALSE
102577 at	-0.105	2487	1421790 a at	-0.125	2635.5	102577 at	0.040	6790	1421790 a at	0.192	3534	3861.625	2006.298	FALSE	potassium voltage-gated channel, shaker-related subfamily, beta member 3	221413 at	-0.034	29264	5.302E-01	FALSE
103243 at	0.041	6383	1433670 at	-0.172	2584	103243 at	-0.218	791	1425273 s at	-0.104	5693	3862.75	2631.37	FALSE	epithelial membrane protein 2	225078 at	0.349	1895	3.214E-06	FALSE
100395 at	0.094	5122	1446086 s at	0.067	5541	100395 at	0.112	2201	1446086 s at	-0.263	2589	3863.25	1711.343	FALSE	GLI-Kruppel family member GLI2	207034 s at	0.127	7764	2.789E-03	FALSE
92656 at	0.077	3568	1436382 at	-0.006	8344.5	92656 at	-0.135	1364	1436382 at	0.301	2184	3865.125	3121.6924	FALSE	zinc finger and BTB domain containing 12	233843 at	0.029	32022	6.324E-01	FALSE
92697 at	0.096	4594	1418496 at	0.204	1020	92697 at	0.143	1751	1418496 at	0.022	8099	3866	3215.65	TRUE	forkhead box A1	204667 at	0.071	16104	9.301E-02	FALSE
161754 f at	0.379	1078	1416205 at	0.006	8280.5	161754 f at	0.058	4533	1416205 at	0.280	1574	3866.375	3314.5591	TRUE	galactosidase, beta 1	201576 s at	0.036	30934	5.918E-01	FALSE
160759 at	-0.086	3612	1417503 at	0.109	2181	160759 at	0.054	5269	1457638 x at	0.158	4406	3867	1311.9637	FALSE	replication factor C (activator 1) 2	203696 s at	-0.072	16028	9.152E-02	FALSE
93506 at	0.059	4829	1416300 a at	-0.059	5204	93506 at	0.054	4419	1416300 a at	0.224	1020	3868	1925.5408	FALSE	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	200030 s at	-0.259	8235	3.779E-03	FALSE
100602 at	0.074	4147	1416089 at	0.117	3353	100602 at	0.120	1801	1416089 at	0.072	6171	3868	1818.3659	TRUE	ribosomal protein S15	NA	NA	NA	NA	
98594 at	-0.098	5485	1433581 at	0.146	2631	98594 at	0.160	4384	1433582 at	0.217	2974	3868.5	1317.8706	FALSE	RIKEN cDNA 1190002N15 gene	226464 at	0.484	3176	2.924E-05	FALSE
95137 at	-0.164	831	1416376 at	0.070	4219	95137 at	0.024	6871	1416376 at	0.170	3553	3868.5	2480.8468	FALSE	transmembrane protein 97	212279 at	-0.139	12021	2.619E-02	FALSE
94504 at	0.151	1081	1450410 a at	-0.160	1752	94504 at	-0.042	5556	1450409 a at	-0.043	7087	3869	2912.9668	FALSE	RIKEN cDNA 4930570C03 gene	NA	NA	NA	NA	
99045 at	-0.314	626	1418829 a at	-0.156	1882	99045 at	-0.091	6063	1418829 a at	-0.044	6907	3869.5	3082.6556	TRUE	enolase 2, gamma neuronal	201313 at	-0.679	1912	3.314E-06	TRUE
93732 f at	-0.079	4039	1422763 at	-0.012	8249	93732 f at	0.176	686	1422763 at	0.274	2504	3869.5	3225.3172	FALSE	GIPC PDZ domain containing family, member 1	207525 s at	-0.075	19554	1.865E-01	FALSE
92941 at	0.075	3788	1436187 at	0.170	1210	92941 at	-0.002	8386	1436187 at	-0.166	2097	3870.25	3194.7931	FALSE	RIKEN cDNA 1110054M08 gene	NA	NA	NA	NA	
103609 at	0.179	1370	1422652 at	0.056	5966	103609 at	0.077	5505	1454333 at	-0.201	2641	3870.5	2223.127	FALSE	crystallin, gamma A	207587 at	-0.011	40183	8.824E-01	FALSE
162415 f at	-0.034	6507	1433709 at	-0.121	2546.5	162415 f at	0.063	4477	1421476 a at	0.201	1955	3871.375	2060.8322	FALSE	calcium activated nucleotidase 1	46323 at	0.057	21680	2.572E-01	FALSE
98867 at	0.116	3495	1427563 at	0.147	1710	97654 at	0.209	2934	1427563 at	0.062	7349	3872	2434.868	TRUE	distal-less homeobox 6, antisense	NA	NA	NA	NA	
93088 at	-0.257	6103	1449289 a at	0.219	3631	93088 at	0.251	1938	1449289 a at	-0.502	3819	3872.75	1710.6144	FALSE	beta-2 microglobulin	201891 s at	0.138	20918	2.310E-01	FALSE
93453 at	0.078	4378	1448996 at	-0.058	5413	161525 f at	0.241	197	1448996 at	0.168	5506	3873.5	2503.7498	FALSE	rod outer segment membrane protein 1	205806 at	0.309	6150	7.924E-04	FALSE
94088 at	0.354	928	1423471 at	0.076	5489	94088 at	-0.091	4769	1423471 at	0.102	4308	3873.5	2022.9122	FALSE	polypyrimidine tract binding protein 2	218683 at	0.045	35103	7.333E-01	FALSE
96522 at	-0.059	5927	1417366 s at	-0.207	1776	96522 at	0.045	5287	1433592 at	-0.221	2505	3873.75	2040.1914	FALSE	calmodulin 1	211984 at	-0.462	920	3.660E-07	FALSE
102759 at	-0.189	620	1418463 at	-0.060	5250	102759 at	-0.038	7206	1418463 at	-0.187	2424	3875	2926.1244	TRUE	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	207105 s at	-0.211	7199	1.870E-03	TRUE
93539 at	-0.231	1158	1452586 at	0.137	2453	93539 at	0.144	3517	1452586 at	-0.009	8373	3875.25	3149.8328	FALSE	anaphase promoting complex subunit 13	215282 at	-0.033	22836	2.961E-01	FALSE
101293 at	0.075	4330	1422326 at	0.078	5018	101293 at	0.121	2400	1422326 at	0.150	3754	3875.5	1111.1164	TRUE	glucose-6-phosphate dehydrogenase 2	NA	NA	NA	NA	
161885 f at	-0.100	5035	1428737 s at	0.042	6659	93484 at	-0.106	2586	1428736 at	-0.236	1225	3876.25	2434.4932	FALSE	GRAM domain containing 3	238049 at	0.834	239	2.611E-08	FALSE
96658 at	-0.035	7197	1433480 at	0.243	1020	96658 at	0.070	5330	1433480 at	0.400	1959	3876.5	2885.295	FALSE	RIKEN cDNA 2900010J23 gene	232218 at	-0.046	23144	3.067E-01	FALSE
104757 at	0.007	8133	1424891 a at	0.158	963	104757 at	-0.072	3364	1431747 at	0.147	3051	3877.75	3030.4221	FALSE	ZW10 homolog (Drosophila), centromere/kinetochore protein	204812 at	0.017	37332	8.002E-01	FALSE
104565 at	-0.158	3011	1451665 a at	0.128	2680	104565 at	0.161	1900	1451665 a at	0.024	7920	3877.75	2734.7846	FALSE	adaptor-related protein complex AP-4, sigma 1	NA	NA	NA	NA	
99977 at	0.081	4898	1450682 at	0.155	1071.5	160886 i at	0.146	1227	1450682 at	0.007	8317	3878.375	3447.1903	TRUE	fatty acid binding protein 6, ileal (gastrotropin)	210445 at	-0.323	4328	1.252E-04	FALSE
96254 at	0.058	6439	1416756 at	-0.150	3661	96254 at	0.125	3672	1416755 at	0.248	1744	3879	1932.3732	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 1	200666 s at	0.442	14691	6.499E-02	FALSE
92387 at	0.089	3558	1416827 at	0.055	5906	162136 r at	0.201	523	1416827 at	-0.132	5530	3879.25	2463.0812	FALSE	thromboxane A synthase 1, platelet	236345 at	-0.039	29080	5.236E-01	FALSE
98890 at	-0.153	1295	1452919 a at	-0.045	6239	98890 at	0.074	3570	1452919 a at	0.124	4416	3880	2051.8692	FALSE	RIKEN cDNA 1700012G19 gene	NA	NA	NA	NA	
104010 at	0.119	2587	1452610 at	0.095	2619	104010 at	0.002	8412	1443495 at	-0.186	1903	3880.25	3039.1623	FALSE	zinc finger protein 99	214714 at	0.066	19599	1.873E-01	FALSE
94643 at	0.032	7200	1423904 a at	0.327	77.5	94643 at	-0.086	4442	1423905 at	0.157	3804	3880.875	2932.7475	FALSE	poliovirus receptor	NA	NA	NA	NA	
160436 at	0.021	7234	1430388 a at	-0.206	491	160436 at	0.065	5760	1447602 x at	0.231	2041	3881.5	3143.8272	FALSE	sulfatase 2	233555 s at	-0.124	16724	1.067E-01	FALSE
93970 at	-0.062	5910	1454955 at	-0.059	5694.5	93970 at	0.200	2144	1458165 at	0.191	1778	3881.625	2224.5149	FALSE	importin 7	200995 at	0.141	14364	5.923E-02	FALSE
103544 at	0.097	2995	1418869 a at	0.080	3509	103544 at	0.040	5442	1418869 a at	0.186	3583	3882.25	1072.2094	TRUE	pseudouridine synthase 1	218670 at	-0.095	20846	2.279E-01	FALSE
95288 i at	0.123	5359	1437216 at	0.064	6726	95288 i at	-0.260	374	1437216 at	0.133	3072	3882.75	2782.8059	FALSE	RIKEN cDNA A430106J12 gene	219387 at	0.336	7227	1.902E-03	FALSE
96752 at	-0.155	2011	1424067 at	0.030	7703.5	96752 at	0.129	1059	1424067 at	-0.178	4758	3882.875	2991.1651	FALSE	intercellular adhesion molecule	202637 s at	0.135	13622	4.564E-02	FALSE
103299 at	0.140	4380	1433678 at	-0.012	8169	162043 i at	0.151	1542	1433678 at	-0.516	1441	3883	3165.4621	FALSE	phospholipase D family, member 4	235802 at	-0.007	42238	9.404E-01	FALSE
95002 at	-0.384	192	1460741 x at	-0.123	4151.5	95002 at	-0.092	4487	1439182 at	-0.055	6705	3883.875	2709.4938	TRUE	DNA segment, Chr 17, Wayne State University 92, expressed	217924 at	-0.188	4922	2.488E-04	TRUE
92636 f at	0.071	6851	1423090 x at	0.367	1333	92636 f at	0.514	846	1423090 x at	0.097	6507	3884.25	3236.2665	TRUE	SEC61, gamma subunit	203484 at	-0.046	36820	7.863E-01	FALSE
95121 at	-0.035	7171	1423372 at	0.254	493	95122 g at	-0.065	5677	1423372 at	0.231	2197	3884.5	3074.8478	FALSE	polymerase (DNA-directed), epsilon 4 (p12 subunit)	225844 at	-0.268	3818	6.822E-05	FALSE
103010 at	0.045	6991	1429041 at	0.057	5899	161462 r at	0.203	2431	1440184 at	-0.504	224	3886.25	3120.922	FALSE	RIKEN cDNA 2610005L07 gene	NA	NA	NA	NA	
94419 at	0.102	2388	1448132 at	0.136	1677	94419 at	0.024	6853	1420138 at	0.098	4628	3886.5	2343.5967	TRUE	solute carrier family 19 (sodium/hydrogen exchanger), member 1	211576 s at	0.096	16136	9.376E-02	FALSE
161882 f at	-0.125	1675	1433799 at	0.123	3818	94765 at	0.131	1917	1433799 at	0.023	8136	3886.5	2990.6858	FALSE	Retinol dehydrogenase 13 (all-trans and 9-cis)	225449 at	-0.071	16414	9.987E-02	FALSE
161073 at	-0.128	1735	1427057 at	-0.101	3274	161073 at	-0.058	5549	1443558 s at	0.123	4990	3887	1730.6767	FALSE	RIKEN cDNA C630002B14 gene	NA	NA	NA	NA	
101844 at	-0.055	5067	1449374 at	-0.157	1544	101844 at	-0.060	5595	1449374 at	-0.207	3345	3887.75	1834.2187	TRUE	pipecolic acid oxidase	221605 s at	0.109	14172	5.560E-02	FALSE
100718 at	-0.150	3884	1423455 at	-0.218	1414.5	100718 at	-0.176	3467	1423455 at	-0.092	6786	3887.875	2213.1323	TRUE	prothymosin alpha	211921 x at	0.622	507	1.077E-07	FALSE
98392 at	-0.198	963	1449911 at	0.036	7130	98392 at	-0.038	6195	1449911 at	-0.515	1267	3888.75	3227.9032	FALSE	lymphocyte-activation gene 3	206486 at	0.020	36079	7.652E-01	FALSE
102038 at	-0.144	1977	1450251 a at	0.023	7489	102038 at	0.066	4002	1450251 a at	0.333	2091	3889.75	2573.0212	FALSE	ligand of numb-protein X 1	223611 s at	-1.073	320	4.376E-08	FALSE
95528 at	0.110	3468	1419840 at	0.090	2977	95528 at	0.137	2683	1419840 at	0.075	6432	3890	1725.3276	TRUE	expressed sequence AI507495	NA	NA	NA	NA	
98993 at	-0.121	4229	1434205 at	-0.302	440	98993 at	-0.015	7992	1425725 s at	0.154	2901	3890.5	3152.8794	FALSE	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	214083 at	0.161	8037	3.338E-03	FALSE
95782 at	0.213	2229	1450293 at	0.062	5528	95782 at	-0.040	6488	1450293 at	-0.225	1317	3890.5	2504.1231	FALSE	melanoma antigen, family B, 3	NA	NA	NA	NA	
99096 at	-0.176	2903	1415713 a at	-0.103	4285.5	99096 at	-0.089	6457	1441631 at	-0.225	1917	3890.625	1967.4692	TRUE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	200694 s at	-0.211	8909	5.476E-03	TRUE
100529 at	0.143	1186	1418631 at	-0.082	5017	100529 at	-0.087	5129	1428791 at	0.110	4231	3890.75	1846.9023	FALSE	ubiquitin-conjugating enzyme E2H	222421 at	0.209	5516	4.519E-04	FALSE
93740 at	-0.074	6090	1418624 at	-0.257	1221.5	93740 at	0.044	5476	1430720 at	0.214	2777	3891.125	2288.7444	FALSE	Y box protein 1	208628 s at	0.239	8361	4.069E-03	FALSE
94246 at	-0.147	3334	1416268 at	-0.117	3821	94246 at	0.177	3287	1437809 x at	0.080	5123	3891.25	855.91837	FALSE	E26 avian leukemia oncogene 2, 3' domain	201328 at	0.273	9607	8.212E-03	FALSE
103742 at	0.066	4428	1419592 at	-0.070	5023.5	103742 at	-0.053	5284	1439174 at	-0.975	831	3891.625	2071.6316	FALSE	unc-5 homolog C (C. elegans)	206189 at	0.077	15174	7.408E-02	FALSE
98610 at	-0.184	1061	1452585 at	0.199	1484	98610 at	0.050	5778	1452585 at	0.050	7249	3893	3089.7393	FALSE	mitochondrial ribosomal protein S28	237854 at	0.094	12448	3.087E-02	FALSE
100886 f at	-0.221	2248	1423492 at	0.092	4847	100886 f at	0.194	1533	1423492 at	0.050	6945	3893.25	2483.3073	FALSE	mitochondrial ribosomal protein L45	224479 s at	-0.163	9955	9.880E-03	FALSE
104293 at	-0.089	2996	1428081 at	-0.044	6525	104293 at	-0.122	1582	1428081 at	-0.154	4473	3894	2114.1704	TRUE	kelch-like 21 (Drosophila)	203068 at	0.355	2515	9.809E-06	FALSE
92203 s at	-0.195	859	1451910 a at	0.031	7401	92203 s at	-0.107	2653	1451910 a at	0.128	4666	3894.75	2807.51	FALSE	CD6 antigen	213958 at	0.051	23511	3.206E-01	FALSE
160897 at	-0.044	6361	1424460 s at	0.093	2970.5	160897 at	-0.055	5343	1424459 at	0.246	907	3895.375	2446.8145	FALSE	acyltransferase like 2	241511 at	-0.064	23755	3.294E-01	FALSE
103616 at	-0.131	2265	1423578 at	-0.087	4882.5	103616 at	0.048	5530	1423578 at	-0.315	2908	3896.375	1557.7166	FALSE	procollagen, type XI, alpha 2	213870 at	0.055	25531	3.897E-01	FALSE
101873 at	0.154	1313	1425750 a at	-0.009	8230	101873 at	0.098	3499	1425750 a at	-0.153	2545	3896.75	3024.2494	FALSE	Janus kinase 3	227677 at	0.088	20272	2.090E-01	FALSE
161427 f at	0.046	7045	1417878 at	0.112	3076	161427 f at	0.126	1350	1447840 x at	0.147	4121	3898	2388.9556	TRUE	E2F transcription factor 1	2028 s at	0.048	23665	3.262E-01	FALSE
100061 f at	0.128	2535	1448107 x at	0.153	3759	100061 f at	0.114	3342	1448107 x at	-0.106	5957	3898.25	1463.5239	FALSE	kallikrein 1	NA	NA	NA	NA	
162316 f at	0.068	5175	1418295 s at	0.039	7258.5	104371 at	0.092	3008	1445229 at	0.694	152	3898.375	3041.2884	TRUE	diacylglycerol O-acyltransferase 1	203669 s at	-0.034	31893	6.272E-01	FALSE
160255 at	0.091	4583	1452217 at	-0.082	4307	160255 at	-0.068	6561	1452217 at	-0.475	144	3898.75	2696.9482	FALSE	AHNAK nucleoprotein (desmoyokin)	211986 at	0.759	114	9.854E-09	FALSE
100773 at	0.077	4569	1425454 a at	0.153	3224	100773 at	0.084	3479	1425454 a at	0.139	4325	3899.25	648.69118	TRUE	interleukin 12a	207160 at	0.025	33295	6.752E-01	FALSE
161928 at	0.037	7087	1453089 at	0.168	2307.5	161928 at	0.074	4233	1453089 at	0.203	1970	3899.375	2347.2546	TRUE	RIKEN cDNA 3110079O15 gene	232299 at	0.280	6367	9.568E-04	TRUE
93493 at	0.465	982	1433809 at	0.170	1431.5	93493 at	0.010	8204	1454793 x at	-0.159	4982	3899.875	3381.4867	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	200033 at	0.187	16213	9.562E-02	FALSE
98763 at	0.064	4718	1427644 at	-0.130	3034	98763 at	-0.025	7011	1427644 at	0.328	837	3900	2612.7489	FALSE	DNA segment, KIST 4	NA	NA	NA	NA	
95881 f at	0.243	2074	1419236 at	0.145	2635.5	95400 i at	0.027	6997	1419235 s at	-0.157	3894	3900.125	2200.3546	FALSE	helicase (DNA) B	NA	NA	NA	NA	
160672 at	0.196	2145	1423612 at	0.066	4828.5	160672 at	-0.258	202	1423612 at	0.005	8429	3901.125	3565.0702	FALSE	expressed sequence AI462438	229496 at	-0.054	21722	2.593E-01	FALSE
160066 at	0.192	502	1422731 at	-0.102	4565	160066 at	0.030	6229	1422731 at	-0.147	4310	3901.5	2420.8099	FALSE	LIM domains containing 1	222762 x at	0.245	5309	3.672E-04	FALSE
93781 at	0.141	2495	1416460 at	0.088	3679	93781 at	-0.036	5768	1416460 at	0.145	3671	3903.25	1361.9458	FALSE	myo-inositol oxygenase	224179 s at	-0.021	32500	6.472E-01	FALSE
102114 f at	0.097	3531	1417130 s at	0.114	3271.5	96118 at	0.105	2405	1453410 at	0.055	6408	3903.875	1737.4504	TRUE	angiopoietin-like 4	221009 s at	0.300	15701	8.400E-02	FALSE
92493 at	0.146	1926	1421956 at	0.090	3709	92493 at	-0.016	7724	1421956 at	0.171	2257	3904	2661.7988	FALSE	recombining binding protein suppressor of hairless-like (Drosophila)	221377 s at	-0.013	39757	8.711E-01	FALSE
96353 at	-0.301	609	1416479 a at	0.069	4870	96353 at	-0.047	5862	1416479 a at	-0.099	4278	3904.75	2292.2928	FALSE	transmembrane protein 14C	223106 at	0.251	9482	7.723E-03	FALSE
98873 at	0.068	4833	1420595 at	0.082	5125	98873 at	-0.079	4610	1427641 at	-0.340	1051	3904.75	1914.1512	FALSE	distal-less homeobox 4	210259 s at	-0.059	27640	4.672E-01	FALSE
160934 s at	-0.054	6491	1451626 x at	0.106	4243.5	160934 s at	-0.826	355	1451626 x at	-0.555	4530	3904.875	2568.7288	FALSE	Gag	NA	NA	NA	NA	
96761 at	0.095	5165	1416596 at	0.116	3238	162285 r at	0.211	1703	1416596 at	0.095	5514	3905	1776.7174	TRUE	solute carrier family 44, member 4	205597 at	-0.007	41234	9.137E-01	FALSE
95095 at	-0.002	8448	1448559 at	0.123	2700	95095 at	0.136	4090	1448559 at	0.303	383	3905.25	3392.6186	FALSE	flotillin 1	213819 s at	0.058	21924	2.658E-01	FALSE
100780 at	0.167	4947	1416276 a at	0.246	1936.5	100780 at	0.106	2693	1416276 a at	-0.061	6045	3905.375	1915.6635	FALSE	ribosomal protein S4, X-linked	213347 x at	0.113	13561	4.482E-02	FALSE
98486 at	-0.323	394	1418105 at	-0.083	3736.5	98486 at	0.088	4863	1418105 at	0.068	6632	3906.375	2627.4067	FALSE	stathmin-like 4	221236 s at	-0.076	35518	7.466E-01	FALSE
100747 at	0.209	521	1420155 at	0.067	5508	100747 at	0.094	4584	1420155 at	-0.088	5013	3906.5	2288.359	FALSE	expressed sequence AA408954	NA	NA	NA	NA	

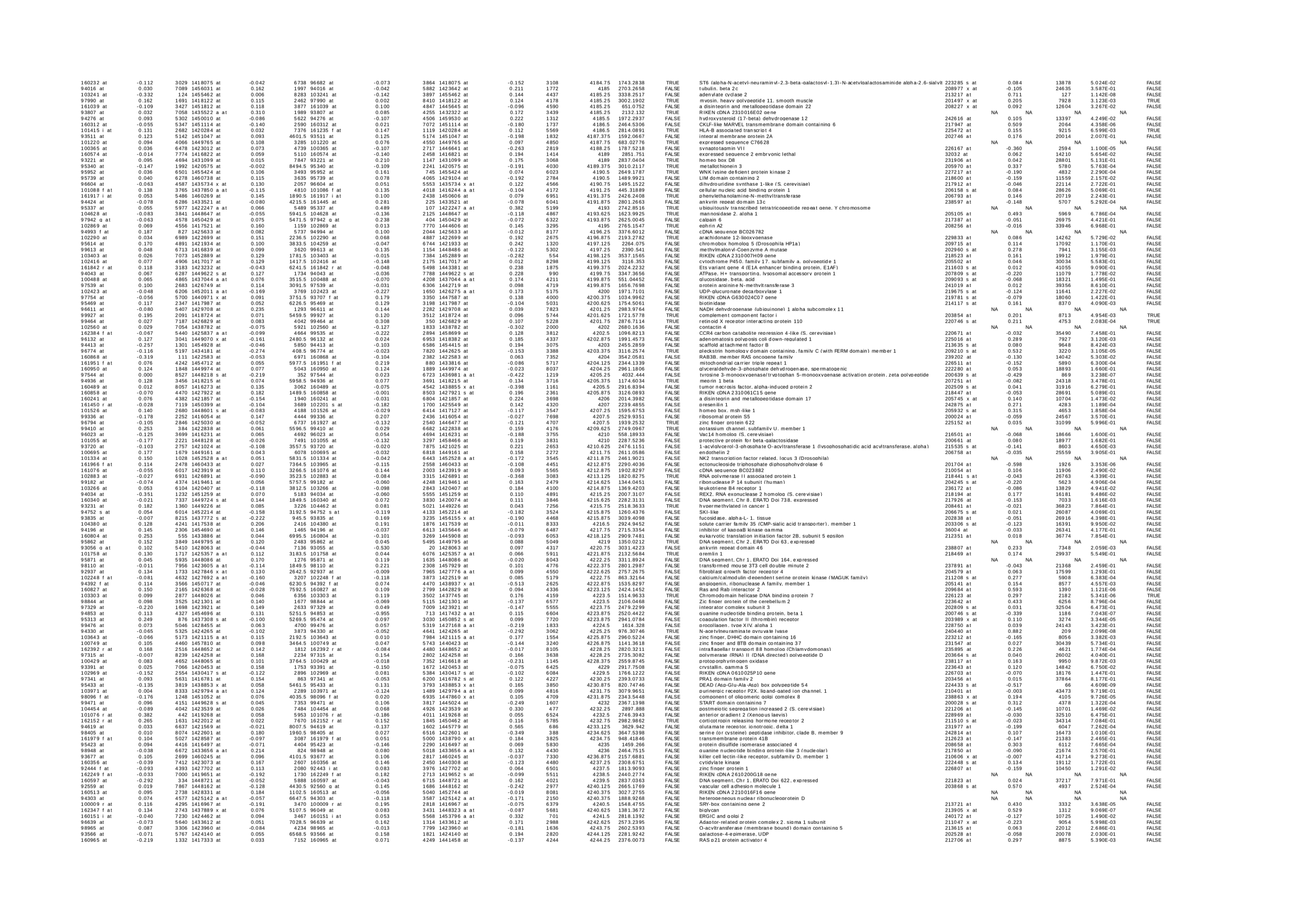
98322 at	0.131	1460	1450395 at	0.058	6034	98322 at	0.029	7025	1450395 at	-0.265	1111	3907.5	3057.8575	FALSE	solute carrier family 22 (organic cation transporter), member 5	205074 at	0.253	4263	1.165E-04	FALSE
102053 at	0.039	6175	1448961 at	0.084	3252	102053 at	0.078	3794	1448961 at	-0.191	2411	3908	1614.8922	FALSE	phospholipid scramblase 2	NA	NA	NA	NA	
96945 at	0.040	6384	1420897 at	-0.102	3684.5	96945 at	0.105	1897	1420898 at	-0.148	3672	3909.375	1851.1562	FALSE	synaptosomal-associated protein 23	209130 at	0.611	3132	2.740E-05	FALSE
100505 at	0.484	351	1448125 at	0.131	3529	102083 at	-0.099	3769	1460166 at	0.025	7990	3909.75	3134.641	FALSE	Ras-like without CAAX 2	206984 s at	-0.991	283	3.396E-08	FALSE
95482 at	-0.192	2133	1419920 s at	-0.011	8086.5	95481 at	-0.084	2782	1454948 at	0.152	2640	3910.375	2797.9853	FALSE	ubiquitin specific peptidase 7	201498 at	0.111	21271	2.426E-01	FALSE
95427 at	0.182	961	1423293 at	0.099	3727.5	95427 at	-0.068	5675	1441240 at	-0.127	5279	3910.625	2138.4801	FALSE	replication protein A1	201528 at	0.238	9277	6.874E-03	FALSE
93884 at	0.099	2625	1425582 a at	0.051	6400	93884 at	-0.056	4859	1425582 a at	-0.211	1760	3911	2111.431	FALSE	endomucin	222885 at	0.187	15459	7.894E-02	FALSE
160395 at	-0.182	2772	1449140 at	0.059	6342	160395 at	0.080	4587	1418566 s at	0.209	1944	3911.25	1960.7096	FALSE	NudC domain containing 2	226643 s at	0.050	24418	3.515E-01	FALSE
160278 at	-0.140	2859	1418702 a at	0.276	488.5	160278 at	0.065	4245	1418702 a at	0.019	8053	3911.375	3166.9086	FALSE	RIKEN cDNA 2810428I15 gene	NA	NA	NA	NA	
160591 at	0.085	4775	1418967 a at	0.079	5001.5	160591 at	-0.049	5331	1418967 a at	0.287	539	3911.625	2259.9756	FALSE	Suppression of tumorigenicity 7	207871 s at	0.190	10180	1.114E-02	FALSE
100748 at	0.060	4933	1446971 at	0.087	3824	100748 at	0.099	2850.5	1446971 at	0.132	4039	3911.625	855.00403	TRUE	DNA segment, Chr 10, Wayne State University 159, expressed	NA	NA	NA	NA	
94425 at	-0.194	4527	1422903 at	0.118	3601	94425 at	0.167	1790	1422903 at	-0.291	5729	3911.75	1661.2564	FALSE	lymphocyte antigen 86	205859 at	0.133	17248	1.207E-01	FALSE
99974 at	0.111	3455	1450185 a at	0.107	3611	99974 at	0.091	2728	1435354 at	-0.080	5853	3911.75	1350.1588	FALSE	potassium inwardly-rectifying channel, subfamily J, member 15	211806 s at	0.041	29280	5.308E-01	FALSE
95076 at	-0.145	3218	1452584 at	0.156	986.5	95076 at	0.034	6294	1452584 at	0.114	5149	3911.875	2326.9636	FALSE	RIKEN cDNA 1500032L24 gene	225795 at	-0.279	6532	1.073E-03	FALSE
98079 at	0.136	1521	1450725 s at	-0.195	1771	98079 at	0.041	6534	1450725 s at	-0.163	5822	3912	2634.625	FALSE	carbonic anhydrase 14	219464 at	-0.081	23568	3.227E-01	FALSE
97900 at	-0.107	4610	1436951 x at	0.303	637	97900 at	0.067	6737	1436108 at	-0.175	3665	3912.25	2533.4076	FALSE	thioredoxin domain containing 9	211758 x at	-0.171	17816	1.357E-01	FALSE
95972 at	0.257	699	1459891 at	-0.071	4684	95972 at	-0.107	2289	1459891 at	0.026	7977	3912.25	3166.3705	FALSE	expressed sequence C78444	NA	NA	NA	NA	
99140 at	-0.175	2783	1450880 at	0.098	3339.5	99140 at	0.065	5534	1450880 at	0.155	3994	3912.625	1188.8375	FALSE	mitochondrial ribosomal protein L16	217980 s at	0.028	33403	6.784E-01	FALSE
92186 at	-0.023	7481	1420926 at	-0.129	1578	92186 at	0.063	3775	1420926 at	0.192	2817	3912.75	2543.1679	FALSE	aristaless related homeobox gene (Drosophila)	231020 at	0.061	23351	3.147E-01	FALSE
160443 at	0.064	4555	1415835 at	0.059	6018	160443 at	0.165	2944	1415835 at	0.173	2134	3912.75	1726.9425	TRUE	chorionic somatomammotropin hormone 2	NA	NA	NA	NA	
160269 at	0.019	7330	1426995 a at	0.095	2755	160269 at	0.107	1881	1426995 a at	0.136	3686	3913	2394.2574	TRUE	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	204660 at	-0.084	19152	1.734E-01	FALSE
101909 f at	0.120	3623	1427631 x at	-0.048	5613	101910 f at	0.134	2562	1427631 x at	0.133	3855	3913.25	1265.2621	FALSE	major urinary protein 3	NA	NA	NA	NA	
99502 at	-0.254	645	1449068 at	-0.046	5982	99502 at	-0.012	7924	1441701 at	0.434	1104	3913.75	3602.739	FALSE	zinc finger protein 148	203318 s at	0.200	12157	2.752E-02	FALSE
160665 at	-0.057	5844	1417678 at	-0.142	1960.5	160665 at	-0.058	5630	1417678 at	-0.207	2224	3914.625	2108.8557	TRUE	matrix metallopeptidase 24	213171 s at	-0.088	15437	7.860E-02	FALSE
98410 at	-0.387	1777	1417793 at	0.032	7459	98410 at	0.077	4146	1417793 at	-0.676	2277	3914.75	2573.4144	FALSE	interferon inducible GTPase 2	NA	NA	NA	NA	
100100 at	-0.020	7494	1416318 at	-0.159	1785.5	100100 at	-0.112	2207	1416318 at	-0.151	4173	3914.875	2603.0648	TRUE	serine (or cysteine) peptidase inhibitor, clade B, member 1a	212268 at	0.281	10696	1.468E-02	FALSE
104746 at	0.078	4537	1416803 at	0.193	1733	104746 at	0.024	7338	1416803 at	0.224	2052	3915	2603.5684	TRUE	FK506 binding protein 7	223667 at	-0.082	13897	5.052E-02	FALSE
92542 at	0.082	4794	1417001 a at	0.137	3958.5	92542 at	0.399	772.5	1448538 a at	0.107	6136	3915.25	2279.0846	TRUE	DNA segment, Chr 4, Wayne State University 53, expressed	209006 s at	-0.328	12099	2.690E-02	FALSE
160362 at	0.021	7963	1423667 at	-0.289	437.5	160362 at	-0.060	4379	1433576 at	-0.199	2882	3915.375	3149.6928	FALSE	methionine adenosyltransferase II, alpha	200768 s at	0.475	518	1.107E-07	FALSE
98911 at	0.029	7455	1433804 at	-0.313	723	98911 at	-0.112	3114	1433804 at	0.197	4370	3915.5	2802.9204	FALSE	Janus kinase 1	201648 at	0.210	7754	2.769E-03	FALSE
103969 at	-0.009	8225	1427236 a at	0.154	2642.5	103969 at	0.234	4392	1439108 at	0.395	404	3915.875	3304.0381	FALSE	myeloid/lymphoid or mixed-lineage leukemia 5	NA	NA	NA	NA	
102000 f at	0.023	7884	1435757 a at	0.106	5399	102000 f at	0.388	333	1428631 a at	0.197	2049	3916.25	3379.7382	TRUE	ubiquinol cytochrome c reductase core protein 2	200883 at	-0.582	3391	3.947E-05	FALSE
101760 at	0.165	1255	1450246 at	0.053	5481	101760 at	0.103	3088	1434862 at	-0.091	5843	3916.75	2154.7666	FALSE	fucosyltransferase 2	210608 s at	0.088	14167	5.556E-02	FALSE
93997 at	0.110	3664	1418115 s at	0.109	3615	93997 at	0.030	6822	1458364 s at	-0.176	1567	3917	2169.2347	FALSE	interferon alpha responsive gene	214801 at	0.164	5510	4.508E-04	FALSE
93728 at	-0.158	2532	1454758 a at	-0.154	1556	93728 at	0.067	5544	1425742 a at	-0.076	6037	3917.25	2208.6251	FALSE	TSC22 domain family, member 1	235315 at	-0.065	23907	3.349E-01	FALSE
104169 at	0.234	3920	1423477 at	-0.355	4824	104169 at	0.867	1862	1439627 at	-0.729	5065	3917.75	1456.4323	FALSE	zinc finger protein of the cerebellum 1	206373 at	0.259	13183	3.955E-02	FALSE
94958 at	-0.359	563	1454893 at	-0.075	5795.5	94958 at	-0.154	2448	1454893 at	-0.060	6866	3918.125	2923.0484	TRUE	RIKEN cDNA 1110013L07 gene	203550 s at	-0.122	8683	4.862E-03	TRUE
93776 at	0.158	864	1428226 at	0.176	948	93776 at	-0.036	7017	1428226 at	0.043	6844	3918.25	3479.1327	FALSE	RIKEN cDNA 1500001L15 gene	216263 s at	0.062	14888	6.864E-02	FALSE
96817 at	-0.022	7291	1457303 at	-0.068	6363	96817 at	-0.139	1235	1457303 at	-0.366	786	3918.75	3384.4283	TRUE	Ankyrin repeat and sterile alpha motif domain containing 3	227303 at	0.060	19783	1.938E-01	FALSE
161020 r at	-0.012	8066	1426925 at	0.166	779	161020 r at	-0.027	6468	1438268 at	0.801	363	3919	3924.2726	FALSE	membrane associated DNA binding protein	220202 s at	-0.278	3782	6.572E-05	FALSE
160818 at	0.085	3631	1436510 a at	0.100	4226	160818 at	0.032	6096	1436378 at	-0.173	1726	3919.75	1800.5341	FALSE	leucine rich repeat (in FLII) interacting protein 2	218364 at	0.223	6202	8.341E-04	FALSE
92850 at	-0.059	6067	1452767 at	-0.243	2001.5	92850 at	0.142	3078	1426123 a at	-0.143	4535	3920.375	1767.997	FALSE	ribosome binding protein 1	201204 s at	0.415	1731	2.342E-06	FALSE
97795 at	0.043	5788	1418489 a at	-0.140	4092	97795 at	0.158	613	1425814 a at	-0.127	5190	3920.75	2314.3145	FALSE	calcitonin receptor-like	206331 at	0.010	39836	8.725E-01	FALSE
93112 at	0.108	2314	1448777 at	-0.116	1832	93112 at	0.014	7983	1448777 at	-0.166	3556	3921.25	2803.5358	FALSE	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	202107 s at	0.107	14651	6.409E-02	FALSE
97813 at	0.109	2151	1419536 a at	-0.121	3265	97813 at	0.004	8294	1419536 a at	-0.199	1976	3921.5	2970.3753	FALSE	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	201783 s at	0.334	640	1.601E-07	FALSE
160877 at	0.317	373	1419663 at	-0.045	7302.5	99549 at	0.073	4126	1419663 at	-0.283	3886	3921.875	2832.319	FALSE	osteoglycin	218730 s at	-0.017	34813	7.256E-01	FALSE
96770 at	0.033	7109	1423320 at	0.107	2646.5	96770 at	-0.055	4998	1423320 at	-0.393	934	3921.875	2699.987	FALSE	deoxyribonuclease 1-like 2	207192 at	-0.029	35389	7.431E-01	FALSE
101894 s at	0.104	5696	1423364 a at	-0.154	2780	101894 s at	-0.101	3574	1423364 a at	-0.123	3639	3922.25	1245.3156	FALSE	fused toes	223894 s at	-0.236	10801	1.562E-02	FALSE
100684 at	-0.119	3619	1416339 a at	0.006	8267	100684 at	-0.190	1016	1416339 a at	-0.147	2788	3922.5	3093.0904	FALSE	protein kinase C substrate 80K-H	214080 x at	0.084	15309	7.671E-02	FALSE
161295 r at	-0.045	6116	1448050 s at	0.096	3101	161295 r at	0.089	3344	1440609 at	0.205	3132	3923.25	1465.8166	FALSE	mitogen-activated protein kinase kinase kinase 4	218181 s at	0.721	1062	5.465E-07	FALSE
101588 at	0.082	3625	1415802 at	-0.146	4379	101588 at	0.084	3558	1415802 at	-0.136	4131	3923.25	397.16862	FALSE	solute carrier family 16 (monocarboxylic acid transporters), member 1	202235 at	0.203	5680	5.169E-04	FALSE
160459 r at	0.045	6698	1423517 at	0.096	4012.5	162279 f at	0.109	3648	1423517 at	0.194	1337	3923.875	2196.3343	TRUE	chaperonin subunit 6a (zeta)	201326 at	-0.132	18044	1.419E-01	FALSE
94025 at	-0.095	4864	1417052 at	0.120	4591.5	94025 at	0.180	1446	1417052 at	0.136	4794	3923.875	1655.9529	FALSE	proteasome (prosome, macropain) subunit, beta type 3	201400 at	-0.030	36179	7.673E-01	FALSE
99191 at	0.257	1398	1448405 a at	0.084	5885	99191 at	-0.006	8350	1448406 at	0.718	63	3924	3861.0445	FALSE	CREBBP/EP300 inhibitory protein 1	208669 s at	-0.379	7901	3.073E-03	FALSE
92573 at	0.069	4867	1455929 x at	0.098	2344.5	92573 at	-0.128	4266	1415819 a at	0.111	4220	3924.375	1093.7167	FALSE	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	200695 at	-0.439	1563	1.629E-06	FALSE
93711 at	0.174	3115	1423347 at	-0.017	8036.5	104709 at	0.217	1493	1423347 at	0.133	3053	3924.375	2842.2725	FALSE	SEC23A (S. cerevisiae)	204344 s at	-0.286	4457	1.462E-04	FALSE
160754 at	-0.170	2865	1448602 at	-0.234	583	160754 at	-0.041	6596	1448602 at	-0.165	5656	3925	2733.9328	TRUE	muscle glycogen phosphorylase	205577 at	0.239	17277	1.214E-01	FALSE
95505 at	-0.099	3228	1417820 at	0.046	6742	95505 at	-0.082	5569	1417820 at	0.454	162	3925.25	2903.1134	FALSE	torsin family 1, member B	209593 s at	0.044	24921	3.694E-01	FALSE
103751 at	0.085	5025	1426996 at	-0.096	3971	103751 at	-0.049	5155	1452273 at	-0.205	1551	3925.5	1669.4202	FALSE	expressed sequence AA409316	NA	NA	NA	NA	
98123 at	0.016	7883	1418519 at	0.111	2932.5	98123 at	-0.081	3416	1418519 at	-0.251	1477	3927.125	2763.0048	FALSE	aminoadipate aminotransferase	223593 at	0.065	15185	7.427E-02	FALSE
96665 at	0.024	7677	1420495 a at	0.152	1701	96665 at	0.202	219	1420495 a at	0.076	6115	3928	3538.0871	TRUE	vacuolar protein sorting 26 homolog A (yeast)	243316 x at	0.094	12072	2.663E-02	TRUE
95061 at	-0.147	3280	1418234 s at	0.154	3430	95061 at	0.157	2765	1437262 x at	-0.183	6250	3931.25	1571.848	FALSE	breast carcinoma amplified sequence 2	203053 at	-0.314	7265	1.949E-03	FALSE
97330 at	-0.018	7533	1452429 s at	-0.139	3421	97330 at	-0.092	4286	1452236 at	0.391	486	3931.5	2899.9168	FALSE	ATP-binding cassette, sub-family F (GCN20), member 1	200045 at	-0.030	31775	6.237E-01	FALSE
161731 at	0.097	4105	1415878 at	0.110	2459	161731 at	0.076	3541	1448127 at	-0.113	5622	3931.75	1317.6543	FALSE	ribonucleotide reductase M1	201477 s at	0.137	14955	7.019E-02	FALSE
100309 at	0.166	1613	1422990 at	0.162	2434.5	100309 at	0.080	3560	1422990 at	0.024	8120	3931.875	2903.9051	TRUE	met proto-oncogene	203510 at	0.133	15371	7.751E-02	FALSE
95133 at	0.148	1685	1433966 x at	0.155	3250	95133 at	-0.086	3301	1451095 at	-0.036	7492	3932	2489.0356	FALSE	asparagine synthetase	205047 s at	-0.334	7286	1.978E-03	FALSE
95742 at	-0.170	3072	1422459 a at	0.162	1849.5	95742 at	0.014	7897	1422459 a at	0.325	2913	3932.875	2697.8998	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	201232 s at	0.071	28607	5.058E-01	FALSE
99469 at	0.025	7257	1451226 at	-0.122	1903.5	99469 at	0.043	5960	1456302 at	-0.381	615	3933.875	3177.2995	FALSE	peroxisomal biogenesis factor 6	320 at	0.154	15073	7.235E-02	FALSE
100501 at	0.135	1885	1448911 at	0.113	3122.5	100501 at	0.057	6305	1448911 at	0.152	4424	3934.125	1890.2094	TRUE	ATPase, H+/K+ exchanging, beta polypeptide	207546 at	0.107	18291	1.487E-01	FALSE
93626 at	0.124	3404	1422906 at	0.006	8333	93626 at	0.189	1675	1422906 at	-0.163	2325	3934.25	3017.9498	FALSE	ATP-binding cassette, sub-family G (WHITE), member 2	209735 at	0.004	44008	9.848E-01	FALSE
100737 at	0.045	6487	1421447 at	0.155	2450	100737 at	-0.039	6696	1450252 at	0.443	107	3935	3214.272	FALSE	one cut domain, family member 1	210745 at	0.033	33163	6.708E-01	FALSE
97099 at	0.078	5638	1423443 at	-0.059	5863	97099 at	0.085	3974	1423443 at	0.373	266	3935.25	2587.1783	FALSE	solute carrier family 4 (anion exchanger), member 8	228935 at	-0.267	3084	2.573E-05	FALSE
97250 at	0.008	8312	1423210 a at	0.228	798	97250 at	0.262	605	1423211 at	-0.093	6027	3935.5	3849.8598	FALSE	nucleolar protein family A, member 3	217962 at	-0.140	14738	6.574E-02	FALSE
103861 s at	0.127	1535	1418132 a at	-0.086	4757.5	103861 s at	-0.135	2033	1448968 at	-0.045	7417	3935.625	2718.9724	FALSE	DNA segment, Chr 7, Wayne State University 128, expressed	224878 at	-0.067	19388	1.808E-01	FALSE
103529 at	-0.145	1854	1449125 at	-0.063	5570	103529 at	-0.215	245	1449125 at	0.018	8074	3935.75	3547.356	FALSE	tumor necrosis factor, alpha-induced protein 8-like 1	227420 at	0.059	22921	2.988E-01	FALSE
97234 at	0.094	4417	1417889 at	0.262	275	97236 r at	0.122	4295	1417889 at	-0.054	6757	3936	2690.7994	FALSE	apolipoprotein B editing complex 2	206160 at	0.035	30388	5.709E-01	FALSE
97224 at	-0.128	3394	1433668 at	-0.138	3412	97224 at	-0.152	1483	1438524 x at	-0.032	7461	3937.5	2517.3508	TRUE	proline-rich nuclear receptor coactivator 1	209034 at	-0.019	37569	8.078E-01	FALSE
100476 at	0.084	3837	1417484 at	0.086	4528.5	100476 at	0.144	1940	1417485 at	0.085	5445	3937.625	1485.7034	TRUE	integrin binding sialoprotein	236028 at	-0.089	10699	1.468E-02	FALSE
97950 at	0.124	2805	1451006 at	0.035	7278	97950 at	-0.078	3288	1451006 at	-0.359	2382	3938.25	2257.0574	FALSE	xanthine dehydrogenase	241994 at	0.039	27203	4.503E-01	FALSE
104315 at	-0.156	1610	1424307 at	-0.126	1581.5	104315 at	-0.039	6784	1424307 at	0.096	5779	3938.625	2736.2792	FALSE	Rho GTPase activating protein 1	202117 at	0.244	3830	6.925E-05	FALSE
160253 at	-0.160	5013	1423754 at	0.193	3171.5	160253 at	0.078	4175	1423754 at	-0.825	3397	3939.125	835.06331	FALSE	interferon induced transmembrane protein 3	212203 x at	0.557	6820	1.346E-03	FALSE
104015 at	-0.203	2122	1426836 s at	0.077	4408	161413 f at	-0.045	5427	1426836 s at	0.133	3801	3939.5	1384.9954	FALSE	methionyl aminopeptidase 1	212673 at	-0.132	8753	5.052E-03	FALSE
99651 at	-0.091	4332	1415714 a at	0.178	486	99651 at	0.068	5191	1460697 s at	0.073	5753	3940.5	2375.9734	FALSE	RIKEN cDNA 2610209M04 gene	241699 at	-0.374	3087	2.600E-05	FALSE
161186 f at	-0.045	6352	1450484 a at	0.103	3597.5	103066 at	0.245	203	1450484 a at	-0.154	5611	3940.875	2750.3004	FALSE	thymidylate kinase family LPS-inducible member	226702 at	-0.576	233	2.485E-08	FALSE
93750 at	-0.293	2624	1437171 x at	-0.336	795	93750 at	0.059	7434	1415812 at	-0.122	4911	3941	2873.6593	FALSE	gelsolin	200696 s at	0.428	6068	7.372E-04	FALSE
104696 at	0.114	2750	1418989 at	0.210	1825	104696 at	-0.033	6146	1418989 at	0.106	5043	3941	1997.6958	FALSE	cathepsin E	205927 s at	0.039	27446	4.595E-01	FALSE
101967 at	0.129	3129	1416857 at	0.129	2692	101967 at	0.042	5522	1416857 at	0.151	4422	3941.25	1284.5579	TRUE	stromal cell derived factor 2	203090 at	-0.041	25775	3.957E-01	FALSE
97258 at	0.057	4958	1425141 at	0.104	2274.5	97258 at	-0.036	6332	1425141 at	0.150	2204	3942.125	2044.9577	FALSE	lactamase, beta 2	222714 s at	0.119	23252	3.103E-01	FALSE
92510 at	-0.104	3371	1426431 at	-0.113	4322.5	92510 at	-0.120	3548	1426431 at	-0.120	4527	3942.125	568.12035	TRUE	jagged 2	209784 s at	-0.040	31558	6.150E-01	FALSE
102354 at	-0.095	4641	1423809 at	0.081	4427	102354 at	0.077	4169	1443795 at	0.170	2532	3942.25	959.76642	FALSE	transcription factor 19	NA	NA	NA	NA	
99640 at	-0.003	8379	1455787 x at	0.130	1413	99640 at	-0.071	4700	1423265 at	0.258	1278	3942.5	3354.3141	FALSE	multiple inositol polyphosphate histidine phosphatase 1	209585 s at	-0.036	33326	6.761E-01	FALSE
103314 at	0.120	4266	1451474 a at	0.141	1876	103314 at	0.159	3279	1451474 a at	0.074	6351	3943	1881.1502	TRUE	poly (ADP-ribose) polymerase family, member 8	219033 at	0.049	23694	3.271E-01	FALSE
96661 at	0.025	7551	1449716 s at	0.159	1376	96661 at	-0.093	3546	1424391 at	0.141	3301	3943.5	2593.3842	FALSE	nardilysin, N-arginine dibasic convertase, NRD convertase 1	242235 x at	0.244	3082	2.572E-05	FALSE
102683 at	-0.187	667	1460654 at	0.022	7571	102683 at	-0.048	6223	1460654 at	0.289	1316	3944.25	3463.8169	FALSE	solute carrier family 30 (zinc transporter), member 3	207035 at	0.026	33525	6.834E-01	FALSE
102849 at	0.064	5375	1418142 at	0.059	5495	102849 at	-0.071	3525	1418142 at	-0.211	1384	3944.75	1930.6752	FALSE	potassium inwardly-rectifying channel, subfamily J, member 8	205303 at	0.311	3736	6.194E-05	FALSE
95703 at	-0.104	5112	1430021 a at	-0.098	2657	95703 at	0.070	6267	1444424 at	0.242	1746	3945.5	2101.4374	FALSE	ubiquitin-like 1 (sentrin) activating enzyme E1A	241185 at	-0.045	22096	2.713E-01	FALSE
160525 f at	-0.043	6605	1426730 a at	0.124	2795.5	160525 f at	-0.065	4181	1426730 a at	0.192	2205	3946.625	1956.2068	FALSE	prolactin-like protein K	NA	NA	NA	NA	
102715 at	-0.037	7418	1418157 at	-0.173	4451.5	102715 at	0.551	1659	1418157 at	0.477	2259	3946.875	2606.8275	FALSE	nuclear receptor subfamily 2, group F, member 1	209505 at	0.813	1045	5.166E-07	FALSE
98914 at	0.015	7727	1423511 at	0.132	3241	98914 at	0.180	884	1423511 at	0.130	3936	3947	2838.3637	TRUE	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	203428 s at	-0.253	8783	5.123E-03	FALSE
95974 at	0.072	5666	1420549 at	0.099	4361.5	95974 at	0.212	473	1420549 at	0.120	5295	3948.875	2381.3538	TRUE	guanylate nucleotide binding protein 1	202748 at	0.380	11393	2.013E-02	TRUE
160285 at	0.092	4395	1428267 at	0.096	4059.5	160285 at	-0.050	6564	1457839 at	0.376	779	3949.375	2387.3452	FALSE	DEAH (Asp-Glu-Ala-His) box polypeptide 40	218277 s at	0.350	7499	2.307E-03	FALSE
99807 r at	0.169	2959	1422279 at	0.041	7239	99807 r at	0.134	2142	1422279 at	0.272	3459	3949.75	2259.0224	TRUE	Friend virus susceptibility 1	NA	NA	NA	NA	
98732 at	0.065	5110	1450549 s at	0.177	1327	98732 at	-0.061	4613	1422233 at	0.096	4752	3950.5	1761.4862	FALSE	ELK4, member of ETS oncogene family	205994 at	-0.024	31750	6.228E-01	FALSE
103596 at	0.176	695	1418578 at	0.032	7053.5	103596 at	0.218	390	1418578 at	0.040	7666	3951.125	3945.8412	TRUE	diacylglycerol kinase, alpha	203385 at	-0.191	5051	2.801E-04	FALSE
93515 at	0.044	5948	1448906 at	0.118	2792.5	93515 at	-0.072	4373	1448906 at	0.144	2694	3951.875	1537.1252	FALSE	cadherin 16	206517 at	0.019	36658	7.824E-01	FALSE
100908 at	-0.100	3045	1425340 a at	-0.090	4338	100908 at	-0.122	4080	1447467 at	-0.154	4348	3952.75	617.74934	TRUE	protein tyrosine phosphatase, receptor type, A	233313 at	0.216	1886	3.170E-06	FALSE
161035 at	0.076	3865	1420395 a at	0.189	546	92490 at	-0.089	3000	1420395 a at	0.006	8403	3953.5	3282.5854	FALSE	kinesin family member 9	231319 x at	0.241	9884	9.489E-03	FALSE
94203 at	0.088	3233	1459928 at	0.040	6747	94203 at	-0.126	2556	1443779 s at	-0.157	3280	3954	1891.1522	FALSE	RIKEN cDNA A630025C20 gene	226520 at	0.368	4721	2.008E-04	FALSE
94869 at	0.033	6777	1434080 at	-0.136	2371.5	94869 at	-0.088	4441	1437743 at	-0.520	2229	3954.625	2135.9173	FALSE	AE binding protein 2	225889 at	0.155	17855	1.369E-01	FALSE
161011 at	0.148	1312	1429168 at	0.053	6617	161011 at	0.014	7669	1454884 at	-0.605	221	3954.75	3733.1062	FALSE	BTB (POZ) domain containing 4	NA	NA	NA	NA	
101189 at	-0.027	7095	1450366 at	-0.102	4832.5	101189 at	-0.137	3870	1439854 at	-0.630	22	3954.875	2949.8768	TRUE	harakiri, BCL2 interacting protein (contains only BH3 domain)	206864 s at	0.057	21083	2.363E-01	FALSE
92317 at	-0.222	2517	1421881 a at	-0.221	2255	92317 at	-0.011	8089	1421881 a at	0.196	2959	3955	2771.2702	FALSE	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	208427 s at	-0.096	10279	1.184E-02	FALSE
104262 at	-0.182	1605	1422324 a at	-0.128	3423	104262 at	-0.089	3292	1422324 a at	-0.082	7502	3955.5	2505.0816	TRUE	parathyroid hormone-like peptide	210355 at	-0.053	12896	3.577E-02	TRUE
100755 at	0.150	1939	1422928 at	0.151	2651.5	100755 at	-0.122	3456	1422928 at	0.042	7776	3955.625	2621.2216	FALSE	elastase 2, neutrophil	206871 at	-0.008	40182	8.824E-01	FALSE
96134 at	-0.014	7740	1430128 a at	0.144	1303	96134 at	-0.144	1024	1430128 a at	-0.136	5756	3955.75	3326.3438	FALSE	receptor accessory protein 6	226597 at	-0.077	15104	7.273E-02	FALSE
160113 at	-0.063	4819	1416739 a at	-0.164	2115	160113 at	-0.126	1930	1416739 a at	0.074	6961	3956.25	2399.2187	FALSE	BRCA1 associated protein	213473 at	0.092	17701	1.324E-01	FALSE
104741 at	-0.077	3950	1454787 at	-0.238	1264	104741 at	-0.022	7535	1454787 at	-0.159	3078	3956.75	2634.8322	TRUE	zinc finger, DHHC domain containing 9	222451 s at	0.253	13798	4.875E-02	FALSE
98574 at	-0.226	2048	1422453 at	-0.111	2766.5	98574 at	-0.077	6137	1422453 at	-0.103	4876	3956.875	1884.899	TRUE	pre-mRNA processing factor 8	200000 s at	-0.021	37471	8.043E-01	FALSE
99021 at	0.048	5594	1432129 a at	0.122	3071	99021 at	-0.045	6118	1425528 at	-0.283	1048	3957.75	2352.0888	FALSE	paired related homeobox 1	226695 at	0.471	4255	1.153E-04	FALSE
92498 at	-0.030	7211	1417757 at	0.229	564	92498 at	0.013	7810	1417757 at	0.542	246	3957.75	4111.6944	FALSE	unc-13 homolog B (C. elegans)	202893 at	-0.144	11855	2.435E-02	FALSE
92997 g at	0.078	3605	1429177 x at	-0.183	3030	92996 at	-0.050	5414	1421657 a at	-0.206	3782	3957.75	1022.5303	FALSE	SRY-box containing gene 17	219993 at	0.005	42413	9.443E-01	FALSE
96494 at	0.083	4763	1451793 at	-0.057	7342.5	96494 at	-0.191	3059	1451793 at	0.546	669	3958.375	2812.3885	FALSE	kelch-like 24 (Drosophila)	206551 x at	0.268	2703	1.383E-05	FALSE
96599 at	0.266	1844	1435420 at	0.044	7206	96599 at	0.204	750	1435420 at	-0.348	6034	3958.5	3142.1616	FALSE	RIKEN cDNA C330016K18 gene	234976 x at	0.077	19495	1.848E-01	FALSE
99012 at	0.046	5686	1424817 at	0.046	6513	93475 at	0.143	1495	1424817 at	0.155	2141	3958.75	2508.7756	TRUE	sperm flagellar 1	NA	NA	NA	NA	
92744 at	-0.189	2573	1450497 at	-0.070	6752	102582 at	-0.066	5811	1455231 s at	-0.296	704	3960	2813.4658	TRUE	adenomatosis polyposis coli 2	227965 at	0.069	17713	1.327E-01	FALSE
102970 at	-0.006	8218	1425271 at	0.158	918	102970 at	0.154	1766	1425271 at	0.101	4940	3960.5	3324.5733	FALSE	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	213951 s at	0.094	13372	4.216E-02	FALSE
162487 f at	0.113	3798	1448912 at	0.079	3553.5	161549 f at	-0.114	1784	1448912 at	-0.056	6708	3960.875	2039.4414	FALSE	C1q and tumor necrosis factor related protein 1	220975 s at	0.194	6405	9.832E-04	FALSE
93967 at	-0.058	5961	1417326 a at	0.181	1903.5	93967 at	0.057	6481	1447897 x at	0.192	1499	3961.125	2623.3026	FALSE	anaphase promoting complex subunit 11 homolog (yeast)	226414 s at	0.041	31157	6.017E-01	FALSE

95694_at	0.093	4232	1423474_at	0.011	8245	95694_at	0.117	2058	1438495_at	-0.305	1310	3961.25	3113.1606	FALSE	topoisomerase (DNA) I	239404_at	0.145	7184	1.843E-03	FALSE
160881_at	-0.050	5515	1417115_at	-0.149	2356.5	160881_at	0.038	6255	1456565_s_at	-0.227	1720	3961.625	2256.3874	FALSE	mitogen activated protein kinase kinase kinase 12	205447_s_at	-0.104	11595	2.183E-02	FALSE
92475_g_at	0.152	1480	1425739_at	-0.081	4573.5	101628_g_at	-0.116	2770	1437113_s_at	0.057	7025	3962.125	2403.9613	FALSE	phospholipase D1	226636_at	0.188	11324	1.967E-02	FALSE
160121_at	-0.059	5949	1455798_at	0.117	3573.5	160121_at	-0.088	3164	1438642_at	-0.208	3162	3962.125	1338.6442	FALSE	galactokinase 2	242965_at	-0.104	12017	2.614E-02	FALSE
95872_at	0.130	2930	1420164_at	0.066	5675	95872_at	0.096	2742	1420164_at	-0.108	4502	3962.25	1387.9713	FALSE	DNA segment, Chr 7, ERATO Doi 183, expressed	NA	NA	NA	NA	
104488_at	-0.005	8238	1427070_at	0.153	866	104488_at	0.076	3763	1427070_at	0.260	2987	3963.5	3101.5915	FALSE	RIKEN cDNA 5730407K14 gene	226595_at	-0.050	20030	2.013E-01	FALSE
104086_at	0.139	2843	1452311_at	0.107	3346	104086_at	-0.070	5150	1452311_at	-0.132	4516	3963.75	1056.7032	FALSE	dimethylglycine dehydrogenase precursor	231790_at	-0.036	23609	3.241E-01	FALSE
92650_at	0.068	4726	1420977_at	-0.119	2152	92650_at	-0.006	8187	1446565_at	0.699	792	3964.25	3253.68	FALSE	mannosidase, alpha, class 1A, member 2	214242_at	-0.037	30790	5.862E-01	FALSE
161836_r_at	0.207	1154	1448875_at	-0.051	6970	161836_r_at	-0.052	6500	1448875_at	-0.230	1235	3964.75	3204.7294	FALSE	zinc fingers and homeoboxes protein 1	223214_s_at	0.221	9958	9.906E-03	FALSE
97865_g_at	0.051	5389	1423216_a_at	0.281	1837.5	97865_g_at	0.044	6028	1423217_a_at	0.169	2610	3966.125	2053.1294	TRUE	RIKEN cDNA 2510049I19 gene	201863_at	-0.041	25847	3.988E-01	FALSE
97496_f_at	-0.264	277	1423771_at	0.132	3110	97496_f_at	-0.060	4816	1423771_at	0.036	7662	3966.25	3094.3159	FALSE	protein kinase C, delta binding protein	213010_at	-0.017	38785	8.437E-01	FALSE
100460_at	0.148	2645	1422679_s_at	0.059	5387	100460_at	-0.120	3874	1422681_at	0.194	3960	3966.5	1121.4248	FALSE	SH2 domain binding protein 1 (tetratricopeptide repeat containing)	202060_at	0.059	31144	6.015E-01	FALSE
95646_at	0.010	7950	1416772_at	-0.108	2711.5	161978_r_at	0.159	539	1447820_x_at	-0.109	4667	3966.875	3145.4599	FALSE	carnitine palmitoyltransferase 2	204264_at	0.160	5096	2.991E-04	FALSE
160916_at	-0.113	3326	1417877_at	0.023	7800	160916_at	-0.091	2701	1447828_x_at	0.221	2042	3967.25	2608.3936	FALSE	RIKEN cDNA 2310005P05 gene	225630_at	-0.184	5056	2.813E-04	FALSE
97735_at	0.156	1897	1449572_at	0.060	5101	97735_at	0.133	4171	1449572_at	0.154	4700	3967.25	1431.7543	TRUE	thyrotropin releasing hormone receptor	211438_at	0.055	26036	4.051E-01	FALSE
97170_at	-0.084	3556	1443001_at	0.097	3093	97170_at	0.210	1478	1443001_at	-0.025	7742	3967.25	2669.4908	FALSE	expressed sequence C78344	NA	NA	NA	NA	
161037_at	-0.019	7491	1418219_at	0.039	6564.5	161037_at	0.123	1202	1418219_at	-0.422	612	3967.375	3562.1544	FALSE	interleukin 15	205992_s_at	0.127	7438	2.180E-03	FALSE
161374_f_at	0.005	8297	1426375_s_at	0.110	3150.5	161374_f_at	0.142	2082	1447816_x_at	0.225	2341	3967.625	2921.9099	TRUE	oxidoreductase NAD-binding domain containing 1	227686_at	-0.133	4748	2.066E-04	FALSE
94273_at	0.125	5382	1449142_a_at	0.092	4972	94273_at	-0.119	4219	1444289_at	-0.290	1299	3968	1843.3641	FALSE	Yip1 domain family, member 5	NA	NA	NA	NA	
94855_at	0.044	5998	1448563_at	0.011	8116	94855_at	-0.243	193	1435144_at	-0.425	1565	3968	3712.6737	FALSE	prohibitin	NA	NA	NA	NA	
100948_at	-0.126	3452	1450627_at	-0.247	496.5	100948_at	0.140	4549	1450627_at	-0.047	7377	3968.625	2844.668	FALSE	progressive ankylosis	220076_at	-0.322	2363	7.576E-06	FALSE
96968_at	0.078	5567	1427216_at	0.103	2846.5	96968_at	-0.106	2470	1427216_at	-0.130	4991	3968.625	1538.9493	FALSE	interferon zeta	NA	NA	NA	NA	
104428_s_at	-0.210	434	1432329_a_at	-0.171	2564	104428_s_at	0.015	7684	1432329_a_at	0.118	5194	3969	3150.2434	FALSE	megakaryocyte-associated tyrosine kinase	206267_s_at	-0.328	722	2.117E-07	FALSE
95325_at	0.050	5781	1448997_at	-0.200	1667	95325_at	-0.105	3485	1457095_at	0.100	4943	3969	1804.2062	FALSE	pleckstrin homology, Sec7 and coiled-coil domains 1	202880_s_at	0.147	16103	9.298E-02	FALSE
97407_at	-0.201	1709	1416963_at	-0.113	3200	97407_at	0.022	7240	1446898_at	-0.114	3729	3969.5	2342.0789	FALSE	ubiquitin associated domain containing 1	202151_s_at	0.094	15288	7.645E-02	FALSE
102979_at	-0.146	1644	1436167_at	-0.043	6121	102979_at	-0.130	3868	1436167_at	-0.182	4246	3969.75	1836.9954	TRUE	Src homology 2 domain containing F	NA	NA	NA	NA	
100998_at	-0.407	2397	1450648_s_at	0.088	4384	100998_at	-0.006	8176	1450648_s_at	-0.462	925	3970.5	3141.5593	FALSE	histocompatibility 2, class II antigen A, beta 1	215536_at	0.072	12056	2.653E-02	FALSE
98972_at	-0.048	6657	1422883_at	-0.038	6518	98972_at	-0.107	1772	1446807_at	0.438	936	3970.75	3041.3062	FALSE	ubiquitin specific peptidase 8	202745_at	0.256	5879	6.242E-04	FALSE
98303_at	0.111	2882	1421004_at	0.140	3360	98303_at	-0.021	7168	1435779_at	0.163	2473	3970.75	2162.102	FALSE	centrosomal protein 110	NA	NA	NA	NA	
97474_r_at	-0.096	4265	1416211_a_at	-0.136	3996	97474_r_at	-0.132	3516	1443809_at	-0.139	4107	3971	322.79095	TRUE	pleiotrophin	209466_x_at	-0.202	14676	6.473E-02	FALSE
100685_at	0.133	1600	1422481_at	0.084	4444	100685_at	0.000	8505	1422481_at	0.365	1338	3971.75	3333.4273	FALSE	keratin complex 2, basic, gene 1	205900_at	-0.019	37396	8.018E-01	FALSE
103934_at	0.063	4765	1424338_at	0.111	2016.5	103934_at	-0.055	5432	1424338_at	-0.167	3676	3972.375	1491.3131	FALSE	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	207184_at	0.024	36198	7.676E-01	FALSE
160793_at	-0.324	691	1452844_at	-0.073	5446	161390_r_at	-0.083	4808	1444751_at	0.098	4945	3972.5	2204.7873	FALSE	POU domain, class 6, transcription factor 1	216330_s_at	-0.063	19569	1.867E-01	FALSE
160709_at	-0.100	4100	1435755_at	0.333	1305	160709_at	0.123	2177	1435755_at	-0.018	8311	3973.25	3118.6649	FALSE	RIKEN cDNA 1110001A16 gene	NA	NA	NA	NA	
161863_r_at	-0.111	2126	1422828_at	0.051	6509	161863_r_at	0.126	1361	1422828_at	-0.098	5902	3974.5	2606.804	FALSE	CD3 antigen, delta polypeptide	213539_at	0.011	40744	9.005E-01	FALSE
100024_at	-0.006	8207	1454211_a_at	0.124	2504.5	100024_at	0.086	2739	1422629_s_at	0.259	2452	3975.625	2823.6748	FALSE	shroom	225548_at	0.164	13485	4.372E-02	FALSE
160127_at	-0.308	615	1450016_at	-0.122	2619	160127_at	0.091	5726	1450016_at	0.064	6947	3976.75	2888.316	FALSE	cyclin G1	208796_s_at	0.152	16522	1.024E-01	FALSE
102056_f_at	-0.188	2602	1438154_x_at	-0.068	5282.5	102056_f_at	0.077	6838	1431003_a_at	-0.216	1185	3976.875	2554.4432	FALSE	RIKEN cDNA 2610002J02 gene	229113_s_at	0.157	7882	3.025E-03	FALSE
162341_r_at	0.130	2227	1456590_x_at	0.198	903.5	162341_r_at	0.033	6708	1437133_x_at	0.097	6071	3977.375	2849.0992	TRUE	aldo-keto reductase family 1, member B3 (aldose reductase)	201272_at	-0.266	8899	5.441E-03	FALSE
102716_at	0.116	3365	1420933_a_at	0.084	5233	102716_at	-0.080	3547	1441543_at	-0.163	3765	3977.5	852.82335	FALSE	eyes absent 3 homolog (Drosophila)	234547_at	-0.015	35212	7.371E-01	FALSE
97875_at	-0.107	3965	1419263_a_at	-0.098	4183.5	97875_at	-0.157	1540	1419263_a_at	-0.067	6226	3978.625	1918.3105	TRUE	adhesion regulating molecule 1	201281_at	-0.011	40527	8.934E-01	FALSE
101521_at	0.068	4651	1424278_a_at	-0.017	7998	101521_at	0.133	1896	1424278_a_at	0.227	1372	3979.25	3040.7939	FALSE	baculoviral IAP repeat-containing 5	202095_s_at	-0.060	20715	2.243E-01	FALSE
97142_at	-0.003	8384	1443589_at	-0.208	1574.5	97142_at	-0.061	5342	1443589_at	0.610	617	3979.375	3575.2136	FALSE	DNA segment, Chr X, ERATO Doi 242, expressed	NA	NA	NA	NA	
101567_at	0.160	1190	1423044_at	-0.065	6788	101568_at	-0.062	4625	1441685_at	0.202	3315	3979.5	2347.141	FALSE	Proline synthetase co-transcribed	209384_at	-0.069	23100	3.050E-01	FALSE
94563_at	0.075	5694	1427561_a_at	0.142	1114	94563_at	0.146	1001	1427561_a_at	-0.014	8111	3980	3516.2174	FALSE	afamin	206840_at	0.022	32879	6.609E-01	FALSE
161700_i_at	-0.085	3892	1416412_at	-0.015	7814.5	161700_i_at	0.269	243	1416412_at	-0.150	3971	3980.125	3091.7301	FALSE	neutral sphingomyelinase (N-SMase) activation associated factor	203269_at	-0.144	12277	2.892E-02	FALSE
92982_at	0.115	3996	1449873_at	0.105	3150.5	92982_at	0.144	2726	1449873_at	-0.075	6048	3980.125	1476.1963	FALSE	bone morphogenetic protein 8a	NA	NA	NA	NA	
100537_at	0.010	7914	1455006_at	0.183	2457	162301_f_at	0.167	2521	1455006_at	0.145	3031	3980.75	2634.7147	TRUE	RIKEN cDNA 2310016M24 gene	225772_s_at	-0.235	7031	1.612E-03	FALSE
96938_at	0.133	2770	1416833_at	0.130	2251	96938_at	-0.014	7657	1416833_at	-0.149	3253	3982.75	2483.4364	FALSE	kidney expressed gene 1	NA	NA	NA	NA	
93442_at	0.162	910	1450151_at	0.079	5604.5	93442_at	0.020	7291	1450151_at	0.442	2130	3983.875	2969.2345	TRUE	zinc finger protein 316	NA	NA	NA	NA	
102017_at	-0.006	8321	1451909_a_at	0.103	2394	102017_at	-0.334	843	1425498_at	-0.103	4381	3984.75	3233.2211	FALSE	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	202127_at	0.210	13402	4.252E-02	FALSE
160952_r_at	-0.092	3316	1420660_at	0.083	3889	160952_r_at	-0.036	6279	1420660_at	-0.225	2460	3986	1637.5626	FALSE	leucine rich repeat containing 6 (testis)	206483_at	0.112	23905	3.348E-01	FALSE
102289_r_at	0.192	655	1425289_a_at	-0.010	8205.5	102289_r_at	0.058	4227	1425289_a_at	0.155	2858	3986.375	3174.3874	FALSE	complement receptor 2	244097_at	-0.078	11643	2.228E-02	FALSE
104395_at	0.061	5021	1435272_at	-0.072	4762	104395_at	0.082	3278	1441058_at	-0.263	2885	3986.5	1062.5229	FALSE	inositol 1,4,5-trisphosphate 3-kinase B	203723_at	1.013	35	3.349E-09	FALSE
93082_at	0.181	3617	1422032_a_at	0.142	3146	93082_at	0.192	3938	1422031_a_at	0.095	5245	3986.5	899.84165	TRUE	zinc finger, A20 domain containing 3	239757_at	0.351	1976	3.634E-06	TRUE
103803_at	0.076	5818	1419767_at	0.079	5967.5	103803_at	-0.119	2164	1419767_at	0.185	1997	3986.625	2202.9049	FALSE	peptidyl arginine deiminase, type III	220779_at	0.000	44665	9.995E-01	FALSE
93179_at	0.259	1071	1455350_at	0.138	1627.5	93179_at	-0.015	7698	1455350_at	0.081	5557	3988.375	3178.4016	FALSE	transmembrane protein 62	218776_s_at	0.061	17170	1.190E-01	FALSE
92235_g_at	0.089	4897	1454773_at	-0.110	4031	92234_at	-0.113	2017	1454773_at	-0.084	5014	3989.75	1386.3182	FALSE	retinoid X receptor alpha	202449_s_at	0.631	584	1.312E-07	FALSE
104284_at	-0.064	4704	1454786_at	-0.176	1903.5	104284_at	0.010	7772	1454786_at	-0.234	1580	3989.875	2885.302	FALSE	RIKEN cDNA 5031439G07 gene	217118_s_at	0.446	1200	7.224E-07	FALSE
99564_at	0.172	897	1415810_at	0.089	4817	99564_at	0.038	6447	1439227_at	0.221	3802	3990.75	2332.5786	TRUE	ubiquitin-like, containing PHD and RING finger domains, 1	225655_at	0.376	2337	7.173E-06	TRUE
93294_at	-1.202	1	1416953_at	-0.150	4243.5	93294_at	0.164	4220	1416953_at	0.278	7500	3991.125	3074.0515	FALSE	connective tissue growth factor	209101_at	0.346	15281	7.631E-02	FALSE
99962_at	-0.076	6445	1450052_at	0.140	2230	99962_at	0.078	5481	1454107_a_at	0.273	1810	3991.5	2316.6137	FALSE	Kinesin family member 2A	203087_s_at	0.040	37938	8.202E-01	FALSE
92877_at	-0.084	3846	1448123_s_at	-0.057	6447.5	92877_at	0.080	3614	1437463_x_at	-0.283	2059	3991.625	1819.356	FALSE	transforming growth factor, beta induced	201506_at	0.178	13562	4.483E-02	FALSE
97816_at	-0.017	8044	1428907_at	0.152	3540.5	97816_at	0.160	4315	1425523_at	0.696	68	3991.875	3272.3417	FALSE	RIKEN cDNA 2600011C06 gene	212027_at	0.137	12213	2.807E-02	FALSE
94548_at	0.054	5516	1424129_at	0.140	2173	94548_at	0.104	2462	1437055_x_at	0.074	5821	3993	1942.2902	TRUE	major facilitator superfamily domain containing 1	240936_at	-0.115	14882	6.850E-02	FALSE
97441_at	-0.047	6500	1421197_a_at	0.139	1480	97441_at	0.116	2756	1416568_a_at	0.303	5237	3993.25	2286.039	FALSE	apoptotic chromatin condensation inducer 1	243249_at	0.358	780	2.571E-07	FALSE
94422_at	-0.235	1903	1434038_at	0.055	6154	94422_at	0.029	7812	1445337_at	0.686	110	3994.75	3591.6783	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 13	212467_at	0.087	11772	2.360E-02	FALSE
102345_at	0.076	4045	1417638_at	0.049	6434	102345_at	-0.184	3101	1417638_at	-0.195	2399	3994.75	1760.4614	FALSE	left right determination factor 1	206268_at	-0.028	30065	5.586E-01	FALSE
94954_at	-0.034	6938	1423931_s_at	0.095	2853	94954_at	0.324	643	1423931_s_at	0.085	5550	3996	2805.9067	FALSE	anaphase promoting complex subunit 4	226917_s_at	0.332	510	1.080E-07	FALSE
99499_at	0.171	1623	1419122_at	0.138	4119.5	99499_at	-0.077	3488	1419122_at	0.050	6755	3996.375	2122.6183	FALSE	methyltransferase-like 1	204027_s_at	-0.072	22716	2.923E-01	FALSE
94683_at	0.099	2728	1419785_at	0.100	4143.5	94683_at	-0.006	8315	1459595_at	-0.357	800	3996.625	3188.4038	FALSE	expressed sequence AA516738	NA	NA	NA	NA	
101089_at	-0.070	5537	1449178_at	0.061	5067.5	101089_at	0.122	3770	1449178_at	0.267	1612	3996.625	1756.6373	FALSE	PDZ and LIM domain 3	NA	NA	NA	NA	
94032_at	0.051	5295	1415727_at	0.212	598	161359_s_at	0.141	2691	1415727_at	-0.047	7405	3997.25	2975.349	FALSE	apolipoprotein A-I binding protein	225427_s_at	0.007	42120	9.380E-01	FALSE
160254_at	0.005	8302	1424254_at	0.108	3133.5	160254_at	0.077	3722	1424254_at	-0.254	833	3997.625	3128.6406	FALSE	interferon induced transmembrane protein 1	NA	NA	NA	NA	
103943_at	-0.031	6639	1428578_s_at	-0.149	1273	103943_at	0.008	7939	1428577_at	-0.407	142	3998.25	3864.3983	FALSE	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	NA	NA	NA	NA	
94141_at	0.130	3549	1451713_a_at	0.155	2074	94141_at	0.083	3099	1451713_a_at	-0.035	7272	3998.5	2267.9398	FALSE	Fc receptor, IgE, low affinity II, alpha polypeptide	206760_s_at	-0.041	29402	5.356E-01	FALSE
162039_f_at	0.049	6520	1448404_at	-0.095	4252	104365_at	0.090	3318	1416611_at	-0.181	1905	3998.75	1938.0443	FALSE	secretory carrier membrane protein 2	NA	NA	NA	NA	
160325_r_at	-0.017	7659	1451100_a_at	0.193	1029.5	160326_at	0.353	69	1415704_a_at	0.035	7241	3999.625	4007.0352	FALSE	carnitine deficiency-associated gene expressed in ventricle 3	212010_s_at	0.187	11895	2.478E-02	FALSE
104728_at	0.197	2005	1426246_at	0.003	8437	104728_at	0.099	4225	1426246_at	-0.327	1332	3999.75	3206.0278	FALSE	protein S (alpha)	207808_s_at	0.302	10726	1.492E-02	FALSE
98845_at	0.073	4221	1426186_a_at	0.102	3409	98845_at	0.030	6752	1438883_at	0.261	1619	4000.25	2132.3529	TRUE	fibroblast growth factor 5	208378_x_at	-0.036	29147	5.258E-01	FALSE
100030_at	0.177	1022	1448562_at	0.034	7026	161325_at	-0.024	7027	1448562_at	-0.247	926	4000.25	3494.6323	FALSE	uridine phosphorylase 1	203234_at	0.007	42712	9.529E-01	FALSE
160075_at	-0.014	7698	1417468_at	0.067	4135	160075_at	-0.083	2751	1417469_at	-0.291	1418	4000.5	2703.0941	FALSE	nitrilase 1	241395_at	0.141	6299	9.132E-04	FALSE
93620_at	0.123	3335	1456066_a_at	0.047	6531	161379_at	0.050	5315	1446439_at	0.344	821	4000.5	2495.5595	TRUE	RNA polymerase 1-4	222704_at	0.021	31520	6.137E-01	FALSE
97460_at	-0.205	2157	1415768_a_at	-0.003	8445	97460_at	0.206	2587	1443742_x_at	-0.148	2815	4001	2975.2011	FALSE	ubiquitin-conjugating enzyme E2R 2	226954_at	-0.112	11297	1.945E-02	FALSE
93674_at	0.029	6951	1437369_at	0.078	4444	93674_at	0.200	1632	1459278_at	0.196	2982	4002.25	2276.6397	TRUE	FYVE, RhoGEF and PH domain containing 1	228639_at	0.099	7576	2.440E-03	TRUE
97862_s_at	-0.080	5540	1451145_s_at	-0.079	4313	97862_s_at	-0.084	3398	1451145_s_at	-0.145	2760	4002.75	1206.8613	TRUE	transmembrane protein 111	217882_at	-0.214	7549	2.392E-03	TRUE
96850_at	-0.085	6065	1426833_at	-0.186	1431.5	96850_at	-0.073	6719	1446145_at	0.221	1796	4002.875	2775.6057	FALSE	eukaryotic translation initiation factor 4 gamma, 3	243149_at	0.262	7616	2.499E-03	FALSE
92762_at	0.303	270	1425406_at	0.138	2646.5	92762_at	0.069	5780	1425406_at	-0.043	7317	4003.375	3157.8318	FALSE	C-type lectin domain family 4, member a2	219947_at	0.052	19615	1.877E-01	FALSE
161926_r_at	0.081	3940	1437465_a_at	-0.192	2255	161926_r_at	-0.028	6406	1437465_a_at	-0.125	3413	4003.5	1749.4743	FALSE	prolyl 4-hydroxylase, beta polypeptide	200654_at	0.156	10634	1.423E-02	FALSE
94806_at	-0.117	3530	1416090_at	0.150	2571	94806_at	0.086	5781	1416090_at	0.140	4133	4003.75	1348.1512	FALSE	pyruvate dehydrogenase (lipoamide) beta	208911_s_at	-0.261	5631	4.943E-04	FALSE
99368_at	-0.039	6753	1423037_at	-0.124	2613	99368_at	-0.084	3697	1423037_at	0.134	2954	4004.25	1887.5585	FALSE	angiotensin receptor-like 1	213592_at	0.959	1913	3.317E-06	FALSE
104650_at	0.115	3493	1422635_at	-0.143	3328	104650_at	-0.125	2443	1422635_at	-0.102	6753	4004.25	1889.6048	FALSE	acetylcholinesterase	205377_s_at	-0.389	3829	6.906E-05	FALSE
103444_at	0.161	815	1452210_at	0.074	4792	103444_at	0.043	5517	1438817_at	-0.117	4894	4004.5	2150.3436	FALSE	DNA2 DNA replication helicase 2-like (yeast)	213647_at	0.018	36126	7.667E-01	FALSE
98398_s_at	0.030	7083	1451755_a_at	0.177	1351.5	98398_s_at	0.096	2943	1451755_a_at	0.226	4641	4004.625	2452.7186	TRUE	apolipoprotein B editing complex 1	207158_at	-0.018	36191	7.676E-01	FALSE
96102_i_at	-0.050	6814	1450903_at	-0.223	2072	96102_i_at	-0.079	6527	1456822_at	0.686	607	4005	3137.6136	FALSE	RAD23b homolog (S. cerevisiae)	201223_s_at	-0.186	8007	3.299E-03	FALSE
95677_at	0.175	1112	1452713_a_at	-0.047	6915	95677_at	0.158	2794	1452713_a_at	-0.223	5201	4005.5	2564.7927	FALSE	WD repeat domain 57 (U5 snRNP specific)	NA	NA	NA	NA	
100489_at	0.074	5992	1450933_at	0.219	2987	100489_at	-0.040	6599	1451839_a_at	0.565	446	4006	2850.7196	FALSE	phosphodiesterase 7A	223359_s_at	-0.056	21326	2.442E-01	FALSE
102286_at	0.087	3209	1426602_at	0.017	8042	102286_at	-0.104	3296	1440764_at	-0.225	1480	4006.75	2817.1664	FALSE	v-raf murine sarcoma 3611 viral oncogene homolog	201895_at	0.184	865	3.201E-07	FALSE
101224_at	0.159	3213	1445125_at	0.256	310	101224_at	0.046	6082	1445125_at	0.062	6423	4007	2854.2907	TRUE	DNA segment, Chr 8, ERATO Doi 107, expressed	NA	NA	NA	NA	
97721_at	0.189	479	1418376_at	0.052	6339	97721_at	0.022	7399	1418376_at	0.201	1812	4007.25	3376.8179	TRUE	fibroblast growth factor 15	223761_at	-0.025	29915	5.543E-01	FALSE
94046_at	0.095	2675	1423518_at	0.045	6146.5	162504_at	0.133	2795	1439744_at	0.222	4413	4007.375	1631.5089	TRUE	c-src tyrosine kinase	202329_at	0.154	8658	4.793E-03	TRUE
100696_at	0.141	3138	1450415_at	0.086	3751.5	100696_at	-0.100	2415	1450415_at	0.055	6725	4007.375	1892.3027	FALSE	phosphodiesterase 6A, cGMP-specific, rod, alpha	206623_at	0.022	37669	8.106E-01	FALSE
101431_at	0.147	2142	1418808_at	-0.071	4944	101431_at	0.084	4149	1418808_at	-0.505	4798	4008.25	1291.2568	FALSE	retinol dehydrogenase 5	210106_at	0.172	7112	1.728E-03	FALSE
94707_s_at	0.090	4580	1451614_a_at	0.037	6883	94707_s_at	-0.120	3384	1451614_a_at	-0.236	1187	4008.5	2376.2874	FALSE	amelogenin X chromosome	208410_x_at	0.005	41106	9.101E-01	FALSE
97798_at	0.122	2615	1426655_a_at	0.076	3481	97798_at	-0.050	5938	1437551_at	-0.109	4003	4009.25	1407.4915	FALSE	RIKEN cDNA 4930504E06 gene	226062_x_at	0.496	227	2.245E-08	FALSE
102146_at	0.104	3779	1421380_at	0.079	4812.5	102146_at	-0.161	935	1421380_at	-0.063	6516	4010.625	2340.4435	FALSE	insulin receptor	207851_s_at	-0.071	24856	3.673E-01	FALSE
102822_at	0.243	1140	1418679_at	0.088	3770	102822_at	-0.067	3747	1418679_at	0.035	7392	4012.25	2569.1485	FALSE	granzyme F	NA	NA	NA	NA	
101689_at	0.412	226	1419831_at	-0.044	5925	101689_at	-0.105	3262	1419831_at	-0.050	6638	4012.75	2912.7157	FALSE	expressed sequence AA416453	NA	NA	NA	NA	
93580_at	-0.039	6737	1418017_at	-0.169	2742.5	93580_at	0.126	2385	1418017_at	-0.121	4187	4012.875	1976.1078	FALSE	pumilio 2 (Drosophila)	201493_s_at	0.155	16311	9.761E-02	FALSE
95428_at	0.065	4467	1426214_at	0.072	4553.5	162197_at	0.126	1807	1426214_at	-0.140	5226	4013.375	1509.532	FALSE	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	212411_at	-0.268	3414	4.119E-05	FALSE
162073_r_at	-0.113	2978	1422043_at	0.079	5767.5	162073_r_at	0.144	1499	1439989_at	0.182	5809	4013.375	2136.61	FALSE	Tuberous sclerosis 1	209390_at	-0.047	27873	4.758E-01	FALSE
160191_at	-0.123	1614	1452120_at	-0.027	7579.5	160191_at	-0.117	3378	1452120_at	-0.193	3483	4013.625	2527.1358	TRUE	N-acetyltransferase 11	222369_at	0.181	6803	1.331E-03	FALSE
160132_at	0.109	3333	1415805_at	0.157	1749	160132_at	0.033	6307	1438612_a_at	-0.109	4668	4014.25	1939.0333	FALSE	colipase, pancreatic	206131_at	-0.008	40919	9.047E-01	FALSE
101564_at	0.126	3954	1430519_a_at	-0.082	6160	101564_at	-0.566	75	1430519_a_at	-0.106	5870	4014.75	2802.9372	FALSE	CCR4-NOT transcription complex, subunit 7	225053_at	-0.163	13923	5.113E-02	FALSE
101395_at	0.000	8522	1419641_at	-0.132	5040	101395_at	0.188	1512	1419641_at	0.378	986	4015	3502.5478	FALSE	Purine rich element binding protein B	235711_at	-0.063	15935	8.940E-02	FALSE
96653_at	-0.124	4452	1456012_x_at	0.116	4902.5	96653_at	0.225	2421	1431785_at	-0.155	4285	4015.125	1094.2823	FALSE	ribonuclease T2	239388_at	-0.158	4242	1.130E-04	FALSE
101611_at	0.143	2971	1449759_at	0.153	1805.5	101611_at	-0.017	7211	1420173_at	-0.121	4073	4015.125	2323.0444	FALSE	DNA segment, Chr 11, ERATO Doi 326, expressed	NA	NA	NA	NA	
161031_at	-0.015	7650	1453175_at	0.068	4890	161031_at	0.175	1855	1453175_at	-0.179	1666	4015.25	2837.9717	FALSE	zinc finger and BTB domain containing 25	230846_at	-0.984	787	2.619E-07	FALSE
97395_at	-0.123	3092	1449635_at	-0.077	6383	97395_at	-0.332	1447	1460633_at	0.234	5139	4015.25	2184.594	FALSE	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	203103_s_at	-0.058	24715	3.623E-01	FALSE
160732_at	0.129	2257	1434507_at	0.123	1857	160732_at	0.074	4305	1434507_at	-0.025	7643	4015.5	2645.374	FALSE	aminopeptidase-like 1	235033_at	-0.268	2809	1.626E-05	FALSE
102790_at	0.023	7201	1424283_at	0.155	1985	102790_at	0.097	3361	1424283_at	0.146	3516	4015.75	2232.2045	TRUE	jumping translocation breakpoint	210927_x_at	-0.123	11336	1.974E-02	FALSE
102644_at	0.093	4984	1427040_at	0.010	8301	102644_at	0.176	1175	1427040_at	-0.536	1604	4016	3326.0223	FALSE	MyoD family inhibitor domain containing	211675_s_at	0.485	3951	8.254E-05	FALSE
93719_at	0.011	8124	1426139_a_at	0.080	4581.5	93719_at	0.109	2219	1437669_x_at	-0.257	1141	4016.375	3092.4795	FALSE	chemokine (C-C motif) receptor-like 1	220351_at	0.059	19550	1.864E-01	FALSE
161859_f_at	0.106	4190	1417788_at	0.146	2979	104280_at	0.075	4035	1417788_at	-0.272	4862	4016.5	779.25627	FALSE	synuclein, gamma	209877_at	-0.155	13988	5.204E-02	FALSE
99078_at	-0.140	2547	1417322_at	0.116	2922.5	99078_at	0.055	5771	1417322_at	0.144	4826	4016.625	1537.2949	FALSE	deoxyhypusine hydroxylase/monooxygenase	208141_s_at	0.141	17117	1.174E-01	FALSE
103881_at	-0.190	2765	1424488_a_at	0.136	2408	103881_at	0.153	4937	1424488_a_at	0.078	5958	4017	1709.8017	FALSE	pyrophosphatase (inorganic) 2	220741_s_at	-0.024	35546	7.478E-01	FALSE
95462_at	-0.025	6960	1423456_at	0.121	4299	95462_at	-0.140	3354	1443227_at	0.431	1456	4017.25	2290.4921	FALSE	basic leucine zipper and W2 domains 2	217809_at	-0.421	464	9.144E-08	FALSE
160175_at	0.101	2447	1417614_at	0.139	2962	161569_f_at	-0.131	2396	1417614_at	0.009	8265	4017.5	2843.183	FALSE	creatine kinase, muscle	204810_s_at	-0.046	27959	4.789E-01	FALSE

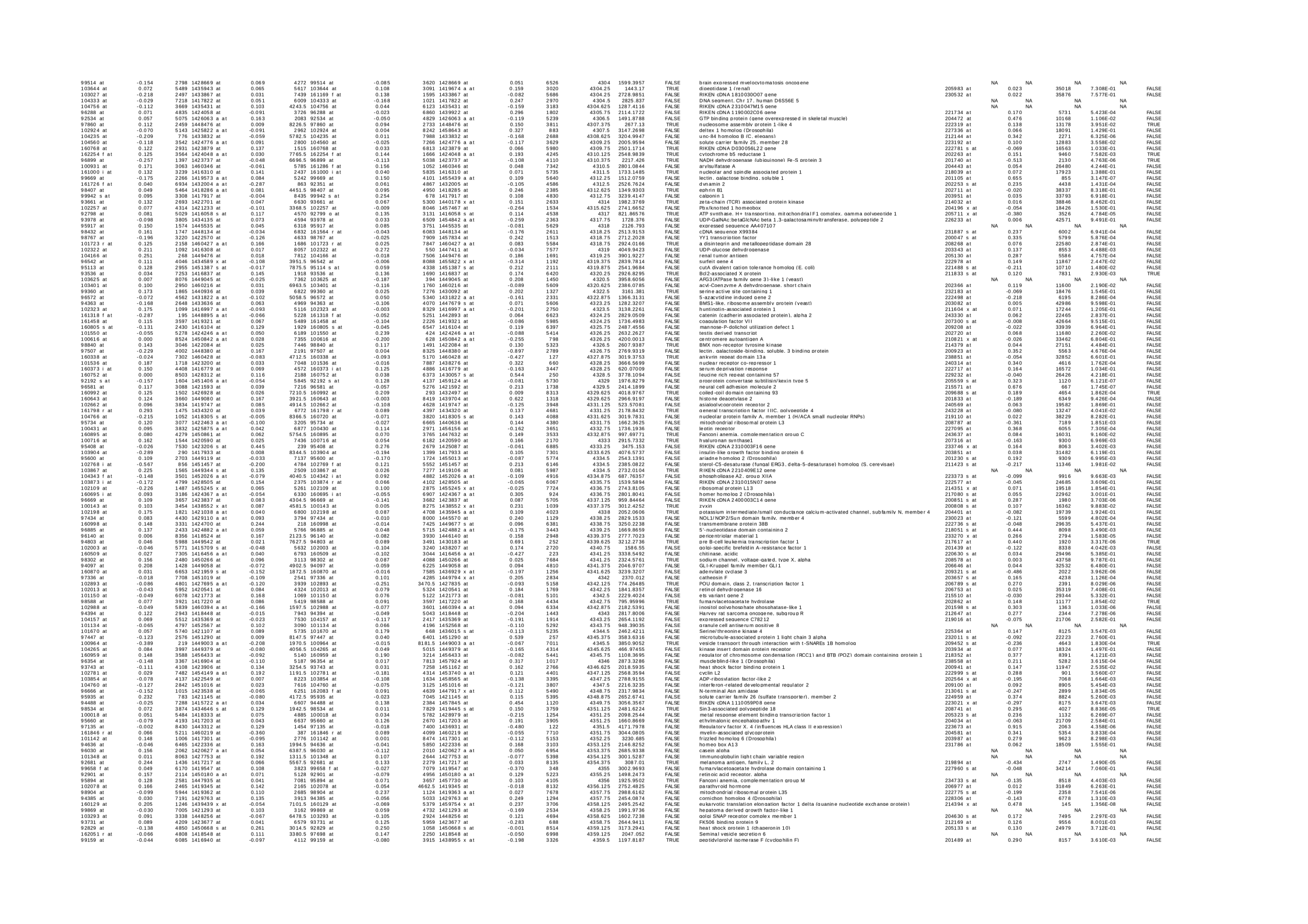
103543 at	-0.256	1789	1424764 at	-0.111	5663	103543 at	-0.237	5031	1424764 at	0.159	3588	4017.75	1721.0011	FALSE	seizure related 6 homolog like	231650 s at	-0.190	10305	1.201E-02	FALSE
160779 at	0.061	4923	1429939 at	0.134	1740	160779 at	0.001	8467	1454030 at	0.350	942	4018	3428.4927	TRUE	SAPS domain family, member 3	228105 at	0.481	953	3.904E-07	TRUE
98340 at	-0.033	6813	1449750 at	-0.089	3711.5	98340 at	-0.157	1567	1449750 at	-0.204	3983	4018.625	2153.6474	TRUE	expressed sequence AA407331	NA	NA	NA	NA	
93147 f at	-0.080	4387	1426930 at	-0.230	3792	93147 f at	0.123	2499	1426929 at	0.120	5403	4020.25	1212.8208	FALSE	bruno-like 4, RNA binding protein (Drosophila)	223653 x at	-0.332	3240	3.197E-05	FALSE
160661 at	-0.024	7038	1420040 at	0.122	2573.5	160661 at	0.147	703	1454621 s at	0.082	5768	4020.625	2901.6477	FALSE	RIKEN cDNA 5730472N09 gene	226356 at	-0.017	37662	8.105E-01	FALSE
161344 r at	0.071	5529	1420023 at	-0.086	4397.5	161344 r at	0.239	1638	1440629 at	-0.095	4519	4020.875	1667.584	FALSE	eukaryotic translation termination factor 1	201573 s at	0.051	30754	5.844E-01	FALSE
160485 r at	-0.023	7308	1426384 a at	0.087	4680	160485 r at	-0.178	875	1440841 at	0.290	3221	4021	2694.1892	FALSE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	210317 s at	-0.559	6015	6.990E-04	FALSE
98373 at	-0.005	8305	1450291 s at	0.166	2239	98373 at	0.196	581	1420671 x at	-0.092	4964	4022.25	3378.9063	FALSE	membrane-spanning 4-domains, subfamily A, member 4C	NA	NA	NA	NA	
94684 at	0.138	2681	1449598 at	0.129	3777.5	94684 at	0.004	8332	1446948 at	0.270	1303	4023.375	3045.6042	TRUE	Density-regulated protein	234915 s at	-0.124	9213	6.592E-03	FALSE
94403 at	-0.110	3030	1432027 a at	-0.157	1110.5	94403 at	0.017	7477	1449772 at	0.132	4476	4023.375	2683.5319	FALSE	TBC1 domain family, member 14	224622 at	0.083	13982	5.202E-02	FALSE
93672 at	0.150	2032	1422006 at	0.138	1689.5	93672 at	0.041	6128	1440866 at	-0.282	6248	4024.375	2502.7282	FALSE	eukaryotic translation initiation factor 2-alpha kinase 2	204211 x at	0.025	27589	4.656E-01	FALSE
102269 at	0.082	5661	1426039 a at	0.019	7753.5	161947 f at	0.129	1568	1445579 at	-0.642	1115	4024.375	3218.8588	FALSE	arachidonate lipoxygenase, epidermal	NA	NA	NA	NA	
96668 at	-0.099	2834	1438656 x at	0.164	1882	96668 at	-0.056	4740	1438656 x at	0.109	6644	4025	2111.9751	FALSE	translocase of inner mitochondrial membrane 17b	203342 at	-0.151	4685	1.940E-04	FALSE
92198 s at	0.169	1940	1430457 at	-0.103	4770	92198 s at	0.060	6106	1430457 at	0.154	3284	4025	1805.7216	FALSE	decay accelerating factor 2	NA	NA	NA	NA	
98120 at	0.069	6164	1415690 at	0.147	2870	98120 at	0.231	470	1415690 at	0.058	6597	4025.25	2896.1212	TRUE	mitochondrial ribosomal protein L27	224330 s at	0.050	28873	5.161E-01	FALSE
97512 at	0.084	5629	1428258 at	0.211	1271.5	97512 at	0.224	1026	1428258 at	-0.014	8176	4025.625	3482.3066	FALSE	RIKEN cDNA 2010107E04 gene	NA	NA	NA	NA	
161904 f at	-0.073	4431	1420579 s at	0.050	5952	94757 at	0.170	746	1427767 a at	0.109	4974	4025.75	2275.2732	FALSE	cystic fibrosis transmembrane conductance regulator homolog	205043 at	-0.083	19608	1.874E-01	FALSE
162204 r at	0.057	5270	1418634 at	-0.081	3782.5	97497 at	0.168	1104	1418634 at	-0.075	5947	4025.875	2147.491	FALSE	Notch gene homolog 1 (Drosophila)	218902 at	0.531	13	2.124E-09	FALSE
103624 at	0.079	4051	1431752 a at	0.089	3647.5	103624 at	-0.160	1103	1431753 x at	0.047	7302	4025.875	2544.2741	FALSE	RIKEN cDNA 2900073H19 gene	208101 s at	0.039	24925	3.694E-01	FALSE
102124 f at	-0.195	1924	1448322 a at	0.047	6158.5	102124 f at	0.343	236	1448322 a at	0.022	7788	4026.625	3534.7184	FALSE	cytochrome c oxidase subunit IV isoform 1	202698 x at	-0.351	786	2.614E-07	FALSE
93579 at	0.063	6167	1417064 at	0.120	3004	93579 at	-0.147	2090	1417064 at	0.129	4846	4026.75	1830.1966	FALSE	jagunal homolog 1 (Drosophila)	223104 at	-0.080	17849	1.368E-01	FALSE
102143 at	0.132	3078	1417951 at	-0.040	7204	102143 at	0.110	2376	1417951 at	0.143	3452	4027.5	2164.1284	FALSE	Enolase 3, beta muscle	204483 at	0.080	14768	6.651E-02	FALSE
95305 at	0.096	5353	1460745 at	0.208	937	95305 at	0.065	3717	1460745 at	-0.090	6103	4027.5	2288.5404	FALSE	RIKEN cDNA A630098A13 gene	NA	NA	NA	NA	
160228 at	0.069	6805	1431293 a at	-0.135	2791	160228 at	-0.055	5696	1437399 at	0.326	820	4028	2727.3544	FALSE	claudin domain containing 1	209143 s at	0.206	9358	7.165E-03	FALSE
97491 at	0.061	6521	1452030 a at	-0.142	3825	97491 at	-0.265	4019	1438807 at	0.574	1747	4028	1954.4223	FALSE	heterogeneous nuclear ribonucleoprotein R	208765 s at	0.098	14891	6.866E-02	FALSE
160329 at	0.140	1915	1437233 x at	0.113	3859.5	160329 at	0.049	6600	1455974 at	0.123	3739	4028.375	1931.4818	TRUE	RIKEN cDNA 1110049F12 gene	223123 s at	-0.149	15825	8.661E-02	FALSE
103539 at	0.107	4088	1460204 at	0.156	1210	103539 at	0.006	8227	1441524 at	0.141	2590	4028.75	3035.5761	TRUE	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	206301 at	-0.013	39596	8.674E-01	FALSE
102040 at	-0.006	8220	1450480 a at	-0.065	5790	102040 at	0.173	912	1450480 a at	0.323	1196	4029.5	3578.0432	FALSE	G protein-coupled receptor kinase 6	210981 s at	0.143	11858	2.438E-02	FALSE
100553 at	0.091	3395	1456375 x at	0.143	1266	100553 at	-0.025	6959	1415815 at	0.105	4501	4030.25	2369.5149	FALSE	tripartite motif protein 27	212118 at	0.068	15651	8.315E-02	FALSE
101975 at	0.187	1219	1449939 s at	-0.395	4302	101975 at	0.128	2359	1449939 s at	0.025	8243	4030.75	3083.143	FALSE	delta-like 1 homolog (Drosophila)	209560 s at	-0.102	17638	1.306E-01	FALSE
104564 at	-0.143	4747	1448628 at	-0.143	2756	162237 f at	0.158	1683	1448628 at	0.047	6938	4031	2316.753	FALSE	secretogranin III	219196 at	-0.530	2419	8.282E-06	FALSE
93492 at	-0.094	3009	1450103 a at	0.025	7265	93492 at	0.066	4388	1450103 a at	0.282	1465	4031.75	2464.0781	FALSE	pleckstrin homology, Sec7 and coiled-coil domains 2	209158 s at	-0.185	7514	2.330E-03	FALSE
100369 at	0.123	2285	1423115 at	0.041	6207	100369 at	-0.272	2318	1423115 at	0.174	5318	4032	2030.9461	FALSE	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialylt	222571 at	-0.219	7255	1.936E-03	FALSE
160150 f at	-0.158	4684	1436836 x at	-0.295	1014.5	160150 f at	0.058	6854	1426724 at	-0.209	3576	4032.125	2429.1309	FALSE	calponin 3, acidic	228297 at	0.295	16054	9.219E-02	FALSE
101705 at	0.208	1916	1421800 at	0.069	5497.5	101705 at	-0.079	4575	1421800 at	0.135	4141	4032.375	1520.0741	FALSE	per-hexamer repeat gene 1	NA	NA	NA	NA	
160390 at	-0.074	3881	1448367 at	0.010	8313	160390 at	-0.235	561	1455584 at	-0.122	3375	4032.5	3205.6851	FALSE	stromal cell derived factor 4	232032 x at	0.134	12304	2.926E-02	FALSE
102702 at	-0.063	5061	1435358 at	0.087	4410	102702 at	0.130	2778	1443455 at	-0.172	3884	4033.25	965.42542	FALSE	CUE domain containing 1	219468 s at	0.323	5322	3.704E-04	FALSE
103597 at	0.233	775	1418028 at	0.094	5081	103597 at	-0.019	7270	1418028 at	-0.160	3009	4033.75	2783.2601	FALSE	dopachrome tautomerase	205337 at	-0.080	11447	2.059E-02	FALSE
102746 at	0.138	2531	1456100 at	0.130	2042	102746 at	0.105	3047	1456100 at	0.001	8515	4033.75	3015.5487	TRUE	cDNA sequence BC089491	NA	NA	NA	NA	
101420 at	-0.101	5065	1422756 at	-0.145	3153.5	101420 at	-0.113	5644	1422756 at	-0.169	2274	4034.125	1584.0814	TRUE	solute carrier family 32 (GABA vesicular transporter), member 1	240532 at	-1.084	1092	5.772E-07	TRUE
100885 at	0.074	4363	1417299 at	0.131	3553.5	100885 at	-0.035	6219	1437579 at	-0.264	2001	4034.125	1755.6039	FALSE	NIMA (never in mitosis gene a)-related expressed kinase 2	211080 s at	-0.058	18833	1.646E-01	FALSE
94289 r at	0.277	444	1426306 a at	-0.007	8331	94289 r at	0.243	331	1426306 a at	0.112	7031	4034.25	4244.468	FALSE	melanoma antigen, family D, 2	213627 at	0.201	5794	5.832E-04	FALSE
98552 at	0.179	2195	1416707 a at	0.148	1805.5	98552 at	0.057	5037	1416707 a at	0.055	7100	4034.375	2500.2998	TRUE	polyamine-modulated factor 1	202337 at	0.046	25981	4.033E-01	FALSE
97411 at	0.058	5615	1419513 a at	0.069	5406.5	97411 at	0.129	1449	1419513 a at	0.122	3668	4034.625	1932.1402	TRUE	ect2 oncogene	219787 s at	-0.025	29549	5.403E-01	FALSE
100949 at	-0.040	6468	1417688 at	-0.223	315	100949 at	0.009	7881	1417688 at	-0.234	1475	4034.75	3701.4954	FALSE	cDNA sequence BC004044	NA	NA	NA	NA	
99579 at	-0.192	1973	1423126 at	-0.145	2416	99579 at	-0.011	8054	1423126 at	-0.160	3697	4035	2777.2654	TRUE	ATPase, Na+/K+ transporting, beta 3 polypeptide	242836 at	-0.166	15624	8.270E-02	FALSE
99386 at	-0.287	2228	1422165 at	0.136	2280.5	99386 at	-0.064	7008	1422165 at	-0.238	4625	4035.375	2275.2544	FALSE	POU domain, class 3, transcription factor 4	207694 at	-0.103	15448	7.874E-02	FALSE
96795 at	-0.085	3488	1421969 a at	0.057	6519	96795 at	-0.128	6037	1421969 a at	0.578	101	4036.25	2941.3046	FALSE	fatty acid amide hydrolase	204231 s at	-0.178	11940	2.528E-02	FALSE
94622 at	0.126	2949	1421530 a at	0.057	6045	94622 at	0.034	7013	1421530 a at	0.627	139	4036.5	3123.3949	TRUE	glutamate receptor, metabotropic 8	216992 s at	-0.169	8790	5.145E-03	FALSE
101471 at	0.089	4784	1421258 a at	0.081	3744	101471 at	0.129	2530	1421258 a at	-0.110	5088	4036.5	1157.5127	FALSE	pyruvate kinase liver and red blood cell	210451 at	0.048	28981	5.198E-01	FALSE
103717 at	0.080	4217	1448146 at	0.048	6122.5	103717 at	0.099	2406	1438482 at	-0.137	3407	4038.125	1574.671	FALSE	WW domain containing E3 ubiquitin protein ligase 2	204022 at	0.237	3700	5.947E-05	FALSE
103068 at	0.068	5578	1417826 at	0.068	5239.5	103068 at	0.190	2646	1417826 at	0.167	2691	4038.625	1588.2143	TRUE	aldo-keto reductase family 1, member E1	223856 at	-0.016	33590	6.856E-01	FALSE
95636 at	-0.160	2653	1428679 s at	0.041	6873	95636 at	0.121	1267	1429252 at	0.097	5366	4039.75	2542.7979	FALSE	RIKEN cDNA 0610010K14 gene	NA	NA	NA	NA	
161023 at	0.073	4331	1448681 at	0.063	5531	161023 at	0.062	4139	1448681 at	0.169	2160	4040.25	1396.6582	TRUE	interleukin 15 receptor, alpha chain	207375 s at	0.106	12719	3.393E-02	TRUE
96096 f at	0.194	1030	1426856 at	-0.044	6924	96095 i at	0.263	71	1426856 at	-0.027	8138	4040.75	4079.3839	FALSE	hydroxysteroid dehydrogenase like 2	215436 at	0.364	1255	8.153E-07	FALSE
98838 at	0.004	8353	1421247 at	0.094	2927	98838 at	0.161	621	1421246 at	0.112	4263	4041	3244.4837	TRUE	paired box gene 9	231145 at	-0.071	18388	1.518E-01	FALSE
93523 at	-0.073	3938	1417606 a at	-0.217	884	93523 at	0.019	7402	1417606 a at	-0.188	3940	4041	2663.5678	FALSE	calreticulin	212953 x at	0.097	19080	1.712E-01	FALSE
102865 at	0.049	5501	1451873 a at	-0.096	3573.5	102865 at	-0.047	5598	1421047 at	0.189	1492	4041.125	1938.3675	FALSE	MAD homolog 5 (Drosophila)	225219 at	0.547	365	5.392E-08	FALSE
92329 at	0.121	3447	1422178 a at	0.071	5129	92329 at	-0.078	2869	1422178 a at	-0.108	4720	4041.25	1060.0636	FALSE	RAB17, member RAS oncogene family	218931 at	0.004	42804	9.542E-01	FALSE
102011 at	0.148	1322	1421949 a at	0.099	3284	102011 at	-0.014	7413	1421948 a at	-0.126	4148	4041.75	2539.5433	FALSE	RIKEN cDNA 2610507L03 gene	232106 s at	-0.024	31942	6.290E-01	FALSE
100944 at	-0.280	1933	1434372 at	0.067	5520	100944 at	0.036	5852	1434372 at	-0.416	2863	4042	1940.6619	FALSE	expressed sequence AW112010	NA	NA	NA	NA	
92934 at	0.114	4366	1449126 at	0.143	3630	92934 at	0.350	475	1440334 at	-0.032	7697	4042	2964.0757	FALSE	zinc finger protein 90	NA	NA	NA	NA	
96892 at	0.058	5726	1415695 at	0.201	2629.5	96892 at	0.129	4031	1415695 at	0.129	3791	4044.375	1277.2512	TRUE	proteasome (prosome, macropain) subunit, alpha type 1	210759 s at	-0.390	3609	5.306E-05	FALSE
101034 at	-0.091	3738	1449111 a at	-0.026	7502.5	101034 at	-0.191	1047	1449111 a at	0.117	3892	4044.875	2649.5263	FALSE	growth factor receptor bound protein 2	215075 s at	-0.244	268	3.166E-08	FALSE
95594 at	0.103	5534	1449697 s at	0.160	1718	162387 f at	0.106	3477	1426773 at	0.114	5451	4045	1819.4789	TRUE	mitofusin 1	236417 at	0.300	5348	3.816E-04	TRUE
94945 at	-0.061	5108	1451369 at	0.256	178	94945 at	0.005	8243	1419989 at	0.223	2651	4045	3447.2258	FALSE	COMM domain containing 5	224387 at	0.116	9035	5.937E-03	FALSE
98821 at	0.083	4377	1422174 at	0.163	918	98821 at	0.080	2937	1422173 at	0.018	7949	4045.25	2964.0756	TRUE	insulin promoter factor 1, homeodomain transcription factor	210938 at	-0.068	23839	3.323E-01	FALSE
94850 at	0.081	4024	1418073 at	-0.024	7637	160171 f at	0.131	2122	1418073 at	0.155	2401	4046	2536.636	FALSE	acyl-CoA thioesterase 9	NA	NA	NA	NA	
161367 f at	0.113	3509	1448408 at	0.049	6370	93901 at	-0.055	5017	1448408 at	-0.353	1291	4046.75	2177.3232	FALSE	Hermansky-Pudlak syndrome 1 homolog (human)	203309 s at	-0.088	12143	2.734E-02	FALSE
101615 at	0.225	1596	1420149 at	0.049	7129	101615 at	-0.089	2903	1454749 at	0.114	4559	4046.75	2385.8615	FALSE	Pericentrin (kendrin)	NA	NA	NA	NA	
160140 at	-0.247	547	1428282 at	0.042	6599.5	160140 at	0.076	6436	1428282 at	-0.200	2605	4046.875	2975.0037	FALSE	tubulin-specific chaperone e	203715 at	-0.012	36367	7.737E-01	FALSE
96651 at	0.061	6589	1422675 at	0.093	5074	96651 at	0.175	1168	1430822 at	0.211	3357	4047	2329.609	TRUE	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member	211988 at	0.101	20224	2.078E-01	FALSE
95642 at	0.000	8511	1456530 x at	-0.251	221	95642 at	-0.054	5669	1425676 a at	-0.267	1788	4047.25	3754.9761	TRUE	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	57163 at	0.244	16168	9.458E-02	FALSE
101280 at	0.183	1037	1460313 at	0.094	2863	101280 at	-0.020	7086	1460313 at	-0.093	5206	4048	2648.3173	FALSE	olfactory receptor 2	221465 at	0.050	27245	4.519E-01	FALSE
95491 at	-0.233	1799	1456194 a at	0.294	667.5	95491 at	-0.024	7811	1416526 a at	0.093	5916	4048.375	3373.197	FALSE	Parkinson disease (autosomal recessive, early onset) 7	200006 at	-0.027	35317	7.406E-01	FALSE
98505 i at	0.311	365	1422492 at	0.100	4541	98506 r at	-0.030	7644	1422492 at	-0.156	3644	4048.5	2994.5489	FALSE	coproporphyrinogen oxidase	234059 at	0.173	11397	2.018E-02	FALSE
97446 at	-0.235	1961	1453251 at	0.235	916	162140 i at	0.030	6969	1453251 at	-0.068	6349	4048.75	3054.6049	FALSE	DEAH (Asp-Glu-Ala-His) box polypeptide 30	204355 at	-0.258	4577	1.660E-04	FALSE
96803 at	0.057	5973	1420654 a at	-0.095	4234	96803 at	0.250	1556	1458767 at	0.174	4432	4048.75	1834.6424	FALSE	glucan (1,4-alpha-), branching enzyme 1	203282 at	0.221	9630	8.322E-03	FALSE
93853 at	-0.037	6356	1451177 at	0.073	5664.5	93853 at	-0.124	2028	1439524 at	-0.187	2148	4049.125	2282.5666	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 4	203811 s at	-0.111	19317	1.785E-01	FALSE
98337 at	0.037	6420	1426177 a at	0.085	4277	98337 at	-0.084	3951	1426177 a at	-0.180	1550	4049.5	1994.0101	FALSE	NK1 transcription factor related, locus 2 (Drosophila)	NA	NA	NA	NA	
101522 at	-0.155	2209	1450958 at	0.058	6418.5	101522 at	-0.096	2157	1439925 at	-0.099	5419	4050.875	2195.1978	FALSE	transmembrane 4 superfamily member 1	209386 at	0.201	22302	2.784E-01	FALSE
94718 at	0.270	704	1422398 at	0.036	6655	94718 at	0.083	5152	1443209 at	0.155	3693	4051	2537.9513	TRUE	histone 1, H1e	208553 at	-0.024	29446	5.368E-01	FALSE
98460 at	0.079	4673	1448223 at	-0.174	1580	98460 at	-0.109	5626	1430829 s at	-0.103	4327	4051.5	1736.8098	FALSE	fatso	209702 at	-0.322	2416	8.244E-06	FALSE
97529 at	0.098	4997	1425789 s at	0.104	2811.5	97529 at	0.088	4180	1417732 at	-0.128	4222	4052.625	908.68911	FALSE	annexin A8	203074 at	-0.040	28792	5.130E-01	FALSE
162332 f at	-0.163	2079	1427079 at	0.192	1256.5	162332 f at	0.080	5428	1427079 at	0.069	7449	4053.125	2894.8534	FALSE	microtubule-associated protein, RP/EB family, member 3	214270 s at	-0.620	1303	8.957E-07	FALSE
104094 at	-0.108	2095	1417928 at	-0.037	6623	162494 at	-0.104	4092	1417928 at	-0.233	3408	4054.5	1902.2969	TRUE	PDZ and LIM domain 4	214175 x at	0.305	8731	4.987E-03	FALSE
103877 at	-0.065	4698	1420054 s at	0.100	3464.5	103877 at	-0.122	1803	1420055 at	0.115	6253	4054.625	1885.4572	FALSE	solute carrier family 35, member C2	219447 s at	0.103	10647	1.436E-02	FALSE
160885 at	0.163	4461	1444953 at	0.102	4652	160885 at	-0.113	5045	1444952 a at	0.262	2063	4055.25	1350.2356	FALSE	nuclear casein kinase and cyclin-dependent kinase substrate 1	229353 s at	0.395	1791	2.614E-06	FALSE
95042 at	-0.060	4755	1424196 at	-0.130	2143	95042 at	-0.045	5288	1424196 at	-0.168	4035	4055.25	1374.3402	TRUE	Yip1 domain family, member 1	214733 s at	0.077	15924	8.919E-02	FALSE
97789 at	0.047	5999	1437779 at	0.112	2928.5	97789 at	-0.065	5622	1422213 s at	0.205	1675	4056.125	2095.0754	FALSE	forkhead box H1	231407 s at	-0.054	22717	2.924E-01	FALSE
93547 at	0.167	1470	1460716 a at	-0.040	6595	93547 at	0.065	4235	1442617 at	-0.132	3925	4056.25	2096.276	FALSE	core binding factor beta	202370 s at	0.547	1411	1.157E-06	FALSE
93891 at	-0.180	1424	1421312 a at	-0.044	7289.5	93890 at	0.104	2849	1426493 a at	-0.144	4664	4056.625	2530.4451	FALSE	kinesin family member C2	226791 at	-0.909	48	3.857E-09	FALSE
95479 at	0.233	1445	1448505 at	0.469	743	95479 at	0.016	8125	1416887 at	0.090	5915	4057	3549.9262	TRUE	nuclear DNA binding protein	200056 s at	-0.247	11473	2.081E-02	FALSE
103072 at	0.232	1721	1448453 at	0.153	3138	161261 f at	-0.074	3453	1448453 at	0.026	7916	4057	2680.6811	FALSE	hydroxysteroid dehydrogenase-1, delta<5>-3-beta	233791 at	-0.045	22108	2.721E-01	FALSE
103765 at	-0.132	1496	1418200 at	0.064	5701	103765 at	-0.068	4014	1418200 at	-0.096	5019	4057.5	1842.8917	FALSE	GLI-Kruppel family member HKR3	NA	NA	NA	NA	
102123 at	0.076	4572	1423141 at	0.072	4782.5	102123 at	0.081	4004	1423141 at	-0.240	2873	4057.875	855.61619	FALSE	Lysosomal acid lipase 1	201847 at	0.081	32393	6.443E-01	FALSE
160094 at	-0.055	5879	1423588 at	-0.194	970	160094 at	-0.021	7183.5	1423588 at	0.269	2201	4058.375	2947.8231	FALSE	actin related protein 2/3 complex, subunit 4	211672 s at	-0.275	12701	3.361E-02	FALSE
162232 r at	0.082	5799	1418281 at	0.130	3321	104527 at	-0.113	3181	1418281 at	-0.130	3933	4058.5	1205.4049	FALSE	RAD51 homolog (S. cerevisiae)	205023 at	0.069	7114	1.731E-03	FALSE
103559 at	0.108	4353	1450519 a at	-0.067	5988.5	103559 at	-0.142	1426	1450519 a at	-0.137	4467	4058.625	1906.8787	FALSE	protein kinase, cAMP dependent, catalytic, alpha	202801 at	-0.044	27275	4.526E-01	FALSE
104388 at	0.140	2008	1417936 at	0.137	2320	104388 at	0.013	7753	1448898 at	-0.105	4154	4058.75	2638.5212	FALSE	chemokine (C-C motif) ligand 9	NA	NA	NA	NA	
102904 at	-0.111	2484	1422891 at	0.121	3409	102904 at	0.025	6621	1422891 at	0.132	3724	4059.5	1786.9148	FALSE	histocompatibility 2, class II antigen E alpha	208894 at	0.389	15570	8.145E-02	FALSE
98076 at	-0.063	6264	1453634 a at	0.160	1194	161755 at	0.097	3559	1453634 a at	0.085	5222	4059.75	2211.5467	FALSE	endoplasmic reticulum protein 29	201216 at	0.002	44156	9.882E-01	FALSE
162471 i at	0.156	1863	1428874 at	0.100	4049.5	162471 i at	-0.083	4616	1428874 at	0.114	5712	4060.125	1619.1725	FALSE	RIKEN cDNA 1110019N10 gene	218074 at	0.087	19755	1.930E-01	FALSE
100703 at	0.092	3764	1417489 at	-0.031	6944.5	162037 f at	-0.337	1578	1417489 at	-0.362	3954	4060.125	2204.5042	FALSE	neuropeptide Y receptor Y2	210730 s at	0.017	36947	7.894E-01	FALSE
100577 at	0.030	7086	1416336 s at	0.529	669	100577 at	-0.146	3136	1416336 s at	-0.111	5350	4060.25	2779.2944	FALSE	small nuclear ribonucleoprotein D1	202691 at	-0.124	10416	1.269E-02	FALSE
96746 at	0.066	5914	1452005 at	0.095	4610.5	96745 at	0.121	2095	1452005 at	0.116	3622	4060.375	1611.7728	TRUE	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	213149 at	-0.279	1733	2.345E-06	FALSE
160147 r at	0.241	1518	1416518 at	0.101	3523.5	160147 r at	0.177	3341	1416518 at	-0.031	7860	4060.625	2689.8919	FALSE	H1 histone family, member O, oocyte-specific	NA	NA	NA	NA	
93278 at	0.063	6092	1419974 at	0.199	1191.5	95787 s at	-0.028	7004	1419974 at	-0.231	1960	4061.875	2911.7256	FALSE	sterol carrier protein 2, liver	211733 x at	0.274	13293	4.105E-02	FALSE
104518 at	0.125	3004	1450671 at	0.119	3071	104518 at	0.138	2346	1450671 at	-0.026	7827	4062	2531.2267	FALSE	crystallin, beta A1	206982 at	-0.012	37312	7.999E-01	FALSE
93085 at	-0.378	1918	1450696 at	0.029	6868	93085 at	0.041	5686	1450696 at	-0.675	1781	4063.25	2601.9674	FALSE	proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	204279 at	0.358	6598	1.128E-03	FALSE
95750 at	0.063	4839	1426654 at	0.078	6176	95750 at	0.068	4082	1426654 at	0.201	1157	4063.5	2122.274	TRUE	zinc finger, C3HC type 1	223163 s at	0.005	41510	9.208E-01	FALSE
104119 at	0.165	3313	1434620 s at	0.086	6204	104119 at	0.093	6045	1442897 at	0.341	693	4063.75	2609.7	TRUE	RIKEN cDNA 2610024E20 gene	218518 at	-0.379	5963	6.733E-04	FALSE
104725 at	-0.109	4625	1427918 a at	-0.108	2041	104725 at	-0.106	5256	1440925 at	0.251	4334	4064	1402.4994	FALSE	ras homolog gene family, member O	239258 at	0.300	8883	5.407E-03	FALSE
98583 at	0.211	1859	1426520 at	0.041	6504	98583 at	0.103	3848	1426520 at	-0.111	4047	4064.5	1902.8548	FALSE	B-cell translocation gene 4	220766 at	0.012	40222	8.838E-01	FALSE
98994 at	0.132	3513	1416854 at	0.136	2386.5	98994 at	0.098	4178	1416854 at	0.080	6182	4064.875	1593.3742	TRUE	solute carrier family 34 (sodium phosphate), member 2	NA	NA	NA	NA	
161611 f at	0.217	1155	1449581 at	0.066	4973.5	93689 at	-0.049	5910	1449581 at	-0.140	4223	4065.375	2059.3252	FALSE	EMI domain containing 1	213779 at	0.194	5382	3.938E-04	FALSE
94810 at	-0.107	5053	1436884 x at	0.113	3031	94810 at	0.043	6865	1425919 at	-0.290	1313	4065.5	2412.3849	FALSE	Ewing sarcoma breakpoint region 1	229966 at	0.191	6136	7.834E-04	FALSE
96847 at	-0.050	7151	1448447 at	0.156	1841	96847 at	0.112	4881	1448447 at	0.167	2389	4065.5	2445.7039	FALSE	vacuolar protein sorting 28 (yeast)	218679 s at	0.090	25058	3.748E-01	FALSE
92961 at	0.058	5848	1450428 at	-0.108	3447	92961 at	-0.052	5509	1421951 at	0.211	1460	4066	2035.6956	FALSE	LIM homeobox protein 1	206230 at	-0.037	31654	6.186E-01	FALSE
101582 at	-0.153	1018	1426579 at	0.084	4257	101582 at	-0.089	3003	1426579 at	0.017	7987	4066.25	2934.3367	FALSE	guanine nucleotide binding protein-like 2 (nucleolar)	201948 at	0.103	11677	2.255E-02	FALSE
104716 at	-0.196	3341	1448754 at	-0.106	6927	104716 at	0.326	2229	1448754 at	-0.380	3770	4066.75	2014.3757	FALSE	retinol binding protein 1, cellular	203423 at	0.125	22543	2.864E-01	FALSE
95360 at	0.143	1489	1448037 at	0.030	7103	95360 at	-0.091	3643	1448037 at	0.111	4037	4068	2312.5781	FALSE	zinc finger, CCHC domain containing 6	220933 s at	0.153	5418	4.075E-04	FALSE
104322 at	0.060	5399	1434748 at	0.145	1093.5	104322 at	-0.097	3336	1434748 at	0.073	6448	4069.125	2367.8	FALSE	cytoskeleton associated protein 2	218252 at	-0.118	9976	1.002E-02	FALSE
102766 at	0.037	6617	1427939 s at	0.232	891	102766 at	0.077	3515	1427938 at	0.118	5254	4069.25	2470.0289	TRUE	c-myc binding protein	203360 s at	0.155	11816	2.399E-02	TRUE
102572 at	-0.076	3601	1421621 at	-0.090	2942.5	102572 at	-0.122	2147	1421621 at	0.051	7590	4070.125	2420.7124	FALSE	RAS protein-specific guanine nucleotide-releasing factor 2	228109 at	-0.380	10823	1.576E-02	FALSE
99029 at	-0.117	2781	1422581 at	-0.153	3694	99029 at	0.000	8517	1422581 at	-0.198	1292	4071	3124.9526	FALSE	protein inhibitor of activated STAT 1	222371 at	0.207	4730	2.027E-04	FALSE
99557 at	-0.052	5996	1439398 x at	-0.049	6618	99557 at	-0.147	3427	1442706 at	0.340	244	4071.25	2901.3502	FALSE	nasal embryonic LHRH factor	221214 s at	0.039	33192	6.718E-01	FALSE
97508 at	0.116	4951	1454925 x at	0.073	4296	97508 at	-0.087	3726	1434319 at	0.156	3313	4071.5	711.48038	FALSE	malate dehydrogenase 1, NAD (soluble)	200978 at	-0.875	826	2.933E-07	FALSE

101713 at	0.081	3889	1420413 at	0.024	7510	101713 at	-0.079	4155	1443536 at	-0.421	732	4071.5	2769.8268	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	209921 at	0.558	3703	5.953E-05	FALSE
104266 at	0.027	6847	1439506 at	-0.136	1932	104266 at	0.027	6427	1439506 at	-0.346	1082	4072	2986.9912	FALSE	gene model 98, (NCBI)	204073 s at	0.453	8238	3.779E-03	FALSE
95537 at	0.041	6220	1417846 at	0.100	3228	95537 at	0.107	3253	1417847 at	0.129	3591	4073	1440.8745	TRUE	Unc-51 like kinase 2 (C. elegans)	204062 s at	-0.173	12811	3.502E-02	FALSE
92417 at	-0.156	1174	1417858 at	0.039	6405	92417 at	-0.066	5793	1417858 at	0.184	2923	4073.75	2457.8665	FALSE	RAS protein activator like 1 (GAP1 like)	233144 s at	-0.122	9299	6.960E-03	FALSE
93866 s at	-0.004	8401	1448416 at	0.094	5537	93866 s at	0.269	1706	1448416 at	-0.449	651	4073.75	3567.8028	FALSE	matrix Gla protein	202291 s at	0.214	16710	1.065E-01	FALSE
95610 at	-0.090	3023	1428092 at	-0.053	5852.5	95610 at	-0.097	2523	1428092 at	0.103	4898	4074.125	1565.4861	FALSE	cell division cycle 5-like (S. pombe)	209055 s at	-0.127	9458	7.572E-03	FALSE
160945 at	0.080	5189	1437786 at	0.105	2509	160945 at	0.047	5827	1458895 at	0.133	2773	4074.5	1679.0929	TRUE	expressed sequence C80008	210603 at	0.021	37021	7.915E-01	FALSE
101605 at	0.115	1872	1446008 at	0.032	6948	101605 at	-0.085	2994	1446008 at	-0.115	4484	4074.5	2194.1725	FALSE	DNA segment, Chr 3, ERATO Doi 246, expressed		NA	NA	NA	NA
95104 at	0.089	3894	1448545 at	-0.045	6540	95104 at	-0.092	3128	1417011 at	-0.148	2737	4074.75	1712.3122	FALSE	syndecan 2	212157 at	-0.158	10490	1.321E-02	FALSE
96696 at	0.238	2148	1452787 a at	0.156	5875	96696 at	-0.211	1616	1452787 a at	0.123	6662	4075.25	2562.0681	FALSE	protein arginine N-methyltransferase 1	206445 s at	-0.220	6210	8.399E-04	FALSE
160991 at	-0.097	4152	1428503 a at	0.191	2823	160991 at	0.090	5248	1428503 a at	0.131	4082	4076.25	991.5316	FALSE	NFKB inhibitor interacting Ras-like protein 1	225930 at	-0.349	4050	9.009E-05	FALSE
94878 at	0.154	3430	1455286 at	0.065	6339	94878 at	0.257	1691	1455286 at	0.096	4845	4076.25	1984.7813	TRUE	BTB (POZ) domain containing 1	217945 at	0.055	33567	6.850E-01	FALSE
100744 at	0.149	2270	1441134 at	0.056	6403	100744 at	0.082	3807	1452340 at	0.114	3826	4076.5	1713.8091	TRUE	RIKEN cDNA 6820424L24 gene	230715 at	-0.081	18252	1.477E-01	FALSE
103997 at	-0.290	221	1423344 at	-0.092	3976	103997 at	0.009	7951	1423344 at	-0.132	4161	4077.25	3156.6791	FALSE	erythropoietin receptor	37986 at	0.104	8218	3.751E-03	FALSE
104132 at	-0.099	4376	1448677 at	0.064	5862	104132 at	-0.108	2623	1434952 at	-0.127	3449	4077.5	1388.5394	FALSE	COX4 neighbor	227363 s at	0.120	11977	2.570E-02	FALSE
104003 at	-0.035	6562	1430492 at	0.117	1945	104003 at	0.021	7283	1437941 at	0.708	520	4077.5	3349.1956	FALSE	phosphorylase kinase alpha 2	209438 at	-0.061	27395	4.577E-01	FALSE
104593 at	0.077	4075	1437592 x at	0.042	7014	104593 at	0.112	1978	1451166 a at	0.241	3247	4078.5	2138.5872	TRUE	coiled-coil domain containing 101	221822 at	0.139	10518	1.336E-02	TRUE
101871 f at	0.052	5642	1425324 x at	-0.058	5939.5	101870 at	0.062	4242	1442544 at	0.273	491	4078.625	2503.6468	FALSE	immunoglobulin heavy chain 4 (serum IgG1)		NA	NA	NA	NA
96699 at	0.053	5857	1422495 a at	-0.083	5169	96699 at	-0.060	4846	1422495 a at	-0.335	445	4079.25	2459.243	FALSE	high mobility group nucleosomal binding domain 1	200944 s at	0.244	7384	2.110E-03	FALSE
98538 at	-0.159	2259	1455905 at	-0.285	1656	98538 at	-0.007	8023	1455905 at	0.187	4383	4080.25	2876.9703	FALSE	RIKEN cDNA 2610507B11 gene	201729 s at	-0.069	25119	3.767E-01	FALSE
97483 at	-0.169	3496	1416219 at	0.089	5731	97483 at	0.227	315	1416219 at	0.050	6779	4080.25	2859.2938	FALSE	ribosomal protein L19		NA	NA	NA	NA
161110 at	0.086	4224	1420065 at	0.048	5961.5	161110 at	0.089	2970	1420065 at	-0.184	3166	4080.375	1369.7048	FALSE	transketolase-like 1	214183 s at	-0.011	41224	9.136E-01	FALSE
98866 at	-0.095	3777	1452507 at	-0.183	2632	98866 at	-0.159	1591	1452507 at	-0.017	8322	4080.5	2965.2542	TRUE	distal-less homeobox 6		NA	NA	NA	NA
98909 at	-0.046	6765	1418700 at	0.086	3850	98909 at	0.177	4537	1447027 s at	0.221	1171	4080.75	2304.579	FALSE	lipoic acid synthetase	214045 at	-0.036	27324	4.546E-01	FALSE
95712 at	0.049	5997	1417037 at	0.156	2476	95712 at	0.179	937	1417037 at	0.046	6914	4081	2837.7048	TRUE	origin recognition complex, subunit 6-like (S. cerevisiae)	219105 x at	0.053	19228	1.758E-01	FALSE
99175 at	-0.002	8444	1450649 at	0.326	648.5	99175 at	0.090	3815	1450649 at	0.146	3429	4084.125	3230.7711	FALSE	guanine nucleotide binding protein (G protein), gamma 10	201921 at	-0.182	13999	5.220E-02	FALSE
92420 at	-0.083	3814	1450803 at	0.124	1861	92420 at	-0.100	4965	1434802 s at	-0.094	5699	4084.75	1673.2217	FALSE	neurotrophin 3	206706 at	0.062	23269	3.110E-01	FALSE
102364 at	-0.125	2864	1449117 at	-0.084	4648	102364 at	0.053	5025	1459964 at	0.126	3803	4085	961.06434	FALSE	Jun proto-oncogene related gene d1	229117 s at	0.097	16386	9.930E-02	FALSE
95549 at	0.024	7391	1418036 at	0.214	772.5	95549 at	-0.071	5621	1418036 at	0.203	2556	4085.125	2977.6629	FALSE	DNA primase, p58 subunit	215708 s at	0.023	28451	4.990E-01	FALSE
95045 at	-0.094	5608	1417711 at	0.142	2322	95045 at	0.059	5022	1417710 at	-0.165	3389	4085.25	1504.447	FALSE	RIKEN cDNA 0610012D09 gene	222447 at	-0.701	148	1.368E-08	FALSE
94070 at	0.126	2331	1419372 at	-0.066	5732	99986 at	-0.187	2334	1419372 at	-0.095	5946	4085.75	2026.3633	FALSE	golgi SNAP receptor complex member 2	243880 at	-0.129	6901	1.467E-03	FALSE
99894 at	0.148	3325	1421319 at	0.100	4412	99894 at	0.078	4078	1421319 at	0.138	4528	4085.75	541.8563	TRUE	prostaglandin F2 receptor negative regulator	224950 at	0.053	20276	2.091E-01	FALSE
93350 f at	0.172	849	1451244 a at	0.086	3509	93350 f at	-0.076	5983	1451244 a at	0.063	6008	4087.25	2456.5413	FALSE	zinc finger protein 422	218005 at	0.313	3007	2.219E-05	FALSE
100394 at	0.121	3864	1448688 at	-0.075	4896	100394 at	0.124	2930	1448688 at	-0.108	4660	4087.5	889.04199	FALSE	podocalyxin-like	201578 at	0.322	10014	1.016E-02	FALSE
95927 f at	-0.034	7401	1439516 at	0.233	828	95927 f at	0.491	1146	1439516 at	0.072	6977	4088	3587.2577	FALSE	RIKEN cDNA 2610201A13 gene		NA	NA	NA	NA
160660 r at	-0.103	3083	1423836 at	0.083	5333.5	160660 r at	0.073	3659	1423836 at	-0.170	4284	4089.875	963.28227	FALSE	zinc finger protein 503	227195 at	-0.382	2595	1.100E-05	FALSE
97712 at	0.205	1109	1422994 at	0.021	8029	97712 at	-0.051	5540	1446974 at	0.223	1683	4090.25	3281.1701	FALSE	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	213111 at	0.217	10355	1.232E-02	FALSE
97141 s at	0.180	878	1441147 at	0.173	1781.5	97141 s at	-0.043	5978	1441147 at	0.046	7725	4090.625	3287.5464	FALSE	DNA segment, Chr 3, ERATO Doi 229, expressed		NA	NA	NA	NA
103868 at	0.197	967	1448802 at	0.111	2831	161685 r at	0.063	4638	1448802 at	0.024	7927	4090.75	2964.292	TRUE	nuclear fragile X mental retardation protein interacting protein 1	205135 s at	-0.038	26203	4.114E-01	FALSE
104040 at	0.099	4140	1434702 at	0.089	3840	104040 at	-0.184	513	1434702 at	0.028	7870	4090.75	3008.2291	FALSE	RIKEN cDNA 2600009E05 gene	218159 at	-0.018	36664	7.824E-01	FALSE
161894 r at	0.246	1479	1423751 at	0.072	5103	99567 at	0.014	7734	1459766 x at	-0.171	2048	4091	2903.5602	FALSE	splicing factor 1	210172 at	0.687	3340	3.675E-05	FALSE
92270 at	0.119	3265	1421201 a at	0.067	6310	92270 at	0.224	1040	1426016 a at	0.116	5749	4091	2426.5065	TRUE	trophinin	211700 s at	0.212	14410	6.004E-02	FALSE
100461 at	-0.081	4671	1417720 at	0.094	5190.5	100461 at	0.119	2066	1417720 at	0.137	4438	4091.375	1386.4023	FALSE	polymerase (RNA) II (DNA directed) polypeptide J	212782 x at	-0.007	41948	9.338E-01	FALSE
160845 at	0.076	5926	1424971 at	0.149	2410	160845 at	0.117	2760	1424971 at	0.154	5271	4091.75	1766.0639	TRUE	coiled-coil domain containing 99	221685 s at	-0.010	39147	8.555E-01	FALSE
94461 at	-0.040	7181	1417190 at	0.054	6114	94461 at	-0.202	695	1417190 at	-0.160	2379	4092.25	3060.7397	FALSE	pre-B-cell colony-enhancing factor 1	243296 at	0.576	11228	1.891E-02	FALSE
160283 at	0.196	2177	1456383 at	0.063	6052	162003 at	0.151	1203	1456383 at	0.047	6939	4092.75	2826.1017	TRUE	ribosomal L1 domain containing 1	212018 s at	-0.130	10123	1.074E-02	FALSE
162274 f at	-0.125	1946	1451255 at	0.005	8353	162274 f at	0.058	4515	1447690 at	0.205	1559	4093.25	3128.1757	FALSE	lipolysis stimulated lipoprotein receptor	208190 s at	0.200	4015	8.711E-05	FALSE
97893 at	0.225	871	1431415 a at	0.011	8092	97893 at	-0.102	4417	1434907 at	0.169	2993	4093.25	3037.9961	FALSE	TATA box binding protein-like 1	208398 s at	-0.157	11454	2.069E-02	FALSE
102366 at	0.106	3062	1449182 at	0.089	3923	102366 at	-0.072	3572	1449182 at	0.081	5818	4093.75	1202.6256	FALSE	resistin	220570 at	0.047	22979	3.008E-01	FALSE
102620 at	-0.084	4129	1450436 s at	-0.138	2586	102620 at	-0.253	2192	1421961 a at	0.058	7469	4094	2400.2443	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 5	207453 s at	-0.141	10297	1.193E-02	FALSE
95954 at	0.193	1235	1444292 at	-0.034	7319.5	95954 at	0.053	5163	1444292 at	-0.152	2660	4094.375	2694.2437	FALSE	DNA segment, Chr 7, ERATO Doi 143, expressed		NA	NA	NA	NA
102073 at	0.144	1286	1420755 a at	0.131	3592	102073 at	-0.024	7119	1426135 a at	0.128	4384	4095.25	2406.3518	FALSE	parkin	207058 s at	-0.136	8852	5.334E-03	FALSE
98848 at	0.187	656	1419329 at	0.065	5580	98848 at	-0.120	2484	1419329 at	0.027	7664	4096	3128.6325	FALSE	sorbin and SH3 domain containing 3	209253 at	0.161	11036	1.746E-02	FALSE
99188 at	-0.110	4175	1423817 s at	0.147	2184.5	99187 f at	0.300	1998	1453430 at	-0.018	8028	4096.375	2800.1369	FALSE	RIKEN cDNA 2010315L10 gene	219348 at	0.072	22444	2.831E-01	FALSE
97750 at	-0.051	5447	1416196 at	0.078	3457.5	97750 at	0.092	3111	1416196 at	-0.133	4373	4097.125	1045.5991	FALSE	ribosomal protein SA	213801 x at	-0.073	20800	2.268E-01	FALSE
98329 at	-0.004	8316	1422092 at	-0.101	6187.5	98329 at	-0.192	1042	1429486 at	-0.269	844	4097.375	3745.4499	TRUE	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	209992 at	0.302	9168	6.448E-03	FALSE
101426 at	-0.380	559	1434034 at	-0.147	2597.5	101426 at	0.060	5303	1434034 at	0.031	7930	4097.375	3209.9984	FALSE	ceramide kinase	218421 at	0.078	18865	1.653E-01	FALSE
94253 at	0.122	5397	1452662 a at	0.208	923	94253 at	0.080	4484	1452662 a at	0.092	5586	4097.5	2170.3429	TRUE	eukaryotic translation initiation factor 2, subunit 1 alpha	201142 at	-0.133	14964	7.042E-02	FALSE
103816 at	0.065	4965	1436374 x at	-0.032	7350	103816 at	0.079	3158	1424595 at	-0.439	920	4098.25	2727.0544	FALSE	F11 receptor	226482 s at	-0.431	3988	8.460E-05	FALSE
98809 s at	-0.007	8211	1438067 at	0.087	4148	98809 s at	-0.087	2560	1452525 a at	0.190	1476	4098.75	2952.9417	FALSE	neurofibromatosis 1	204325 s at	-0.192	2562	1.065E-05	FALSE
93230 at	0.196	1150	1450836 at	0.040	6328	93230 at	-0.131	3302	1450836 at	0.088	5615	4098.75	2352.198	FALSE	neurogenin 1	208497 x at	-0.037	29748	5.483E-01	FALSE
104635 r at	0.133	2150	1449094 at	-0.074	5712.5	104635 r at	0.127	4359	1447787 x at	0.172	4174	4098.875	1469.1503	FALSE	gap junction membrane channel protein alpha 7	228776 at	0.386	5237	3.457E-04	FALSE
102062 at	-0.329	312	1423417 at	-0.064	5424.5	102062 at	0.026	7156	1455246 at	-0.246	3504	4099.125	2932.4389	FALSE	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member	201074 at	0.312	740	2.247E-07	FALSE
99123 s at	-0.089	3085	1417916 a at	0.154	2274.5	99124 at	0.046	5615	1448887 x at	0.100	5423	4099.375	1674.1393	FALSE	fractured callus expressed transcript 1	222481 at	0.180	7280	1.967E-03	FALSE
104519 at	0.136	2416	1417618 at	0.050	6275.5	104519 at	0.106	2460	1417618 at	-0.090	5246	4099.375	1963.9731	FALSE	inter-alpha trypsin inhibitor, heavy chain 2	204987 at	-0.085	24886	3.683E-01	FALSE
97117 at	-0.106	2940	1419845 at	0.009	8305	97117 at	-0.087	4723	1419845 at	-0.413	432	4100	3310.0845	FALSE	distal-less homeobox 1, antisense		NA	NA	NA	NA
103553 at	0.184	1188	1433408 a at	0.116	3854.5	103553 at	-0.052	6452	1454244 at	-0.114	4906	4100.125	2215.2166	FALSE	minichromosome maintenance deficient 10 (S. cerevisiae)	222962 s at	0.039	25585	3.910E-01	FALSE
97270 at	0.149	1646	1422465 a at	0.076	4203.5	97270 at	0.036	6565	1422465 a at	-0.159	3991	4101.375	2010.052	FALSE	nucleoredoxin	219489 s at	0.414	827	2.934E-07	FALSE
102898 at	0.085	4167	1451866 a at	0.102	3106	102898 at	0.063	3973	1451866 a at	0.128	5161	4101.75	843.47747	TRUE	hepatocyte growth factor	209960 at	0.073	16650	1.048E-01	FALSE
102060 at	-0.058	6412	1417674 s at	-0.044	6195	102060 at	0.190	3380	1448803 at	0.557	421	4102	2815.895	FALSE	golgi autoantigen, golgin subfamily a, 4	215203 at	0.286	5374	3.898E-04	FALSE
93532 at	0.142	2932	1438608 at	0.281	294	93532 at	0.025	7297	1416889 at	-0.082	5885	4102	3122.8661	FALSE	troponin I, skeletal, fast 2	206393 at	0.006	42205	9.393E-01	FALSE
104287 at	-0.120	3992	1448866 at	-0.071	4427	104287 at	-0.152	1255	1448866 at	-0.052	6737	4102.75	2248.4333	TRUE	SUMO/sentrin specific peptidase 3	215113 s at	-0.140	11903	2.486E-02	TRUE
94799 at	0.153	3686	1449558 at	0.145	2650	94799 at	0.103	3104	1449558 at	0.060	6972	4103	1959.1035	TRUE	coagulation factor VIII	205756 s at	-0.310	4686	1.944E-04	FALSE
102629 at	0.094	4510	1419607 at	0.153	1381.5	102629 at	0.098	4020	1419607 at	0.056	6502	4103.375	2108.2616	TRUE	tumor necrosis factor	207113 s at	-0.023	35436	7.443E-01	FALSE
102895 at	-0.140	3485	1453576 at	0.094	4165	102895 at	0.014	7904	1430309 at	0.669	861	4103.75	2906.5404	FALSE	Nipped-B homolog (Drosophila)	212483 at	0.370	839	2.971E-07	FALSE
162385 i at	-0.036	7231	1415958 at	0.152	2148	162385 i at	0.171	1297	1415958 at	-0.093	5739	4103.75	2837.6363	FALSE	solute carrier family 2 (facilitated glucose transporter), member 4	206603 at	0.017	37505	8.052E-01	FALSE
92328 at	0.171	1008	1427655 a at	-0.040	6934	92328 at	-0.054	4656	1459400 at	0.151	3818	4104	2448.1705	FALSE	RIKEN cDNA A630038E17 gene		NA	NA	NA	NA
97354 at	-0.187	1652	1434066 at	-0.014	7868	97354 at	-0.068	4880	1434066 at	-0.180	2017	4104.25	2894.6931	TRUE	general transcription factor III C 1	239540 at	-0.028	29623	5.433E-01	FALSE
103795 f at	0.119	4033	1418766 s at	0.091	4720	97335 at	0.122	2197	1418765 at	0.090	5468	4104.5	1400.1953	TRUE	T-cell immunoglobulin and mucin domain containing 2		NA	NA	NA	NA
104364 at	-0.156	1441	1417016 at	0.046	6520.5	104364 at	0.045	6515	1439828 at	-0.230	1943	4104.875	2793.6762	FALSE	MAP kinase-activated protein kinase 5	212871 at	-0.115	15789	8.587E-02	FALSE
99473 at	0.113	3211	1451988 s at	-0.068	5593.5	99472 at	0.124	2317	1426240 at	-0.092	5299	4105.125	1595.5614	FALSE	Chromatin modifying protein 4B	225498 at	-0.173	13034	3.733E-02	FALSE
98555 at	-0.061	6063	1416484 at	-0.348	442	98555 at	-0.060	5854	1441684 at	-0.357	4062	4105.25	2602.0622	TRUE	tetratricopeptide repeat domain 3	208664 s at	-0.436	3350	3.698E-05	TRUE
161040 at	0.237	370	1422985 at	0.097	3453.5	161040 at	0.028	6412	1422985 at	0.067	6194	4107.375	2832.009	TRUE	frizzled homolog 1 (Drosophila)	204452 s at	-0.075	21377	2.463E-01	FALSE
93609 at	0.114	2208	1424875 at	-0.146	1165	93609 at	-0.029	7388	1424875 at	-0.121	5669	4107.5	2913.5528	FALSE	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	236600 at	0.345	3915	7.953E-05	FALSE
99141 at	-0.064	6129	1416188 at	-0.147	1134.5	99141 at	0.138	1747	1448241 at	-0.037	7420	4107.625	3134.2095	FALSE	GM2 ganglioside activator protein	212737 at	0.274	5108	3.072E-04	FALSE
96731 at	0.126	4450	1434697 at	-0.052	6994	96731 at	-0.162	3200	1434697 at	-0.232	1790	4108.5	2209.3398	FALSE	RIKEN cDNA 1110001P04 gene		NA	NA	NA	NA
97112 at	0.114	2268	1422245 a at	-0.029	7302.5	97112 at	0.209	1407	1459665 s at	-0.158	5457	4108.625	2751.0986	FALSE	MRV integration site 1	226047 at	0.567	2066	4.358E-06	FALSE
98896 at	-0.179	1416	1424028 at	-0.193	1532	98896 at	-0.017	7952	1424028 at	-0.160	5535	4108.75	3198.7134	TRUE	RIKEN cDNA 5830457O10 gene		NA	NA	NA	NA
95498 at	-0.068	7004	1456109 a at	0.165	1744	95498 at	-0.017	7308	1430100 at	0.539	381	4109.25	3563.9788	FALSE	mitochondrial ribosomal protein S15	221437 s at	-0.160	4430	1.411E-04	FALSE
162491 f at	0.063	5344	1428706 at	0.111	2196	162491 f at	0.082	3138	1428706 at	-0.086	5762	4110	1718.5304	FALSE	proline-rich polypeptide 6	226611 s at	-0.372	4475	1.505E-04	FALSE
102754 at	0.030	7037	1419562 at	0.079	4141	102754 at	0.156	4561	1427488 a at	0.319	702	4110.25	2606.7959	TRUE	baculoviral IAP repeat-containing 6	242068 at	0.202	7364	2.079E-03	TRUE
99518 at	0.022	7471	1449082 at	0.180	2151	99517 at	-0.182	824	1418454 at	-0.088	5998	4111	3135.62	FALSE	microfibrillar associated protein 5	213764 s at	0.067	12950	3.644E-02	FALSE
101664 at	-0.117	4344	1422475 a at	0.208	2231	101664 at	0.129	2185	1422475 a at	-0.025	7686	4111.5	2587.0697	FALSE	ribosomal protein S3a	212391 x at	-0.090	19326	1.787E-01	FALSE
94371 at	0.094	3624	1417237 at	-0.089	3941	94371 at	-0.005	8245	1417237 at	-0.328	637	4111.75	3131.8098	FALSE	phospholipase D2	209643 s at	0.127	9006	5.837E-03	FALSE
99439 at	-0.092	4644	1422936 at	-0.059	4855	99439 at	-0.142	2804	1422936 at	-0.237	4144	4111.75	921.40486	TRUE	MAS1 oncogene	208210 at	0.013	40368	8.893E-01	FALSE
93012 at	0.086	4743	1416908 s at	0.112	2727	93012 at	0.008	7997	1416907 at	-0.221	983	4112.5	3011.1045	FALSE	translin	201504 s at	-0.252	8970	5.685E-03	FALSE
104735 at	-0.054	7345	1434881 s at	-0.132	4639	104735 at	-0.291	1950	1434881 s at	-0.150	2521	4113.75	2445.0992	TRUE	potassium channel tetramerisation domain containing 12	212188 at	0.245	10666	1.458E-02	FALSE
94995 at	-0.093	2690	1435695 a at	0.248	1827.5	94995 at	-0.016	7995	1445855 at	-0.122	3943	4113.875	2729.3015	FALSE	RIKEN cDNA A030007L17 gene	215380 s at	-0.123	14911	6.908E-02	FALSE
162179 r at	0.213	1197	1438961 s at	0.097	3662.5	162221 i at	0.080	3529	1439325 at	0.018	8071	4114.875	2870.1227	TRUE	Bleomycin hydrolase	202179 at	-0.091	11894	2.478E-02	FALSE
96910 at	0.147	1902	1427224 at	0.139	1529	96910 at	-0.019	7344	1456190 a at	-0.082	5688	4115.75	2856.8942	FALSE	acyl-CoA synthetase medium-chain family member 2	244723 at	-0.027	27465	4.602E-01	FALSE
102036 at	-0.071	4169	1452069 a at	0.117	2565.5	102036 at	-0.048	5211	1426429 at	-0.198	4520	4116.375	1120.8776	FALSE	THAP domain containing 7	218492 s at	0.113	12205	2.800E-02	FALSE
98417 at	0.060	5893	1451905 a at	0.178	1619	98417 at	0.051	5948	1451905 a at	-0.206	3006	4116.5	2158.7852	FALSE	myxovirus (influenza virus) resistance 1		NA	NA	NA	NA
160421 r at	0.101	3993	1448220 at	0.108	3394.5	160421 r at	0.091	4788	1448220 at	-0.134	4291	4116.625	582.49426	FALSE	chymotrypsinogen B1	214411 x at	-0.051	24688	3.610E-01	FALSE
161079 at	0.093	4200	1422671 s at	0.069	5904	161079 at	0.110	1627	1422671 s at	-0.217	4739	4117.5	1806.2153	FALSE	N-acetylated alpha-linked acidic dipeptidase 2	222161 at	-0.138	10441	1.289E-02	FALSE
99600 at	-0.030	7372	1416945 at	0.125	2444	99599 s at	-0.145	3961	1438058 s at	-0.183	2693	4117.5	2269.0721	FALSE	prostate tumor over expressed gene 1	235665 at	-0.058	25787	3.960E-01	FALSE
93413 at	-0.212	2332	1421147 at	-0.059	7030.5	93413 at	0.087	4706	1421147 at	0.175	2402	4117.625	2233.2974	FALSE	telomeric repeat binding factor 2	203611 at	-0.227	5193	3.347E-04	FALSE
160062 i at	-0.024	7394	1449108 at	0.169	1807	92587 at	0.325	565	1449108 at	0.078	6706	4118	3434.8435	FALSE	Ferredoxin 1	203646 at	-0.055	26115	4.082E-01	FALSE
92736 at	0.075	4930	1426008 a at	0.153	1638	92736 at	-0.027	6945	1422648 at	-0.266	2961	4118.5	2319.5058	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	225516 at	0.898	2076	4.377E-06	FALSE
99028 at	-0.346	243	1424120 at	0.007	8240.5	99028 at	-0.137	4389	1424120 at	-0.118	3602	4118.625	3283.8152	FALSE	ring finger protein 8		NA	NA	NA	NA
102848 f at	0.105	2791	1429244 at	0.066	6505	102848 f at	0.171	2694	1429244 at	0.132	4487	4119.25	1790.9615	TRUE	RIKEN cDNA 2610524H06 gene		NA	NA	NA	NA
161009 at	0.095	3391	1434436 at	-0.021	7898	161009 at	0.085	3480	1434436 at	-0.248	1711	4120	2646.8602	FALSE	microrchidia 4	219038 at	0.216	1218	7.535E-07	FALSE
92825 at	0.128	2096	1416717 at	-0.004	8372.5	92825 at	0.113	1882	1416717 at	-0.109	4136	4121.625	3010.494	FALSE	cysteine-rich secretory protein 2	210262 at	-0.015	36429	7.756E-01	FALSE
99821 at	0.014	7691	1443711 at	0.085	3490	99821 at	-0.121	2984	1457712 at	0.270	2322	4121.75	2427.0853	FALSE	Chromodomain helicase DNA binding protein 8	212571 at	0.192	4668	1.896E-04	FALSE
102813 f at	0.243	1145	1451973 at	0.022	7636	102812 i at	0.155	959	1435247 at	0.066	6747	4121.75	3563.9827	TRUE	ubiquitin-activating enzyme E1-domain containing 1	218289 s at	-0.117	14044	5.309E-02	FALSE
161639 f at	0.506	1180	1422915 at	0.058	6061.5	161639 f at	0.067	6001	1422915 at	0.156	3249	4122.875	2360.07	TRUE	gastrin	208138 at	-0.005	42694	9.524E-01	FALSE
98326 f at	0.104	3123	1419306 at	0.169	1776	98326 f at	-0.084	3923	1419306 at	0.032	7670	4123	2525.181	FALSE	coiled-coil domain containing 96	238682 at	-0.044	32351	6.433E-01	FALSE
102738 s at	0.154	3548	1451924 a at	0.162	1903.5	102737 at	0.028	6781	1451924 a at	0.128	4262	4123.625	2028.2249	TRUE	endothelin 1	218995 s at	0.211	14895	6.883E-02	FALSE
94059 at	-0.002	8380	1423864 at	0.123	2307.5	94059 at	-0.197	297	1423864 at	0.123	5510	4123.625	3558.0956	FALSE	nuclear receptor binding protein	217765 at	0.037	26032	4.051E-01	FALSE
100521 at	-0.199	647	1426526 s at	0.093	5232	100521 at	-0.064	4557	1426526 s at	0.094	6059	4123.75	2397.8398	FALSE	oviductal glycoprotein 1	205432 at	-0.052	26921	4.402E-01	FALSE
96613 at	-0.032	7112	1416633 a at	0.178	2026	96613 at	0.140	2469	1416634 at	0.088	4893	4125	2356.5603	FALSE	RIKEN cDNA 5730536A07 gene	224779 s at	-0.103	19177	1.742E-01	FALSE
96819 at	0.051	5479	1432295 a at	-0.091	2731.5	96819 at	-0.065	3969	1432295 a at	-0.124	4323	4125.625	1131.1788	FALSE	RIKEN cDNA 2310035K24 gene	219706 at	-0.016	36281	7.705E-01	FALSE
160200 at	0.191	3289	1416856 at	0.024	7547	160200 at	0.103	3825	1416856 at	0.239	1842	4125.75	2429.7508	TRUE	RIKEN cDNA 3230401D17 gene	221954 at	0.027	31828	6.258E-01	FALSE
102117 at	-0.105	2658	1424648 at	0.066	5276	102117 at	0.079	3530	1434299 x at	-0.144	5048	4128	1249.3742	FALSE	RAB, member of RAS oncogene family-like 4	213784 at	0.060	28265	4.922E-01	FALSE
92792 at	0.084	5267	1448188 at	-0.201	1572	92792 at	0.005	8237	1459740 s at	-0.319	1437	4128.25	3263.7309	FALSE	uncoupling protein 2 (mitochondrial, proton carrier)	208997 s at	-0.092	22020	2.688E-01	FALSE
94316 at	0.177	1651	1422588 at	0.116	4509	94316 at	-0.001	8498	1422588 at	-0.226	1855	4128.25	3190.8264	FALSE	keratin complex 2, basic, gene 6b		NA	NA	NA	NA
101924 at	0.113	2734	1425944 a at	0.155	1622.5	101924 at	0.036	6431	1425944 a at	-0.098	5726	4128.375	2315.0363	FALSE	RAD51-like 3 (S. cerevisiae)	37793 r at	-0.027	36526	7.781E-01	FALSE
102815 at	-0.277	280	1418468 at	0.089	3421	102815 at	-0.128	5997	1418468 at	-0.103	6818	4129	2945.9696	FALSE	annexin A11	206200 s at	-0.140	14329	5.834E-02	FALSE
98876 at	0.053	5759	1437131 x at	0.186	1229.5	98876 at	0.101	3982	1438080 at	0.083	5546	4129.125	2089.1384	TRUE	mitochondrial ribosomal protein L11	219162 s at	-0.033	29767	5.490E-01	FALSE

100739 at	0.040	6584	1427834 at	0.137	1539	100739 at	0.063	4735	1427834 at	0.144	3660	4129.5	2107.3143	TRUE	serine protease inhibitor 16	NA	NA	NA	NA	
94149 at	0.166	2601	1450132 at	0.087	4689	94149 at	0.018	7718	1458802 at	0.349	1511	4129.75	2731.4969	TRUE	human immunodeficiency virus type I enhancer binding protein 3	244764 at	-0.056	23323	3.132E-01	FALSE
95501 at	-0.181	2828	1460362 at	-0.043	6530	95501 at	-0.183	653	1460362 at	0.087	6509	4130	2898.5269	FALSE	RIKEN cDNA 2410001C21 gene	233842 x at	0.153	13751	4.773E-02	FALSE
100073 at	-0.108	4866	1435270 x at	0.190	566	100073 at	0.037	6800	1435269 at	-0.112	4289	4130.25	2607.5514	FALSE	RIKEN cDNA 2510005D08 gene	227054 at	0.073	13395	4.247E-02	FALSE
99156 at	0.111	4360	1451269 at	0.106	4792	99156 at	0.102	2743	1453518 at	-0.197	4626	4130.25	941.79417	FALSE	PDZ domain containing 11	223037 at	-0.060	20516	2.170E-01	FALSE
161077 f at	-0.080	4020	1448401 at	-0.054	6084	161077 f at	0.254	1852	1448401 at	-0.135	4568	4131	1752.269	FALSE	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member	201827 at	0.210	3775	6.513E-05	FALSE
97090 at	-0.082	3434	1421909 at	-0.051	6271	97090 at	-0.273	609	1442042 at	-0.080	6211	4131.25	2695.4463	TRUE	transcription factor 20	238667 at	-0.041	28483	5.001E-01	FALSE
160495 at	-0.107	4195	1450695 at	0.094	3714	160495 at	-0.265	389	1450695 at	-0.012	8228	4131.5	3212.7847	FALSE	aryl-hydrocarbon receptor	202820 at	0.113	15880	8.808E-02	FALSE
92412 s at	-0.087	4836	1433892 at	0.061	4448	92412 s at	0.061	5670	1433892 at	0.184	1573	4131.75	1780.3929	FALSE	sperm associated antigen 5	203145 at	-0.066	21558	2.519E-01	FALSE
92813 at	-0.054	5689	1417952 at	0.104	4027.5	92813 at	-0.047	5423	1440691 at	-0.295	1389	4132.125	1968.5781	FALSE	cytochrome P450, family 2, subfamily i, polypeptide 6	205073 at	0.468	739	2.245E-07	FALSE
92262 at	-0.205	1361	1449353 at	-0.265	539.5	92262 at	-0.072	6215	1449353 at	-0.005	8415	4132.625	3797.6955	TRUE	wild-type p53-induced gene 1	219628 at	-0.316	6326	9.317E-04	TRUE
103235 at	-0.764	15	1419127 at	-0.066	6642	103235 at	-0.134	4756	1419127 at	0.157	5118	4132.75	2864.2252	FALSE	neuropeptide Y	206001 at	-0.400	13783	4.833E-02	FALSE
92248 at	-0.879	6	1450750 a at	0.052	7249	92249 g at	-0.255	2900	1447863 s at	0.522	6376	4132.75	3331.3122	FALSE	nuclear receptor subfamily 4, group A, member 2	204622 x at	0.157	19059	1.705E-01	FALSE
101748 at	0.142	1678	1450586 at	-0.052	6575	101748 at	-0.064	4408	1450586 at	0.141	3872	4133.25	2011.1468	FALSE	bradykinin receptor, beta 1	207510 at	-0.002	43820	9.802E-01	FALSE
160082 s at	0.086	6188	1439367 x at	0.121	2517	160082 s at	-0.289	1725	1457348 at	-0.114	6105	4133.75	2346.7514	FALSE	ADP-ribosylation factor 4	201096 s at	-0.451	8390	4.120E-03	FALSE
97176 at	0.140	3896	1420075 at	0.081	5771.5	97176 at	-0.059	5625	1420075 at	-0.250	1243	4133.875	2107.0526	FALSE	ATPase, class I, type 8B, member 1	214594 x at	0.444	3019	2.275E-05	FALSE
95056 r at	0.072	5206	1449929 at	0.119	4838	95056 r at	-0.074	4811	1420614 at	0.179	1685	4135	1643.2413	FALSE	dynein light chain Tctex-type 3	203303 at	-0.420	2688	1.358E-05	FALSE
96882 at	-0.026	7797	1451076 s at	0.177	3200	96882 at	0.119	4736	1457898 at	-0.654	807	4135	2928.0969	FALSE	dendritic cell protein GA17	202232 s at	-0.186	19568	1.867E-01	FALSE
98240 at	0.151	1753	1418166 at	0.077	5070.5	98240 at	0.165	1492	1418166 at	-0.014	8227	4135.625	3176.948	FALSE	interleukin 12 receptor, beta 1	206890 at	0.017	37692	8.111E-01	FALSE
160518 at	-0.135	2477	1460706 s at	0.084	4670	160518 at	0.158	2454	1460660 x at	0.057	6943	4136	2140.5459	FALSE	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	NA	NA	NA	NA	
104306 at	-0.067	5315	1431594 at	0.118	4072.5	104306 at	-0.091	3019	1448215 a at	0.120	4139	4136.375	938.39769	FALSE	dipeptidylpeptidase 3	232510 s at	0.096	11733	2.316E-02	FALSE
98360 at	0.142	1536	1425812 a at	0.018	7884	98360 at	-0.056	5818	1425812 a at	0.355	1308	4136.5	3247.2661	FALSE	calcium channel, voltage-dependent, N type, alpha 1B subunit	235781 at	-0.670	1940	3.427E-06	FALSE
160572 at	0.103	3662	1416145 at	-0.089	4282.5	160572 at	-0.042	5797	1416145 at	-0.148	2805	4136.625	1261.8265	FALSE	DEAH (Asp-Glu-Ala-His) box polypeptide 15	201385 at	0.149	13542	4.455E-02	FALSE
103774 at	-0.036	6552	1448008 at	0.193	875.5	103774 at	0.017	7267	1419867 a at	0.368	1853	4136.875	3239.5042	FALSE	ankyrin repeat and KH domain containing 1	NA	NA	NA	NA	
102315 at	-0.147	3905	1423884 at	0.061	5081	102315 at	-0.220	3096	1423884 at	0.101	4466	4137	843.97512	FALSE	cirrhosis, autosomal recessive 1A (human)	230656 s at	-0.370	2273	6.382E-06	FALSE
97983 s at	-0.104	3867	1420506 a at	-0.465	328	97983 s at	-0.131	4999	1420505 a at	0.057	7355	4137.25	2925.7448	FALSE	syntaxin binding protein 1	202260 s at	-0.754	1392	1.121E-06	FALSE
99167 at	-0.021	7695	1417006 at	0.118	2114	99167 at	-0.066	5058	1417006 at	0.178	1684	4137.75	2805.7881	FALSE	COMM domain containing 4	209132 s at	0.056	26953	4.414E-01	FALSE
103620 s at	-0.358	811	1426596 a at	0.023	7495.5	103620 s at	-0.087	3534	1426596 a at	-0.110	4712	4138.125	2771.0424	FALSE	survival motor neuron 1	203852 s at	0.067	23235	3.098E-01	FALSE
92867 at	0.037	6452	1437239 x at	-0.087	2870	92867 at	0.085	4007	1416048 at	-0.183	3225	4138.5	1613.8101	FALSE	polyhomeotic-like 2 (Drosophila)	200919 at	0.084	17674	1.316E-01	FALSE
98533 at	-0.223	1268	1416727 a at	0.153	3405.5	98533 at	0.066	6388	1416727 a at	-0.079	5494	4138.875	2285.8032	FALSE	cytochrome b-5	215726 s at	0.109	20515	2.170E-01	FALSE
99924 at	-0.162	1054	1417144 at	-0.148	3387.5	99924 at	-0.096	4236	1417144 at	-0.027	7883	4140.125	2834.8379	TRUE	tubulin, gamma 1	201714 at	-0.163	9787	8.985E-03	TRUE
96166 at	-0.144	3666	1450965 at	0.035	6877	101517 at	0.147	1610	1450965 at	0.143	4410	4140.75	2174.8289	FALSE	testis expressed gene 261	212083 at	0.231	1779	2.531E-06	FALSE
96272 at	-0.081	3504	1420842 at	-0.119	3100	96272 at	0.043	7115	1420843 at	-0.228	2845	4141	2001.1448	FALSE	protein tyrosine phosphatase, receptor type, F	200636 s at	0.210	5569	4.698E-04	FALSE
100084 at	-0.287	1566	1456725 x at	0.120	4109	100084 at	-0.073	4254	1450850 at	-0.127	6637	4141.5	2071.5882	FALSE	villin 2	208623 s at	0.846	1034	4.943E-07	FALSE
102164 at	0.153	3141	1422328 at	0.125	3372	102164 at	0.175	1562	1422328 at	-0.004	8491	4141.5	3009.1583	FALSE	gap junction membrane channel protein alpha 10	NA	NA	NA	NA	
101777 at	0.097	2856	1427783 at	0.046	6432	101777 at	-0.055	5120	1446211 at	-0.166	2162	4142.5	1981.1427	FALSE	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	233498 at	0.199	6475	1.029E-03	FALSE
104387 at	-0.060	5409	1450404 at	0.102	2916	104387 at	0.028	6335	1450404 at	-0.190	1911	4142.75	2073.24	FALSE	solute carrier family 23 (nucleobase transporters), member 1	223732 at	-0.013	39894	8.747E-01	FALSE
160375 at	0.002	8445	1460256 at	0.138	2280.5	160375 at	0.045	5245	1453588 at	0.296	601	4142.875	3451.39	TRUE	carbonic anhydrase 3	204865 at	0.007	37687	8.110E-01	FALSE
101325 r at	-0.223	421	1425276 at	0.049	6772	101325 r at	-0.073	3270	1451645 at	0.097	6111	4143.5	2909.7581	FALSE	fibrosin 1	238771 at	0.130	13249	4.045E-02	FALSE
97853 at	0.206	2044	1460403 at	-0.106	5433	97853 at	-0.030	7737	1460403 at	-0.212	1362	4144	2984.4427	FALSE	PC4 and SFRS1 interacting protein 1	210758 at	-0.188	8182	3.667E-03	FALSE
97284 at	0.061	4602	1424406 at	0.057	5988.5	97284 at	-0.083	2956	1429539 at	0.193	3032	4144.625	1444.5104	FALSE	BCL2-like 13 (apoptosis facilitator)	226798 at	0.078	11542	2.135E-02	FALSE
94699 at	0.122	2112	1421771 a at	0.093	3332.5	94699 at	-0.020	7188	1421771 a at	0.161	3947	4144.875	2167.3562	FALSE	IAP promoted placental gene	219843 at	0.240	5340	3.765E-04	FALSE
98508 s at	-0.031	7157	1422619 at	0.109	3380.5	96043 at	0.089	3644	1422620 s at	0.247	2400	4145.375	2077.8699	FALSE	phosphatidic acid phosphatase 2a	243442 x at	0.315	2102	4.561E-06	FALSE
100965 at	0.137	1996	1455167 at	0.047	6059.5	161475 f at	0.224	730	1455167 at	0.026	7796	4145.375	3330.4422	TRUE	cytochrome c oxidase, subunit VIIc	NA	NA	NA	NA	
101601 at	0.086	5050	1419885 at	0.064	5364	101601 at	0.142	3313	1419886 at	0.231	2857	4146	1245.813	TRUE	DNA segment, Chr X, ERATO Doi 223, expressed	NA	NA	NA	NA	
94374 at	0.024	7849	1425490 a at	-0.194	1597.5	94374 at	-0.045	5738	1425490 a at	-0.241	1400	4146.125	3177.1078	FALSE	WD repeat domain 13	222138 s at	-0.051	29569	5.409E-01	FALSE
95749 at	-0.038	7235	1428112 at	0.096	6630	95749 at	0.173	734	1459455 at	-0.267	1987	4146.5	3266.762	FALSE	arginine-rich, mutated in early stage tumors	202655 at	0.062	30614	5.791E-01	FALSE
104698 at	0.165	1745	1425464 at	0.070	4374	104698 at	0.107	3076	1425464 at	-0.042	7393	4147	2415.5531	FALSE	GATA binding protein 6	210002 at	-0.048	18839	1.648E-01	FALSE
97097 at	-0.100	3094	1436307 at	0.077	4971	97097 at	-0.011	7796	1441567 at	0.512	730	4147.75	2987.6899	FALSE	myosin IXa	219027 s at	-0.118	18802	1.635E-01	FALSE
93821 at	-0.119	2232	1417195 at	-0.168	3141	93821 at	0.030	6889	1448611 at	0.107	4332	4148.5	2019.2442	FALSE	WW, C2 and coiled-coil domain containing 2	218775 s at	0.146	12549	3.188E-02	FALSE
99655 at	-0.118	2983	1418223 at	0.213	1253	99655 at	0.030	7366	1418223 at	0.106	4997	4149.75	2634.044	FALSE	Sec11-like 1 (S. cerevisiae)	201290 at	0.402	2149	4.909E-06	FALSE
94914 at	0.083	5341	1451441 at	0.129	3764.5	94914 at	0.182	529	1451441 at	0.046	6965	4149.875	2744.8714	TRUE	RIKEN cDNA 2210415F13 gene	NA	NA	NA	NA	
102018 at	-0.032	6707	1435965 at	-0.074	4254	102018 at	-0.223	855	1435965 at	-0.182	4784	4150	2436.3939	TRUE	CCR4-NOT transcription complex, subunit 3	229143 at	0.139	13577	4.505E-02	FALSE
96743 at	-0.078	6385	1428554 a at	0.572	720	96743 at	0.317	1594	1428554 a at	0.031	7902	4150.25	3529.4364	FALSE	RIKEN cDNA 1810035L17 gene	221434 s at	-0.524	6324	9.285E-04	FALSE
92333 at	-0.084	3714	1418640 at	0.174	1938	92333 at	-0.014	7661	1458538 at	0.169	3289	4150.5	2459.7751	FALSE	Sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	218878 s at	0.220	6698	1.233E-03	FALSE
98143 at	-0.031	7352	1460319 at	-0.080	4135	98143 at	-0.124	3595	1442483 at	0.324	1521	4150.75	2413.3443	FALSE	fucosyltransferase 8	203988 s at	0.214	12992	3.684E-02	FALSE
96071 at	0.016	7928	1430978 at	0.195	1137	96071 at	0.257	1002	1430978 at	-0.058	6536	4150.75	3603.4405	FALSE	ribosomal protein S25	200091 s at	0.051	29082	5.238E-01	FALSE
102706 i at	0.102	3242	1421564 at	0.151	3707	102706 i at	0.106	3624	1421564 at	-0.097	6033	4151.5	1270.5732	FALSE	serine (or cysteine) peptidase inhibitor, clade A, member 3C	NA	NA	NA	NA	
162354 f at	0.032	7039	1423377 at	0.109	2494.5	92349 at	0.172	933	1423377 at	-0.135	6140	4151.625	2909.5349	FALSE	insulin-like growth factor binding protein-like 1	227760 at	-0.615	258	2.870E-08	FALSE
103810 at	0.064	5125	1452027 a at	0.112	2672	103810 at	0.037	6053	1418158 at	-0.227	2757	4151.75	1702.6406	FALSE	transformation related protein 63	209863 s at	0.129	12496	3.127E-02	FALSE
95077 at	0.047	6472	1419553 a at	0.169	1622.5	95077 at	0.201	810	1419553 a at	0.030	7705	4152.375	3443.5226	TRUE	RAB geranylgeranyl transferase, b subunit	213704 at	0.094	25207	3.801E-01	FALSE
98133 at	-0.201	1128	1448738 at	0.099	5799	98133 at	-0.013	8157	1417504 at	-0.207	1526	4152.5	3405.5389	FALSE	calbindin-28K	205625 s at	-1.941	459	8.814E-08	FALSE
97169 f at	0.089	4288	1425427 at	0.062	5358	97169 f at	0.052	4825	1425427 at	0.173	2139	4152.5	1411.6219	TRUE	hypothetical protein LOC639910	NA	NA	NA	NA	
162208 f at	-0.201	1142	1422921 at	0.062	6073	162208 f at	0.117	4780	1422921 at	0.106	4616	4152.75	2110.2937	FALSE	pre-B lymphocyte gene 3	220068 at	-0.037	29669	5.451E-01	FALSE
98573 r at	0.094	5380	1422547 at	0.148	3051.5	98573 r at	0.218	1699	1422547 at	0.057	6482	4153.125	2172.9541	TRUE	RAN binding protein 1	202483 s at	-0.196	12067	2.659E-02	FALSE
94349 at	0.142	3028	1434163 at	0.079	4510.5	94349 at	0.085	4341.5	1434163 at	-0.126	4733	4153.25	767.10783	FALSE	expressed sequence AU024076	220513 at	-0.260	4511	1.591E-04	FALSE
98550 at	-0.178	2571	1426854 a at	-0.072	6377.5	98550 at	0.372	1432	1426854 a at	0.079	6235	4153.875	2529.1426	FALSE	SET translocation	200630 x at	0.140	7768	2.803E-03	FALSE
103493 at	-0.097	3158	1419405 at	-0.057	5580	103493 at	0.037	6391	1419405 at	-0.308	1490	4154.75	2245.481	FALSE	neuromedin B	205204 at	0.177	6431	9.975E-04	FALSE
92617 at	0.136	2883	1427543 s at	0.073	5298	92617 at	-0.083	3349	1427543 s at	0.114	5090	4155	1217.6882	FALSE	ubiquitin-activating enzyme E1, Chr Y 1	NA	NA	NA	NA	
96573 at	-0.121	2216	1415779 s at	-0.142	2282.5	96573 at	-0.056	5173	1415779 s at	-0.044	6950	4155.375	2317.6371	TRUE	actin, gamma, cytoplasmic 1	211995 x at	-0.128	22731	2.926E-01	FALSE
96296 at	-0.194	1448	1425189 a at	0.097	3451	96296 at	-0.012	7982	1430798 x at	0.241	3741	4155.5	2747.1676	FALSE	mitochondrial ribosomal protein L15	NA	NA	NA	NA	
96091 at	0.256	769	1454067 a at	-0.114	5132.5	96091 at	-0.095	4568	1454067 a at	0.101	6153	4155.625	2351.1043	FALSE	RIKEN cDNA 4931406C07 gene	229851 s at	0.231	9667	8.544E-03	FALSE
103890 at	0.034	6488	1415866 at	0.063	5934	103890 at	-0.077	3372	1415866 at	0.275	830	4156	2599.7718	FALSE	unc-45 homolog A (C. elegans)	207499 x at	0.125	12278	2.893E-02	FALSE
95424 at	0.050	6799	1422457 s at	0.171	678.5	95424 at	0.148	4626	1422457 s at	0.094	4522	4156.375	2545.1464	TRUE	SMT3 suppressor of mif two 3 homolog 3 (yeast)	200739 s at	-0.410	1696	2.135E-06	FALSE
99037 at	0.085	5064	1425393 a at	-0.061	6064	99037 at	-0.128	2393	1457182 at	-0.176	3106	4156.75	1700.5484	FALSE	mitogen activated protein kinase kinase 7	226053 at	0.128	11508	2.105E-02	FALSE
92190 at	-0.109	3541	1418605 at	-0.067	5445	92190 at	-0.037	6159	1446194 at	0.198	1482	4156.75	2097.7789	FALSE	nuclear receptor subfamily 2, group C, member 1	204791 at	0.169	15135	7.334E-02	FALSE
101297 at	0.118	4779	1422124 a at	-0.001	8518.5	101048 at	0.165	436	1422124 a at	-0.447	2896	4157.375	3408.1044	FALSE	protein tyrosine phosphatase, receptor type, C	212587 s at	0.265	9824	9.162E-03	FALSE
101421 at	-0.171	2243	1422888 at	0.006	8277	101421 at	-0.101	1740	1422888 at	0.150	4372	4158	2973.5448	FALSE	ring finger protein 5	209111 at	-0.154	13754	4.779E-02	FALSE
104017 at	0.109	2962	1433531 at	0.123	5439.5	102381 at	0.198	4730	1418911 s at	0.208	3501	4158.125	1130.1167	TRUE	acyl-CoA synthetase long-chain family member 4	202422 s at	-0.186	8679	4.839E-03	FALSE
99677 at	0.036	6688	1438206 a at	-0.006	8294.5	99677 at	0.210	388	1450057 at	-0.284	1265	4158.875	3919.7737	FALSE	RIKEN cDNA 2610042O14 gene	NA	NA	NA	NA	
92346 at	-0.240	1272	1422520 at	-0.484	164.5	92346 at	0.009	8143	1422520 at	0.076	7058	4159.375	4023.5662	FALSE	neurofilament 3, medium	205113 at	-1.260	587	1.322E-07	FALSE
93140 at	0.121	4090	1420439 at	0.087	4493.5	93140 at	0.131	3391	1420439 at	0.109	4665	4159.875	566.42392	TRUE	testis specific X-linked gene	NA	NA	NA	NA	
95805 at	-0.144	2040	1418841 s at	0.052	5896	99961 s at	-0.256	434	1418841 s at	-0.010	8270	4160	3572.2669	FALSE	cell division cycle 2-like 1	NA	NA	NA	NA	
94049 at	0.103	4275	1450624 at	0.126	2248	94049 at	0.089	3927	1450624 at	-0.095	6193	4160.75	1618.265	FALSE	betaine-homocysteine methyltransferase	230309 at	0.091	12569	3.225E-02	FALSE
94247 at	0.119	1755	1435493 at	0.028	7601	161892 r at	0.288	336	1427610 at	-0.068	6952	4161	3653.4341	FALSE	desmoplakin	200606 at	0.075	22182	2.743E-01	FALSE
161093 at	0.090	3463	1449407 at	0.110	3304	102215 at	-0.080	2806	1419286 s at	0.051	7073	4161.5	1961.0729	FALSE	intraflagellar transport 81 homolog (Chlamydomonas)	219372 at	0.187	17124	1.177E-01	FALSE
97242 at	-0.210	498	1427878 at	0.051	6271	97242 at	0.031	6418	1441883 at	-0.137	3461	4162	2796.0516	FALSE	RIKEN cDNA 0610010O12 gene	224707 at	0.185	9423	7.424E-03	FALSE
160318 at	-0.143	3587	1434412 x at	0.099	3633	160318 at	0.128	2171	1429069 at	0.050	7259	4162.5	2173.0129	FALSE	STIP1 homology and U-Box containing protein 1	217934 x at	-0.097	11021	1.736E-02	FALSE
96135 at	-0.096	5138	1426964 at	0.401	476	96135 at	-0.061	6976	1426964 at	0.125	4064	4163.5	2736.6258	FALSE	RIKEN cDNA 3110003A17 gene	223361 at	-0.435	4625	1.788E-04	FALSE
98038 at	-0.120	2795	1416155 at	-0.091	4631.5	98038 at	0.135	5736	1416155 at	-0.126	3493	4163.875	1292.8189	FALSE	high mobility group box 3	225601 at	0.201	3996	8.541E-05	FALSE
97710 f at	-0.287	340	1448028 at	-0.040	6990.5	97710 f at	-0.015	8225	1442325 at	0.391	1105	4165.125	4019.1738	FALSE	TBC1 domain family, member 24	227908 at	-0.138	16372	9.916E-02	FALSE
96692 at	0.014	7712	1427526 at	-0.078	6219	96692 at	-0.392	139	1423591 at	-0.190	2591	4165.25	3439.2963	FALSE	FGFR1 oncogene partner 2	236808 at	0.301	6734	1.266E-03	FALSE
104095 at	-0.026	6875	1426699 at	-0.226	692	104095 at	-0.073	4145	1452150 at	-0.095	4953	4166.25	2583.7419	TRUE	expressed sequence AU040320	222468 at	-0.035	30696	5.825E-01	FALSE
95903 at	0.063	6460	1447959 at	0.123	3053	95903 at	0.082	3730	1430626 at	0.195	3423	4166.5	1553.8499	TRUE	zinc finger protein 398	226202 at	-0.077	19278	1.770E-01	FALSE
101310 at	0.137	1573	1450517 at	0.121	4003	101310 at	-0.008	7996	1460309 at	-0.135	3094	4166.5	2742.7663	FALSE	T-cell acute lymphocytic leukemia 2	231759 at	0.029	29927	5.546E-01	FALSE
98615 at	-0.045	7436	1425780 a at	0.195	2611	98615 at	-0.060	6203	1450904 at	0.392	417	4166.75	3230.8561	FALSE	RIKEN cDNA 0610041E09 gene	226276 at	-0.296	12452	3.093E-02	FALSE
160224 at	-0.060	5656	1456013 x at	0.081	6049	160224 at	0.083	2706	1420199 at	-0.168	2263	4168.5	1959.4874	FALSE	Solute carrier family 35, member A4	224626 at	0.129	7472	2.255E-03	FALSE
160803 at	-0.078	5636	1454006 a at	-0.047	6068	160803 at	0.155	3443	1454006 a at	0.274	1528	4168.75	2102.3992	FALSE	UBX domain containing 6	215983 s at	-0.107	13419	4.278E-02	FALSE
160303 at	-0.007	8119	1429581 at	0.097	3694	160303 at	-0.111	2133	1444394 at	0.245	2733	4169.75	2710.1977	FALSE	acyl-Coenzyme A dehydrogenase family, member 9	239976 at	-0.053	19292	1.775E-01	FALSE
94744 at	0.137	2187	1420421 s at	0.135	3452	94744 at	-0.048	6334	1420421 s at	0.105	4710	4170.75	1772.2215	FALSE	killer cell lectin-like receptor subfamily B member 1B	214470 at	0.082	21524	2.508E-01	FALSE
99025 at	-0.065	5209	1417927 at	-0.058	5618.5	99025 at	-0.135	3834	1417927 at	-0.230	2022	4170.875	1623.2139	TRUE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	202577 s at	0.115	12610	3.280E-02	FALSE
98539 at	0.245	1525	1423459 at	0.040	7427.5	98540 g at	0.103	4644	1423459 at	0.158	3090	4171.625	2516.5053	TRUE	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	202467 s at	-0.152	20307	2.100E-01	FALSE
98817 at	-0.037	7265	1421365 at	-0.150	3771.5	98817 at	-0.065	5637	1434458 at	-1.376	13	4171.625	3118.2556	TRUE	follistatin	226847 at	-0.040	24284	3.464E-01	FALSE
96151 at	-0.133	2212	1429352 at	0.069	5197	161830 f at	0.092	3532	1429352 at	-0.117	5746	4171.75	1610.3106	FALSE	molybdenum cofactor sulfurase	219959 at	-0.040	23450	3.187E-01	FALSE
96099 at	0.123	1927	1416728 at	0.150	1793	96099 at	-0.009	7865	1416728 at	0.101	5110	4173.75	2899.2957	FALSE	casein kinase II, beta subunit	201390 s at	-0.051	21974	2.675E-01	FALSE
97386 at	-0.161	834	1436026 at	-0.024	7273	97386 at	0.076	4574	1439891 at	0.171	4015	4174	2642.2643	FALSE	zinc finger protein 703	222760 at	0.239	6506	1.049E-03	FALSE
92564 at	-0.068	4411	1448487 at	0.057	5815	92563 at	-0.070	5344	1433842 at	-0.445	1128	4174.5	2113.1387	FALSE	leucine rich repeat (in FLII) interacting protein 1	NA	NA	NA	NA	
94698 at	-0.005	8352	1422024 at	0.056	5760	94698 at	-0.107	2166	1441584 at	-0.322	423	4175.25	3562.4495	FALSE	Friend leukemia integration 1	244592 at	0.243	2074	4.375E-06	FALSE
162239 at	0.194	1538	1427980 at	-0.069	6551	103748 at	-0.070	5754	1460032 at	0.171	2860	4175.75	2367.9533	FALSE	RIKEN cDNA 4933407C03 gene	243720 at	0.119	9993	1.011E-02	FALSE
101734 at	0.059	5467	1421436 at	0.062	4930	101734 at	-0.055	5717	1459245 s at	0.369	591	4176.25	2412.6129	FALSE	glutamate receptor, ionotropic, delta 2	221364 at	-0.098	16401	9.970E-02	FALSE
101037 at	-0.037	6760	1423177 a at	-0.263	573	101037 at	0.010	7927	1423177 a at	-0.243	1446	4176.5	3705.022	FALSE	abl-interactor 1	NA	NA	NA	NA	
97817 at	-0.129	1746	1428132 at	-0.091	3682	97817 at	0.007	8235	1428132 at	-0.134	3044	4176.75	2822.8732	FALSE	CDC42 small effector 1	218157 x at	0.262	2265	6.275E-06	FALSE
161582 r at	-0.035	6819	1415799 at	-0.157	2414	98617 at	-0.150	2489	1415799 at	-0.116	4985	4176.75	2128.422	TRUE	WW domain binding protein 11	217821 s at	-0.261	7876	3.017E-03	TRUE
103071 at	0.045	6533	1452241 at	0.056	5915	103071 at	0.242	665	1458480 at	0.131	3594	4176.75	2661.166	TRUE	topoisomerase (DNA) II beta binding protein	202633 at	-0.115	15406	7.805E-02	FALSE
93078 at	-0.225	2094	1417185 at	0.017	8136	93078 at	0.207	524	1417185 at	-0.300	5960	4178.5	3489.7975	FALSE	lymphocyte antigen 6 complex, locus A	NA	NA	NA	NA	
102928 at	-0.010	7935	1425969 a at	0.031	7003.5	102927 s at	-0.163	474	1435539 at	-0.259	1302	4178.625	3833.601	FALSE	Huntington disease gene homolog	202390 s at	-0.102	14093	5.427E-02	FALSE
100089 at	0.069	5625	1416498 at	0.137	3461.5	100089 at	-0.070	4482	1416498 at	-0.180	3149	4179.375	1119.2901	FALSE	peptidylprolyl isomerase C	204517 at	0.186	9212	6.589E-03	FALSE
99026 at	-0.138	1889	1420887 a at	-0.106	4634.5	99026 at	-0.089	4927	1426191 a at	-0.099	5268	4179.625	1548.871	TRUE	Bcl2-like 1	212312 at	0.244	5506	4.458E-04	FALSE
93500 at	-0.111	3193	1455282 x at	0.074	3546	93500 at	-0.077	5011	1455282 x at	-0.110	4969	4179.75	946.78522	FALSE	aminolevulinic acid synthase 1	205633 s at	-0.310	5441	4.177E-04	FALSE
93693 at	-0.226	1341	1436341 at	-0.076	5387	93693 at	-0.094	5237	1436341 at	-0.162	4754	4179.75	1911.6742	TRUE	homeobox containing 1	219269 at	0.465	6689	1.229E-03	FALSE
101309 at	0.123	2754	1450577 at	-0.084	6460	101309 at	0.041	6303	1441603 at	0.393	1203	4180	2620.5301	FALSE	somatostatin receptor 3	214491 at	-0.008	42095	9.374E-01	FALSE
162409 r at	-0.095	4032	1417791 a at	0.092	4581.5	99999 at	0.111	4111	1447983 at	-0.162	3996	4180.125	271.85976	FALSE	zinc finger, matrin-like	235493 at	0.363	3525	4.769E-05	FALSE
160966 at	0.050	6795	1457285 at	-0.045	7288	160966 at	-0.172	1139	1457285 at	-0.194	1501	4180.75	3312.7335	FALSE	zinc finger protein 187	213218 at	0.084	19167	1.738E-01	FALSE
97807 at	-0.158	2600	1416327 at	0.126	2711.5	97807 at	-0.125	3049	1416327 at	0.008	8364	4181.125	2795.1091	FALSE	ubiquitin-fold modifier conjugating enzyme 1	217797 at	-0.081	22447	2.832E-01	FALSE
161653 f at	0.036	6612	1429388 at	0.045	6304	161072 at	0.117	2420	1429388 at	-0.194	1390	4181.5	2665.0635	FALSE	Nanog homeobox	220184 at	-0.264	8267	3.832E-03	FALSE
94223 at	0.000	8526	1421321 a at	0.040	6914	94223 at	0.188	918	1421321 a at	0.356	372	4182.5	4143.4267	FALSE	neuroepithelial cell transforming gene 1	201829 at	0.432	2115	4.626E-06	FALSE
101727 at	0.049	6510	1431843 a at	0.087	4146.5	101727 at	-0.141	2215	1431843 a at	-0.174	3861	4183.125	1769.4603	FALSE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	203927 at	0.164	4504	1.587E-04	FALSE
104137 at	0.092	3356	1449302 at	-0.150	1620.5	104137 at	-0.067	4719	1449302 at	0.048	7041	4184.125	2288.0698	FALSE	ATP-binding cassette, sub-family A (ABC1), member 2	212772 s at	0.287	9355	7.149E-03	FALSE

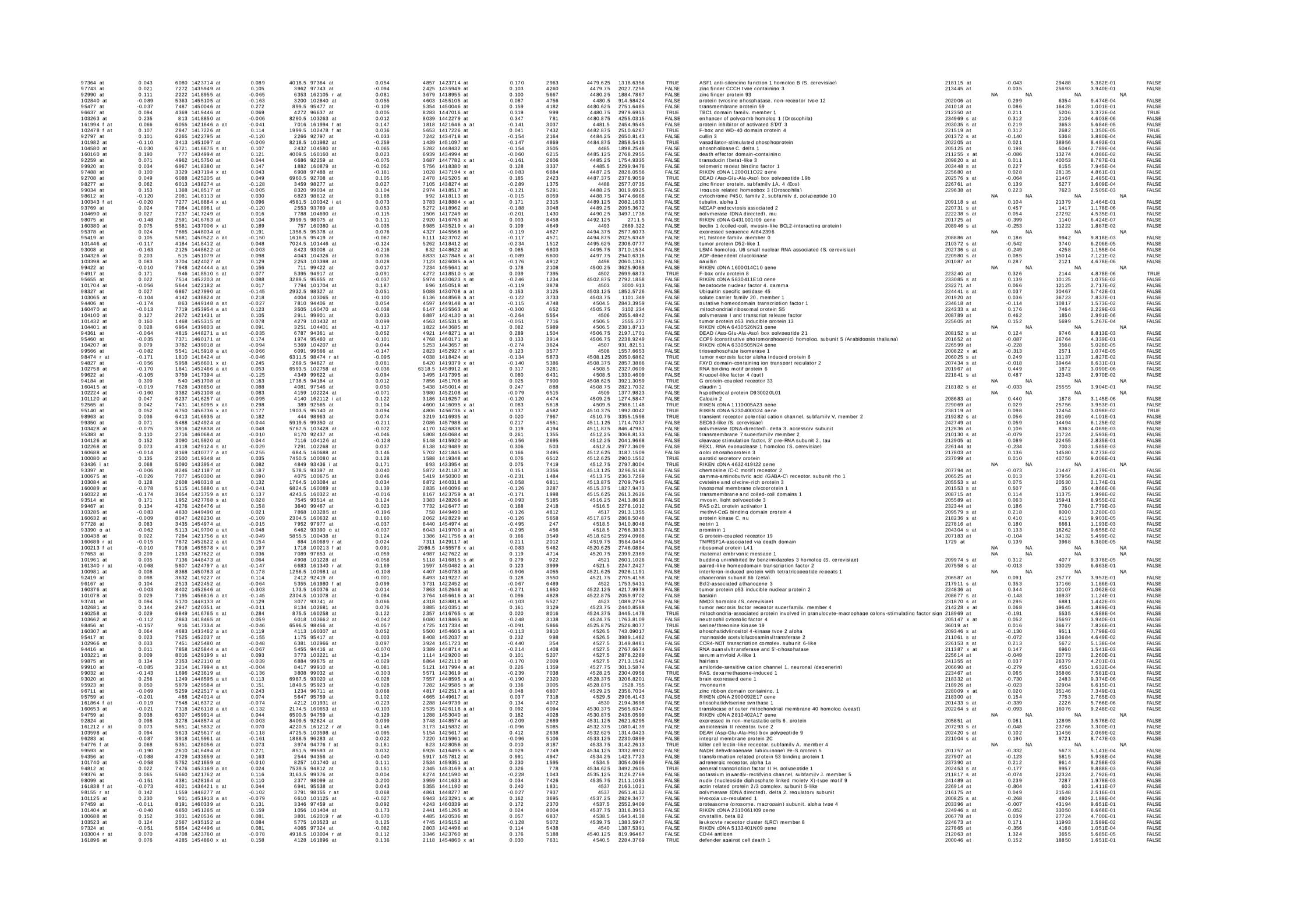


100525 at	-0.059	5204	1448115 at	0.066	5265	100525 at	0.123	1378	1453995 a at	0.151	5131	4244.5	1911.7849	FALSE	HpaII tiny fragments locus 9c	218475 at	0.065	20759	2.255E-01	FALSE
103427 at	-0.035	7175	1427471 at	-0.221	454.5	103427 at	-0.006	8205	1441561 at	0.383	1144	4244.625	4010.4277	FALSE	F-box and leucine-rich repeat protein 3	242829 x at	0.354	3546	4.938E-05	FALSE
160516 at	0.212	458	1436849 x at	0.056	6512	162441 i at	0.110	2779	1419428 a at	-0.041	7230	4244.75	3190.6133	FALSE	glucosidase, alpha, acid	202812 at	0.154	8685	4.864E-03	FALSE
92860 at	0.038	6256	1416112 at	0.092	3662.5	92860 at	0.182	2531	1416112 at	0.109	4537	4246.625	1571.2497	TRUE	cytochrome c oxidase, subunit VIIIa	201119 s at	-0.137	10966	1.688E-02	FALSE
99080 at	-0.168	2632	1428311 at	-0.133	2374	99080 at	-0.024	7354	1428311 at	0.133	4632	4248	2303.4774	FALSE	coiled-coil domain containing 6	225010 at	-0.361	7785	2.831E-03	FALSE
162302 f at	0.193	3207	1450995 at	-0.126	5845	162302 f at	0.151	945	1450995 at	-0.382	6995	4248	2713.5406	FALSE	folate receptor 1 (adult)	211074 at	0.251	18547	1.565E-01	FALSE
94302 at	-0.088	5194	1418874 a at	0.128	1606.5	94302 at	0.020	7651	1425859 a at	0.349	2542	4248.375	2730.2798	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	211609 x at	-0.076	20616	2.207E-01	FALSE
103704 at	-0.103	3895	1435376 at	-0.029	7444	103704 at	0.100	5393	1457209 at	0.359	263	4248.75	3029.3164	FALSE	DDHD domain containing 2	212690 at	-0.480	1775	2.509E-06	FALSE
102573 at	0.073	4957	1459921 at	-0.191	1080	102573 at	-0.095	4298	1436718 at	0.100	6661	4249	2335.5206	FALSE	neurexophilin 1	232377 at	-0.263	13443	4.304E-02	FALSE
93076 at	-0.056	6123	1428537 at	-0.090	5084	99650 at	-0.113	4668	1456216 at	0.488	1122	4249.25	2172.7702	FALSE	casein kinase 1, alpha 1	208866 at	0.246	7276	1.962E-03	FALSE
98154 at	-0.041	6914	1428449 at	-0.105	4158	98154 at	-0.128	3985	1440307 at	-0.251	1940	4249.25	2042.1951	TRUE	general transcription factor IIIC, polypeptide 2, beta	210620 s at	0.018	34564	7.166E-01	FALSE
102780 at	0.062	6800	1451680 at	-0.278	166.5	102780 at	0.150	3869	1426875 s at	0.078	6162	4249.375	2998.7984	FALSE	sulfiredoxin 1 homolog (S. cerevisiae)	225252 at	-0.001	44415	9.948E-01	FALSE
103668 at	-0.099	3897	1417628 at	-0.087	5387	103668 at	-0.043	5618	1417628 at	-0.296	2096	4249.5	1625.6811	TRUE	suppressor of Ty 6 homolog (S. cerevisiae)	208420 x at	-0.063	17298	1.218E-01	FALSE
103660 at	0.072	4564	1419365 at	0.132	1842.5	103660 at	-0.047	4946	1449442 at	0.141	5646	4249.625	1666.1216	FALSE	peroxisomal biogenesis factor 11a	205160 at	0.258	5478	4.363E-04	FALSE
103565 at	0.031	6927	1417886 at	0.295	260	103565 at	0.132	2889	1417886 at	0.071	6925	4250.25	3270.7988	TRUE	RIKEN cDNA 1810009A15 gene		NA	NA	NA	NA
104548 at	0.149	1659	1417837 at	0.117	3775.5	104548 at	0.003	8374	1417837 at	0.194	3193	4250.375	2890.3896	TRUE	pleckstrin homology-like domain, family A, member 2	209803 s at	0.068	15474	7.923E-02	FALSE
160308 at	-0.095	4913	1450379 at	-0.113	3474.5	160308 at	0.004	8308	1450379 at	-0.387	307	4250.625	3319.4166	FALSE	moesin	200600 at	0.460	4313	1.224E-04	FALSE
102243 at	-0.078	4912	1419475 a at	0.081	4749.5	102243 at	0.100	3962	1419474 a at	0.132	3381	4251.125	713.1723	FALSE	ets homologous factor	225645 at	0.398	8512	4.384E-03	FALSE
92277 at	0.072	5531	1449753 at	0.072	5188.5	92277 at	0.164	955	1449753 at	-0.079	5331	4251.375	2202.0689	FALSE	myosin IE	203072 at	0.258	6141	7.871E-04	FALSE
104427 at	0.000	8506	1443762 s at	0.098	2388.5	104427 at	0.080	5894	1443160 at	0.746	218	4251.625	3675.9791	FALSE	SET binding factor 2	226169 at	0.224	7907	3.080E-03	FALSE
160721 at	0.127	1899	1417540 at	0.019	7986	160721 at	-0.047	6120	1417540 at	-0.306	1005	4252.5	3342.2446	FALSE	E74-like factor 1	233931 at	0.349	2385	7.964E-06	FALSE
104004 at	0.055	5140	1428875 at	-0.025	7517.5	104004 at	0.268	681	1428875 at	-0.168	3673	4252.875	2860.0299	FALSE	golgi phosphoprotein 4	238002 at	0.770	1344	9.882E-07	FALSE
96359 at	-0.037	6578	1419869 s at	-0.158	1468.5	96359 at	-0.059	6110	1419869 s at	-0.148	2855	4252.875	2487.4296	TRUE	high density lipoprotein (HDL) binding protein	240152 at	0.114	8263	3.826E-03	FALSE
160449 at	0.103	3156	1416019 at	-0.111	2950	160449 at	0.002	8413	1416019 at	0.232	2498	4254.25	2786.0867	FALSE	down-regulator of transcription 1	209188 x at	-0.163	14107	5.446E-02	FALSE
160888 at	0.102	2835	1416216 at	-0.101	5504	160888 at	0.106	2261	1440822 x at	0.084	6417	4254.25	2018.8015	FALSE	RalBP1 associated Eps domain containing protein	215201 at	0.092	15330	7.704E-02	FALSE
103635 at	0.130	2213	1424526 a at	0.021	7760	103635 at	-0.237	423	1424526 a at	-0.071	6624	4255	3500.0559	FALSE	TDP-glucose 4,6-dehydratase	208249 s at	0.132	7440	2.181E-03	FALSE
104663 at	-0.071	5470	1426009 a at	0.036	6614.5	104663 at	-0.260	85	1426009 a at	0.112	4855	4256.125	2874.7383	FALSE	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	235646 at	0.175	9978	1.003E-02	FALSE
93718 at	0.112	3145	1452113 a at	0.063	4987	93718 at	-0.045	6919	1452113 a at	0.188	1975	4256.5	2165.1182	FALSE	RAB23, member RAS oncogene family	223463 at	0.412	4281	1.188E-04	FALSE
92218 at	0.171	718	1425153 at	0.040	7315.5	92218 at	-0.014	7742	1425153 at	0.214	1251	4256.625	3788.5883	FALSE	myosin, heavy polypeptide 2, skeletal muscle, adult	204631 at	-0.001	43849	9.809E-01	FALSE
101788 f at	0.107	3994	1450564 x at	0.082	4792	101788 f at	-0.051	5979	1450564 x at	0.246	2270	4258.75	1556.5812	FALSE	interferon alpha family, gene 1	208261 x at	0.043	23543	3.215E-01	FALSE
102193 at	0.108	2622	1435390 at	0.166	1849.5	102193 at	0.021	7418	1440673 at	-0.130	5148	4259.375	2533.447	FALSE	exonuclease domain containing 1		NA	NA	NA	NA
102373 at	0.204	638	1448649 at	0.019	7856	102373 at	0.204	782	1448649 at	0.042	7764	4260	4099.7805	TRUE	glutamyl aminopeptidase	204844 at	0.063	21983	2.676E-01	FALSE
95290 at	-0.206	507	1427782 a at	-0.048	6278	95290 at	0.098	3837	1418810 at	0.118	6418	4260	2768.4668	FALSE	corticotropin releasing hormone receptor 1	208593 x at	0.037	28423	4.977E-01	FALSE
161857 r at	0.138	2315	1427176 s at	-0.033	7189	161008 at	-0.030	6666	1427176 s at	-0.267	870	4260	3143.4059	FALSE	expressed sequence AI428936	235515 at	0.017	36026	7.633E-01	FALSE
103985 at	0.012	8080	1450244 a at	-0.084	3981	103985 at	0.195	685	1434833 at	-0.140	4294	4260	3025.0081	FALSE	mitogen activated protein kinase kinase kinase kinase 2	204936 at	0.016	38369	8.330E-01	FALSE
98311 at	0.120	2893	1420737 at	0.115	3565	98311 at	0.058	5242	1420737 at	0.103	5345	4261.25	1223.8269	TRUE	polyamine modulated factor 1 binding protein 1	221022 s at	0.047	28764	5.120E-01	FALSE
97204 s at	-0.051	5721	1416910 at	0.185	3804	97204 s at	0.158	2495	1416910 at	0.158	5027	4261.75	1419.6195	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 15	218435 at	0.276	6545	1.087E-03	FALSE
92689 at	-0.045	6284	1450424 a at	0.057	6368.5	92689 at	-0.127	2159	1450424 a at	-0.201	2236	4261.875	2384.1918	FALSE	interleukin 18 binding protein	224283 x at	0.033	29654	5.442E-01	FALSE
160957 at	-0.111	4892	1427941 at	0.087	4510.5	160957 at	0.054	4948	1427941 at	0.176	2698	4262.125	1060.7143	FALSE	Dicer1, Dcr-1 homolog (Drosophila)	213229 at	0.496	1046	5.174E-07	FALSE
97803 at	0.015	7813	1450919 at	0.068	4160.5	97803 at	-0.074	3851	1423243 at	0.350	1227	4262.875	2708.0156	FALSE	membrane protein, palmitoylated	202974 at	-0.248	3672	5.779E-05	FALSE
102400 at	-0.106	4106	1433663 s at	0.102	3339.5	102400 at	0.098	3960	1433663 s at	-0.091	5647	4263.125	980.60631	FALSE	expressed sequence AU014645	236197 at	0.114	11328	1.969E-02	FALSE
93129 at	-0.130	1822	1450181 at	-0.014	8094.5	93129 at	0.083	3603	1447500 at	0.266	3542	4265.375	2682.927	FALSE	cut-like 2 (Drosophila)	213920 at	0.014	36986	7.902E-01	FALSE
93083 at	0.147	2206	1425567 a at	0.027	7920.5	93083 at	0.285	465	1425567 a at	0.105	6471	4265.625	3507.544	TRUE	annexin A5	200782 at	0.405	3806	6.725E-05	TRUE
103944 at	0.067	5008	1430486 at	0.180	2609.5	103944 at	0.025	6762	1439301 at	-0.183	2683	4265.625	2002.5368	FALSE	RAD51-like 1 (S. cerevisiae)	242737 at	0.198	6208	8.369E-04	FALSE
161322 r at	-0.062	5049	1437343 x at	0.053	6684.5	104103 at	0.180	568	1456541 x at	0.182	4762	4265.875	2606.6231	FALSE	ATPase family, AAA domain containing 3A	227237 x at	-0.046	20995	2.332E-01	FALSE
98429 at	-0.136	2593	1417433 at	0.107	2184.5	98429 at	-0.079	4079	1417433 at	0.012	8208	4266.125	2751.1152	FALSE	lysophospholipase 2	215566 x at	-0.111	11076	1.776E-02	FALSE
104205 at	0.160	2749	1449827 at	-0.024	7486	104205 at	0.119	2107	1449827 at	-0.158	4725	4266.75	2418.1018	FALSE	aggrecan 1	205679 x at	0.132	12219	2.816E-02	FALSE
99958 at	-0.162	1375	1449989 at	0.141	2680	99958 at	-0.072	4654	1449989 at	0.010	8358	4266.75	3042.383	FALSE	mast cell protease 2		NA	NA	NA	NA
104091 at	0.071	4728	1428197 at	-0.144	2168.5	104091 at	0.068	3698	1443361 at	0.084	6475	4267.375	1808.7977	FALSE	tetraspanin 9	220968 s at	0.065	20479	2.155E-01	FALSE
97433 at	-0.078	4482	1448711 at	-0.062	5184	97433 at	-0.063	4354	1448711 at	-0.160	3060	4270	885.34287	TRUE	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	215582 x at	0.112	14405	5.992E-02	FALSE
97198 at	0.155	1231	1421840 at	0.051	6239	94354 at	0.500	2167	1421839 at	0.054	7444	4270.25	3033.6648	TRUE	ATP-binding cassette, sub-family A (ABC1), member 1	203505 at	0.559	3110	2.635E-05	TRUE
100952 at	0.070	5023	1436945 x at	0.062	5330.5	100952 at	0.115	4294	1436945 x at	0.173	2435	4270.625	1298.6491	TRUE	stromal interaction molecule 1	202764 at	-0.200	3180	2.940E-05	FALSE
160334 at	0.064	5381	1421993 a at	0.126	2274.5	95090 at	-0.040	5485	1421993 a at	0.107	3945	4271.375	1505.3442	FALSE	transmembrane protein 134	233018 at	0.110	12355	2.982E-02	FALSE
160165 at	-0.109	2857	1425858 at	0.121	1998	160165 at	0.034	6454	1425858 at	-0.106	5782	4272.75	2176.7348	FALSE	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	203109 at	-0.423	850	3.097E-07	FALSE
95902 at	0.066	5453	1440963 at	0.154	1784	95902 at	0.031	6610	1440964 s at	-0.133	3245	4273	2168.3999	TRUE	expressed sequence AI465270		NA	NA	NA	NA
93581 at	-0.017	7887	1448198 a at	0.248	232.5	93581 at	0.084	4426	1448198 a at	0.176	4547	4273.125	3135.0237	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	201226 at	-0.347	1185	7.041E-07	FALSE
93187 at	0.093	3043	1426784 at	-0.071	5070.5	161484 r at	0.387	1050	1426784 at	-0.029	7929	4273.125	2938.422	FALSE	tripartite motif protein 47	225868 at	0.612	2191	5.407E-06	FALSE
160772 i at	-0.055	6781	1425489 at	0.127	3318	160772 i at	-0.203	2094	1420030 at	-0.093	4900	4273.25	2028.4032	FALSE	DNA segment, Chr 11, ERATO Doi 730, expressed	231718 at	0.006	42961	9.591E-01	FALSE
160417 at	-0.012	8287	1418429 at	-0.251	4101.5	160417 at	-0.455	1008	1418429 at	-0.220	3699	4273.875	3007.2859	TRUE	kinesin family member 5B	201991 s at	0.390	2563	1.068E-05	FALSE
101180 at	0.186	1439	1421205 at	0.093	4589	101180 at	-0.099	4693	1421205 at	0.055	6375	4274	2059.6288	FALSE	ataxia telangiectasia mutated homolog (human)	210858 x at	0.247	6296	9.122E-04	FALSE
102136 r at	0.183	3780	1445047 at	0.013	7925	102136 r at	0.142	2673	1445047 at	-0.150	2719	4274.25	2486.9702	FALSE	expressed sequence C79246		NA	NA	NA	NA
92212 at	-0.071	4155	1426965 at	-0.165	1297	92212 at	0.002	8426	1426965 at	0.140	3220	4274.5	3012.5686	FALSE	RAS related protein 2a	214487 s at	-0.319	1830	2.840E-06	FALSE
101311 at	0.111	2537	1427849 a at	0.046	6354	99798 at	0.046	5650	1426159 x at	0.431	2557	4274.5	2015.3604	TRUE	T-cell receptor beta, variable 13		NA	NA	NA	NA
95470 at	-0.256	1009	1423766 at	0.138	1718	95470 at	0.002	8434	1430875 a at	0.075	5938	4274.75	3524.5735	FALSE	PAK1 interacting protein 1	218886 at	0.057	23229	3.097E-01	FALSE
161341 f at	0.025	7609	1419761 a at	0.028	7609.5	103318 at	-0.129	1136	1436232 a at	-0.258	746	4275.125	3853.2068	FALSE	GA repeat binding protein, beta 1	204618 s at	0.116	8440	4.206E-03	FALSE
95920 at	0.109	4038	1448048 at	0.091	4268	95920 at	-0.055	5356	1448048 at	-0.115	3440	4275.5	800.41718	FALSE	cDNA sequence BC016495	219147 s at	0.069	30759	5.846E-01	FALSE
102313 at	-0.041	6586	1420499 at	0.115	2106	102313 at	-0.097	4160	1420499 at	-0.095	4251	4275.75	1831.1272	FALSE	GTP cyclohydrolase 1	204224 s at	-0.448	2601	1.110E-05	FALSE
99666 at	0.038	6949	1422577 at	-0.290	228	99666 at	-0.100	4521	1422577 at	0.091	5407	4276.25	2879.2602	FALSE	citrate synthase	208660 at	-0.123	9840	9.216E-03	FALSE
96758 s at	-0.136	1482	1424530 at	0.049	6230.5	96758 s at	-0.200	1196	1424530 at	0.011	8197	4276.375	3487.4607	FALSE	SEC14-like 2 (S. cerevisiae)	204541 at	0.252	7142	1.786E-03	FALSE
96700 r at	0.012	8013	1435518 at	-0.318	716	96700 r at	0.163	1484	1455349 at	0.049	6894	4276.75	3709.8048	FALSE	RAS related protein 1b	200833 s at	0.295	8100	3.495E-03	FALSE
98309 at	-0.018	7868	1422111 at	0.054	6934	98309 at	-0.111	1798	1422111 at	-0.280	508	4277	3665.4118	FALSE	chemokine binding protein 2	239452 at	-0.023	32946	6.635E-01	FALSE
92857 at	-0.135	2361	1448398 s at	0.033	6759	92857 at	0.179	723	1453118 s at	-0.038	7266	4277.25	3235.0382	FALSE	ribosomal protein L22	221726 at	-0.137	11896	2.479E-02	FALSE
98280 at	-0.036	6678	1437568 at	-0.048	6350.5	98280 at	-0.096	2732	1440161 at	0.202	1351	4277.875	2646.5513	FALSE	matrix metallopeptidase 16	208167 s at	-0.036	20181	2.063E-01	FALSE
93940 at	-0.071	4990	1419298 at	0.104	3978	93940 at	-0.060	5010	1419298 at	-0.222	3135	4278.25	901.70519	FALSE	paraoxonase 3	213695 at	0.207	11611	2.199E-02	FALSE
100047 at	-0.155	2019	1416828 at	-0.210	1790.5	100047 at	0.017	7496	1416828 at	0.090	5808	4278.375	2827.6705	FALSE	synaptosomal-associated protein 25	202507 s at	-1.535	772	2.502E-07	FALSE
97772 at	0.077	4946	1422139 at	0.088	3932	97772 at	0.039	6190	1422138 at	0.215	2046	4278.5	1751.5238	TRUE	plasminogen activator, urokinase	211668 s at	-0.087	21330	2.445E-01	FALSE
100979 at	0.320	495	1419369 at	0.062	5841.5	99529 f at	-0.065	4922	1419369 at	0.107	5862	4280.125	2561.2103	FALSE	ring finger protein 138	218738 s at	0.285	9673	8.584E-03	FALSE
98512 at	0.028	6881	1452462 a at	0.109	3547.5	98512 at	0.063	4892	1452462 a at	0.228	1801	4280.375	2146.4499	TRUE	Btg3 associated nuclear protein	228928 x at	0.359	2092	4.508E-06	TRUE
104163 at	0.064	6937	1452185 at	0.110	4964	104163 at	0.148	2929	1459203 at	0.185	2292	4280.5	2105.932	TRUE	importin 8	225528 at	0.241	3913	7.878E-05	TRUE
93621 at	0.108	3259	1434400 at	0.070	4725.5	93621 at	-0.046	5506	1434400 at	0.238	3632	4280.625	1026.9517	FALSE	TGFB-induced factor 2	218724 s at	0.116	6005	6.953E-04	FALSE
161488 r at	0.229	2147	1422819 at	0.060	5323.5	96098 at	0.082	4657	1422819 at	0.100	4996	4280.875	1448.3742	TRUE	mitochondrial ribosomal protein L36	224331 s at	-0.092	19492	1.847E-01	FALSE
101733 at	0.121	4538	1422349 at	0.127	3626.5	101733 at	0.107	2826	1422349 at	0.074	6134	4281.125	1419.5132	TRUE	chemokine (C-C motif) receptor 1-like 1		NA	NA	NA	NA
96831 at	-0.086	3934	1424650 at	-0.081	5604.5	96831 at	-0.055	5124	1424650 at	-0.228	2463	4281.375	1400.9323	TRUE	protein disulfide isomerase associated 5	203857 s at	0.000	44421	9.948E-01	FALSE
101347 at	0.008	8233	1427858 at	0.171	1324	101347 at	0.073	3758	1452537 at	0.233	3814	4282.25	2878.2961	TRUE	Immunoglobulin kappa chain variable 1 (V1)		NA	NA	NA	NA
103462 at	-0.025	7649	1422808 s at	0.025	7567	103462 at	0.130	1502	1422808 s at	-0.410	412	4282.5	3865.7993	FALSE	dedicator of cyto-kinesis 2	235236 at	0.128	21168	2.387E-01	FALSE
104165 at	-0.056	6457	1418486 at	0.196	1248.5	104165 at	-0.028	6508	1418486 at	0.155	2917	4282.625	2630.022	FALSE	vanin 1	205844 at	0.014	36474	7.768E-01	FALSE
161396 f at	-0.398	261	1433765 at	-0.013	7934	97739 at	-0.234	1031	1433765 at	0.021	7905	4282.75	4211.1231	FALSE	ubiquitin-conjugating enzyme E2O	218141 at	-0.102	13578	4.505E-02	FALSE
100127 at	-0.124	3299	1451191 at	0.042	7038	100127 at	-0.065	6069	1451191 at	-0.297	728	4283.5	2851.0876	FALSE	cellular retinoic acid binding protein II	202575 at	-0.103	17053	1.157E-01	FALSE
103818 at	-0.008	8129	1417392 a at	0.126	2758	103818 at	0.095	4348	1417392 a at	-0.281	1901	4284	2756.5368	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	204588 s at	0.096	17352	1.231E-01	FALSE
95729 at	0.065	4751	1417610 at	0.072	4501	95728 g at	-0.082	2838	1417610 at	0.105	5046	4284	989.40015	FALSE	apolipoprotein A-V	224244 s at	-0.047	22333	2.795E-01	FALSE
100074 at	-0.087	4941	1448268 at	0.157	1919	100074 at	-0.181	2797	1439448 x at	0.033	7480	4284.25	2479.9502	FALSE	transmembrane emp24 protein transport domain containing 9	205812 s at	0.162	10163	1.099E-02	FALSE
92311 s at	0.044	5950	1421023 at	-0.052	7076.5	92312 at	-0.262	282	1443655 s at	-0.120	3830	4284.625	2988.6302	FALSE	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide	241905 at	0.281	12144	2.735E-02	FALSE
94112 at	0.066	5439	1420412 at	0.105	4206.5	94112 at	-0.041	6566	1439680 at	-0.245	928	4284.875	2436.5473	FALSE	tumor necrosis factor (ligand) superfamily, member 10	200687 s at	-0.069	22404	2.818E-01	FALSE
101108 at	0.035	6515	1416042 s at	0.013	7958.5	101108 at	0.195	634	1442728 at	0.158	2033	4285.125	3505.6529	TRUE	nuclear autoantigenic sperm protein (histone-binding)	201970 s at	0.391	3379	3.870E-05	TRUE
160657 at	-0.066	5438	1436802 at	0.063	4520.5	160657 at	-0.118	4898	1460669 at	-0.157	2284	4285.125	1386.1985	FALSE	interleukin enhancer binding factor 3	211375 s at	0.123	18224	1.466E-01	FALSE
94318 at	0.149	1241	1416677 at	0.071	4325	94318 at	-0.024	6925	1447719 at	0.206	4650	4285.25	2335.9767	FALSE	apolipoprotein H	205216 s at	0.040	29024	5.212E-01	FALSE
97282 at	0.056	5059	1456456 x at	0.158	1613	97282 at	-0.001	8487	1433438 x at	0.199	1982	4285.25	3198.9203	FALSE	melanoma antigen		NA	NA	NA	NA
95275 at	0.132	3056	1421570 at	-0.031	7462	95275 at	0.125	1619	1421570 at	-0.119	5007	4286	2531.9693	FALSE	interleukin 9 receptor	217212 s at	0.059	19566	1.866E-01	FALSE
102639 at	-0.161	3087	1422758 at	-0.080	6957	102639 at	-0.235	420	1460070 at	-0.092	6685	4287.25	3123.726	TRUE	carbohydrate sulfotransferase 2	203921 at	-0.234	9132	6.300E-03	TRUE
101085 at	-0.033	7259	1438563 s at	0.268	720	101085 at	0.154	1265	1438563 s at	0.025	7907	4287.75	3820.696	FALSE	mitochondrial ribosomal protein S24	224948 at	-0.083	19222	1.755E-01	FALSE
97248 at	-0.075	6303	1433991 x at	0.232	2970.5	97248 at	0.147	4879	1422432 at	-0.260	3004	4289.125	1611.8275	FALSE	diazepam binding inhibitor	202428 x at	0.451	2671	1.334E-05	FALSE
93799 at	0.141	1269	1433629 s at	0.118	1471	93799 at	0.036	7175	1433629 s at	0.052	7243	4289.5	3372.271	TRUE	expressed sequence AI316787	225374 at	-0.019	33877	6.950E-01	FALSE
95425 at	0.270	1164	1448987 at	-0.040	6975.5	95425 at	0.091	5254	1448987 at	-0.206	3768	4290.375	2462.0835	FALSE	acyl-Coenzyme A dehydrogenase, long-chain	206068 s at	0.080	18098	1.430E-01	FALSE
160231 at	-0.022	7154	1424907 a at	0.028	7625	160231 at	-0.189	975	1445003 at	0.389	1409	4290.75	3587.6689	FALSE	phenylalanine-tRNA synthetase-like, alpha subunit	216602 s at	-0.376	2960	2.040E-05	FALSE
97526 at	0.009	8020	1448309 at	-0.145	2091	97526 at	-0.091	2684	1458092 at	0.147	4369	4291	2666.7067	FALSE	adaptor-related protein complex 3, mu 1 subunit	222516 at	0.147	13807	4.907E-02	FALSE
92885 at	0.234	1143	1450118 a at	0.105	3008	92885 at	0.051	5628	1450118 a at	-0.039	7386	4291.25	2764.211	FALSE	troponin T3, skeletal, fast	205693 at	-0.023	36372	7.738E-01	FALSE
104065 at	-0.010	8033	1451218 at	0.085	4902.5	104065 at	0.142	1999	1451218 at	0.171	2231	4291.375	2820.9549	FALSE	ER degradation enhancer, mannosidase alpha-like 1	203279 at	-0.158	6023	7.066E-04	FALSE
93681 at	-0.094	3252	1418532 at	-0.101	3078.5	93681 at	-0.094	3619	1418533 s at	0.058	7218	4291.875	1963.7199	FALSE	frizzled homolog 2 (Drosophila)	210220 at	-0.069	26326	4.171E-01	FALSE
161528 r at	0.093	5808	1448187 at	0.035	6740.5	161528 r at	0.145	1220	1456055 x at	-0.173	3402	4292.625	2484.7998	FALSE	polymerase (DNA directed), delta 1, catalytic subunit	203422 at	0.051	23628	3.246E-01	FALSE
102695 at	0.077	4351	1427608 a at	0.086	4370	102695 at	0.112	3585	1427608 a at	0.108	4866	4293	528.79927	TRUE	T-cell receptor gamma, constant region		NA	NA	NA	NA
93059 at	-0.098	3574	1428966 at	0.183	1330	93059 at	0.092	6184	1428966 at	0.063	6085	4293.25	2315.4175	FALSE	RIKEN cDNA 2610204K14 gene	225208 s at	-0.087	11114	1.813E-02	FALSE
96255 at	0.240	2933	1448525 a at	-0.170	2533	96255 at	0.026	7696	1416923 a at	-0.132	4012	4293.5	2352.7692	FALSE	BCL2/adenovirus E1B interacting protein 3-like	221479 s at	0.116	17957	1.395E-01	FALSE
94291 at	0.041	6855	1452543 a at	0.059	6165	94291 at	0.147	2174	1452543 a at	-0.157	1981	4293.75	2575.7672	FALSE	secretoglobin, family 1A, member 1 (uteroglobin)	205725 at	-0.045	27844	4.747E-01	FALSE
160227 s at	-0.187	544	1450742 at	0.017	7709	160227 s at	-0.078	3810	1422767 at	0.109	5114	4294.25	2979.4508	FALSE	bystin-like	203612 at	0.000	44534	9.971E-01	FALSE
160557 at	0.118	2215	1427661 a at	0.005	8307	160557 at	-0.083	3300	1427661 a at	0.241	3359	4295.25	2725.721	FALSE	tumor-suppressing subchromosomal transferable fragment 4	218612 s at	0.097	9679	8.599E-03	FALSE
93483 at	-0.048	6607	1449455 at	0.075	5548	93483 at	0.085	4138	1446553 at	-0.251	891	4296	2485.1032	FALSE	hemopoietic cell kinase	208018 s at	0.163	20891	2.300E-01	FALSE
92377 at	-0.126	2163	1455279 at	0.053	6069.5	92377 at	0.054	5074	1455279 at	0.146	3881	4296.875	1680.5254	FALSE	gene model 1060, (NCBI)		NA	NA	NA	NA
93894 f at	-0.160	1125	1425436 x at	0.074	5330.5	93894 f at	0.099	3997	1425436 x at	0.078	6739	4297.875	2393.2591	FALSE	killer cell lectin-like receptor, subfamily A, member 3		NA	NA	NA	NA
104314 r at	0.741	1338	1417211 a at	0.280	1728	104314 r at	-0.079	6274	1445336 at	0.030	7857	4299.25	3262.7979	FALSE	RIKEN cDNA 1110032A03 gene	222785 x at	-0.398	1914	3.317E-06	FALSE
96939 at	-0.046	6514	1452670 at	0.069	5701	96939 at	0.119	1685	1452670 at	-0.333	3298	4299.5	2214.1082	FALSE	myosin, light polypeptide 9, regulatory	201058 s at	0.242	11805	2.389E-02	FALSE
160638 at	0.124	2761	1416868 at	0.103	2992	160638 at	-0.017	7337	1439164 at	0.116	4112	4300.5	2108.5617	FALSE	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	204159 at	0.246	3833	6.965E-05	FALSE
94551 at	0.085	4306	1424103 at	-0.032	7588	94551 at	-0.117	1848	1424103 at	0.132	3464	4301.5	2416.7589	FALSE	autophagy-related 4B (yeast)	212280 x at	0.117	15850	8.719E-02	FALSE
99112 at	0.169	2400	1416954 at	0.028	7310	99112 at	-0.063	5226	1416955 at	-0.286	2271	4301.75	2425.1739	FALSE	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	218275 at	0.024	35558	7.481E-01	FALSE
161078 at	0.198	3019	1439625 at	0.096	4069	161078 at	0.061	4933	1439625 at	0.153	5186	4301.75	979.795	TRUE	Keratin associated protein 5-5		NA	NA	NA	NA
101972 at	-0.020	7618	1423590 at	0.127	2852	101972 at	0.129	3833	1423590 at	0.142	2907	4302.5	2255.6847	FALSE	napsin A aspartic peptidase	223806 s at	-0.027	31404	6.096E-01	FALSE
99995 at	0.117	4573	1453881 x at	0.142	2689.5	99995 at	-0.002	8461	1423203 a at	-0.219	1487	4302.625	3049.3224	FALSE	centrin 1	207209 at	0.002	43766	9.789E-01	FALSE
161983 f at	0.125	1894	1451201 s at	0.063	5094	100621 at	0.088	2883	1451201 s at	0.067	7341	4303	2427.2622	TRUE	ribonuclease/angiogenin inhibitor 1	216798 at	0.073	17056	1.160E-01	FALSE
100951 at	0.097	4535	1417753 at	0.080	4872	100951 at	-0.225	1988	1441870 s at	-0.080	5819	4303.5	1636.5681	FALSE	polycystic kidney disease 2	203688 at	0.292	6368	9.595E-04	FALSE



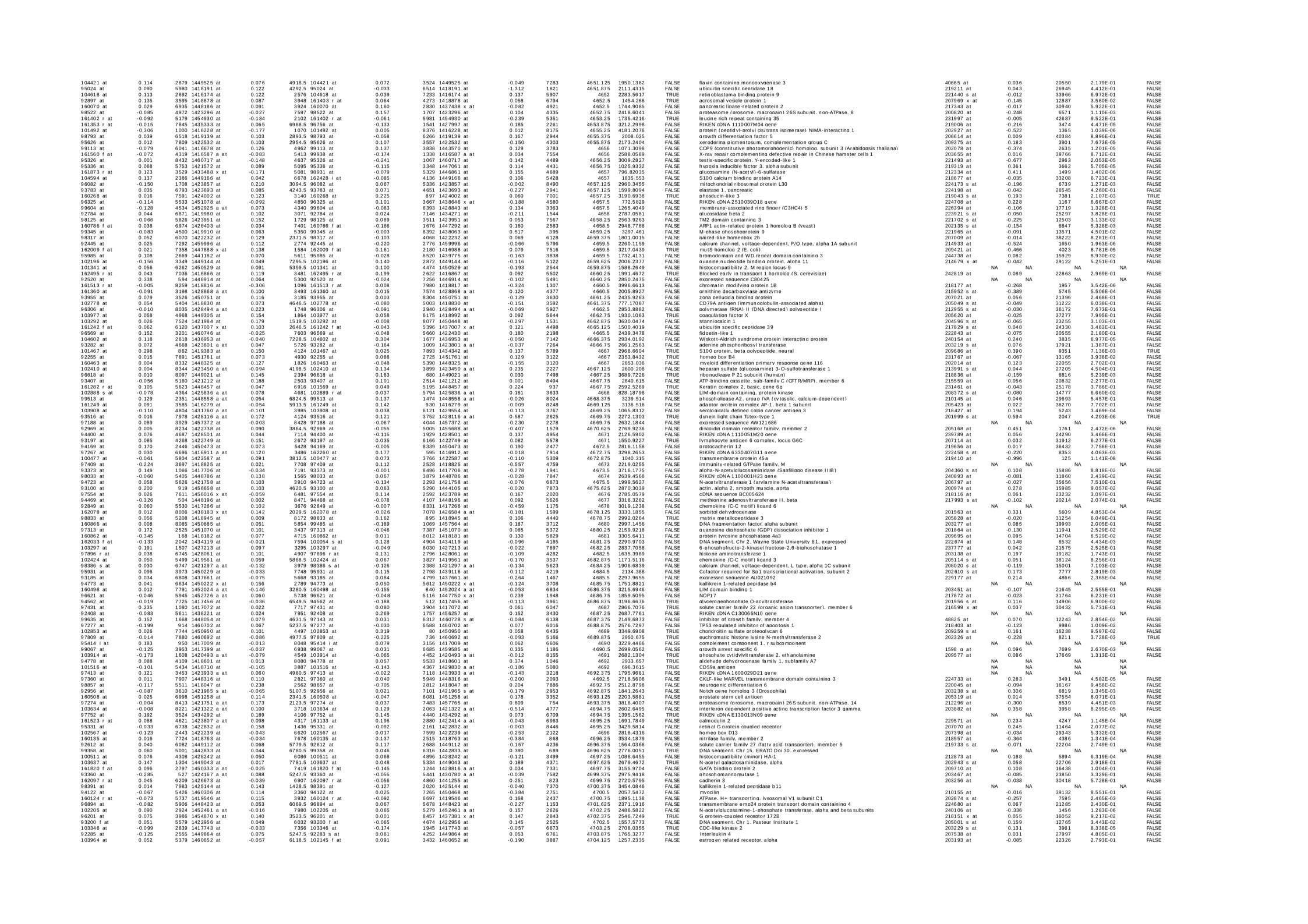
101436 at	-0.784	2261	1418652 at	0.071	3932	101436 at	0.004	8297	1456907 at	-0.177	2949	4359.75	2712.9243	FALSE	chemokine (C-X-C motif) ligand 9	203915 at	0.057	33229	6.729E-01	FALSE
94641 at	0.056	6347	1425092 at	0.103	3686	94641 at	-0.164	4040	1425092 at	0.147	3367	4360	1352.8851	FALSE	cadherin 10	220115 s at	-0.050	28533	5.030E-01	FALSE
160778 at	-0.074	4022	1433737 at	0.012	8123	160778 at	0.313	1360	1433737 at	-0.123	3935	4360	2796.1305	FALSE	similar to U2AF homology motif (UHM) kinase 1	NA	NA	NA	NA	
102208 at	0.055	5953	1449079 s at	-0.110	3885	102208 at	-0.044	6151	1443740 at	0.257	1452	4360.25	2192.9751	FALSE	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	210942 s at	-0.110	18461	1.539E-01	FALSE
93066 at	-0.160	2217	1456567 x at	0.085	5858.5	93066 at	0.145	3365	1448148 at	-0.097	6004	4361.125	1873.5623	FALSE	granulin	200678 x at	0.117	10515	1.335E-02	FALSE
101778 at	0.071	5869	1422192 at	0.119	2746.5	101778 at	0.058	4737	1429101 at	-0.153	4092	4361.125	1303.1259	FALSE	gap junction membrane channel protein alpha 5	226701 at	-0.058	21184	2.392E-01	FALSE
93953 at	-0.281	206	1420388 at	0.074	4927	93953 at	0.012	7590	1420388 at	0.454	4726	4362.25	3062.8985	FALSE	protease, serine, 12 neurotrypsin (motopsin)	213802 at	-0.042	18611	1.583E-01	FALSE
101926 at	0.064	4623	1417216 at	0.087	3339.5	101926 at	0.086	4135	1417216 at	0.086	5353	4362.625	846.01727	TRUE	proviral integration site 2	204269 at	-0.098	12321	2.941E-02	FALSE
102012 at	0.231	241	1418895 at	0.100	3896	102012 at	0.022	7174	1460623 at	-0.070	6142	4363.25	3070.0453	FALSE	src family associated phosphoprotein 2	242598 at	0.117	10462	1.303E-02	FALSE
96243 f at	0.242	1126	1437398 a at	0.034	7293	96243 f at	0.289	3051	1437398 a at	0.090	5984	4363.5	2793.5672	TRUE	aldehyde dehydrogenase 9, subfamily A1	201612 at	0.276	5820	5.966E-04	TRUE
103527 at	-0.017	7648	1434167 at	0.099	3415	103527 at	0.181	2208	1439118 at	-0.144	4184	4363.75	2335.665	FALSE	solute carrier family 35, member E4	231238 at	0.225	7982	3.253E-03	FALSE
161345 f at	-0.127	3050	1421075 s at	0.147	957.5	161345 f at	-0.020	7262	1446995 at	0.067	6187	4364.125	2889.785	FALSE	Cytochrome P450, family 7, subfamily b, polypeptide 1	235438 at	-0.099	22283	2.781E-01	FALSE
96742 at	0.195	953	1418511 at	0.031	7173	96742 at	0.135	3400	1418511 at	-0.064	5933	4364.75	2763.8413	FALSE	dermatopontin	207977 s at	0.024	29822	5.506E-01	FALSE
96160 at	-0.052	5732	1431812 a at	-0.205	775	96160 at	-0.056	4453	1431812 a at	-0.112	6506	4366.5	2539.5803	TRUE	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	207043 s at	0.141	10573	1.378E-02	FALSE
162057 f at	0.126	4586	1455932 at	0.055	5967.5	93802 at	-0.027	6475	1456548 at	0.406	441	4367.375	2736.5855	FALSE	Metadherin	212251 at	0.220	9768	8.915E-03	FALSE
97486 at	-0.134	4517	1422509 at	0.199	1075	97486 at	0.085	3607	1422509 at	0.013	8274	4368.25	2983.3989	FALSE	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	202858 at	0.234	3161	2.882E-05	FALSE
103567 at	0.151	1421	1415758 at	-0.086	5003	103567 at	0.028	7444	1444520 at	0.136	3606	4368.5	2525.2362	FALSE	furry homolog-like (Drosophila)	212548 s at	0.475	1170	6.726E-07	FALSE
99639 at	-0.167	1404	1448230 at	-0.081	4697	99639 at	-0.111	3227	1448230 at	-0.013	8146	4368.5	2855.9121	TRUE	ubiquitin specific peptidase 10	209137 s at	-0.117	8498	4.350E-03	TRUE
97533 at	-0.034	6843	1416978 at	-0.110	3257	97533 at	-0.040	5346	1416978 at	-0.247	2032	4369.5	2142.6866	TRUE	Fc receptor, IgG, alpha chain transporter	218831 s at	0.320	1182	6.977E-07	FALSE
161255 at	0.034	6811	1415990 at	0.084	5091	161255 at	0.113	2196	1415990 at	0.125	3382	4370	2015.0055	TRUE	voltage-dependent anion channel 2	211662 s at	-0.215	9222	6.615E-03	FALSE
161603 r at	0.168	1176	1449167 at	0.008	8231	92231 at	0.147	1156	1449167 at	-0.062	6917	4370	3738.358	FALSE	erythrocyte protein band 4.1-like 4a	228256 s at	-0.103	17570	1.285E-01	FALSE
103447 at	-0.061	5917	1434445 at	0.083	4211	103447 at	-0.226	2193	1457004 at	0.100	5165	4371.5	1611.4005	FALSE	DNA segment, Chr 15, Wayne State University 169, expressed	227876 at	0.155	7327	2.036E-03	FALSE
100103 f at	0.039	6884	1422436 at	0.165	1656	100103 f at	0.075	3206	1422435 at	0.110	5743	4372.25	2375.2892	TRUE	RIKEN cDNA 2210010C04 gene	213421 x at	-0.237	6167	8.039E-04	FALSE
102828 at	0.079	4533	1426850 a at	0.033	6643	102829 s at	0.086	4421	1459292 at	-0.217	1893	4372.5	1943.4679	FALSE	mitogen activated protein kinase kinase 6	205698 s at	-0.054	28723	5.109E-01	FALSE
96060 at	-0.092	6115	1450138 a at	0.099	4581.5	96060 at	0.350	1573	1446417 at	-0.252	5221	4372.625	1969.5295	FALSE	serine (or cysteine) peptidase inhibitor, clade B, member 6a	211474 s at	0.476	1174	6.772E-07	FALSE
96347 at	0.134	1498	1424382 at	-0.204	4749.5	96347 at	0.074	4942	1424382 at	-0.072	6302	4372.875	2037.3332	FALSE	reticulocalbin 3, EF-hand calcium binding domain	61734 at	0.066	20897	2.302E-01	FALSE
93513 at	0.212	693	1417317 s at	0.442	672	93513 at	0.006	8202	1417317 s at	0.020	7926	4373.25	4263.2089	TRUE	ribosomal protein L35a	215208 x at	0.258	4028	8.848E-05	TRUE
92895 at	0.074	5221	1449967 at	0.089	4311	92895 at	0.190	548	1420736 at	-0.042	7413	4373.25	2863.2832	FALSE	single-minded homolog 1 (Drosophila)	206876 at	-0.025	31673	6.195E-01	FALSE
161490 at	-0.041	6267	1439267 x at	0.114	4480.5	161490 at	0.157	1134	1439267 x at	0.105	5614	4373.875	2282.5418	FALSE	cytochrome c oxidase, subunit Va	203663 s at	-0.319	9156	6.400E-03	FALSE
102050 at	0.111	2414	1419976 s at	-0.043	6525	102050 at	0.043	6485	1419976 s at	-0.165	2072	4374	2464.6789	FALSE	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	210555 s at	0.175	7910	3.084E-03	FALSE
160844 at	0.143	2626	1450660 at	0.213	1186.5	160844 at	0.031	7343	1450660 at	0.094	6341	4374.125	2938.237	TRUE	6-pyruvoyl-tetrahydropterin synthase	209694 at	-0.311	4864	2.359E-04	FALSE
103483 at	0.151	1010	1450935 at	0.038	6520.5	161777 f at	0.082	4900	1457713 at	-0.101	5067	4374.375	2358.0276	FALSE	excision repair cross-complementing rodent repair deficiency, complementation group 5	202414 at	0.162	8652	4.764E-03	FALSE
94920 at	0.053	5619	1415793 at	0.081	4130.5	94920 at	0.065	6125	1415793 at	0.281	1623	4374.375	2020.1748	TRUE	pyridoxine 5'-phosphate oxidase	218511 s at	-0.020	34666	7.207E-01	FALSE
97908 at	-0.136	4356	1426884 at	-0.136	3311.5	97908 at	-0.063	6322	1444195 at	-0.295	3512	4375.375	1374.4054	TRUE	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	212479 s at	0.079	14747	6.600E-02	FALSE
102251 at	0.071	6062	1437531 at	0.147	1849.5	102251 at	0.018	7213	1437445 at	0.226	2377	4375.375	2662.7283	TRUE	transient receptor potential cation channel, subfamily M, member 1	214410 at	-0.072	17580	1.289E-01	FALSE
99154 s at	0.052	5605	1451381 at	0.234	983.5	99154 s at	0.091	3688	1451381 at	0.047	7226	4375.625	2684.2343	TRUE	RIKEN cDNA 1810020D17 gene	221599 at	0.262	2334	7.121E-06	TRUE
160166 r at	0.126	2515	1438094 x at	0.094	4993	160166 r at	0.159	3986	1430053 a at	0.083	6011	4376.25	1491.0103	TRUE	RIKEN cDNA 2810409H07 gene	219293 s at	-0.383	1451	1.271E-06	FALSE
100082 at	0.052	6044	1421234 at	0.062	5725	100082 at	0.085	3913	1421234 at	0.269	1823	4376.25	1943.7252	TRUE	transcription factor 1	216930 at	-0.039	21801	2.613E-01	FALSE
95725 at	0.079	4422	1448539 a at	0.063	6076	95725 at	-0.072	4017	1448539 a at	0.189	2991	4376.5	1283.1239	FALSE	aspartoacylase (aminoacylase) 3	230481 at	-0.020	36098	7.658E-01	FALSE
94121 at	0.139	1713	1422240 s at	0.264	415	94121 at	0.019	7315	1422240 s at	0.022	8065	4377	3874.1678	TRUE	small proline-rich protein 2H	NA	NA	NA	NA	
103842 at	0.865	2191	1426439 at	0.053	5469	103842 at	1.310	1750	1426439 at	0.232	8098	4377	2984.2939	TRUE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	NA	NA	NA	NA	
160869 at	-0.249	892	1417892 a at	0.015	8086.5	160869 at	0.097	4361	1417892 a at	0.201	4170	4377.375	2941.0157	FALSE	sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae)	221562 s at	-0.210	4232	1.121E-04	FALSE
96570 at	0.022	7153	1427973 s at	0.069	5273	96570 at	-0.058	4679	1429940 at	0.406	406	4377.75	2850.0898	FALSE	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	222320 at	0.128	3694	5.891E-05	FALSE
162041 f at	0.215	2745	1419387 s at	0.086	5158	98000 at	0.087	3440	1419386 at	-0.067	6168	4377.75	1566.2091	FALSE	mucin 13, epithelial transmembrane	222712 s at	-0.080	18616	1.584E-01	FALSE
101735 f at	0.142	2774	1422415 at	0.026	7849	101735 f at	0.093	3503	1422415 at	0.186	3385	4377.75	2336.1172	TRUE	angiogenin, ribonuclease A family, member 2	NA	NA	NA	NA	
103449 at	-0.230	1556	1455155 at	-0.054	6830	103449 at	-0.101	5790	1455155 at	-0.138	3339	4378.75	2383.9219	TRUE	LSM14 homolog B (SCD6, S. cerevisiae)	219653 at	-0.028	31951	6.294E-01	FALSE
104268 at	0.097	3420	1452416 at	0.084	3870	104268 at	0.094	3461	1452416 at	-0.063	6767	4379.5	1604.5798	FALSE	interleukin 6 receptor, alpha	205945 at	0.229	3995	8.515E-05	FALSE
101417 at	0.336	983	1427252 at	0.080	4347	101417 at	0.062	5415	1427252 at	-0.065	6775	4380	2473.0513	FALSE	DMRT-like family B with proline-rich C-terminal, 1	240313 at	0.007	41457	9.191E-01	FALSE
160223 at	0.044	5850	1452665 at	0.187	1242.5	160223 at	0.149	2791	1452665 at	0.030	7637	4380.125	2894.6949	TRUE	RIKEN cDNA 2610511O17 gene	244248 at	0.096	12107	2.699E-02	TRUE
102242 at	0.042	6485	1421087 at	-0.131	2987	102242 at	-0.012	7855	1442243 at	-0.591	195	4380.5	3462.2403	FALSE	period homolog 3 (Drosophila)	221045 s at	0.217	10347	1.228E-02	FALSE
160462 f at	-0.112	3875	1415978 at	-0.294	499.5	160462 f at	-0.075	5688	1415978 at	0.039	7462	4381.125	2973.3756	FALSE	tubulin, beta 3	213476 x at	-0.314	9588	8.152E-03	FALSE
103080 at	-0.014	7955	1434438 at	0.117	4177	103080 at	0.129	1538	1418131 at	-0.129	3856	4381.5	2656.6498	FALSE	SAM domain and HD domain, 1	241268 x at	0.181	2998	2.203E-05	FALSE
103672 at	-0.069	5459	1428997 at	0.067	4989	103672 at	0.120	3812	1428997 at	0.130	3266	4381.5	1016.3223	FALSE	PHD finger protein 23	NA	NA	NA	NA	
96329 at	-0.072	6037	1416438 at	0.105	3632	96329 at	-0.121	3709	1430705 at	0.175	4150	4382	1126.6881	FALSE	RIKEN cDNA 2410104I19 gene	209899 s at	0.153	10806	1.565E-02	FALSE
160305 at	-0.254	2017	1456059 at	0.034	6567	160305 at	0.054	6956	1429370 a at	0.202	1989	4382.25	2751.9311	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	208777 s at	0.074	23789	3.306E-01	FALSE
94298 at	-0.016	7645	1448495 at	0.047	5935	94298 at	-0.138	1984	1448495 at	-0.184	1965	4382.25	2866.5467	FALSE	tissue specific transplantation antigen P35B	36936 at	0.035	24889	3.684E-01	FALSE
102218 at	0.038	6606	1450297 at	0.090	4156	102218 at	0.089	3604	1450297 at	-0.167	3164	4382.5	1536.8864	FALSE	interleukin 6	205207 at	0.085	19770	1.933E-01	FALSE
160887 at	-0.066	4860	1418102 at	-0.061	5985.5	160887 at	-0.070	5082	1418102 at	0.277	1606	4383.375	1914.4942	FALSE	hairy and enhancer of split 1 (Drosophila)	203394 s at	0.196	12451	3.088E-02	FALSE
160668 at	0.054	5413	1422511 a at	-0.077	3896	160668 at	0.140	1140	1422511 a at	-0.056	7085	4383.5	2524.2769	FALSE	opioid growth factor receptor	211513 s at	-0.092	20216	2.076E-01	FALSE
103541 at	0.083	4950	1430773 a at	0.087	5371	103541 at	-0.042	6649	1425009 at	-0.291	564	4383.5	2646.8314	FALSE	t-complex-associated testis expressed 2	NA	NA	NA	NA	
96094 at	0.067	4932	1438840 x at	0.115	1541.5	96094 at	-0.005	8263	1419233 x at	0.211	2801	4384.375	2940.1043	FALSE	apolipoprotein A-I	204450 x at	0.059	28112	4.852E-01	FALSE
102104 f at	-0.082	5519	1450234 at	0.074	4620.5	102104 f at	0.113	2231	1450234 at	-0.142	5177	4386.875	1484.1813	FALSE	membrane-spanning 4-domains, subfamily A, member 6C	NA	NA	NA	NA	
104522 at	-0.020	7402	1421192 a at	-0.154	632.5	104522 at	0.007	8055	1421192 a at	-0.248	1461	4387.625	3881.6746	FALSE	intersectin 1 (SH3 domain protein 1A)	35776 at	0.459	2127	4.758E-06	FALSE
99531 at	-0.025	7577	1418875 at	0.097	4528.5	99531 at	0.153	1204	1418875 at	0.146	4243	4388.125	2604.3772	FALSE	synaptogyrin 4	206719 at	-0.029	33014	6.659E-01	FALSE
160943 at	0.104	3058	1460229 at	0.064	5868.5	160943 at	0.076	4308	1460229 at	-0.108	4319	4388.375	1150.6434	FALSE	stromal antigen 3	219753 at	0.023	32012	6.320E-01	FALSE
92215 at	0.101	4035	1450536 s at	0.086	3703	92215 at	-0.054	5062	1450536 s at	0.123	4755	4388.75	627.90571	FALSE	keratin associated protein 12-1	NA	NA	NA	NA	
97256 at	0.043	6836	1433513 x at	0.197	2063	97256 at	-0.017	7571	1418814 s at	-0.280	1087	4389.25	3287.6746	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	223244 s at	-0.300	4961	2.575E-04	FALSE
92923 g at	-0.080	4504	1421995 at	0.061	5779.5	92922 at	0.091	2391	1426048 s at	0.119	4884	4389.625	1435.7046	FALSE	transcription factor AP-2, alpha	204654 s at	-0.052	20418	2.137E-01	FALSE
96734 at	0.089	3726	1448853 at	0.050	6525	101548 at	-0.107	3399	1448853 at	0.129	3910	4390	1438.935	FALSE	synaptojanin 2 binding protein	219156 at	0.158	8202	3.709E-03	FALSE
98997 f at	0.165	1882	1420409 at	0.089	4969	98997 f at	0.113	3028	1420409 at	0.026	7683	4390.5	2537.9911	TRUE	keratin complex 1, acidic, gene 24	216921 s at	-0.026	32554	6.488E-01	FALSE
101143 at	0.070	4468	1450043 at	0.089	4670	101143 at	0.045	5140	1450043 at	0.133	3286	4391	788.62665	TRUE	frizzled homolog 7 (Drosophila)	203706 s at	0.243	13905	5.064E-02	FALSE
97279 at	0.225	1794	1423780 at	0.064	5647	97279 at	0.000	8527	1442848 at	0.229	1598	4391.5	3328.1271	FALSE	3-hydroxyisobutyrate dehydrogenase	215316 at	0.050	16106	9.309E-02	FALSE
103322 at	0.047	5722	1418337 at	0.139	2536	103322 at	0.074	3472	1418337 at	0.073	5837	4391.75	1648.0353	TRUE	ribose 5-phosphate isomerase A	212973 at	0.142	5075	2.899E-04	TRUE
94840 at	-0.077	6040	1449024 a at	-0.038	7517.5	94840 at	-0.208	1704	1449024 a at	-0.153	2306	4391.875	2832.0425	TRUE	hexosaminidase A	215155 at	0.160	7228	1.903E-03	FALSE
94818 at	0.034	7688	1436780 at	0.219	2388.5	94818 at	-0.084	5719	1436780 at	0.407	1775	4392.625	2798.0496	FALSE	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acety	207564 x at	-0.253	12722	3.396E-02	FALSE
96191 at	0.170	3237	1415711 at	0.022	7519	96191 at	0.112	4003	1444175 at	0.198	2812	4392.75	2141.6406	TRUE	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	236742 at	0.142	6724	1.257E-03	TRUE
103836 at	0.081	3658	1419374 at	-0.064	5489	103836 at	0.034	6873	1419375 at	-0.183	1560	4395	2303.4549	FALSE	WW domain binding protein 4	203599 s at	-0.104	14902	6.890E-02	FALSE
96486 at	0.088	4800	1421455 at	0.172	2464	93384 at	-0.021	6924	1446258 at	-0.147	3394	4395.5	1939.9851	FALSE	Syntrophin, basic 1	214708 at	0.133	10128	1.079E-02	FALSE
103656 at	-0.164	2499	1427012 at	0.050	5956	103656 at	-0.293	1247	1427011 a at	-0.020	7884	4396.5	3061.2935	FALSE	LanC (bacterial lantibiotic synthetase component C)-like 1	202019 s at	-0.261	5702	5.274E-04	FALSE
101457 at	-0.044	6430	1421065 at	-0.173	1224	101457 at	0.039	7093	1421066 at	-0.167	2839	4396.5	2822.3393	FALSE	Janus kinase 2	205841 at	-0.064	12458	3.099E-02	FALSE
104332 at	-0.026	6941	1423769 at	0.089	3254.5	104332 at	-0.092	2789	1458108 at	0.099	4604	4397.125	1862.4138	FALSE	pentatricopeptide repeat domain 2	NA	NA	NA	NA	
101422 at	0.136	2511	1423191 at	0.086	4725.5	101422 at	0.174	3636	1438700 at	0.117	6717	4397.375	1791.315	TRUE	formin binding protein 4	242472 x at	0.071	13516	4.427E-02	TRUE
162289 at	0.143	1391	1421855 at	-0.070	5150.5	97949 at	0.083	3704	1421854 at	0.036	7345	4397.625	2501.6494	FALSE	fibrinogen-like protein 2	204834 at	0.056	25746	3.951E-01	FALSE
99917 at	0.052	6338	1416544 at	0.073	4599.5	99917 at	0.050	5182	1416544 at	-0.273	1472	4397.875	2080.0909	FALSE	enhancer of zeste homolog 2 (Drosophila)	215006 at	0.020	34280	7.073E-01	FALSE
160251 at	-0.077	5430	1427877 at	-0.030	7392	160251 at	-0.067	3720	1427877 at	0.277	1050	4398	2689.3523	FALSE	RIKEN cDNA 2610312B22 gene	201595 s at	-0.417	5317	3.692E-04	FALSE
92777 at	0.104	4613	1438133 a at	0.045	6709.5	92777 at	0.065	5214	1416039 x at	-0.242	1057	4398.375	2395.6484	FALSE	cysteine rich protein 61	201289 at	0.782	9127	6.259E-03	FALSE
95963 at	0.012	8032	1419968 at	0.082	5145	95963 at	-0.080	3721	1419968 at	0.353	697	4398.75	3050.6662	FALSE	expressed sequence C77370	244370 at	-0.617	3705	5.986E-05	FALSE
161043 r at	0.047	6598	1449623 at	0.116	2998	161043 r at	-0.064	4565	1449623 at	0.200	3438	4399.75	1607.2209	FALSE	thioredoxin reductase 3	NA	NA	NA	NA	
93461 at	0.122	2234	1425298 a at	0.086	3779.5	93461 at	0.047	6568	1425298 a at	-0.097	5018	4399.875	1840.1743	FALSE	baculoviral IAP repeat-containing 1a	204861 s at	0.217	11842	2.422E-02	FALSE
104460 at	0.148	2023	1423365 at	-0.066	6797	104460 at	0.189	2926	1423365 at	0.164	5854	4400	2286.3749	FALSE	calcium channel, voltage-dependent, T type, alpha 1G subunit	NA	NA	NA	NA	
95604 at	-0.060	5691	1433618 at	0.042	6995.5	95604 at	0.180	715	1433618 at	0.152	4200	4400.375	2709.3988	FALSE	RIKEN cDNA C330006A16 gene	224962 at	-0.242	1882	3.164E-06	FALSE
98918 at	0.074	4228	1451091 at	0.090	3404	98918 at	-0.045	5246	1456172 at	0.159	4727	4401.25	784.05756	FALSE	thioredoxin domain containing 5	221253 s at	0.204	8994	5.771E-03	FALSE
100280 at	0.058	5364	1450608 at	0.131	3311.5	100280 at	-0.104	4251	1450608 at	-0.121	4679	4401.375	859.10083	FALSE	histone 1, H1t	207982 at	0.001	44112	9.868E-01	FALSE
98297 at	-0.095	2678	1450988 at	-0.035	7022	98297 at	0.049	4951	1450988 at	0.180	2957	4402	2018.7457	FALSE	leucine rich repeat containing G protein coupled receptor 5	213880 at	0.250	13114	3.850E-02	FALSE
102962 at	-0.017	7526	1449898 at	0.139	2452	102962 at	0.105	3254	1449898 at	0.123	4378	4402.5	2227.1323	FALSE	septin 1	227552 at	-0.071	16653	1.048E-01	FALSE
96085 at	0.029	6968	1416368 at	0.142	3269	96085 at	0.165	2727	1416368 at	0.200	4648	4403	1891.5762	TRUE	glutathione S-transferase, alpha 4	NA	NA	NA	NA	
93288 at	-0.212	2180	1437148 at	-0.081	5567.5	93288 at	-0.122	6115	1442295 at	0.208	3757	4404.875	1793.1383	FALSE	actin related protein 2/3 complex, subunit 2	208679 s at	-0.481	1834	2.853E-06	FALSE
100392 at	0.106	2900	1451038 at	-0.141	2538.5	100392 at	-0.069	3983	1451038 at	0.012	8200	4405.375	2603.1363	FALSE	apelin	244166 at	0.136	8582	4.581E-03	FALSE
160814 at	0.060	5369	1424052 at	0.098	3203	160814 at	-0.042	5417	1458185 at	-0.110	3634	4405.75	1153.6439	FALSE	THAP domain containing 4	220417 s at	-0.084	14616	6.336E-02	FALSE
97973 at	0.159	1504	1449389 at	-0.012	8086.5	97973 at	0.151	866	1449389 at	0.042	7167	4405.875	3747.1058	FALSE	T-cell acute lymphocytic leukemia 1	206283 s at	0.257	1785	2.576E-06	FALSE
93985 at	0.041	6298	1426721 s at	-0.082	4423	93985 at	-0.038	6362	1452160 at	-0.937	541	4406	2729.1094	FALSE	TCDD-inducible poly(ADP-ribose) polymerase	212665 at	0.330	9911	9.629E-03	FALSE
98291 at	0.104	2534	1435252 at	-0.103	2970.5	98291 at	0.044	6042	1440340 at	-0.122	6078	4406.125	1918.0827	FALSE	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	226427 s at	0.125	11925	2.506E-02	FALSE
161142 at	-0.091	4278	1422628 at	0.102	4040.5	161142 at	-0.038	5965	1447137 at	-0.122	3343	4406.625	1112.1185	FALSE	RIKEN cDNA 4632417K18 gene	218248 at	0.298	4194	1.081E-04	FALSE
98780 at	0.180	710	1427605 at	0.104	3717	98780 at	-0.057	5886	1427605 at	-0.048	7315	4407	2874.4747	FALSE	homeo box B3	228904 at	-0.049	25444	3.876E-01	FALSE
94194 s at	-0.168	3988	1421154 at	-0.110	2704	94195 r at	-0.058	4966	1421154 at	-0.087	5979	4409.25	1397.5472	TRUE	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	207592 s at	-0.403	923	3.676E-07	TRUE
161388 f at	-0.039	6963	1418682 at	0.092	4343.5	97661 at	-0.103	2266	1418682 at	0.114	4066	4409.625	1935.3986	FALSE	testis nuclear RNA binding protein	240299 at	0.069	17093	1.170E-01	FALSE
160079 i at	0.113	4653	1451495 at	-0.062	5716	160079 i at	0.087	6205	1451494 at	0.335	1067	4410.25	2321.0887	FALSE	WW domain containing adaptor with coiled-coil	230154 at	-0.272	4578	1.680E-04	FALSE
92988 i at	0.209	3136	1448955 s at	-0.043	7564	92988 i at	-0.149	5471	1458298 at	0.206	1473	4411	2665.9881	FALSE	Ca<2+>dependent activator protein for secretion	233950 at	-0.275	6655	1.185E-03	FALSE
99009 at	0.131	1988	1456573 x at	-0.156	5286	99009 at	0.021	6905	1416105 at	-0.141	3468	4411.75	2140.548	FALSE	nicotinamide nucleotide transhydrogenase	202783 at	-0.276	3243	3.203E-05	FALSE
101199 at	0.080	4606	1426072 at	0.103	2950	101199 at	0.158	2488	1456887 at	-0.040	7606	4412.5	2315.0587	FALSE	chemokine-like receptor 1	207652 s at	0.076	21323	2.441E-01	FALSE
104202 at	-0.155	2136	1435430 at	-0.087	3955.5	104202 at	0.134	3824	1435430 at	0.026	7738	4413.375	2366.1911	FALSE	transmembrane protein 1	215269 at	0.209	10528	1.341E-02	FALSE
97484 at	-0.275	1943	1426532 at	-0.143	3867	97484 at	-0.076	6366	1444461 at	0.090	5479	4413.75	1945.0432	FALSE	zinc finger, MYND domain containing 11	202136 at	0.096	15650	8.313E-02	FALSE
98454 at	-0.290	467	1423967 at	-0.096	5162	98454 at	-0.034	6844	1422034 a at	-0.219	5184	4414.25	2746.8839	TRUE	paralemmin	203859 s at	-0.208	7449	2.197E-03	TRUE
94267 i at	0.028	7757	1416848 at	0.002	8479	94268 f at	0.415	326	1416848 at	0.219	1096	4414.5	4298.0903	TRUE	ubiquitin-like 5	218011 at	-0.214	8464	4.251E-03	FALSE
92459 at	0.048	6512	1419684 at	0.083	4564	92459 at	0.073	4447	1419684 at	-0.299	2135	4414.5	1790.6268	FALSE	chemokine (C-C motif) ligand 8	NA	NA	NA	NA	
102007 at	0.043	5967	1420889 at	-0.070	4734	160573 at	-0.135	2510	1420889 at	0.119	4450	4415.25	1430.7008	FALSE	holocytochrome c synthetase	203745 at	-0.236	6154	7.945E-04	FALSE
93587 at	-0.009	8025	1416137 at	0.128	2378	93587 at	0.044	5461	1416138 at	0.178	1797	4415.25	2894.2189	FALSE	annexin A7	242027 at	0.043	22219	2.756E-01	FALSE
99236 at	0.173	1817	1419336 at	0.028	7559	99236 at	0.155	1996	1419336 at	0.071	6292	4416	2944.4312	TRUE	lipocalin 5	NA	NA	NA	NA	
95599 at	0.082	4065	1425668 a at	-0.056	5716	95599 at	0.118	2660	1447458 at	0.113	5224	4416.25	1360.0981	FALSE	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	215710 at	0.038	25591	3.912E-01	FALSE
92414 at	0.083	4011	1421171 at	0.087	5401.5	92414 at	-0.009	7785	1421172 at	-0.428	468	4416.375	3058.9813	FALSE	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	215613 at	-0.093	15586	8.183E-02	FALSE
99893 at	0.072	5929	1418497 at	-0.039	7378	99893 at	-0.432	622	1418497 at	0.127	3740	4417.25	2939.0485	FALSE	fibroblast growth factor 13	205110 s at	-1.618	295	3.690E-08	FALSE
93764 at	-0.072	6124	1430713 s at	0.198	2158	93764 at	0.137	2059	1430713 s at	0.039	7328	4417.25	2711.1507	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	220864 s at	-0.158	17151	1.182E-01	FALSE
95715 at	-0.288	650	1452674 a at	0.130	4154	95715 at	0.110	4717	1452674 a at	-0.017	8152	4418.25	3071.3557	FALSE	eukaryotic translation initiation factor 3, subunit 12	210501 x at	-0.150	10343	1.227E-02	FALSE
160279 at	-0.028	7299	1427882 at	0.062	6482	160279 at	0.127	2754	1427882 at	0.298	1140	4418.75	2948.1313	FALSE	deoxynucleotidyltransferase, terminal, interacting protein 2	202776 at	0.028	32761	6.566E-01	FALSE
160092 at	-0.175	1531	1416067 at	-0.053	7017	160092 at	0.017	8038	1416067 at	0.228	1094	4420	3616.7633	FALSE	interferon-related developmental regulator 1	202146 at	0.579	2722	1.408E-05	FALSE
100039 at	0.033	6841	1437783 x at	0.348	1365	100039 at	0.109	2238	1448372 a at	0.050	7238	4420.5	3049.3996	TRUE	transmembrane protein 4	209796 s at	-0.295	8627	4.706E-03	FALSE
96109 at	0.054	6189	1448890 at	-0.142	3838	96109 at	-0.158	1211	1448890 at	-0.102	6445	4420.75	2440.3817	FALSE	Kruppel-like factor 2 (lung)	219371 s at	0.375	3666	5.713E-05	FALSE
97897 at	0.094	5867	1433475 a at	-0.090	4806	97897 at	-0.081	3392	1433476 at	-0.137	3621	4421.5	1145.7139	FALSE	expressed sequence C78339	203420 at	-0.062	21486	2.492E-01	FALSE

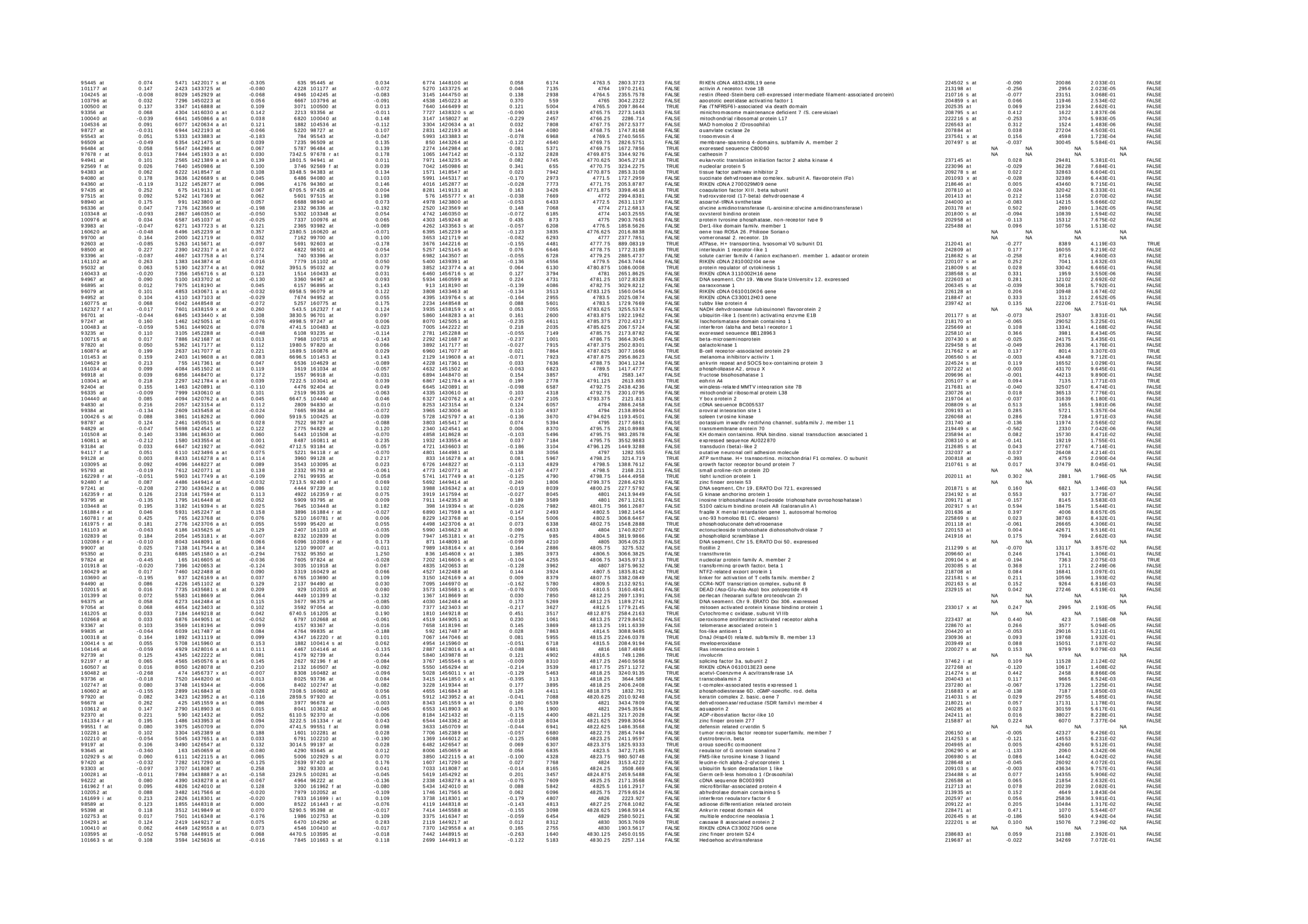
103062 at	0.141	3825	1423083 at	-0.085	4867	103062 at	0.199	1420	1423083 at	0.027	7575	4421.75	2550.0227	FALSE	RAB33B, member of RAS oncogene family	221014 s at	0.098	12816	3.503E-02	FALSE
160741 at	0.056	5633	1418339 at	0.135	1452	160741 at	-0.006	8130	1439047 s at	0.277	2474	4422.25	3045.8381	FALSE	RecQ protein-like	212917 x at	0.420	1231	7.604E-07	FALSE
95913 at	-0.009	8271	1457265 at	0.129	1485	95913 at	-0.040	7031	1457686 at	0.300	903	4422.5	3769.6601	FALSE	RIKEN cDNA B230333C21 gene	NA	NA	NA	NA	
98803 at	0.062	5884	1420390 s at	0.002	8469	98803 at	-0.276	196	1420390 s at	-0.200	3143	4423	3559.5208	FALSE	zinc finger protein 354A	217715 x at	0.210	5352	3.825E-04	FALSE
104430 at	0.029	6686	1419226 at	0.228	1119	104430 at	-0.045	5177	1419226 at	0.114	4711	4423.25	2358.6044	FALSE	CD96 antigen	206761 at	-0.031	28150	4.868E-01	FALSE
94693 at	0.014	7742	1424413 at	-0.108	5166	94693 at	0.059	4317	1442529 at	0.298	469	4423.5	3011.819	FALSE	Opioid growth factor receptor-like 1	219582 at	0.280	4526	1.609E-04	FALSE
92435 at	-0.036	6402	1418310 a at	0.147	1993	92435 at	-0.201	835	1418310 a at	-0.004	8464	4423.5	3606.6959	FALSE	retinaldehyde binding protein 1	206154 at	-0.099	16120	9.353E-02	FALSE
92430 at	0.070	4937	1424851 at	-0.062	5457	92430 at	-0.031	6663	1451505 at	-0.347	639	4424	2624.8558	FALSE	coiled-coil-helix-coiled-coil-helix domain containing 5	223479 s at	0.062	24413	3.514E-01	FALSE
100760 at	0.114	3332	1421460 at	0.121	2693	100760 at	0.124	3542.5	1421460 at	0.014	8131	4424.625	2497.1794	TRUE	desmocollin 1	207324 s at	0.009	38491	8.362E-01	FALSE
97261 at	0.058	6694	1460179 at	0.079	5243	97261 at	0.122	2816	1437220 x at	0.246	2946	4424.75	1879.1671	TRUE	DnaJ (Hsp40) homolog, subfamily A, member 1	200880 at	-0.088	29853	5.518E-01	FALSE
96641 at	0.135	2617	1433478 at	-0.009	8357.5	96641 at	0.206	2617	1433478 at	0.170	4108	4424.875	2714.3307	FALSE	presenilin associated, rhomboid-like	218271 s at	-0.113	16763	1.078E-01	FALSE
162497 r at	0.085	4305	1448116 at	0.040	6640.5	162497 r at	0.048	4913	1448116 at	0.180	1843	4425.375	1985.5904	TRUE	ubiquitin-activating enzyme E1, Chr X	200964 at	0.119	19254	1.763E-01	FALSE
101698 f at	0.086	4549	1427154 at	0.087	4757.5	101698 f at	0.173	586	1427154 at	-0.031	7812	4426.125	2962.8599	FALSE	keratin complex 2, basic, gene 17	207908 at	0.080	21348	2.452E-01	FALSE
97555 at	0.087	5510	1420039 s at	0.128	3644	97555 at	-0.083	4830	1449713 at	-0.149	3723	4426.75	902.58938	FALSE	chromobox homolog 7	212914 at	-0.195	11770	2.355E-02	FALSE
103804 at	0.035	6524	1450784 at	-0.001	8481	103804 at	0.165	2571	1450784 at	-0.449	131	4426.75	3774.1523	FALSE	reversion-inducing-cysteine-rich protein with kazal motifs	205407 at	0.088	18427	1.531E-01	FALSE
161943 at	0.209	1417	1435622 at	0.033	6734	161943 at	0.078	4774	1435622 at	-0.112	4782	4426.75	2208.2257	FALSE	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	219985 at	-0.028	28677	5.083E-01	FALSE
102686 at	0.127	3020	1424059 at	-0.037	7094	102686 at	-0.046	5580	1424059 at	-0.168	2013	4426.75	2327.3263	FALSE	suppressor of variegation 4-20 homolog 2 (Drosophila)	224431 s at	0.017	36048	7.640E-01	FALSE
161998 f at	-0.020	7217	1436188 a at	-0.140	3246	160819 at	0.062	4545	1436188 a at	-0.139	2702	4427.5	2013.9852	FALSE	N-myc downstream regulated gene 4	209159 s at	-0.794	814	2.833E-07	FALSE
100422 i at	-0.094	3641	1450259 a at	0.104	4806	100422 i at	-0.119	2252	1450259 a at	0.064	7013	4428	2014.899	FALSE	signal transducer and activator of transcription 5A	203010 at	0.149	7667	2.599E-03	FALSE
99842 at	-0.231	460	1421698 a at	-0.058	6146.5	99842 at	-0.096	4869	1421698 a at	0.282	6237	4428.125	2718.1629	FALSE	procollagen, type XIX, alpha 1	211011 at	-0.019	31840	6.259E-01	FALSE
102351 at	0.115	3049	1448730 at	0.024	7528	162348 r at	0.120	3025	1448730 at	-0.181	4114	4429	2127.4901	FALSE	carboxypeptidase A3, mast cell	205624 at	0.005	42622	9.503E-01	FALSE
93084 at	0.084	4337	1424563 at	0.114	3486	93084 at	0.079	3890	1455069 x at	0.075	6007	4430	1107.2961	TRUE	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	214821 at	-0.536	1517	1.447E-06	FALSE
97785 at	0.127	3084	1419419 at	0.007	8298	97785 at	-0.095	3754	1419419 at	-0.195	2584	4430	2622.8376	FALSE	DNA segment, human D6S2654E	NA	NA	NA	NA	
93903 at	-0.115	2394	1419140 at	0.008	8193	93903 at	-0.037	5916	1419140 at	-0.248	1218	4430.25	3205.7555	FALSE	activin receptor IIB	220028 at	0.260	1581	1.698E-06	FALSE
102965 at	-0.268	343	1427091 at	-0.018	7868	102965 at	-0.122	3037	1427091 at	-0.107	6474	4430.5	3398.1268	TRUE	expressed sequence AI481105	225076 s at	0.198	4491	1.548E-04	FALSE
99488 at	0.108	3440	1423509 a at	0.105	5118	99488 at	-0.060	5464	1423509 a at	-0.150	3701	4430.75	1008.9663	FALSE	islet amyloid polypeptide	213878 at	-0.103	26370	4.190E-01	FALSE
93533 at	-0.302	416	1425674 a at	0.096	4322.5	93533 at	-0.027	7502	1441282 at	0.125	5486	4431.625	2981.9491	FALSE	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	223053 x at	-0.217	4382	1.327E-04	FALSE
98484 at	-0.101	2819	1417901 a at	0.085	3896	98484 at	-0.013	7807	1431644 a at	0.139	3205	4431.75	2293.8482	FALSE	islet cell autoantigen 1	210547 x at	-0.277	2495	9.536E-06	FALSE
101469 at	0.018	7414	1422818 at	-0.135	1735	101469 at	0.017	7454	1437132 x at	-0.207	1124	4431.75	3475.7004	FALSE	neural precursor cell expressed, developmentally down-regulated gene 9	233223 at	0.145	18435	1.532E-01	FALSE
93202 at	0.007	8187	1422974 at	0.093	3965	93202 at	-0.141	3995	1428547 at	-0.333	1585	4433	2745.5715	FALSE	5' nucleotidase, ecto	227486 at	0.056	21278	2.428E-01	FALSE
162429 r at	0.062	6018	1416168 at	-0.084	3622	162429 r at	0.108	4387	1416168 at	-0.429	3705	4433	1110.8624	FALSE	serine (or cysteine) peptidase inhibitor, clade F, member 1	202283 at	0.051	28561	5.040E-01	FALSE
160133 at	0.099	4952	1438312 s at	-0.062	5293	160133 at	0.025	7066	1418049 at	-0.322	426	4434.25	2828.2912	FALSE	latent transforming growth factor beta binding protein 3	227308 x at	0.220	1935	3.370E-06	FALSE
96667 at	-0.078	5553	1437901 a at	-0.205	1285.5	96667 at	0.061	4422	1433666 s at	0.058	6477	4434.375	2261.2095	FALSE	vacuolar protein sorting 41 (yeast)	203106 s at	-0.114	7145	1.787E-03	FALSE
93028 at	0.112	3813	1448194 a at	0.228	851.5	93028 at	-0.025	6967	1448194 a at	0.084	6107	4434.625	2734.6519	FALSE	H19 fetal liver mRNA	NA	NA	NA	NA	
97006 s at	0.131	1845	1425107 a at	0.117	2534	104658 at	-0.030	6879	1450207 at	0.112	6481	4434.75	2612.8626	FALSE	leukemia inhibitory factor receptor	225571 at	1.170	331	4.612E-08	FALSE
102229 at	0.109	2149	1423581 at	-0.035	7097	102229 at	-0.014	7791	1444387 at	0.312	703	4435	3535.6565	FALSE	N-myristoyltransferase 2	205005 s at	-0.171	10934	1.659E-02	FALSE
99559 at	0.140	1294	1415776 at	0.035	7120	161401 f at	0.272	1687	1415776 at	0.028	7642	4435.75	3411.3271	TRUE	aldehyde dehydrogenase family 3, subfamily A2	202053 s at	-0.220	6867	1.415E-03	FALSE
94434 at	0.035	6570	1424892 at	0.082	4331	94434 at	-0.117	2276	1430562 at	0.211	4567	4436	1755.728	FALSE	zinc finger protein 95	203731 s at	0.043	22554	2.867E-01	FALSE
97505 at	0.092	5192	1451025 at	-0.084	6146.5	97505 at	-0.075	4510	1447089 at	0.191	1897	4436.375	1821.1116	FALSE	ADP-ribosylation factor-like 1	201658 at	-0.298	2634	1.201E-05	FALSE
93738 at	-0.038	7243	1426599 a at	-0.219	1863	93738 at	-0.111	2925	1434773 a at	-0.129	5715	4436.5	2477.8041	TRUE	solute carrier family 2 (facilitated glucose transporter), member 1	201250 s at	0.221	3377	3.860E-05	FALSE
95517 i at	-0.120	3034	1416608 a at	0.200	1037	95517 i at	0.021	7728	1416608 a at	0.100	5949	4437	2980.2256	FALSE	cDNA sequence BC004004	224988 at	0.015	37115	7.941E-01	FALSE
104087 at	0.076	5406	1449339 at	0.145	950	104087 at	0.003	8282	1419994 s at	-0.154	3112	4437.5	3143.129	FALSE	DNA segment, Chr 10, ERATO Doi 641, expressed	224667 x at	0.213	4161	1.041E-04	FALSE
97375 at	-0.015	7830	1460210 at	0.035	7345	97375 at	-0.196	1382	1460210 at	-0.267	1193	4437.5	3643.509	FALSE	polycystic kidney disease 1 homolog	216949 s at	-0.118	15297	7.654E-02	FALSE
104529 at	-0.075	5546	1417842 at	0.077	3666.5	104529 at	0.088	5361	1417842 at	0.131	3180	4438.375	1191.2694	FALSE	calcium modulating ligand	203538 at	-0.125	16977	1.138E-01	FALSE
101502 at	0.183	2090	1422286 a at	0.080	4569	101502 at	0.066	4416	1422286 a at	-0.067	6681	4439	1876.3257	FALSE	TG interacting factor	203313 s at	0.653	1939	3.423E-06	FALSE
103755 at	0.066	4596	1449084 s at	-0.294	2567	103755 at	0.089	3144	1418461 at	0.072	7450	4439.25	2181.1449	FALSE	SH3 domain protein D19	237157 at	0.221	7508	2.322E-03	FALSE
97889 at	-0.066	5754	1418438 at	0.077	4893	97889 at	0.115	1569	1418438 at	-0.121	5542	4439.5	1948.4052	FALSE	fatty acid binding protein 2, intestinal	207475 at	-0.064	26912	4.397E-01	FALSE
103395 at	0.240	499	1422654 at	0.031	7333	160631 s at	0.029	6627	1422654 at	0.138	3303	4440.5	3161.0477	TRUE	sarcoglycan, alpha (dystrophin-associated glycoprotein)	210632 s at	0.035	33853	6.942E-01	FALSE
94774 at	-0.061	5858	1421551 s at	0.048	6588.5	161173 f at	0.165	1696	1457666 s at	0.338	3625	4441.875	2222.6503	FALSE	interferon activated gene 202B	NA	NA	NA	NA	
92585 at	-0.249	1040	1416351 at	-0.061	6474	92585 at	-0.138	3493	1416351 at	-0.062	6763	4442.5	2707.4138	TRUE	mitogen activated protein kinase kinase 1	202670 at	-0.892	2050	4.249E-06	TRUE
160471 at	0.070	5056	1460168 at	0.123	3715	160471 at	0.064	4734	1430058 at	-0.180	4266	4442.75	583.59882	FALSE	stem-loop binding protein	206052 s at	-0.353	7592	2.463E-03	FALSE
95730 at	0.018	7982	1421971 a at	0.138	1702	95730 at	-0.083	5893	1421971 a at	0.227	2194	4442.75	3010.9856	FALSE	mitochondrial ribosomal protein S34	218112 at	-0.042	28084	4.840E-01	FALSE
94448 at	-0.048	5911	1418970 a at	0.082	4378	94448 at	0.069	4910	1418972 at	0.147	2579	4444.5	1396.6418	FALSE	B-cell leukemia/lymphoma 10	205263 at	0.131	7633	2.535E-03	FALSE
103673 at	-0.139	1569	1416051 at	0.070	5437	103673 at	0.060	5083	1441912 x at	0.155	5691	4445	1933.477	FALSE	complement component 2 (within H-2S)	203052 at	0.013	39233	8.580E-01	FALSE
97166 at	0.003	8360	1428477 at	0.121	2001.5	97166 at	-0.063	3857	1428477 at	0.133	3565	4445.875	2733.6214	FALSE	elaC homolog 2 (E. coli)	201766 at	-0.017	37242	7.984E-01	FALSE
102906 at	-0.846	2664	1449009 at	0.007	8282	102906 at	0.331	1949	1449009 at	-0.567	4889	4446	2847.3191	FALSE	T-cell specific GTPase	NA	NA	NA	NA	
103812 at	0.089	4614	1417853 at	0.076	4700	103812 at	0.030	6358	1417852 x at	0.173	2112	4446	1750.8131	TRUE	chloride channel calcium activated 1	NA	NA	NA	NA	
92717 at	0.009	8022	1426413 at	0.119	2664	92717 at	0.035	6758	1426413 at	0.675	342	4446.5	3566.1117	TRUE	neurogenic differentiation 1	206282 at	-0.008	40862	9.037E-01	FALSE
103799 at	0.066	4922	1452254 at	0.054	6129	103799 at	-0.158	952	1434676 at	0.080	5786	4447.25	2384.8616	FALSE	myotubularin related protein 9	233101 at	0.185	3710	5.994E-05	FALSE
95663 at	-0.024	7463	1416136 at	0.155	2695	161509 at	0.119	3977	1439364 a at	-0.221	3656	4447.75	2082.6537	FALSE	matrix metallopeptidase 2	201069 at	0.187	5259	3.514E-04	FALSE
92704 at	0.076	4362	1448984 at	0.056	5977.5	92704 at	-0.051	5610	1448984 at	-0.164	1846	4448.875	1867.9232	FALSE	excision repair cross-complementing rodent repair deficiency, complementation group 4	210158 at	0.006	42517	9.475E-01	FALSE
92253 at	0.047	6985	1449919 at	0.102	3795	92253 at	0.060	4508	1449919 at	-0.153	2508	4449	1882.3721	FALSE	keratin associated protein 6-2	NA	NA	NA	NA	
103402 at	0.108	3322	1452664 a at	-0.196	2216.5	103402 at	-0.035	7703	1445392 at	-0.122	4555	4449.125	2370.2276	FALSE	transmembrane 7 superfamily member 3	222477 s at	-0.164	11995	2.589E-02	FALSE
96857 at	0.038	6825	1455821 x at	0.159	1370	96857 at	-0.074	5130.5	1455821 x at	0.149	4472	4449.375	2279.6628	FALSE	complement component 1, q subcomponent binding protein	208910 s at	-0.187	20327	2.107E-01	FALSE
101403 at	-0.078	5371	1418777 at	-0.018	7868	101403 at	-0.120	2414	1418777 at	-0.306	2145	4449.5	2707.3533	TRUE	chemokine (C-C motif) ligand 25	206988 at	-0.094	22039	2.696E-01	FALSE
94832 at	0.418	942	1415963 at	0.215	2701	94832 at	-0.159	6216	1415963 at	-0.026	7939	4449.5	3196.714	FALSE	heterogeneous nuclear ribonucleoprotein H2	201132 at	-0.042	37025	7.916E-01	FALSE
104216 at	0.178	1251	1425845 a at	-0.080	4562	104216 at	0.166	4633	1425845 a at	0.055	7357	4450.75	2498.685	FALSE	soc-2 (suppressor of clear) homolog (C. elegans)	202777 at	-0.091	27468	4.602E-01	FALSE
95327 at	0.114	3026	1422163 at	0.052	6054	95327 at	0.030	6859	1422163 at	0.171	1868	4451.75	2385.4129	TRUE	SH3 and PX domains 2A	230767 at	-0.208	4143	1.020E-04	FALSE
99269 g at	0.080	5408	1449337 at	0.163	2667	99269 g at	-0.055	4586	1449337 at	0.109	5146	4451.75	1238.2451	FALSE	tryptophan 2,3-dioxygenase	231702 at	0.002	43610	9.751E-01	FALSE
96807 at	-0.047	5853	1416295 a at	0.049	6245.5	96807 at	0.058	5577	1416296 at	-0.441	132	4451.875	2892.9494	FALSE	interleukin 2 receptor, gamma chain	204116 at	0.042	30192	5.634E-01	FALSE
95878 at	0.074	5476	1459410 at	0.172	2259	95878 at	-0.024	7016	1459410 at	-0.146	3057	4452	2189.2119	FALSE	hypothetical LOC493582	NA	NA	NA	NA	
96356 at	0.025	7015	1416226 at	-0.285	296.5	96356 at	0.058	4902	1416226 at	-0.264	5596	4452.375	2906.7958	FALSE	Actin related protein 2/3 complex, subunit 1B	201954 at	0.336	6999	1.582E-03	FALSE
160174 at	0.006	8193	1448278 at	0.220	170.5	160174 at	-0.115	2992	1436886 x at	-0.057	6455	4452.625	3580.965	FALSE	XPA binding protein 2	218110 at	0.015	37999	8.216E-01	FALSE
99466 at	0.099	4179	1452376 at	0.057	5341.5	99466 at	-0.116	3202	1452376 at	-0.120	5091	4453.375	972.37727	FALSE	zinc finger protein 444	50376 at	0.115	12492	3.125E-02	FALSE
96147 at	-0.147	3910	1448916 at	-0.198	1063	93406 at	-0.072	5268	1448916 at	-0.058	7574	4453.75	2719.7924	TRUE	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	NA	NA	NA	NA	
94241 at	-0.104	3380	1423701 at	0.043	6401	161554 r at	-0.095	2757	1423701 at	-0.105	5281	4454.75	1684.0448	FALSE	Coenzyme A synthase	201913 s at	0.005	42661	9.512E-01	FALSE
97442 at	0.197	1388	1416832 at	0.029	7435	97442 at	0.123	1879	1448482 at	0.080	7121	4455.75	3267.5281	TRUE	solute carrier family 39 (metal ion transporter), member 8	209267 s at	0.179	13648	4.604E-02	TRUE
97717 at	0.107	2850	1449592 at	0.050	6104	97717 at	-0.003	8341	1449592 at	0.261	533	4457	3453.4181	FALSE	transcription factor 15	207306 at	-0.134	22139	2.730E-01	FALSE
95149 at	-0.144	2598	1451825 a at	-0.006	8311	95149 at	-0.163	1828	1451825 a at	-0.081	5093	4457.5	2922.632	TRUE	coatomer protein complex, subunit zeta 1	222386 s at	-0.191	11635	2.224E-02	TRUE
102385 at	-0.031	7011	1428389 s at	0.187	1044	98973 at	0.053	5529	1428390 at	0.113	4247	4457.75	2540.6539	FALSE	WD repeat domain 43	214662 at	0.129	10907	1.642E-02	FALSE
160352 at	0.069	4223	1433658 x at	-0.046	7241	160352 at	-0.139	1437	1433658 x at	-0.130	4932	4458.25	2391.0549	FALSE	poly(rC) binding protein 4	209361 s at	0.317	4347	1.271E-04	FALSE
92960 at	0.049	6728	1421206 at	0.162	1787.5	92960 at	0.055	4635	1450160 at	-0.151	4684	4458.625	2030.3426	FALSE	leukemia inhibitory factor	205266 at	0.021	36921	7.889E-01	FALSE
99900 at	0.070	4759	1449185 at	0.175	1706.5	99900 at	-0.067	4490	1418705 at	-0.053	6879	4458.625	2123.175	FALSE	cone-rod homeobox containing gene	217510 at	-0.011	39741	8.710E-01	FALSE
102399 at	0.023	7602	1455936 a at	0.154	3651	103888 at	0.084	3618	1425652 s at	-0.146	2972	4460.75	2117.3687	FALSE	RNA binding protein gene with multiple splicing	209487 at	0.306	1628	1.869E-06	FALSE
102710 at	-0.083	5573	1425269 at	0.107	2714	102710 at	0.151	2600	1425269 at	-0.048	6956	4460.75	2158.4639	FALSE	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	230925 at	0.267	13742	4.760E-02	FALSE
160831 at	0.098	3081	1448836 s at	0.046	5719	160831 at	-0.149	2976	1448836 s at	0.097	6069	4461.25	1661.1093	FALSE	ATP binding domain 1 family, member B	235058 at	0.090	16844	1.099E-01	FALSE
160873 at	0.172	2866	1448980 at	0.019	8036.5	99534 at	0.091	3347	1448980 at	-0.131	3597	4461.625	2402.479	FALSE	ghrelin	244695 at	-0.059	26238	4.133E-01	FALSE
102304 f at	0.074	4657	1417363 at	0.017	7886	102304 f at	0.182	964	1417363 at	0.138	4340	4461.75	2829.1747	TRUE	zinc finger protein 61	NA	NA	NA	NA	
96076 at	0.016	7720	1419952 at	0.145	1671	96076 at	0.085	3153	1448267 at	-0.088	5304	4462	2634.8112	FALSE	syntaxin 5A	224610 at	0.134	14398	5.986E-02	FALSE
92760 at	-0.043	6609	1419631 at	-0.025	7843.5	92760 at	-0.160	1150	1419631 at	-0.252	2248	4462.625	3261.6606	TRUE	Wiskott-Aldrich syndrome homolog (human)	38964 r at	0.080	12849	3.528E-02	FALSE
96849 at	0.022	7764	1416345 at	0.126	2480.5	96849 at	0.214	1552	1416346 at	0.103	6065	4465.375	2936.3929	TRUE	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	205217 at	-0.096	12508	3.136E-02	FALSE
99409 at	-0.035	6905	1421641 at	0.119	4803	99409 at	-0.041	5682	1460129 at	-0.335	473	4465.75	2797.9156	FALSE	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	215715 at	-0.080	19929	1.981E-01	FALSE
162297 s at	-0.096	4074	1418413 at	0.005	8364.5	99050 at	-0.107	2874	1418413 at	-0.173	2555	4466.875	2679.4495	FALSE	caveolin 3	208204 s at	0.028	31158	6.018E-01	FALSE
95666 at	-0.167	2621	1415934 at	0.108	4381	95666 at	0.034	7032	1415934 at	0.117	3837	4467.75	1861.1139	FALSE	COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)	202143 s at	-0.399	4099	9.618E-05	FALSE
92562 at	-0.030	7118	1416543 at	-0.142	3827	92562 at	0.033	6658	1416543 at	-0.403	270	4468.25	3154.5039	FALSE	nuclear factor, erythroid derived 2, like 2	201146 at	0.359	6270	8.931E-04	FALSE
98924 at	-0.077	3990	1452474 a at	0.105	2699	98924 at	-0.030	6911	1441752 at	0.106	4273	4468.25	1766.7408	FALSE	ADP-ribosyltransferase 3	210147 at	-0.008	41876	9.314E-01	FALSE
160996 at	0.117	2301	1418876 at	-0.050	5961.5	160996 at	0.018	7365	1418877 at	-0.195	2250	4469.375	2597.342	FALSE	forkhead box D1	206307 s at	0.179	3752	6.323E-05	FALSE
103492 at	-0.014	7703	1448901 at	-0.140	1332	103492 at	0.133	2186	1448901 at	0.103	6658	4469.75	3178.2245	FALSE	carboxypeptidase X 1 (M14 family)	227860 at	0.036	27734	4.703E-01	FALSE
161083 at	0.030	7350	1455733 at	0.211	1238	161083 at	0.007	8238	1435964 a at	0.311	1055	4470.25	3855.7435	TRUE	TAO kinase 3	220761 s at	0.113	18425	1.530E-01	FALSE
92244 at	0.087	5078	1418026 at	0.163	2788	92244 at	0.029	7038	1418026 at	0.136	2978	4470.5	2001.6223	TRUE	exonuclease 1	204603 at	-0.009	41905	9.322E-01	FALSE
161474 r at	0.172	2706	1429035 at	0.071	5023.5	161065 at	0.062	4748	1429035 at	0.113	5406	4470.875	1207.1226	TRUE	dipeptidase 3	220179 at	0.017	37256	7.988E-01	FALSE
104406 at	0.107	3476	1449449 at	0.076	4258	104406 at	0.084	3222	1449449 at	0.067	6929	4471.25	1696.7772	TRUE	prostaglandin E synthase	210367 s at	0.100	16101	9.290E-02	FALSE
98414 at	-0.057	6227	1418362 at	0.130	3527	98414 at	-0.073	6232	1418362 at	0.203	1899	4471.25	2136.2722	FALSE	zinc finger protein 42	243161 x at	0.052	16687	1.061E-01	FALSE
92710 at	-0.057	5350	1419458 at	0.019	7932	92710 at	0.085	4512	1419458 at	0.607	91	4471.25	3262.7822	FALSE	Rho-guanine nucleotide exchange factor	NA	NA	NA	NA	
99991 at	-0.159	912	1420904 at	0.035	7076.5	99991 at	0.029	7232	1420905 at	-0.284	2665	4471.375	3180.1398	FALSE	interleukin 17 receptor A	205707 at	-0.234	4509	1.589E-04	FALSE
96813 f at	-0.202	2421	1453865 a at	-0.029	7266.5	94770 at	0.117	1874	1438985 x at	0.064	6324	4471.375	2720.0084	FALSE	OTU domain containing 5	233933 s at	-0.175	6846	1.380E-03	FALSE
102599 at	-0.191	2103	1416642 a at	-0.072	5374	102599 at	0.055	5007	1416643 at	0.098	5402	4471.5	1589.223	FALSE	tumor protein, translationally-controlled 1	216520 s at	-0.081	19030	1.699E-01	FALSE
104325 at	0.223	716	1451371 at	0.090	4109	104325 at	-0.017	7470	1451966 at	0.075	5592	4471.75	2856.6711	FALSE	melanocortin 2 receptor accessory protein	NA	NA	NA	NA	
94359 at	0.104	3734	1417965 at	-0.092	4749.5	162252 f at	0.210	1405	1417965 at	0.019	7999	4471.875	2736.6566	FALSE	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	226247 at	-0.202	11945	2.534E-02	FALSE
102207 at	0.085	4771	1424544 at	-0.102	5052	102207 at	0.173	1519	1424544 at	-0.073	6546	4472	2117.1904	FALSE	nuclear receptor binding protein 2	NA	NA	NA	NA	
161397 r at	0.076	5331	1417581 at	0.046	5779.5	103683 at	-0.172	828	1417582 s at	-0.093	5950	4472.125	2443.4032	FALSE	dihydroorotate dehydrogenase	213632 at	0.035	30131	5.603E-01	FALSE
92482 at	-0.130	2582	1450212 at	0.021	7891	92482 at	-0.116	3858	1450212 at	-0.139	3559	4472.5	2343.2332	FALSE	formin-like 1	204789 at	-0.124	9967	9.952E-03	FALSE
92806 at	-0.140	3075	1428308 at	0.061	5709	92806 at	0.009	8266	1428309 s at	-0.246	840	4472.5	3218.0552	FALSE	p53 and DNA damage regulated 1	225075 at	-0.005	42191	9.392E-01	FALSE
96433 at	-0.001	8456	1427551 at	0.145	2811.5	96433 at	-0.130	1838	1427551 at	-0.114	4785	4472.625	2924.9182	FALSE	ubiquitin specific peptidase 29	220895 at	0.031	33012	6.658E-01	FALSE
104394 at	0.055	5412	1416402 at	0.116	1984	104394 at	0.107	4570	1416402 at	-0.129	5925	4472.75	1750.6718	FALSE	ATP-binding cassette, sub-family B (MDR/TAP), member 10	223320 s at	-0.104	19498	1.848E-01	FALSE
100296 at	0.045	5968	1452213 at	-0.170	1537	100296 at	-0.011	7921	1452213 at	-0.168	2466	4473	2987.2994	FALSE	testis expressed gene 2	218099 at	0.138	12003	2.596E-02	FALSE
94912 at	-0.353	1047	1422451 at	0.063	4940	94912 at	0.130	3474	1422451 at	-0.004	8431	4473	3088.6529	FALSE	mitochondrial ribosomal protein S21	222997 s at	-0.032	34468	7.127E-01	FALSE
101922 at	0.048	5828	1417205 at	-0.061	5517	101922 at	0.078	4297	1417204 at	0.223	2251	4473.25	1622.1612	FALSE	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	NA	NA	NA	NA	
95709 at	0.163	1257	1452770 at	-0.031	7868	95709 at	0.222	596	1452770 at	0.016	8173	4473.5	4106.4912	FALSE	vitamin K epoxide reductase complex, subunit 1	217949 s at	-0.021	33364	6.772E-01	FALSE
92523 at	-0.032	6888	1451868 at	0.116	2843	92523 at	-0.032	6618	1421581 at	-0.186	1546	4473.75	2686.8493	FALSE	potassium inwardly-rectifying channel, subfamily J, member 6	210454 s at	0.011	39865	8.739E-01	FALSE
99578 at	0.011	7986	1427724 at	0.101	2839.5	99578 at	0.050	5846	1427724 at	-0.197	1226	4474.375	3024.2146	FALSE	topoisomerase (DNA) II alpha	237469 at	-0.070	14342	5.872E-02	FALSE
98842 at	0.105	3443	1419346 a at	0.112	3004	98842 at	0.016	7439	1419346 a at	-0.190	4019	4476.25	2018.4227	FALSE	seminal vesicle secretion 5	NA	NA	NA	NA	
92509 at	0.084	4313	1420496 at	0.192	835	92509 at	-0.011	7756	1420496 at	-0.096	5002	4476.5	2847.1345	FALSE	coagulation factor XII (Hageman factor)	205774 at	-0.628	98	6.678E-09	FALSE
97146 g at	0.008	8149	1441344 at	-0.097	3518	97146 g at	-0.071	4049	1441344 at	-0.257	2190	4476.5	2570.1373	FALSE	expressed sequence C80197	NA	NA	NA	NA	
96854 at	0.082	4546	1415706 at	0.015	8077	96854 at	-0.140	2899	1415706 at	-0.143	2386	4477	2570.8057	FALSE	coatomer protein complex subunit alpha	214336 s at	-0.204	9452	7.555E-03	FALSE
96078 g at	0.183	2219	1417280 at	0.008	8332	96077 at	0.188	647	1417280 at	-0.064	6713	4477	3634.473	FALSE	solute carrier family 17 (sodium phosphate), member 1	242536 at	-0.052	17882	1.375E-01	FALSE
100766 at	0.057	5070	1421136 at	0.041	7210.5	100766 at	-0.149	2557	1441923 s at	-0.183	3074	4477.75	2119.6287	FALSE	endothelin 3	217154 s at	-0.074	15804	8.602E-02	FALSE
92455 at	0.139	2722	1450469 at	0.042	7049.5	92455 at	-0.039	6015	1450469 at	0.216	2125	4477.875	2421.7849	FALSE	testis specific protein, Ddc8	NA	NA	NA	NA	

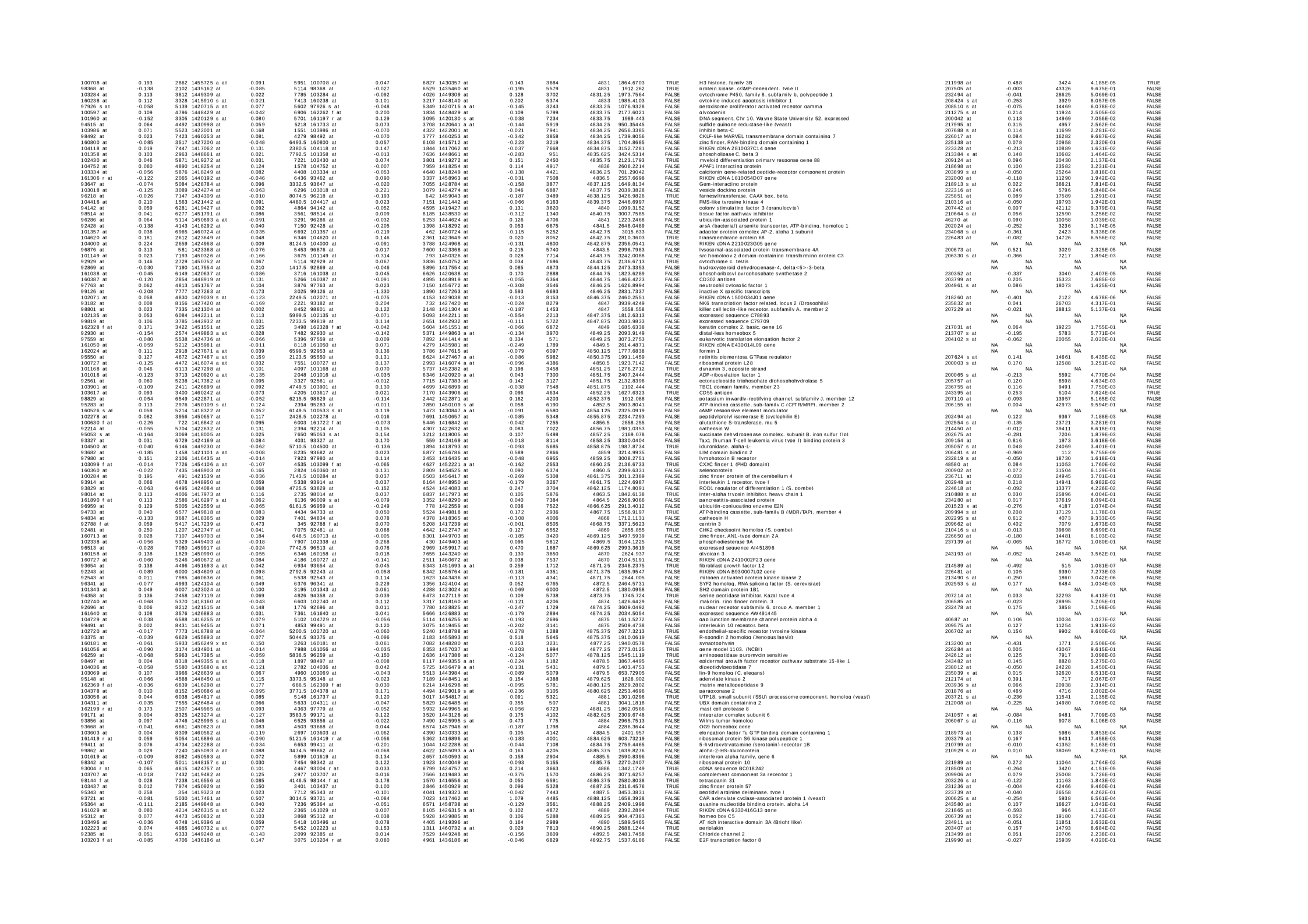


94126 at	0.071	5226	1421465 at	0.101	4757.5	94126 at	-0.069	4703	1421465 at	0.155	3477	4540.875	747.09151	FALSE	wingless related MMTV integration site 2b	206458 s at	-0.224	4268	1.167E-04	FALSE
101708 at	0.058	6283	1421618 at	0.043	6558	101708 at	-0.072	3975	1429524 at	-0.284	1348	4541	2423.39	FALSE	myosin IF	213733 at	0.178	7932	3.135E-03	FALSE
97479 at	0.052	5777	1417907 at	-0.045	6753	97479 at	0.075	3381	1448879 at	0.151	2255	4541.5	2081.0282	FALSE	ubiquitin-conjugating enzyme E2L 3	200676 s at	0.094	19196	1.747E-01	FALSE
92965 at	0.180	936	1420560 at	0.083	5097	92965 at	0.057	4363	1420560 at	0.038	7772	4542	2815.2088	TRUE	cholinergic receptor, nicotinic, epsilon polypeptide	215916 at	0.052	26682	4.312E-01	FALSE
100588 at	-0.026	7420	1417189 at	0.180	820	100588 at	0.115	2502	1417189 at	0.067	7442	4546	3401.3578	FALSE	proteasome (prosome, macropain) 28 subunit, beta		NA	NA	NA	NA
161767 r at	0.223	3366	1416984 at	0.026	7375	94327 at	-0.118	2606	1416984 at	0.189	4839	4546.5	2101.1972	FALSE	mitochondrial ribosomal protein S18A	221693 s at	-0.082	12185	2.780E-02	FALSE
93041 at	0.103	3296	1436708 x at	0.139	1987	93041 at	0.019	7295	1436708 x at	-0.158	5610	4547	2366.4371	FALSE	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	212141 at	-0.179	6254	8.786E-04	FALSE
160324 at	-0.011	8041	1448938 at	0.301	1588.5	160324 at	0.063	4053	1448938 at	-0.125	4507	4547.375	2658.7211	FALSE	replication protein A3	209507 at	-0.330	3356	3.726E-05	FALSE
100464 at	0.196	3359	1428468 at	0.050	6849.5	100464 at	-0.158	4630	1428468 at	-0.140	3354	4548.125	1647.5217	FALSE	RIKEN cDNA 3110043O21 gene	225919 s at	0.228	15563	8.116E-02	FALSE
100636 at	0.187	2327	1417562 at	0.089	4191	100636 at	0.038	6472	1434976 x at	-0.121	5203	4548.25	1750.3419	FALSE	eukaryotic translation initiation factor 4E binding protein 1	221539 at	0.080	20823	2.275E-01	FALSE
162117 f at	-0.069	4292	1417553 at	0.152	2504.5	162117 f at	0.075	3152	1417553 at	0.010	8245	4548.375	2572.8099	FALSE	placental specific protein 1	219702 at	0.033	30280	5.665E-01	FALSE
161636 r at	0.049	5714	1434496 at	-0.032	7364.5	161636 r at	0.087	3055	1434496 at	-0.164	2062	4548.875	2429.0924	FALSE	polo-like kinase 3 (Drosophila)	215462 at	0.097	16383	9.925E-02	FALSE
160785 at	-0.053	6829	1428368 at	-0.174	1803.5	160785 at	-0.065	6840	1445628 at	0.161	2724	4549.125	2665.5504	FALSE	Rho GTPase activating protein 21	224764 at	0.371	6933	1.508E-03	FALSE
160636 at	-0.167	1168	1452599 s at	0.020	8007.5	160636 at	0.042	6098	1452599 s at	0.215	2925	4549.625	3078.374	FALSE	expressed sequence AI413582	226306 at	0.259	5234	3.453E-04	FALSE
99385 at	0.019	7457	1450831 at	0.088	4460.5	99385 at	-0.082	5109	1450831 at	0.279	1173	4549.875	2593.2778	FALSE	POU domain, class 3, transcription factor 2	242455 at	0.475	1737	2.353E-06	FALSE
160208 at	0.120	2558	1415985 at	0.048	5985.5	160208 at	-0.035	6575	1430075 at	-0.156	3082	4550.125	2023.559	FALSE	splicing factor 3b, subunit 3	200688 at	-0.152	8396	4.139E-03	FALSE
93021 at	0.335	216	1428209 at	0.200	1958	93021 at	0.029	7647	1428209 at	-0.006	8381	4550.5	4073.0819	FALSE	brain expressed gene 4	215440 s at	-0.531	3484	4.524E-05	FALSE
96575 at	-0.153	3314	1417762 a at	0.069	6413	96575 at	0.109	2559	1417762 a at	0.075	5917	4550.75	1900.1081	FALSE	ribosomal protein L8	200936 at	0.146	15587	8.189E-02	FALSE
101742 at	0.284	166	1421715 at	-0.005	8335	101742 at	0.122	2720	1421715 at	-0.067	6982	4550.75	3777.5302	FALSE	tissue-type vomeronasal neurons putative pheromone receptor V2R2		NA	NA	NA	NA
99996 at	0.107	3959	1449586 at	0.160	2413	97601 f at	0.067	4129	1449586 at	0.027	7703	4551	2238.6526	TRUE	plakophilin 1	221854 at	-0.070	20063	2.022E-01	FALSE
93341 r at	0.134	3179	1456175 a at	0.095	3222.5	93341 r at	0.060	4223	1452102 at	-0.028	7580	4551.125	2076.0316	FALSE	coatomer protein complex, subunit beta 2 (beta prime)	201098 at	0.045	27188	4.498E-01	FALSE
95960 at	0.285	739	1458011 s at	0.077	4772	95960 at	0.007	8021	1419948 at	0.139	4673	4551.25	2979.7074	TRUE	DNA segment, Chr 4, ERATO Doi 117, expressed		NA	NA	NA	NA
160427 at	-0.074	4669	1428084 at	0.056	5786	98090 at	-0.047	4877	1452658 at	-0.139	2874	4551.5	1218.9822	FALSE	KRR1, small subunit (SSU) processome component, homolog (yeast)	235038 at	0.053	21028	2.344E-01	FALSE
99447 at	0.069	4869	1451700 a at	-0.034	6599.5	99447 at	-0.109	2068	1428528 at	-0.090	4670	4551.625	1868.7719	FALSE	RIKEN cDNA 1110007L15 gene	223811 s at	-0.051	27171	4.490E-01	FALSE
100372 at	0.214	2132	1460408 at	0.099	4143.5	100372 at	0.024	8058	1460408 at	-0.308	3879	4553.125	2501.2152	FALSE	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	241805 at	0.779	2085	4.431E-06	FALSE
99902 at	-0.191	2108	1450193 at	0.038	6734	99902 at	0.019	7805	1450193 at	0.592	1566	4553.25	3174.5057	FALSE	hyperpolarization-activated, cyclic nucleotide-gated K+ 1		NA	NA	NA	NA
104689 at	-0.063	5916	1450464 at	0.123	1426	104689 at	0.057	5520	1450464 at	0.094	5352	4553.5	2098.3634	FALSE	E4F transcription factor 1	218524 at	0.123	12328	2.947E-02	FALSE
160776 at	-0.107	3700	1434133 s at	0.061	5958.5	160776 at	-0.051	6479	1434134 at	-0.177	2078	4553.875	2044.353	FALSE	WD repeat domain 42A	243318 at	0.300	475	9.244E-08	FALSE
160894 at	-0.055	6626	1423233 at	-0.063	6013	160894 at	0.301	2710	1423233 at	-0.289	2869	4554.5	2054.3795	FALSE	CCAAT/enhancer binding protein (C/EBP), delta	203973 s at	0.648	12285	2.911E-02	FALSE
93704 at	0.122	4398	1423013 at	0.112	4234	93704 at	-0.080	4360	1434939 at	-0.091	5227	4554.75	453.61465	FALSE	forkhead box F1a	205935 at	0.156	13509	4.419E-02	FALSE
160569 at	-0.012	8173	1449139 at	0.066	6372	160569 at	0.176	2321	1429898 at	-0.418	1354	4555	3246.9765	FALSE	RIKEN cDNA 2310008M10 gene	223001 at	-0.243	9330	7.086E-03	FALSE
99895 at	0.099	3924	1422291 at	0.141	2348.5	99895 at	-0.022	7051	1422291 at	-0.130	4897	4555.125	1967.552	FALSE	chemokine (C-C motif) receptor 8	208059 at	0.020	37339	8.005E-01	FALSE
101979 at	-0.094	3104	1453851 a at	-0.041	6853	101979 at	0.016	7610	1453851 a at	-0.512	654	4555.25	3262.7714	FALSE	growth arrest and DNA-damage-inducible 45 gamma	204121 at	0.287	5921	6.476E-04	FALSE
160678 at	-0.092	3716	1454604 s at	-0.092	5044.5	160678 at	-0.048	5856	1454604 s at	-0.180	3608	4556.125	1085.1937	TRUE	tetraspanin 12	219274 at	0.032	31319	6.062E-01	FALSE
101369 at	0.055	5572	1433705 at	0.078	5205.5	101369 at	0.024	7112	1438479 at	0.297	338	4556.875	2931.3685	TRUE	zinc finger protein 213	227207 x at	0.024	30952	5.927E-01	FALSE
102199 at	-0.058	5419	1436856 x at	0.104	4061.5	102199 at	-0.170	1609	1431125 a at	-0.052	7139	4557.125	2334.2374	FALSE	threonyl-tRNA synthetase-like 1	221189 s at	0.013	38133	8.261E-01	FALSE
93455 s at	0.114	2814	1422912 at	0.136	3957	93456 r at	0.072	3608	1422912 at	-0.028	7851	4557.5	2247.1526	FALSE	bone morphogenetic protein 4	211518 s at	0.002	43815	9.801E-01	FALSE
101992 at	-0.044	6971	1448822 at	0.140	2578	101992 at	0.218	951	1448822 at	0.025	7732	4558	3307.9548	FALSE	proteasome (prosome, macropain) subunit, beta type 6	208827 at	-0.219	8538	4.450E-03	FALSE
94628 r at	0.126	3815	1424063 at	0.092	4514	94628 r at	0.057	5250	1424063 at	-0.100	4653	4558	589.31429	FALSE	androgen binding protein alpha		NA	NA	NA	NA
160987 r at	0.080	4435	1423440 at	0.122	1903.5	160987 r at	0.039	5875	1458130 at	-0.083	6021	4558.625	1909.3067	FALSE	RIKEN cDNA 1110001A07 gene	225684 at	0.225	5719	5.345E-04	FALSE
94048 at	-0.326	611	1434879 at	-0.013	8031.5	94048 at	-0.139	1927	1434879 at	0.035	7667	4559.125	3839.7938	FALSE	cell division cycle 34 homolog (S. cerevisiae)	241927 x at	0.075	16291	9.715E-02	FALSE
161496 r at	0.127	2810	1420193 at	0.057	6625	92862 f at	0.071	5588	1423227 at	0.141	3214	4559.25	1843.477	TRUE	keratin complex 1, acidic, gene 17	205157 s at	0.030	28114	4.853E-01	FALSE
99051 at	0.033	6837	1424542 at	0.114	2221	99051 at	0.173	1465	1424542 at	-0.052	7715	4559.5	3172.2074	FALSE	S100 calcium binding protein A4	203186 s at	0.279	4235	1.125E-04	FALSE
92458 at	0.134	2606	1422663 at	0.093	4223	92458 at	0.004	8278	1422663 at	0.130	3133	4560	2568.4975	TRUE	origin recognition complex, subunit 1-like (S.cereviaiae)	205085 at	-0.024	29671	5.451E-01	FALSE
104604 at	0.150	2439	1451281 at	0.032	7178	104604 at	0.241	830	1451281 at	0.047	7795	4560.5	3451.1201	TRUE	zinc finger protein 96		NA	NA	NA	NA
94250 at	-0.005	8391	1416661 at	-0.083	5607	94250 at	-0.167	3015	1416660 at	0.295	1232	4561.25	3121.7182	FALSE	eukaryotic translation initiation factor 3, subunit 10 (theta)	200596 s at	0.147	14152	5.534E-02	FALSE
94631 at	0.119	3673	1450327 at	0.149	3046	94631 at	-0.053	5844	1450327 at	-0.075	5682	4561.25	1412.6215	FALSE	purinergic receptor P2X-like 1, orphan receptor	206880 at	-0.023	35965	7.608E-01	FALSE
97726 at	-0.058	5424	1449245 at	-0.181	514.5	97726 at	-0.002	8416	1449245 at	-0.120	3891	4561.375	3287.7984	TRUE	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	210400 at	0.220	7324	2.034E-03	FALSE
96866 at	-0.339	158	1423122 at	0.046	6293	96866 at	0.079	3412	1423122 at	0.006	8386	4562.25	3574.7752	FALSE	arginine vasopressin-induced 1	218631 at	-0.087	14316	5.809E-02	FALSE
102734 at	0.158	2262	1418854 at	0.098	5782.5	102734 at	0.141	2647	1418854 at	0.027	7558	4562.375	2544.462	TRUE	baculoviral IAP repeat-containing 2	202076 at	0.262	7474	2.257E-03	TRUE
100463 at	0.054	6351	1438694 at	0.091	3579.5	100463 at	0.057	5125	1436170 a at	0.127	3194	4562.375	1455.3602	TRUE	casein gamma		NA	NA	NA	NA
98301 at	0.078	6528	1430912 a at	0.112	3311.5	98301 at	0.134	1122	1430912 a at	0.050	7288	4562.375	2869.0057	TRUE	tectorin beta		NA	NA	NA	NA
96643 at	0.197	1253	1424351 at	0.040	6563	96643 at	0.063	5151	1424351 at	-0.315	5283	4562.5	2296.3916	FALSE	WAP four-disulfide core domain 2	203892 at	-0.145	10611	1.404E-02	FALSE
100035 at	0.054	5450	1449160 at	0.111	2912	100035 at	-0.001	8497	1459876 at	-0.232	1391	4562.5	3111.8327	FALSE	natriuretic peptide receptor 1	32625 at	0.088	14987	7.087E-02	FALSE
103247 at	-0.122	2887	1419077 at	-0.049	6181.5	103247 at	0.032	6937	1419077 at	0.284	2247	4563.125	2340.1033	FALSE	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	206186 at	0.029	32938	6.631E-01	FALSE
96223 at	-0.074	4373	1431933 a at	0.096	3654	96223 at	0.046	5866	1422131 at	0.131	4360	4563.25	931.19972	FALSE	decapping enzyme	218508 at	0.087	11890	2.475E-02	FALSE
96200 at	0.011	7961	1456240 x at	0.157	1059.5	162416 at	0.153	2363	1423683 at	0.047	6870	4563.375	3365.6681	TRUE	cell division cycle associated 4	218399 s at	0.001	44006	9.847E-01	FALSE
102048 at	0.016	7723	1420992 at	0.097	3128	102048 at	0.121	2811	1420991 at	-0.093	4592	4563.5	2244.6358	FALSE	ankyrin repeat domain 1 (cardiac muscle)	206029 at	-0.032	30228	5.648E-01	FALSE
97929 r at	0.026	7070	1423386 at	0.181	807	97929 r at	0.008	8150	1444321 at	-0.212	2235	4565.5	3590.6691	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	207805 s at	0.193	10619	1.408E-02	FALSE
92904 at	0.024	7228	1420425 at	0.042	6699	92904 at	0.250	762	1420425 at	0.139	3573	4565.5	3005.1288	TRUE	PR domain containing 1, with ZNF domain	217192 s at	-0.057	25380	3.861E-01	FALSE
101303 at	0.146	3033	1422372 at	0.148	2312.5	101303 at	0.080	4749	1422372 at	-0.013	8170	4566.125	2610.9166	FALSE	olfactory receptor 15	221460 at	0.018	38008	8.219E-01	FALSE
96073 at	0.068	4658	1416534 at	-0.045	6215.5	96073 at	-0.023	6713	1429903 at	-0.347	679	4566.375	2735.4276	FALSE	D4, zinc and double PHD fingers family 2	202116 at	0.265	5210	3.388E-04	FALSE
100287 at	0.027	7510	1430512 a at	0.199	785.5	100287 at	0.132	2245	1430512 a at	0.025	7729	4567.375	3575.4216	TRUE	immunoglobulin (CD79A) binding protein 1b		NA	NA	NA	NA
103876 at	0.068	4837	1417583 a at	0.071	4937.5	103876 at	0.140	1162	1417583 a at	0.037	7335	4567.875	2547.2872	TRUE	charged amino acid rich leucine zipper 1	209486 at	0.013	41320	9.157E-01	FALSE
104411 at	-0.026	7390	1449656 at	0.110	2444	104411 at	0.127	2896	1449656 at	-0.128	5543	4568.25	2325.3149	FALSE	RIKEN cDNA D930048N14 gene		NA	NA	NA	NA
102197 at	-0.228	360	1418355 at	-0.122	5111.5	102197 at	0.040	6928	1418355 at	-0.096	5874	4568.375	2902.7511	FALSE	nucleobindin 2	229838 at	-0.154	6003	6.948E-04	FALSE
160534 at	-0.287	700	1415740 at	0.047	6209.5	161921 f at	0.105	4050	1415740 at	0.043	7314	4568.375	2913.4622	FALSE	protease (prosome, macropain) 26S subunit, ATPase 5	209503 s at	0.018	38494	8.362E-01	FALSE
160679 at	-0.235	1562	1424747 at	0.035	6751	160679 at	0.038	5636	1424747 at	-0.145	4330	4569.75	2235.9771	FALSE	Kinesin family member 1C	209244 s at	0.300	5033	2.768E-04	FALSE
101130 at	0.091	3640	1450857 a at	-0.258	3666.5	101130 at	0.042	5659	1446326 at	0.097	5314	4569.875	1067.8123	FALSE	procollagen, type I, alpha 2	202404 s at	0.107	8820	5.251E-03	FALSE
97823 g at	0.134	1550	1454887 at	-0.026	7350	97822 at	0.069	3571	1434250 at	-0.065	5810	4570.25	2541.9416	FALSE	p21 (CDKN1A)-activated kinase 2	208877 at	0.497	1595	1.756E-06	FALSE
93803 at	-0.003	8403	1438509 at	0.259	399	93803 at	-0.063	6371	1418078 at	-0.195	3109	4570.5	3533.9898	FALSE	proteaseome (prosome, macropain) 28 subunit, 3	200987 x at	-0.232	4234	1.124E-04	FALSE
99380 at	0.123	2059	1422197 at	-0.004	8412.5	99380 at	-0.228	1339	1422197 at	0.126	6472	4570.625	3421.8363	FALSE	potassium voltage-gated channel, shaker-related subfamily, member 2	239118 at	-0.449	4108	9.776E-05	FALSE
94145 at	-0.086	4138	1422305 at	0.083	4432.5	94145 at	-0.135	1424	1422305 at	0.011	8291	4571.375	2825.4014	FALSE	interferon beta 1, fibroblast	208173 at	-0.009	41393	9.177E-01	FALSE
102761 at	0.038	6632	1452262 at	0.054	5795.5	102761 at	-0.216	167	1452262 at	0.087	5694	4572.125	2966.6738	FALSE	GrpE-like 2, mitochondrial	238427 at	-0.087	13230	4.022E-02	FALSE
92371 at	0.123	2654	1419109 at	0.099	4663	92371 at	0.106	2525	1419109 at	-0.003	8449	4572.75	2763.3519	FALSE	histidine rich calcium binding protein	207066 at	0.093	19516	1.852E-01	FALSE
94788 f at	-0.126	2290	1416256 a at	-0.106	4243.5	94789 r at	-0.026	6741	1416256 a at	0.084	5017	4572.875	1845.5369	FALSE	tubulin, beta 5	209026 x at	-0.271	6491	1.039E-03	FALSE
160840 at	-0.206	1983	1424250 a at	0.068	4785	160840 at	0.140	3522	1424250 a at	-0.019	8002	4573	2557.0612	FALSE	Rho guanine nucleotide exchange factor (GEF) 3	218501 at	-0.092	27928	4.777E-01	FALSE
93424 at	-0.210	1551	1434937 at	0.038	7342.5	93424 at	-0.092	6435	1434937 at	0.126	2969	4574.375	2759.3759	FALSE	pam, highwire, rpm 1	201959 s at	-0.237	6637	1.172E-03	FALSE
96139 at	0.085	3194	1422489 at	0.073	4024	96139 at	-0.043	6012	1422489 at	0.126	5069	4574.75	1227.4318	FALSE	glucosidase 1	210627 s at	-0.014	36581	7.801E-01	FALSE
98975 at	0.008	8084	1424291 at	0.201	263	98975 at	-0.069	6130	1424291 at	0.143	3823	4575	3361.0491	FALSE	nucleoporin 93	202188 at	-0.264	1550	1.571E-06	FALSE
160437 at	-0.052	5536	1449097 at	0.100	4052	160437 at	-0.043	5727	1429971 at	0.146	2985	4575	1297.7229	FALSE	thioredoxin reductase 2	210803 at	0.026	31415	6.098E-01	FALSE
101170 at	0.001	8446	1450548 at	0.066	6021	101170 at	0.122	2007	1440422 at	0.233	1829	4575.75	3225.4558	TRUE	5-hydroxytryptamine (serotonin) receptor 1F	221458 at	0.038	35142	7.348E-01	FALSE
100569 at	-0.014	7785	1437691 at	0.150	3241	100569 at	0.208	892	1437691 at	-0.070	6387	4576.25	3105.4513	FALSE	annexin A2	201590 x at	0.552	4726	2.024E-04	FALSE
161301 f at	0.185	1159	1421217 a at	0.071	5229	161301 f at	0.025	7685	1421217 a at	-0.552	4232	4576.25	2701.0192	FALSE	lectin, galactose binding, soluble 9	203236 s at	0.123	14665	6.442E-02	FALSE
161389 f at	-0.106	3927	1430656 a at	0.024	7851	97797 at	0.074	3626	1430656 a at	0.139	2902	4576.5	2224.9795	FALSE	asparagine synthetase domain containing 1	217987 at	-0.017	40689	8.982E-01	FALSE
98825 at	0.086	3417	1420672 at	0.054	5826	98825 at	0.085	4184	1420672 at	-0.130	4880	4576.75	1024.9974	FALSE	potassium voltage-gated channel, Isk-related subfamily, member 1	236407 at	0.066	24129	3.421E-01	FALSE
97426 at	0.047	6416	1416529 at	-0.057	5667	97426 at	0.123	1250	1459171 at	0.098	4976	4577.25	2294.7876	FALSE	epithelial membrane protein 1	201324 at	0.655	11656	2.242E-02	FALSE
101158 at	0.063	5787	1452025 a at	-0.044	6858	101158 at	-0.093	2668	1449913 at	-0.183	2999	4578	2065.7059	FALSE	zinc finger protein 2	207757 at	0.068	15882	8.817E-02	FALSE
160853 at	0.056	5268	1450354 a at	-0.077	4149	160853 at	0.001	8468	1450354 a at	-0.287	433	4579.5	3315.2806	FALSE	phosphatidylserine synthase 2	221005 s at	0.169	7321	2.030E-03	FALSE
93753 at	0.002	8383	1416304 at	-0.228	844.5	93753 at	0.011	8002	1416304 at	-0.292	1090	4579.875	4175.6019	FALSE	LPS-induced TN factor	200706 s at	0.203	13812	4.916E-02	FALSE
103450 at	0.097	3003	1423528 at	-0.164	2625	103450 at	0.014	7760	1428454 at	0.129	4935	4580.75	2348.5724	FALSE	breast carcinoma amplified sequence 3	237412 at	0.047	24985	3.719E-01	FALSE
160169 at	-0.098	4752	1429707 at	0.098	4964	160169 at	0.093	3905	1429707 at	0.129	4703	4581	464.68269	FALSE	phospholipase A2, activating protein	209532 at	-0.035	22553	2.867E-01	FALSE
94906 at	-0.003	8364	1416225 at	0.128	2515	94906 at	-0.059	5080	1416225 at	-0.184	2367	4581.5	2812.4865	FALSE	alcohol dehydrogenase 1 (class I)	209614 at	0.134	5280	3.612E-04	FALSE
104474 s at	-0.008	8178	1422099 a at	-0.152	1751	104474 s at	-0.016	7328	1450486 a at	0.479	1069	4581.5	3689.0586	FALSE	opioid receptor-like 1	206564 at	-0.150	7929	3.125E-03	FALSE
96949 at	-0.218	2771	1415767 at	-0.082	5309	96949 at	-0.209	3333	1437456 x at	0.045	6913	4581.5	1897.5257	FALSE	YTH domain family 1	221741 s at	0.164	12908	3.593E-02	FALSE
92644 s at	-0.164	1386	1421317 x at	-0.042	6705.5	92644 s at	0.045	6971	1421317 x at	-0.306	3264	4581.625	2718.3397	FALSE	myeloblastosis oncogene	215152 at	-0.011	35084	7.327E-01	FALSE
92624 r at	0.083	4443	1448745 s at	0.321	127.5	92624 r at	0.003	8371	1448745 s at	-0.142	5385	4581.625	3408.9696	FALSE	loricrin	207720 at	-0.005	42805	9.542E-01	FALSE
104033 at	-0.180	2585	1426445 at	0.018	7877	104033 at	0.096	6310	1444458 at	-0.241	1555	4581.75	2999.6526	FALSE	meningioma expressed antigen 6 (coiled-coil proline-rich)	204055 s at	0.053	19111	1.722E-01	FALSE
161793 at	0.027	6942	1424808 at	0.250	1231	161793 at	-0.067	3934	1424807 at	0.098	6223	4582.5	2576.2754	FALSE	laminin, alpha 4	202202 s at	0.340	3903	7.710E-05	FALSE
97819 at	0.028	7518	1456036 x at	0.331	374.5	97819 at	0.070	6464	1416531 at	0.171	3977	4583.375	3174.434	TRUE	glutathione S-transferase omega 1	201470 at	-0.199	12113	2.703E-02	FALSE
99542 at	0.088	4329	1450962 at	0.114	3020.5	99542 at	0.083	4001	1450962 at	0.050	6985	4583.875	1694.5252	TRUE	pyruvate dehydrogenase E1 alpha 2	214518 at	0.050	26373	4.191E-01	FALSE
104731 at	0.005	8293	1449510 at	-0.207	1541.5	104731 at	0.018	7323	1449510 at	-0.320	1179	4584.125	3746.5377	FALSE	zinc finger protein 467	214746 s at	-0.330	3335	3.646E-05	FALSE
100956 at	0.515	1843	1423400 at	-0.286	5235	100956 at	0.253	4122	1451892 at	0.048	7138	4584.5	2211.5787	FALSE	klotho	205978 at	-0.517	2148	4.904E-06	FALSE
94084 at	-0.028	7198	1423987 at	0.110	3443	94084 at	0.053	5843	1459540 at	0.214	1854	4584.5	2392.5479	FALSE	cell division cycle 26	225422 at	0.235	10318	1.211E-02	FALSE
101839 at	-0.074	4339	1432301 a at	0.097	4358	101839 at	0.097	2375	1432301 a at	0.038	7268	4585	2016.1543	FALSE	RIKEN cDNA 1700074P13 gene		NA	NA	NA	NA
97681 f at	-0.152	873	1427474 s at	0.119	2924.5	97682 r at	0.038	6549	1427474 s at	0.022	7994	4585.125	3266.7405	FALSE	glutathione S-transferase, mu 3		NA	NA	NA	NA
103759 at	0.005	8267	1449453 at	0.189	2034.5	103759 at	0.052	4851	1449453 at	0.150	3189	4585.375	2713.0392	TRUE	bone marrow stromal cell antigen 1	205715 at	0.010	40594	8.949E-01	FALSE
97278 at	0.041	6289	1438554 x at	-0.056	6423	97278 at	0.094	2630	1436637 at	0.195	3002	4586	2050.1845	FALSE	Williams-Beuren syndrome chromosome region 1 homolog (human)	206621 s at	-0.162	8624	4.692E-03	FALSE
93934 at	0.157	3140	1417232 at	-0.102	3142	93934 at	0.069	4984	1417231 at	-0.259	7080	4586.5	1875.6769	FALSE	claudin 2	223509 at	-0.004	41938	9.334E-01	FALSE
103469 at	0.073	5465	1420722 at	0.080	4304.5	103469 at	0.222	239	1420722 at	0.007	8338	4586.625	3357.8661	TRUE	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	234513 at	-0.026	34093	7.018E-01	FALSE
162486 f at	-0.123	2560	1415745 a at	-0.017	8094.5	101104 at	0.152	1261	1415745 a at	0.084	6436	4587.875	3208.9645	FALSE	Down syndrome critical region gene 3	203635 at	-0.072	16958	1.129E-01	FALSE
102882 at	-0.150	1032	1421169 at	0.097	4435	102882 at	-0.025	6951	1421169 at	0.111	5937	4588.75	2586.6396	FALSE	zinc finger protein 46	226113 at	-0.179	6895	1.458E-03	FALSE
92407 at	0.110	4212	1420693 at	0.089	4507	92407 at	0.108	2631	1420693 at	-0.063	7010	4590	1811.4317	FALSE	myomesin 1	205610 at	0.134	7990	3.267E-03	FALSE
96388 at	0.159	1773	1449680 at	-0.038	6558	96388 at	0.101	3799	1419953 at	-0.062	6230	4590	2245.2761	FALSE	expressed sequence C80678		NA	NA	NA	NA
103757 at	-0.062	5076	1440255 at	0.058	5572.5	161581 r at	0.220	452	1440255 at	0.040	7260	4590.125	2912.8134	FALSE	MBD2-interacting zinc finger	206495 s at	-0.025	34060	7.006E-01	FALSE
160310 at	0.067	4880	1426932 at	-0.046	6570	160310 at	-0.057	4855	1426931 s at	0.196	2057	4590.5	1870.0101	FALSE	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed	203712 at	0.151	4135	1.012E-04	FALSE
100481 at	0.103	3267	1449154 at	0.173	1008.5	100481 at	0.000	8512	1449154 at	0.168	5582	4592.375	3211.6245	TRUE	procollagen, type XI, alpha 1	232805 at	-0.088	9100	6.156E-03	FALSE
103592 at	-0.031	6858	1455941 s at	0.194	399	103592 at	-0.071	4142	1417854 at	-0.044	6975	4593.5	3087.4577	FALSE	mitogen activated protein kinase kinase 5	210482 x at	-0.121	8060	3.397E-03	FALSE
94411 at	0.207	516	1416873 a at	0.004	8381	94411 at	0.093	3369	1447617 at	0.078	6108	4593.5	3404.1285	TRUE	cyclin-dependent kinase 2		NA	NA	NA	NA
104254 at	0.059	5896	1428789 at	0.082	4819.5	104254 at	-0.095	3518	1431704 a at	0.155	4143	4594.125	1017.715	FALSE	Ral GEF with PH domain and SH3 binding motif 2	227533 at	-0.420	2173	5.256E-06	FALSE
100711 at	-0.042	6990	1431177 a at	0.139	3608	100711 at	0.202	1715	1431177 a at	-0.086	6068	4595.25	2392.65	FALSE	ribosomal protein L10A	229562 at	0.051	18975	1.681E-01	FALSE
95647 f at	-0.087	5641	1423782 at	-0.130	3302.5	95647 f at	0.035	7247	1423782 at	-0.161	2191	4595.375	2278.6686	FALSE	MOB1, Mps One Binder kinase activator-like 1B (yeast)	214812 s at	0.276	5476	4.360E-04	FALSE
96287 at	0.054	5766	1419269 at	0.099	3536	96287 at	0.021	7231	1419270 a at	-0.216	1849	4595.5	2379.1969	FALSE	deoxyuridine triphosphatase	209932 s at	0.149	10776	1.538E-02	FALSE
100088 at	0.029	7606	1456462 x at	-0.148	4670	100088 at	-0.095	6107	1431328 at	1.544	1	4596	3289.5148	FALSE	protein phosphatase 1, catalytic subunit, beta isoform	228222 at	-0.243	16210	9.549E-02	FALSE
98049 at	-0.115	2673	1423681 at	-0.031	6949	98049 at	-0.077	4163	1443388 at	0.112	4599	4596	1772.196	FALSE	RIKEN cDNA 1300018I05 gene	212380 at	0.075	16253	9.623E-02	FALSE
161691 at	-0.080	5637	1431058 at	0.118	2241	161691 at	0.130	2324	1454760 at	-0.012	8186	4597	2868.2042	FALSE	HIV TAT specific factor 1	202601 s at	-0.061	22183	2.744E-01	FALSE
161634 r at	0.079	4481	1419204 at	0.002	8449	92931 at	-0.129	1470	1419204 at	-0.137	3990	4597.5	2886.6322	FALSE	delta-like 1 (Drosophila)	224215 s at	0.451	2175	5.273E-06	FALSE
97928 at	0.051	5993	1454837 at	0.061	5167	97928 at	0.080	2810	1454837 at	-0.094	4420	4597.5	1353.811	FALSE	ceroid-lipofuscinosis, neuronal 6	218161 s at	0.073	22393	2.815E-01	FALSE

99478 at	0.067	5659	1448511 at	0.054	6107	99478 at	0.042	5401	1448511 at	0.207	1224	4597.75	2268.0011	TRUE	protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	204960 at	0.053	29173	5.266E-01	FALSE
99810 at	0.073	5432	1449279 at	0.057	5528	99810 at	-0.030	6700	1449279 at	0.279	733	4598.25	2640.523	FALSE	glutathione peroxidase 2	202831 at	-0.047	31414	6.098E-01	FALSE
103631 at	-0.068	5111	1452588 at	0.176	1226.5	103631 at	0.085	3562	1452588 at	-0.002	8495	4598.625	3049.0482	FALSE	zinc finger protein 688	213527 s at	0.266	1471	1.326E-06	FALSE
103674 f at	0.318	4605	1417210 at	0.075	3687	103674 f at	0.511	2325	1431642 at	0.065	7778	4598.75	2317.2467	TRUE	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked		NA	NA	NA	NA
93561 at	-0.013	7819	1423779 at	0.144	1085.5	93561 at	0.048	6236	1438659 x at	0.209	3255	4598.875	3011.0456	FALSE	coiled-coil-helix-coiled-coil-helix domain containing 6	224462 s at	-0.172	8813	5.227E-03	FALSE
102627 at	-0.025	7617	1418761 at	0.094	4551	102627 at	0.126	1726	1449210 at	-0.122	4504	4599.5	2406.5038	FALSE	insulin-like growth factor 2 mRNA binding protein 1	227377 at	-0.052	22171	2.739E-01	FALSE
160099 at	0.091	4401	1451336 at	0.105	2804.5	160099 at	0.009	8032	1451336 at	-0.168	3161	4599.625	2388.3583	FALSE	lectin, galactose binding, soluble 4	204272 at	-0.004	43337	9.677E-01	FALSE
101520 at	0.065	5727	1418651 at	0.095	4080	101520 at	0.021	7153	1418650 at	-0.238	1439	4599.75	2452.907	FALSE	spermatogenesis associated 6	242086 at	0.285	5854	6.107E-04	FALSE
96749 f at	-0.044	6179	1433579 at	-0.030	7567	96749 f at	0.178	1918	1433579 at	0.208	2736	4600	2705.7932	FALSE	transmembrane protein 30B	213285 at	-0.149	6004	6.948E-04	FALSE
92544 f at	-0.029	7850	1448442 a at	0.253	2199.5	92544 f at	0.216	3068	1448442 a at	0.078	5284	4600.375	2525.8517	FALSE	proteasome (prosome, macropain) subunit, alpha type 3	237300 at	0.181	2654	1.263E-05	FALSE
161108 r at	0.110	3297	1455408 at	0.104	2954.5	161108 r at	0.061	6341	1455408 at	-0.074	5814	4601.625	1723.4022	FALSE	phospholipase A2, group IVF	235958 at	-0.008	41428	9.184E-01	FALSE
102934 s at	0.048	6574	1422252 a at	0.108	3082	102935 at	-0.237	731	1422252 a at	-0.021	8021	4602	3310.2561	FALSE	cell division cycle 25 homolog C (S. cerevisiae)	217010 s at	-0.041	29364	5.342E-01	FALSE
101375 at	0.196	1450	1420751 at	0.053	6296	101375 at	-0.057	4901	1420751 at	0.099	5761	4602	2178.4874	FALSE	keratin associated protein 6-1		NA	NA	NA	NA
94909 at	-0.102	5087	1453728 a at	0.090	5614.5	94909 at	0.077	5113	1453728 a at	0.160	2594	4602.125	1360.584	FALSE	mitochondrial ribosomal protein S17	218982 s at	-0.161	13240	4.035E-02	FALSE
103283 at	-0.063	5224	1419555 at	0.026	7802.5	103283 at	-0.083	4301	1419555 at	-0.298	1081	4602.125	2775.9759	FALSE	E74-like factor 5	220625 s at	0.065	19575	1.868E-01	FALSE
94632 at	-0.059	6233	1449320 at	0.075	4604	94632 at	-0.094	3761	1449320 at	-0.119	3813	4602.75	1153.2512	FALSE	probasin		NA	NA	NA	NA
92323 at	-0.088	3739	1449283 a at	0.033	6942	92323 at	0.059	4562	1447823 x at	0.155	3169	4603	1660.8686	FALSE	mitogen-activated protein kinase 12	206106 at	-0.007	42533	9.482E-01	FALSE
97105 at	-0.110	4638	1437111 at	0.050	6785	97105 at	0.063	6581	1437111 at	-0.440	410	4603.5	2958.3825	FALSE	zinc finger CCCH-type containing 12C	231899 at	0.381	3072	2.523E-05	FALSE
161071 at	0.061	5098	1429317 at	0.119	2274.5	161071 at	0.034	5785	1456542 s at	0.123	5257	4603.625	1580.2717	TRUE	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	233089 at	0.050	22338	2.798E-01	FALSE
97465 at	0.088	4291	1451879 a at	0.087	4523.5	97465 at	-0.067	4261	1451879 a at	-0.094	5339	4603.625	504.09083	FALSE	solute carrier family 6 (neurotransmitter transporter), member 18	238215 at	-0.019	34633	7.196E-01	FALSE
103357 at	0.021	7574	1449067 at	0.091	4418	103357 at	-0.059	4398	1449067 at	0.172	2026	4604	2276.2554	FALSE	solute carrier family 2 (facilitated glucose transporter), member 2	206535 at	-0.028	28715	5.106E-01	FALSE
99135 at	-0.043	6046	1416819 at	-0.098	3020.5	99135 at	-0.102	2777	1416819 at	0.064	6573	4604.125	1983.4084	FALSE	cell division cycle 37 homolog (S. cerevisiae)	209953 s at	-0.056	24031	3.393E-01	FALSE
93353 at	0.102	2395	1423607 at	0.141	2178.5	93353 at	0.022	6998	1423607 at	0.077	6845	4604.125	2678.062	TRUE	lumican	201744 s at	0.019	31205	6.029E-01	FALSE
101359 at	0.008	8114	1416513 at	-0.110	3204	101359 at	-0.086	3157	1416513 at	-0.199	3944	4604.75	2367.1014	FALSE	laminin, beta 2	216264 s at	0.395	1853	2.995E-06	FALSE
94983 at	-0.090	5819	1451283 at	0.126	2870	94983 at	-0.024	7497	1424253 at	-0.188	2233	4604.75	2481.5364	FALSE	RIKEN cDNA 1810073G14 gene	218588 s at	0.074	13130	3.877E-02	FALSE
160182 at	0.241	2470	1416721 s at	0.181	1196.5	160182 at	0.004	8316	1447898 s at	0.081	6439	4605.375	3332.2252	TRUE	splicing factor, arginine/serine-rich 6	208804 s at	0.222	8665	4.810E-03	TRUE
94182 at	-0.029	6700	1420596 at	-0.011	8200	94182 at	-0.166	1926	1453363 at	0.210	1597	4605.75	3343.5586	FALSE	calcium channel, voltage-dependent, gamma subunit 2	214495 at	-0.241	4931	2.506E-04	FALSE
95158 at	-0.099	4767	1415744 at	0.120	4066.5	95158 at	0.060	5339	1415744 at	0.173	4253	4606.375	571.22053	FALSE	H2-K region expressed gene 2	242048 at	-0.076	12504	3.134E-02	FALSE
101445 at	-0.091	3171	1435122 x at	0.072	5599	101445 at	-0.046	5220	1435122 x at	-0.113	4436	4606.5	1072.5622	FALSE	DNA methyltransferase (cytosine-5) 1	227684 at	-0.054	25794	3.964E-01	FALSE
161178 at	0.026	7099	1419833 s at	0.075	5290.5	161178 at	-0.056	5142	1419833 s at	-0.460	895	4606.625	2629.4743	FALSE	centaurin, delta 3	235806 at	-0.032	29261	5.300E-01	FALSE
160874 r at	0.161	2822	1416585 at	0.016	8131	99537 at	-0.116	2910	1416585 at	-0.122	4565	4607	2482.3627	FALSE	RuvB-like protein 1	201614 s at	0.070	25648	3.928E-01	FALSE
98285 at	0.011	7996	1422135 at	-0.010	8396	98285 at	-0.485	213	1422135 at	0.273	1827	4608	4198.3121	FALSE	similar to zinc finger protein 146		NA	NA	NA	NA
98292 at	0.200	2405	1449240 at	0.032	7549	98292 at	-0.071	4503	1449240 at	-0.231	3976	4608.25	2153.535	FALSE	G substrate	220231 at	-0.035	29507	5.388E-01	FALSE
100742 at	0.080	4444	1420161 at	0.095	2962	100742 at	-0.037	5657	1420162 at	-0.113	5377	4610	1214.9016	FALSE	expressed sequence AA409749		NA	NA	NA	NA
98604 at	-0.063	6250	1415957 a at	-0.225	1235.5	98604 at	-0.127	3901	1415957 a at	0.096	7054	4610.125	2617.4203	FALSE	novel nuclear protein 1	222733 x at	0.148	7709	2.685E-03	FALSE
160071 at	0.092	4579	1423373 at	0.102	4492	160071 at	0.131	3141	1423373 at	0.082	6231	4610.75	1264.9749	TRUE	ribonuclease P/MRP 30 subunit (human)	203436 at	0.039	24729	3.627E-01	FALSE
162088 r at	-0.051	5791	1418066 at	-0.100	4786.5	162088 r at	0.038	6465	1431432 at	0.476	1402	4611.125	2247.8284	FALSE	cofilin 2, muscle	224352 s at	0.252	11708	2.291E-02	FALSE
103432 at	-0.068	5292	1419569 a at	-0.097	5212.5	103432 at	-0.069	4993	1419569 a at	-0.215	2947	4611.125	1116.5995	TRUE	interferon-stimulated protein	33304 at	0.135	14428	6.032E-02	FALSE
100599 at	-0.002	8439	1439258 at	0.092	3951.5	100599 at	-0.097	4150	1438992 x at	-0.284	1908	4612.125	2745.132	FALSE	activating transcription factor 4	200779 at	0.255	9681	8.599E-03	FALSE
160693 at	-0.347	345	1416387 at	0.045	5779.5	161763 r at	-0.071	5925	1416388 at	0.170	6403	4613.125	2857.8541	FALSE	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	218942 at	0.023	36193	7.676E-01	FALSE
95718 f at	-0.004	8361	1448179 at	0.487	94	95718 f at	0.117	2111	1448179 at	-0.021	7888	4613.5	4141.4367	FALSE	upregulated during skeletal muscle growth 5	225413 at	-0.419	1897	3.237E-06	FALSE
100115 at	0.216	1318	1426289 at	-0.130	6797	100115 at	0.093	4312	1426289 at	-0.077	6028	4613.75	2430.3432	FALSE	RIKEN cDNA 2610028H07 gene	209174 s at	-0.090	13123	3.868E-02	FALSE
92911 at	0.148	2524	1449177 at	-0.059	6114	92911 at	-0.066	4970	1449177 at	-0.097	4847	4613.75	1505.4484	FALSE	cyclin A1	205899 at	-0.090	24440	3.522E-01	FALSE
98559 at	0.139	1984	1452469 a at	0.061	6084	98559 at	0.001	8476	1452469 a at	-0.374	1915	4614.75	3228.9029	FALSE	smoothelin	209427 at	0.192	7710	2.685E-03	FALSE
161222 r at	0.036	6377	1423707 at	-0.222	3124	96340 at	-0.122	2595	1423707 at	-0.065	6367	4615.75	2039.4139	FALSE	transmembrane protein 50B	231696 x at	0.079	14654	6.414E-02	FALSE
104116 at	0.035	6591	1434442 at	0.007	8303.5	104116 at	0.157	1010	1434442 at	0.141	2561	4616.375	3402.1827	TRUE	DNA segment, Chr 5, ERATO Doi 593, expressed	203986 at	0.276	2663	1.304E-05	TRUE
95532 at	0.085	4388	1439771 s at	0.094	3839	95532 at	-0.050	4903	1439771 s at	0.081	5336	4616.5	647.16845	FALSE	DNA segment, Chr 13, ERATO Doi 608, expressed		NA	NA	NA	NA
98485 at	0.154	3829	1434628 a at	-0.050	6675	98485 at	0.088	5998	1431805 a at	-0.328	1967	4617.25	2143.6704	FALSE	rhophilin, Rho GTPase binding protein 2	227196 at	0.220	14854	6.786E-02	FALSE
97791 at	-0.010	7977	1422146 at	-0.183	2657	97791 at	-0.152	1642	1435963 at	-0.172	6195	4617.75	2970.5166	TRUE	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM	223610 at	-0.087	18330	1.499E-01	FALSE
161568 f at	0.161	2153	1450253 a at	-0.011	8101	161568 f at	0.145	1262	1447667 x at	-0.065	6957	4618.25	3412.7785	FALSE	mitogen activated protein kinase kinase kinase 4	204089 x at	0.177	6757	1.286E-03	FALSE
104448 at	0.087	3154	1419399 at	0.055	5754.5	104448 at	0.026	7130	1419400 at	-0.183	2436	4618.625	2198.9539	FALSE	microsomal triglyceride transfer protein		NA	NA	NA	NA
92783 at	-0.214	2986	1460310 a at	-1.033	3966	92783 at	-0.042	6598	1460310 a at	0.113	4927	4619.25	1538.8743	FALSE	growth hormone		NA	NA	NA	NA
100455 at	0.124	4041	1416688 at	-0.089	5421.5	100455 at	-0.032	7958	1459094 at	0.233	1059	4619.875	2875.2164	FALSE	synaptosomal-associated protein 91	204953 at	-0.854	1992	3.816E-06	FALSE
104096 at	-0.014	8009	1453804 a at	0.082	5580	104096 at	-0.144	2172	1431172 at	-0.194	2721	4620.5	2708.3713	FALSE	origin recognition complex, subunit 4-like (S. cerevisiae)	203352 at	-0.077	12625	3.290E-02	FALSE
98114 at	0.032	7473	1423086 at	-0.149	1571	98114 at	0.063	5711	1423086 at	0.144	3732	4621.75	2543.9355	FALSE	Niemann Pick type C1	202679 at	0.340	8700	4.915E-03	FALSE
100320 at	0.193	903	1417974 at	0.047	7330	100320 at	-0.063	5583	1417975 at	-0.158	4671	4621.75	2713.5553	FALSE	karyopherin (importin) alpha 4	209653 at	-0.237	10625	1.417E-02	FALSE
96002 at	-0.029	7050	1428165 at	0.068	4749.5	96002 at	-0.058	5392	1459584 at	-0.281	1297	4622.125	2419.3639	FALSE	vacuolar protein sorting 24 (yeast)	217837 s at	-0.745	1253	8.128E-07	FALSE
92712 at	0.121	3968	1422918 at	0.181	1779	92712 at	0.006	8144	1422918 at	0.108	4598	4622.25	2640.4182	TRUE	RIKEN cDNA 1810009J06 gene		NA	NA	NA	NA
103202 at	-0.210	5490	1418392 a at	0.106	3573.5	103202 at	0.034	6384	1418392 a at	-0.831	3043	4622.625	1575.9293	FALSE	guanylate nucleotide binding protein 4	235574 at	-0.029	27983	4.798E-01	FALSE
94177 at	-0.181	1279	1448865 at	-0.039	7005	94177 at	-0.049	6169	1448865 at	0.149	4038	4622.75	2555.2952	FALSE	hydroxysteroid (17-beta) dehydrogenase 7	220081 x at	0.307	2580	1.084E-05	FALSE
98862 at	-0.173	1091	1460657 at	0.028	7254	98862 at	0.043	5543	1460657 at	0.105	4603	4622.75	2597.6903	FALSE	wingless related MMTV integration site 10a	223709 s at	-0.121	8780	5.119E-03	FALSE
97788 at	0.006	8190	1419231 s at	0.188	1144	97788 at	-0.008	7956	1419231 s at	0.748	1202	4623	3984.9325	FALSE	keratin complex 1, acidic, gene 12	207811 at	-0.039	31646	6.182E-01	FALSE
160650 at	0.019	7359	1424565 at	0.086	4193	160650 at	-0.150	2370	1424565 at	0.147	4570	4623	2061.5054	FALSE	polymerase (RNA) III (DNA directed) polypeptide D	208361 s at	0.013	37465	8.040E-01	FALSE
161727 r at	-0.090	3478	1416602 a at	0.091	5353	161727 r at	0.096	3396	1416602 a at	0.126	6266	4623.25	1419.9651	FALSE	RAD52 homolog (S. cerevisiae)	205647 at	0.212	4478	1.511E-04	FALSE
95588 at	-0.036	6667	1417208 at	0.222	514.5	95588 at	0.023	7052	1417208 at	0.118	4265	4624.625	3004.7686	FALSE	alpha-methylacyl-CoA racemase	209426 s at	-0.065	20906	2.305E-01	FALSE
93564 at	0.080	3546	1460638 at	-0.035	6679	162093 at	0.165	868	1460638 at	-0.039	7406	4624.75	3012.8705	FALSE	tyrosyl-tRNA synthetase	212048 s at	-0.513	1781	2.546E-06	FALSE
101989 at	-0.066	5582	1428782 a at	-0.098	4489	101989 at	-0.227	1716	1428782 a at	-0.074	6716	4625.75	2142.3433	TRUE	ubiquinol-cytochrome c reductase core protein 1	201903 at	-0.196	13311	4.129E-02	TRUE
99569 at	-0.052	6437	1460185 at	-0.003	8448	99569 at	-0.115	1661	1460185 at	0.245	1957	4625.75	3356.6943	FALSE	keratin complex 2, basic, gene 18	207670 at	0.004	42398	9.441E-01	FALSE
99951 at	0.121	2647	1425793 a at	0.132	2635.5	99951 at	0.040	6405	1425792 a at	-0.093	6817	4626.125	2298.1045	FALSE	RAR-related orphan receptor gamma	228806 at	0.090	17360	1.233E-01	FALSE
100578 at	0.058	6389	1415851 a at	0.182	568.5	100578 at	-0.010	8183	1415852 at	0.166	3364	4626.125	3357.3982	FALSE	inosine 5'-phosphate dehydrogenase 2	201892 s at	0.097	18719	1.617E-01	FALSE
104717 at	0.074	6824	1419983 at	0.117	2430	104717 at	-0.026	7899	1436985 at	0.280	1352	4626.25	3218.9659	FALSE	zinc finger protein 644	222580 at	0.238	9148	6.355E-03	FALSE
160317 at	-0.094	3579	1416590 a at	0.166	1259	160317 at	-0.002	8401	1416591 at	0.104	5267	4626.5	3005.24	FALSE	RAB34, member of RAS oncogene family	224710 at	0.394	2608	1.128E-05	FALSE
95440 at	0.121	3580	1423679 at	-0.131	4704.5	95440 at	-0.089	5223.5	1423679 at	0.135	4998	4626.5	729.30732	FALSE	RIKEN cDNA 2810432L12 gene	224458 at	-0.392	6319	9.270E-04	FALSE
160795 at	-0.144	3550	1426775 s at	-0.018	7895.5	160795 at	-0.164	3327	1453054 at	-0.168	3735	4626.875	2185.4584	TRUE	secretory carrier membrane protein 1	212425 at	-0.479	426	7.356E-08	TRUE
97787 at	0.115	3414	1417415 at	0.049	6634.5	97787 at	-0.122	2169	1417415 at	0.091	6290	4626.875	2183.9382	FALSE	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	206836 at	0.017	35651	7.508E-01	FALSE
97180 f at	0.080	5044	1436717 x at	0.098	4222	97180 f at	0.111	2156	1450621 a at	0.050	7086	4627	2040.4604	TRUE	hemoglobin Y, beta-like embryonic chain	217683 at	-0.021	33672	6.876E-01	FALSE
100635 at	0.105	3150	1423720 a at	-0.196	1308	100635 at	0.015	7504	1415696 at	0.067	6548	4627.5	2896.2423	FALSE	SAR1 gene homolog A (S. cerevisiae)	201542 at	0.294	6720	1.253E-03	FALSE
94844 at	-0.043	6061	1450840 a at	0.460	550	94844 at	-0.019	7375	1423032 at	-0.107	4524	4627.5	2957.4988	FALSE	ribosomal protein L39	208695 s at	0.115	13133	3.881E-02	FALSE
95359 at	-0.075	4593	1416365 at	-0.146	4182	95359 at	0.019	7445	1416365 at	0.247	2290	4627.5	2129.3092	FALSE	heat shock protein 90kDa alpha (cytosolic), class B member 1	214359 s at	-0.249	14918	6.926E-02	FALSE
97725 at	0.055	6185	1422872 at	0.041	6963.5	97725 at	0.060	4837	1437312 at	-0.287	530	4628.875	2870.3131	FALSE	bone morphogenetic protein receptor, type 1B	240331 at	0.152	6535	1.077E-03	FALSE
100961 at	-0.026	7035	1449544 a at	-0.189	1065	100961 at	0.076	3376	1449544 a at	-0.118	7040	4629	2936.7704	FALSE	potassium voltage-gated channel, subfamily H (eag-related), member 2	205262 at	-0.519	122	1.080E-08	FALSE
96825 at	0.128	1637	1452264 at	-0.001	8478	96825 at	-0.039	6010	1452264 at	-0.245	2393	4629.5	3197.5887	FALSE	tensin like C1 domain-containing phosphatase	212494 at	0.421	774	2.513E-07	FALSE
161734 r at	-0.024	7575	1430240 a at	0.052	6118.5	161734 r at	0.113	2807	1418617 x at	0.179	2018	4629.625	2647.9256	FALSE	Calmegin	205830 at	-0.041	23869	3.337E-01	FALSE
96266 at	-0.219	2282	1426698 a at	-0.133	3360	96266 at	0.066	6000	1426698 a at	-0.046	6880	4630.5	2165.287	FALSE	heterogeneous nuclear ribonucleoprotein M	230392 at	0.214	6170	8.045E-04	FALSE
96869 at	0.340	1726	1416937 at	0.097	5333.5	96869 at	0.054	5313	1416937 at	0.097	6150	4630.625	1975.265	TRUE	gamma-aminobutyric acid receptor associated protein	200645 at	0.081	17573	1.286E-01	FALSE
96552 at	0.019	7607	1442296 at	0.153	1936.5	96552 at	0.025	7076	1442296 at	-0.287	1906	4631.375	3136.907	FALSE	WD repeat domain 75	224721 at	0.132	9236	6.668E-03	FALSE
101809 at	0.061	5236	1422777 at	-0.081	4924	101809 at	-0.051	6070	1422777 at	-0.149	2298	4632	1629.4662	FALSE	complement component 1, q subcomponent-like 1	214346 at	0.040	24391	3.501E-01	FALSE
94953 at	-0.005	8269	1421546 a at	0.072	5304	94953 at	0.273	337	1451358 a at	0.285	4619	4632.25	3272.4378	FALSE	Rac GTPase-activating protein 1	222077 s at	-0.214	11792	2.374E-02	FALSE
102621 at	0.146	3006	1421452 at	-0.006	8300	102621 at	0.051	6199	1434957 at	-0.269	1025	4632.5	3243.6624	FALSE	cell adhesion molecule-related/down-regulated by oncogenes	207230 at	0.069	17002	1.144E-01	FALSE
104124 at	-0.001	8471	1428580 at	0.172	619.5	104124 at	0.157	1084	1428580 at	-0.009	8356	4632.625	4370.147	FALSE	biliverdin reductase A	211729 x at	0.162	8521	4.420E-03	FALSE
102749 at	0.035	6827	1418709 at	0.067	5152.5	102749 at	0.067	3948	1418709 at	0.341	2604	4632.875	1795.3256	TRUE	cytochrome c oxidase, subunit VIIa 1	204570 at	0.147	21503	2.499E-01	FALSE
102206 at	0.007	8146	1422787 at	0.089	3704	102206 at	0.056	5053	1422787 at	0.279	1629	4633	2732.8023	TRUE	FK506 binding protein-like	219187 at	0.068	17083	1.168E-01	FALSE
94270 at	0.138	1974	1448169 at	-0.159	3448	94270 at	0.062	6047	1448169 at	-0.156	7063	4633	2336.5788	FALSE	keratin complex 1, acidic, gene 18	201596 x at	0.085	17766	1.341E-01	FALSE
99667 at	-0.149	1688	1417607 at	-0.045	5928.5	99667 at	-0.056	4893	1457633 x at	-0.083	6024	4633.375	2029.2713	TRUE	cytochrome c oxidase, subunit VI a, polypeptide 2	206353 at	0.059	25578	3.909E-01	FALSE
93688 at	0.007	8183	1421214 at	0.141	1924.5	93688 at	0.116	2914	1421214 at	0.081	5515	4634.125	2808.9946	TRUE	cytidine monophospho-N-acetylneuraminic acid hydroxylase		NA	NA	NA	NA
101131 at	0.011	8040	1450299 at	0.015	8021	101131 at	-0.137	1585	1450299 at	-0.325	892	4634.5	3931.5633	FALSE	cholinergic receptor, nicotinic, alpha polypeptide 7	210123 s at	-0.022	34216	7.062E-01	FALSE
103409 at	0.007	8136	1424951 at	0.195	607.5	103409 at	0.035	6179	1424951 at	0.474	3616	4634.625	3260.882	TRUE	BAI1-associated protein 2-like 1	222675 s at	0.040	22745	2.929E-01	FALSE
93287 at	0.141	2320	1420362 a at	0.064	5729	93287 at	-0.055	5002	1449836 x at	0.092	5489	4635	1572.6905	FALSE	Bcl2-interacting killer	205780 at	0.056	20104	2.038E-01	FALSE
98804 at	0.067	5972	1420604 at	0.248	809	98804 at	0.062	4747	1420604 at	0.069	7012	4635	2713.4552	TRUE	homeo box gene expressed in ES cells	211267 at	0.044	22783	2.942E-01	FALSE
92614 at	-0.077	5449	1416630 at	-0.107	4089.5	92614 at	-0.001	8509	1416630 at	-0.403	493	4635.125	3322.8605	TRUE	inhibitor of DNA binding 3	207826 s at	0.925	1644	1.933E-06	FALSE
162388 r at	0.121	3857	1424798 a at	0.118	2190	162388 r at	0.067	4777	1424798 a at	-0.035	7719	4635.75	2317.6516	FALSE	a disintegrin and metallopeptidase domain 5		NA	NA	NA	NA
100986 at	-0.266	443	1419184 a at	-0.027	7408	100986 at	-0.016	7601	1419184 a at	0.443	3096	4637	3484.6355	FALSE	four and a half LIM domains 2	202949 s at	-0.075	20431	2.138E-01	FALSE
101394 at	0.056	5390	1437523 s at	0.076	4451.5	101394 at	-0.059	4819	1421254 a at	0.161	3889	4637.375	630.88475	FALSE	sarcoglycan, gamma (dystrophin-associated glycoprotein)	207302 at	-0.061	22053	2.702E-01	FALSE
103838 at	0.139	1658	1449206 at	0.063	5560	103838 at	0.106	4280	1449206 at	0.053	7053	4637.75	2286.9829	TRUE	synaptophysin-like 2		NA	NA	NA	NA
101835 at	-0.114	3080	1448409 at	0.000	8527	101835 at	-0.114	3060	1448409 at	0.157	3885	4638	2620.9908	FALSE	lymphoid-restricted membrane protein	204674 at	0.076	17029	1.152E-01	FALSE
160313 at	-0.016	8007	1456699 s at	0.090	3764.5	160313 at	-0.276	3033	1426827 at	-0.159	3749	4638.375	2271.5273	FALSE	RIKEN cDNA A730098D12 gene		NA	NA	NA	NA
102297 at	0.031	6527	1448920 at	0.149	995.5	102297 at	0.073	4919	1448920 at	0.116	6116	4639.375	2523.1967	TRUE	zinc finger protein 535	226787 at	0.057	18043	1.419E-01	FALSE
94568 at	0.089	3856	1452399 at	0.070	4925	94568 at	0.020	7520.5	1427340 at	0.151	2260	4640.375	2210.3967	TRUE	regulator of G-protein signaling 6	210270 at	0.034	31195	6.026E-01	FALSE
160262 at	-0.105	4814	1448654 at	0.059	5550.5	160262 at	-0.015	7618	1430969 at	0.807	581	4640.875	2955.4046	FALSE	mitochondrial carrier homolog 2 (C. elegans)	242645 at	0.212	6107	7.641E-04	FALSE
103353 f at	0.089	5862	1416194 at	0.156	1768	103353 f at	-0.005	8226	1416194 at	0.201	2710	4641.5	2962.3164	FALSE	cytochrome P450, family 4, subfamily b, polypeptide 1	210096 at	-0.011	38570	8.383E-01	FALSE
97101 at	0.099	2923	1430661 at	0.132	3878	92670 at	-0.056	4992	1430661 at	0.064	6778	4642.75	1655.6621	FALSE	Myosin, light polypeptide 6B	204173 at	-0.469	864	3.197E-07	FALSE
93155 at	0.041	6788	1436243 at	-0.217	290.5	93155 at	0.008	8298	1436243 at	-0.127	3197	4643.375	3605.3304	FALSE	RIKEN cDNA A930004K21 gene	240502 at	0.203	13170	3.940E-02	FALSE
94545 at	-0.061	5077	1429761 at	-0.084	5512	94545 at	-0.356	2105	1429761 at	0.091	5881	4643.75	1724.1039	FALSE	reticulon 1	210222 s at	-0.627	4004	8.632E-05	FALSE
93133 at	0.253	579	1417022 at	0.022	7989	93133 at	0.058	4203	1417022 at	0.209	5804	4643.75	3122.6768	TRUE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	230597 at	0.004	42780	9.540E-01	FALSE
95091 at	0.020	7430	1416241 at	0.130	3187.5	95091 at	0.194	569	1416241 at	0.054	7389	4643.875	3367.6816	TRUE	SEC13-like 1 (S. cerevisiae)	207707 s at	0.008	41683	9.261E-01	FALSE
104016 at	0.081	4076	1449204 at	0.128	2865	104016 at	0.071	5721	1449204 at	0.129	5920	4645.5	1446.3242	TRUE	gap junction membrane channel protein beta 5	206156 at	-0.009	40555	8.945E-01	FALSE
98427 s at	-0.087	4438	1427705 a at	0.027	7207	98427 s at	0.040	6611	1442949 at	0.420	327	4645.75	3115.3903	FALSE	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	239876 at	0.143	4907	2.451E-04	FALSE
161500 i at	0.281	1393	1416583 at	0.056	5861	99670 at	0.034	6374	1416583 at	0.133	4955	4645.75	2246.4564	TRUE	Bcl-associated death promoter	209364 at	0.085	16734	1.069E-01	FALSE
100384 at	0.102	2553	1425786 a at	0.224	1267	100384 at	0.029	6759	1425786 a at	0.023	8007	4646.5	3243.423	TRUE	heat shock transcription factor 4	210977 s at	-0.049	29587	5.417E-01	FALSE
94124 at	0.080	4127	1418597 at	0.135	3014.5	94124 at	0.007	8091	1418597 at	0.145	3355	4646.875	2342.7801	TRUE	topoisomerase (DNA) III alpha	204946 s at	0.049	22093	2.713E-01	FALSE
93355 at	0.015	7847	1417716 at	-0.190	1040	93355 at	0.074	5931	1417716 at	0.150	3775	4648.25	2924.5788	FALSE	glutamate oxaloacetate transaminase 2, mitochondrial	200708 at	-0.168	7989	3.266E-03	FALSE
104230 at	0.167	1452	1432097 a at	0.053	6516	104230 at	-0.037	6643	1432097 a at	-0.136	3982	4648.25	2458.1443	FALSE	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	209804 at	-0.024	31579	6.157E-01	FALSE
101712 at	0.088	5136	1422218 at	0.100	5123	101712 at	-0.032	6299	1419853 a at	-0.271	2036	4648.5	1826.8473	FALSE	purinergic receptor P2X, ligand-gated ion channel, 7	207091 at	0.456	6980	1.561E-03	FALSE
92854 at	0.251	1639	1449256 a at	0.019	8043	92854 at	-0.212	726	1449256 a at	0.012	8188	4649	4020.5218	FALSE	RAB11a, member RAS oncogene family	200863 s at	-0.211	6486	1.035E-03	FALSE
104089 at	0.100	4567	1428529 at	0.296	725	104089 at	0.055	6957	1432738 at	0.064	6348	4649.25	2805.8252	TRUE	RIKEN cDNA 2810026P18 gene		NA	NA	NA	NA
95875 at	-0.012	7976	1459220 at	0.144	2257	95875 at	-0.045	5722	1459220 at	0.167	2642	4649.25	2706.164	FALSE	expressed sequence C78651		NA	NA	NA	NA
160392 at	-0.023	7477	1433448 at	0.109	3609	160392 at	-0.029	6426	1436909 at	0.435	1091	4650.75	2880.756	FALSE	RIKEN cDNA B430110G05 gene	32091 at	-0.142	10750	1.508E-02	FALSE
92313 at	0.143	2192	1427391 a at	0.062	4973.5	92314 at	0.055	5633	1445751 at	-0.087	5805	4650.875	1677.9677	FALSE	Procollagen, type XII, alpha 1	233109 at	-0.090	17771	1.341E-01	FALSE







160423 at	0.054	5154	1420845 at	-0.075	4263	160423 at	0.020	7224	1420846 at	0.166	2930	4892.75	1802.956	FALSE	mitochondrial ribosomal protein S2	218001 at	0.029	34866	7.269E-01	FALSE
92213 at	0.105	2226	1418728 at	0.101	5656	92213 at	-0.025	7147	1418728 at	0.127	4543	4893	2073.4893	FALSE	steroidogenic acute regulatory protein	204548 at	-0.215	6048	7.269E-04	FALSE
92864 at	-0.144	1530	1423147 at	0.083	5479	92864 at	-0.026	7230	1423147 at	0.088	5333	4893	2401.9668	FALSE	methionine adenosyltransferase I, alpha	205813 s at	0.038	30359	5.696E-01	FALSE
99523 at	-0.076	5603	1424585 at	0.067	4234	99523 at	-0.018	7378	1446446 at	0.257	2358	4893.25	2124.4474	FALSE	RAN binding protein 10	53987 at	0.056	15955	9.001E-02	FALSE
93973 at	-0.057	5235	1426674 at	-0.083	5372	161743 i at	0.047	6314	1426674 at	-0.136	2657	4894.5	1566.8794	FALSE	eukaryotic translation initiation factor 3, subunit 9 (eta)	236274 at	0.166	5677	5.149E-04	FALSE
94259 at	0.001	8484	1460221 at	0.070	5547	94259 at	0.301	2372	1460221 at	0.214	3175	4894.5	2746.5101	TRUE	prostaglandin E synthase 3 (cytosolic)	238895 at	0.075	22122	2.724E-01	FALSE
160770 at	-0.097	2627	1448663 s at	-0.052	6339	160770 at	-0.053	5144	1448663 s at	0.108	5471	4895.25	1594.0239	FALSE	mevalonate (diphospho) decarboxylase	203027 s at	-0.047	27930	4.777E-01	FALSE
101186 at	0.057	5466	1420747 at	0.072	4670	101186 at	-0.127	1737	1420747 at	-0.033	7717	4897.5	2470.7144	FALSE	per-pentamer repeat gene	NA	NA	NA	NA	
94662 at	0.061	5915	1456706 at	0.038	7467.5	94662 at	0.221	552	1456706 at	-0.110	5659	4898.375	3005.742	FALSE	RIKEN cDNA 4833441D16 gene	NA	NA	NA	NA	
92242 at	0.052	5428	1419318 at	0.121	2394	92242 at	0.063	5399	1419318 at	0.090	6373	4898.5	1729.8883	TRUE	serum amyloid A 4	207096 at	0.022	34233	7.066E-01	FALSE
99397 at	0.096	2845	1460727 at	0.019	7714	99397 at	-0.074	4492	1460727 at	0.151	4546	4899.25	2035.7962	FALSE	excision repair cross-complementing rodent repair deficiency, complementation group 2	213468 at	-0.046	27879	4.759E-01	FALSE
161111 f at	0.105	4256	1434959 at	0.077	4243.5	161111 f at	-0.121	2611	1422127 at	-0.002	8488	4899.625	2513.8942	FALSE	desert hedgehog	NA	NA	NA	NA	
102121 f at	0.148	1314	1417156 at	0.052	6474	102121 f at	-0.081	4134	1417156 at	0.028	7677	4899.75	2806.8581	FALSE	keratin complex 1, acidic, gene 19	201650 at	0.020	32624	6.514E-01	FALSE
99589 f at	-0.043	6994	1439379 x at	0.080	3719	99589 f at	-0.090	3787	1437054 x at	0.087	5099	4899.75	1533.8369	FALSE	protamine 1	NA	NA	NA	NA	
93589 at	0.017	7549	1438177 x at	0.099	5171	93589 at	0.084	4813	1438177 x at	0.177	2069	4900.5	2244.4577	TRUE	ectonucleoside triphosphate diphosphohydrolase 4	204076 at	-0.161	17172	1.191E-01	FALSE
96562 at	0.094	3781	1420361 at	-0.070	5647	96562 at	0.014	7552	1420361 at	-0.323	2624	4901	2162.055	FALSE	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	210423 s at	0.202	7797	2.859E-03	FALSE
94975 at	0.075	5396	1433527 at	0.103	3724	94975 at	0.008	8258	1458618 at	0.367	2230	4902	2584.1852	TRUE	iron responsive element binding protein 2	242261 at	0.117	16086	9.263E-02	FALSE
95973 at	-0.057	5965	1442566 at	0.046	6425	95973 at	0.140	1412	1442566 at	-0.086	5807	4902.25	2341.5538	FALSE	expressed sequence C78878	NA	NA	NA	NA	
101938 at	0.086	6057	1419500 at	0.083	4119.5	101938 at	0.130	2539	1419500 at	0.048	6896	4902.875	1958.412	TRUE	poly A binding protein, cytoplasmic 2	NA	NA	NA	NA	
160370 at	0.151	1750	1416552 at	0.098	4826	160370 at	-0.020	7538	1416552 at	0.080	5500	4903.5	2397.7052	FALSE	developmental pluripotency associated 5	NA	NA	NA	NA	
100620 at	0.033	7312	1424618 at	0.099	2901.5	100620 at	-0.149	1034	1424618 at	-0.006	8367	4903.625	3501.3206	FALSE	4-hydroxyphenylpyruvic acid dioxygenase	206024 at	-0.011	39942	8.758E-01	FALSE
160126 at	-0.047	5882	1416272 at	0.110	2497.5	160126 at	-0.019	7435	1416272 at	0.127	3800	4903.625	2188.7974	FALSE	mitogen-activated protein kinase kinase 1 interacting protein 1	NA	NA	NA	NA	
102346 at	-0.027	7047	1448497 at	0.141	1874	102346 at	0.085	6531	1448497 at	0.116	4163	4903.75	2378.3439	FALSE	excision repair cross-complementing rodent repair deficiency, complementation group 3	202176 at	-0.061	29726	5.470E-01	FALSE
95855 at	0.139	2496	1448059 at	0.043	6774.5	95855 at	-0.068	4024	1459228 at	-0.071	6323	4904.375	2007.087	FALSE	mirror-image polydactyly gene 1 homolog (human)	NA	NA	NA	NA	
92621 at	-0.094	5836	1435881 at	0.123	2184.5	92621 at	0.164	4076	1421743 a at	-0.041	7525	4905.375	2296.3392	FALSE	poly(rC) binding protein 2	213517 at	0.306	2649	1.240E-05	FALSE
96228 at	-0.002	8440	1448804 at	0.052	6307	96228 at	-0.101	3459	1439947 at	0.530	1417	4905.75	3094.0204	FALSE	cytochrome P450, family 11, subfamily a, polypeptide 1	204309 at	0.147	9778	8.950E-03	FALSE
98772 at	0.202	865	1419728 at	0.025	7582.5	98772 at	0.046	6007	1419728 at	-0.231	5169	4905.875	2873.7144	FALSE	chemokine (C-X-C motif) ligand 5	214974 x at	0.201	9666	8.534E-03	FALSE
94898 at	0.087	5764	1420607 at	-0.128	2887.5	94898 at	-0.060	6525	1420608 at	-0.147	4448	4906.125	1595.9774	FALSE	RNA binding motif protein 18	225236 at	-0.124	13831	4.943E-02	FALSE
99960 at	-0.038	6556	1451982 at	0.023	7785	99960 at	-0.108	4209	1426233 at	0.253	1075	4906.25	2953.7271	FALSE	mitogen activated protein kinase kinase 4	203265 s at	-0.346	2636	1.204E-05	FALSE
98906 at	-0.023	7630	1432211 a at	-0.138	2386.5	98906 at	-0.110	4957	1432211 a at	0.132	4655	4907.125	2147.3746	FALSE	f-box only protein 9	210638 s at	-0.222	4296	1.208E-04	FALSE
101584 at	0.103	2398	1419259 at	0.105	3427	160584 at	-0.059	5418	1419259 at	-0.005	8387	4907.5	2636.7278	FALSE	Ras suppressor protein 1	230490 x at	0.149	3706	5.986E-05	FALSE
98449 at	0.028	6929	1448658 at	0.093	4011	98449 at	0.156	1111	1448658 at	0.027	7581	4908	2969.3539	TRUE	squamous cell carcinoma antigen recognized by T-cells 1	200051 at	0.162	10348	1.229E-02	TRUE
103296 at	0.027	7244	1449285 at	0.200	425.5	103296 at	-0.052	4854	1449285 at	0.068	7119	4910.625	3185.4414	FALSE	cystatin 9	230829 at	-0.059	19339	1.793E-01	FALSE
100282 at	0.159	2250	1422235 at	-0.030	7651	100282 at	-0.053	5238	1422235 at	-0.104	4506	4911.25	2225.5692	FALSE	5-hydroxytryptamine (serotonin) receptor 7	207818 s at	-0.034	21219	2.407E-01	FALSE
103132 at	0.039	6899	1446790 at	0.108	3961	103132 at	0.032	6198	1446790 at	0.175	2587	4911.25	1992.6522	TRUE	expressed sequence C78948	NA	NA	NA	NA	
161006 at	-0.001	8465	1434537 at	-0.281	695	161006 at	-0.076	3390	1434537 at	-0.071	7097	4911.75	3535.4211	TRUE	solute carrier organic anion transporter family, member 3a1	219229 at	0.494	2676	1.338E-05	FALSE
160999 r at	0.015	7732	1429137 at	0.146	1967	160999 r at	-0.012	7675	1429137 at	-0.231	2273	4911.75	3226.1388	FALSE	RIKEN cDNA 2810422O20 gene	213528 at	0.073	19459	1.836E-01	FALSE
92334 at	-0.117	3701	1449295 at	0.084	4213	92334 at	-0.025	7243	1418977 at	0.139	4492	4912.25	1587.9843	FALSE	SAP30 binding protein	222475 at	0.123	6528	1.072E-03	FALSE
94895 at	-0.006	8371	1460357 at	0.115	2394	94895 at	-0.030	7367	1451317 at	0.208	1519	4912.75	3456.6109	FALSE	YTH domain family 2	222430 s at	-0.102	19231	1.759E-01	FALSE
94038 at	0.137	3883	1437450 x at	0.374	841.5	94038 at	0.035	7495	1437450 x at	-0.050	7433	4913.125	3196.6199	FALSE	RIKEN cDNA 2700060E02 gene	217768 at	0.068	29023	5.212E-01	FALSE
160267 at	-0.094	2874	1417912 at	0.033	7171	160267 at	-0.009	7979	1417912 at	0.228	1633	4914.25	3131.2849	FALSE	transmembrane protein 93	221255 s at	-0.017	37001	7.908E-01	FALSE
98374 at	0.079	5014	1450550 at	0.123	3128	98374 at	-0.001	8430	1450550 at	-0.153	3087	4914.75	2509.9787	FALSE	interleukin 5	207952 at	0.024	30002	5.570E-01	FALSE
103884 at	-0.051	5433	1424682 at	0.074	4016	103884 at	-0.007	7994	1424682 at	0.161	2217	4915	2438.3034	FALSE	ATP binding domain 1 family, member C	218461 at	-0.014	37124	7.944E-01	FALSE
104340 at	0.103	4335	1417968 a at	-0.104	5009	104340 at	0.027	6986	1453678 at	0.168	3334	4916	1542.0586	FALSE	methyl-CpG binding domain protein 1	241813 at	-0.098	11103	1.801E-02	FALSE
100327 at	0.136	4666	1420353 at	0.070	5671.5	102630 s at	0.100	3909	1420353 at	0.107	5421	4916.875	796.31468	TRUE	lymphotoxin A	206975 at	-0.058	24277	3.464E-01	FALSE
95329 at	0.178	1873	1450139 at	0.137	4272	95329 at	0.027	6672	1450139 at	0.069	6851	4917	2345.3743	TRUE	endoplasmic reticulum (ER) to nucleus signalling 2	223910 at	0.037	26155	4.095E-01	FALSE
160571 at	0.019	7517	1419821 s at	-0.084	5647	160571 at	0.097	3575	1422433 s at	0.151	2934	4918.25	2083.7584	FALSE	isocitrate dehydrogenase 1 (NADP+), soluble	201193 at	0.199	9936	9.774E-03	FALSE
161033 at	0.121	2668	1449208 at	0.095	5681.5	161033 at	0.077	3489	1449208 at	0.021	7839	4919.375	2325.203	TRUE	poly (A) polymerase beta (testis specific)	242158 at	-0.036	29886	5.530E-01	FALSE
104436 at	0.081	3789	1426507 at	0.162	1924.5	104436 at	0.020	7514	1426507 at	0.065	6450	4919.375	2537.8413	TRUE	interleukin 1 family, member 5 (delta)	222223 s at	-0.014	38058	8.236E-01	FALSE
160321 at	-0.088	5987	1416084 at	-0.064	4857	160321 at	0.006	8379	1416085 s at	0.376	455	4919.5	3318.8031	FALSE	zinc finger, A20 domain containing 2	217741 s at	-0.400	9893	9.553E-03	FALSE
160872 f at	-0.121	1869	1420548 a at	-0.065	5099	160872 f at	0.014	7509	1436541 at	-0.179	5202	4919.75	2318.2671	FALSE	RIKEN cDNA 2310008H09 gene	213237 at	0.087	28877	5.161E-01	FALSE
93319 at	-0.222	1296	1415850 at	-0.003	8431	93319 at	0.086	5746	1415850 at	0.118	4209	4920.5	2980.3967	FALSE	RAS p21 protein activator 3	225562 at	0.288	3415	4.126E-05	FALSE
97792 at	0.082	5670	1422839 at	0.109	4400.5	97792 at	0.011	7942	1422839 at	0.186	1677	4922.375	2612.9097	TRUE	neurogenin 2	215632 at	-0.005	41119	9.104E-01	FALSE
93472 at	0.104	5392	1434479 at	-0.065	5351.5	101080 at	-0.010	7854	1434479 at	0.350	1093	4922.625	2808.5129	FALSE	Procollagen, type V, alpha 1	212488 at	0.204	9241	6.699E-03	FALSE
96802 at	-0.074	4111	1416377 at	0.175	1574.5	96802 at	0.041	5752	1416377 at	0.015	8255	4923.125	2808.3958	FALSE	programmed cell death protein 7	231809 x at	0.251	5312	3.674E-04	FALSE
104476 at	0.018	7750	1425166 at	0.141	2806	104476 at	0.034	6286.5	1425166 at	0.179	2850	4923.125	2491.9925	TRUE	retinoblastoma-like 1 (p107)	NA	NA	NA	NA	
93258 at	-0.054	5549	1426475 at	-0.026	7477.5	93258 at	-0.045	5809	1426475 at	-0.267	859	4923.625	2841.2695	TRUE	hydroxymethylbilane synthase	203040 s at	0.016	36306	7.715E-01	FALSE
100304 at	0.122	5155	1450587 at	0.066	5277	100303 at	0.118	1735	1450587 at	0.045	7530	4924.25	2390.1832	TRUE	histocompatibility 2, M region locus 10.1	NA	NA	NA	NA	
102032 at	0.211	877	1426073 at	0.086	5202	102032 at	0.024	6757	1426073 at	0.066	6862	4924.5	2803.0474	TRUE	twisted gastrulation homolog 1 (Drosophila)	225406 at	0.390	1752	2.439E-06	TRUE
160148 at	0.098	3514	1427439 s at	-0.111	2947	160148 at	0.050	6212	1427439 s at	0.090	7026	4924.75	1997.8301	FALSE	Protein arginine N-methyltransferase 5	217786 at	-0.066	24837	3.669E-01	FALSE
101963 at	0.026	7745	1451310 a at	0.074	5857	101963 at	0.271	499	1451310 a at	0.094	5598	4924.75	3101.7967	TRUE	cathepsin L	210074 at	-0.008	40843	9.030E-01	FALSE
95965 at	0.125	3403	1449654 s at	0.140	2602	95965 at	-0.006	8220	1449654 s at	0.117	5478	4925.75	2508.3623	FALSE	expressed sequence C77545	NA	NA	NA	NA	
93710 at	0.069	4915	1450540 x at	-0.090	4914.5	93710 at	-0.016	7293	1450540 x at	0.180	2593	4928.875	1918.8363	FALSE	keratin associated protein 5-1	NA	NA	NA	NA	
93081 at	-0.164	4354	1415775 at	-0.157	2527	93081 at	-0.061	6897	1415775 at	-0.064	5941	4929.75	1914.6274	TRUE	retinoblastoma binding protein 7	201092 at	-0.268	6604	1.135E-03	TRUE
102418 at	0.080	3799	1417482 at	0.080	5207	102418 at	0.065	6062	1417482 at	0.099	4652	4930	951.24445	TRUE	testis expressed gene 19	NA	NA	NA	NA	
103911 at	0.059	6467	1424604 s at	0.177	3115	103911 at	0.115	3957	1424603 at	0.113	6184	4930.75	1650.8419	TRUE	sulfatase modifying factor 1	226850 at	0.213	9136	6.319E-03	TRUE
98066 r at	-0.027	7100	1423502 at	0.082	4717.5	98066 r at	0.030	6245	1437210 a at	0.296	1663	4931.375	2391.4126	FALSE	bromodomain containing 2	214911 s at	0.235	6902	1.467E-03	FALSE
103889 at	0.092	5296	1422761 at	0.102	4018.5	103889 at	-0.011	7978	1442312 at	0.314	2434	4931.625	2344.1486	FALSE	transducin (beta)-like 1X-linked receptor 1	233633 at	-0.058	15220	7.493E-02	FALSE
102552 at	0.069	4971	1422339 at	-0.002	8465.5	102552 at	-0.092	3651	1439793 at	-0.146	2644	4932.875	2540.541	FALSE	gap junction membrane channel protein alpha 3	208590 x at	0.031	33899	6.954E-01	FALSE
101691 s at	-0.118	2646	1448093 s at	0.035	6843	101692 r at	-0.158	3724	1448093 s at	-0.051	6519	4933	2070.0681	FALSE	expressed sequence C77405	NA	NA	NA	NA	
97924 at	0.123	1616	1448810 at	0.012	8036.5	97924 at	-0.043	5519	1448810 at	0.096	4561	4933.125	2653.0474	FALSE	glucosamine	205042 at	0.020	39059	8.521E-01	FALSE
96045 at	0.120	3868	1426347 at	0.062	6042	96045 at	-0.022	7251	1426347 at	0.163	2572	4933.25	2106.4623	FALSE	RIKEN cDNA 2010321M09 gene	221265 s at	0.071	15159	7.378E-02	FALSE
104279 at	-0.033	7332	1415754 at	0.167	2500	104279 at	0.129	2790	1415754 at	0.084	7111	4933.25	2646.433	FALSE	polymerase (RNA) II (DNA directed) polypeptide F	209511 at	0.098	16176	9.469E-02	FALSE
92932 at	0.051	6339	1423287 at	-0.211	3441	92932 at	0.037	6794	1423288 s at	-0.399	3160	4933.5	1898.2228	FALSE	cerebellin 1 precursor protein	205747 at	-0.057	23746	3.290E-01	FALSE
93482 at	0.027	7163	1425505 at	-0.046	6584.5	93482 at	0.136	2322	1425504 at	-0.167	3666	4933.875	2318.2579	FALSE	myosin, light polypeptide kinase	202555 s at	0.647	490	9.726E-08	FALSE
101499 at	-0.035	7148	1449942 a at	0.043	6574	101499 at	0.072	3795	1449942 a at	-0.213	2219	4934	2328.0852	FALSE	integrin linked kinase	201234 at	0.140	6081	7.493E-04	FALSE
103053 at	0.146	1719	1419391 at	0.068	5181	103053 at	-0.026	6910	1419391 at	0.076	5928	4934.5	2257.5684	FALSE	myogenin	207282 s at	-0.094	21111	2.370E-01	FALSE
104381 at	0.160	1431	1450444 a at	0.024	7751.5	104381 at	0.094	2254	1450444 a at	-0.011	8302	4934.625	3593.2872	FALSE	nuclear receptor subfamily 1, group H, member 3	203920 at	0.134	6432	9.976E-04	FALSE
93503 at	0.141	1555	1448201 at	-0.110	2580.5	93503 at	-0.006	8172	1448201 at	-0.060	7431	4934.625	3350.4355	FALSE	secreted frizzled-related protein 2	223121 s at	0.247	9344	7.107E-03	FALSE
94795 at	0.025	7594	1420531 at	0.107	3380.5	94795 at	0.106	3906	1420531 at	0.118	4859	4934.875	1875.3994	TRUE	hydroxysteroid dehydrogenase-5, delta<5>-3-beta	NA	NA	NA	NA	
93111 at	-0.067	6218	1416925 at	-0.212	524	93111 at	0.039	6965	1434357 a at	0.147	6035	4935.5	2968.3839	FALSE	karyopherin (importin) beta 1	213574 s at	0.241	6347	9.404E-04	FALSE
101538 i at	0.185	1862	1435370 a at	-0.020	7851	101538 i at	0.066	5357	1449081 a at	-0.106	4675	4936.25	2462.5233	FALSE	carboxylesterase 3	209616 s at	0.058	25995	4.036E-01	FALSE
160477 at	0.133	2543	1424085 at	0.252	2680	160477 at	-0.027	7271	1424085 at	0.045	7253	4936.75	2685.56	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	217773 s at	-0.558	1799	2.672E-06	FALSE
160898 at	0.053	5606	1424751 at	0.136	1139.5	160898 at	0.013	7707	1424751 at	0.096	5296	4937.125	2748.9603	TRUE	activator of basal transcription	218405 at	-0.033	26716	4.323E-01	FALSE
92342 at	0.058	5310	1422205 at	0.068	5647	92342 at	-0.138	3237	1422205 at	-0.108	5558	4938	1142.9299	FALSE	SRY-box containing gene 1	240713 s at	-1.205	474	9.244E-08	FALSE
96630 at	0.151	1674	1415938 at	0.052	6296	96630 at	-0.036	6183	1415938 at	0.070	5602	4938.75	2197.6335	FALSE	serine peptidase inhibitor, Kazal type 3	206239 s at	0.045	21511	2.501E-01	FALSE
97010 at	0.059	5733	1420744 at	-0.080	5684	97010 at	-0.125	2135	1441837 at	-0.078	6203	4938.75	1883.7527	FALSE	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	206635 at	0.057	27438	4.590E-01	FALSE
93207 at	0.093	5261	1449895 at	0.194	1513	93207 at	-0.011	7849	1449895 at	-0.107	5136	4939.75	2604.3596	FALSE	preproacrosin	207427 at	-0.052	27834	4.745E-01	FALSE
93330 at	0.130	2825	1416203 at	-0.077	6346	93330 at	-0.038	6832	1416203 at	-0.550	3760	4940.75	1951.2494	FALSE	aquaporin 1	209047 at	1.294	166	1.569E-08	FALSE
101919 at	0.052	6249	1449512 a at	0.102	4610.5	101919 at	0.137	3110	1428046 a at	-0.148	5795	4941.125	1402.6132	FALSE	zinc finger protein X-linked	214678 x at	0.068	8292	3.927E-03	FALSE
99118 at	0.022	7421	1419167 at	0.114	2236.5	99118 at	0.089	3255	1419167 at	0.054	6853	4941.375	2579.6033	TRUE	proline-rich acidic protein 1	243669 s at	-0.055	18169	1.445E-01	FALSE
104475 at	-0.048	6367	1434103 at	-0.068	5152.5	104475 at	-0.393	156	1434103 at	0.015	8094	4942.375	3411.5409	FALSE	expressed sequence AA408278	NA	NA	NA	NA	
104713 at	0.009	8142	1433565 at	0.204	1152.5	104713 at	0.066	5046	1444087 at	-0.112	5430	4942.625	2878.0357	FALSE	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	223230 at	0.241	2831	1.662E-05	FALSE
101624 at	0.062	5827	1421518 at	0.050	5825	101624 at	-0.170	2419	1421518 at	-0.070	5700	4942.75	1683.5483	FALSE	K+ voltage-gated channel, subfamily S, 1	207366 at	-0.090	19039	1.700E-01	FALSE
95351 at	0.154	1981	1423374 at	-0.007	8330	95351 at	-0.220	1857	1423374 at	0.033	7608	4944	3505.7491	FALSE	nuclear receptor coactivator 6	208979 at	0.154	8200	3.708E-03	FALSE
93770 at	0.026	7319	1416809 at	0.154	2156	93770 at	0.036	5902	1416809 at	0.122	4403	4945	2207.8655	TRUE	cytochrome P450, family 3, subfamily a, polypeptide 11	242981 at	-0.058	16818	1.094E-01	FALSE
93683 at	0.057	5617	1450680 at	0.088	4263	93683 at	0.115	3307	1450680 at	0.054	6596	4945.75	1452.0733	TRUE	recombination activating gene 1	206591 at	-0.021	29072	5.233E-01	FALSE
103207 at	-0.011	7896	1419397 at	0.133	2054	103207 at	-0.057	5341	1459319 at	0.171	4493	4946	2410.2142	FALSE	polymerase (DNA directed), alpha 1	204835 at	0.342	447	8.445E-08	FALSE
101419 at	0.020	7353	1423221 at	-0.137	2380.5	101419 at	-0.211	1744	1423221 at	-0.011	8307	4946.125	3362.7649	FALSE	tubulin, beta 4	212664 at	-0.499	4935	2.518E-04	FALSE
96698 at	0.084	4407	1423234 at	0.086	4749.5	96698 at	0.006	8097	1423234 at	0.156	2540	4948.375	2312.7723	TRUE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	203447 at	-0.008	41950	9.339E-01	FALSE
101155 at	0.117	2275	1449306 at	0.074	4480.5	101155 at	0.032	6622	1449306 at	-0.055	6421	4949.625	2027.7639	FALSE	heat shock factor 2	209657 s at	0.105	21228	2.411E-01	FALSE
92602 at	0.073	4270	1423145 a at	0.083	4769	92602 at	-0.053	5222	1423145 a at	0.089	5540	4950.25	552.94507	FALSE	titin-cap	205766 at	0.042	30269	5.659E-01	FALSE
94466 f at	-0.240	1511	1420497 a at	-0.101	5459.5	94467 at	-0.046	6446	1429962 at	-0.068	6386	4950.625	2337.1223	TRUE	CCAAT/enhancer binding protein zeta	203341 at	0.203	9952	9.875E-03	FALSE
96710 at	-0.208	2006	1428029 a at	-0.064	6104	96710 at	0.088	4962	1436596 at	-0.062	6731	4950.75	2095.3086	FALSE	H2A histone family, member V	202487 s at	0.150	9603	8.192E-03	FALSE
103801 at	0.099	3355	1419310 s at	0.074	5489	103801 at	0.038	6269	1425670 at	0.125	4691	4951	1243.836	TRUE	regulatory factor X-associated ankyrin-containing protein	202758 s at	0.222	7025	1.606E-03	TRUE
160910 at	-0.124	2642	1419634 a at	0.063	5373	160910 at	0.078	4890	1419634 a at	-0.044	6900	4951.25	1761.8065	FALSE	growth hormone releasing hormone	214524 at	-0.008	42249	9.407E-01	FALSE
95562 at	-0.169	1002	1429483 at	0.045	6080	95562 at	0.036	6235	1429483 at	0.064	6492	4952.25	2638.9754	FALSE	nuclear domain 10 protein 52	NA	NA	NA	NA	
96532 at	-0.131	1615	1417875 at	0.040	6657	92226 at	0.048	6116	1417875 at	0.078	5422	4952.5	2281.6945	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	221699 s at	0.013	41626	9.242E-01	FALSE
101277 at	0.061	5141	1450230 at	0.083	5131	101277 at	-0.001	8481	1450230 at	-0.322	1058	4952.75	3037.8082	FALSE	DNA segment, Chr 17, human D6S56E 3	221301 at	-0.009	39556	8.658E-01	FALSE
103371 at	-0.101	4871	1416949 s at	-0.119	2360	103371 at	0.015	8072	1416949 s at	0.182	4509	4953	2356.2449	FALSE	solute carrier family 39 (zinc transporter), member 7	202667 s at	0.064	20231	2.081E-01	FALSE
93399 at	-0.083	3800	1452358 at	-0.006	8255	93399 at	0.089	2645	1452358 at	0.146	5119	4954.75	2421.227	FALSE	retinoic acid induced 2	219440 at	0.009	41132	9.105E-01	FALSE
162373 r at	0.171	1336	1448328 at	0.016	7922	92975 at	0.096	3277	1448328 at	-0.061	7286	4955.25	3170.1469	FALSE	SH3-domain binding protein 2	209370 s at	0.203	3845	7.122E-05	FALSE
98328 at	0.053	6316	1428001 at	0.127	2807.5	98328 at	0.055	5591	1421999 at	0.107	5108	4955.625	1515.6935	TRUE	thyroid stimulating hormone receptor	210055 at	-0.072	14246	5.708E-02	FALSE
92596 at	0.066	6162	1452047 at	0.201	2628	92596 at	-0.036	6326	1452047 at	0.107	4708	4956	1713.9063	TRUE	calcyclin binding protein	211761 s at	-0.237	11276	1.934E-02	FALSE
162157 f at	0.068	5118	1426160 a at	0.042	6456	162157 f at	0.093	3552	1426160 a at	0.125	4701	4956.75	1198.9555	TRUE	serine/threonine kinase 16	209622 at	-0.086	17402	1.242E-01	FALSE
99015 at	0.106	3962	1448757 at	0.004	8328	99015 at	-0.020	7260	1456103 at	-0.398	282	4958	3629.1916	FALSE	promyelocytic leukemia	235508 at	0.246	4418	1.393E-04	FALSE
161695 f at	0.120	5436	1417150 at	0.099	4644	161695 f at	0.116	2213	1417150 at	-0.029	7543	4959	2201.8421	FALSE	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	207519 at	-0.016	39621	8.681E-01	FALSE
94415 at	0.098	4959	1440831 at	-0.025	7776	94415 at	0.049	5863	1449311 at	0.370	1239	4959.25	2744.1516	FALSE	BTB and CNC homology 1	204194 at	0.182	6831	1.367E-03	FALSE
101035 at	-0.017	8107	1437053 x at	0.169	692	101035 at	0.091	5168	1437053 x at	0.072	5872	4959.75	3108.8283	FALSE	apoptosis inhibitor 5	214959 s at	-0.272	3679	5.811E-05	FALSE
101589 at	-0.096	5012	1433507 a at	-0.197	3380.5	101589 at	-0.102	6361	1433507 a at	-0.125	5086	4959.875	1221.502	TRUE	high mobility group nucleosomal binding domain 2	231147 at	0.046	25715	3.945E-01	FALSE
162308 f at	-0.036	6782	1416455 a at	-0.471	54	93279 at	-0.064	5634	1434369 a at	-0.046	7372	4960.5	3349.6537	TRUE	crystallin, alpha B	209283 at	0.466	5603	4.819E-04	FALSE
93624 at	0.067	6269	1428776 at	0.098	4541	93624 at	0.185	660	1428776 at	-0.006	8374	4961	3267.7431	FALSE	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	NA	NA	NA	NA	
103405 at	0.048	6159	1428188 at	0.097	5046.5	103405 at	0.002	8389	1438591 at	0.722	251	4961.375	3434.0354	TRUE	RIKEN cDNA 2610019A05 gene	52169 at	0.141	4345	1.270E-04	TRUE
104674 s at	0.110	3406	1425824 a at	0.019	7832	104674 s at	0.107	2311	1425824 a at	-0.070	6297	4961.5	2547.421	FALSE	proprotein convertase subtilisin/kexin type 4	230901 x at	0.003	43320	9.675E-01	FALSE
94026 at	-0.038	6255	1433800 a at	-0.423	4229	94026 at	-0.067	5271	1433800 a at	-0.153	4094	4962.25	1009.6274	TRUE	pro-opiomelanocortin-alpha	205720 at	-0.034	34597	7.185E-01	FALSE
160700 i at	0.064	4979	1451898 a at	0.104	3757.5	160700 i at	0.128	5034	1451898 a at	-0.072	6079	4962.375	949.38255	FALSE	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	208100 x at	-0.078	20077	2.029E-01	FALSE
102328 at	0.097	3348	1424552 at	0.030	7078	102328 at	0.002	8427	1424552 at	-0.311	1002	4963.75	3404.4219	FALSE	caspase 8	213373 s at	0.038	30774	5.852E-01	FALSE
104105 at	-0.051	6332	1422759 a at	-0.047	6252	104105 at	0.089	3226	1422759 a at	0.110	4046	4964	1569.8977	FALSE	exportin 6	211982 x at	0.053	22877	2.972E-01	FALSE

103366 at	-0.096	2934	1436097 x at	0.119	4454	103366 at	0.053	5306	1436097 x at	0.052	7162	4964	1763.4406	FALSE	Rho GTPase activating protein 9	NA	NA	NA	NA	
160252 at	0.095	5502	1454626 at	-0.090	5575	160252 at	-0.047	6963	1439094 at	-0.218	1818	4964.5	2202.7317	FALSE	clathrin, heavy polypeptide (Hc)	200614 at	-0.309	5823	5.981E-04	FALSE
98063 at	0.178	2258	1424825 a at	0.056	5917	98063 at	-0.054	4872	1424825 a at	0.045	6821	4967	1973.7884	FALSE	glycosylation dependent cell adhesion molecule 1	NA	NA	NA	NA	
96221 at	0.152	1222	1448508 at	-0.049	6471	96221 at	0.027	7135	1448508 at	-0.160	5044	4968	2645.3223	FALSE	Traf3 interacting protein 2	215411 s at	0.253	9655	8.475E-03	FALSE
104082 at	-0.154	3411	1427992 a at	0.060	5708	104082 at	0.010	8148	1427992 a at	0.190	2607	4968.5	2493.8972	FALSE	RAB12, member RAS oncogene family	NA	NA	NA	NA	
160280 at	0.039	6274	1449145 a at	0.072	4190	97849 at	-0.037	6727	1449145 a at	-0.198	2686	4969.25	1880.8259	FALSE	caveolin, caveolae protein 1	212097 at	0.490	4404	1.367E-04	FALSE
100311 f at	0.123	2251	1421802 at	0.002	8455.5	100311 f at	0.086	3162	1421802 at	0.072	6009	4969.375	2821.9411	TRUE	eosinophil-associated, ribonuclease A family, member 1	NA	NA	NA	NA	
95363 at	-0.075	4961	1449501 a at	0.108	3496.5	95363 at	0.033	6628	1449501 a at	-0.099	4793	4969.625	1284.7277	FALSE	granzyme M (lymphocyte met-ase 1)	207460 at	0.019	38046	8.232E-01	FALSE
104115 at	0.021	7866	1426824 at	-0.084	3725	104115 at	0.060	6546	1445147 at	0.233	1742	4969.75	2759.2632	FALSE	proteasome (prosome, macropain) activator subunit 4	237180 at	0.219	6409	9.864E-04	FALSE
93322 at	-0.021	7500	1451148 at	-0.262	1220	93322 at	0.074	3611	1441937 s at	-0.054	7549	4970	3107.063	FALSE	PTEN induced putative kinase 1	209018 s at	-0.315	2293	6.645E-06	FALSE
96374 at	-0.032	7290	1449704 at	0.182	1588.5	96374 at	-0.064	4666	1420027 at	-0.073	6339	4970.875	2502.2334	FALSE	expressed sequence C80171	NA	NA	NA	NA	
94012 at	-0.027	7049	1417499 at	0.228	1172	94012 at	0.088	3622	1417499 at	0.021	8047	4972.5	3163.9666	FALSE	translocase of inner mitochondrial membrane 10 homolog (yeast)	218408 at	-0.155	12018	2.614E-02	FALSE
160446 at	0.066	4940	1423719 at	0.091	3902	160446 at	0.012	7885.5	1439423 x at	-0.154	3167	4973.625	2073.0349	FALSE	cDNA sequence U46068	226067 at	-0.014	36683	7.828E-01	FALSE
94763 at	0.008	8208	1450511 at	-0.028	7483	94763 at	-0.161	2468	1450511 at	-0.428	1736	4973.75	3342.5797	FALSE	muscle, skeletal, receptor tyrosine kinase	241122 s at	-0.067	14585	6.280E-02	FALSE
101433 at	0.143	1962	1421898 a at	0.012	8069	101433 at	0.148	2259	1421899 a at	-0.045	7605	4973.75	3313.8374	FALSE	major histocompatibility complex, class I-related	210528 at	0.049	18987	1.687E-01	FALSE
97737 f at	-0.113	2891	1433661 at	-0.047	6399	97737 f at	-0.009	8068	1433661 at	-0.174	2538	4974	2700.3979	TRUE	cDNA sequence BC034204	219680 at	0.138	5477	4.360E-04	FALSE
161332 f at	0.175	1980	1416802 a at	0.080	5269.5	161332 f at	0.057	5042	1448466 at	-0.066	7607	4974.625	2308.5831	FALSE	cell division cycle associated 5	224753 at	-0.016	36346	7.728E-01	FALSE
104121 at	-0.027	7071	1426873 s at	-0.033	6730	104121 at	-0.178	2612	1426873 s at	-0.204	3486	4974.75	2256.408	TRUE	junction plakoglobin	201015 s at	0.336	1641	1.926E-06	FALSE
99838 at	-0.093	4207	1450764 at	-0.039	6922.5	99838 at	-0.116	1717	1460156 at	0.041	7056	4975.625	2538.2214	FALSE	acyloxyacyl hydrolase	205639 at	-0.154	9033	5.932E-03	FALSE
95015 at	0.096	4213	1450455 s at	0.021	7627.5	95015 at	-0.052	6196	1422000 at	-0.180	1867	4975.875	2501.1266	FALSE	aldo-keto reductase family 1, member C12	NA	NA	NA	NA	
97080 at	0.125	4777	1443473 at	0.082	4576	97080 at	0.070	6375	1443473 at	-0.104	4177	4976.25	965.26382	FALSE	expressed sequence C79562	NA	NA	NA	NA	
104274 at	-0.009	8046	1435450 at	0.033	6607	104274 at	0.064	4692	1452814 at	-0.265	562	4976.75	3248.0307	FALSE	copine III	202118 s at	0.514	3630	5.510E-05	FALSE
98730 at	0.132	2203	1456239 at	0.029	7295.5	98730 at	0.073	4443	1456239 at	-0.070	5966	4976.875	2185.8481	FALSE	fibroblast growth factor 17	221376 at	-0.088	20234	2.081E-01	FALSE
98990 at	0.141	1435	1450622 at	0.050	6430	98990 at	-0.043	5458	1450622 at	-0.054	6586	4977.25	2413.6566	FALSE	breast cancer anti-estrogen resistance 1	223116 at	0.085	14068	5.371E-02	FALSE
161642 f at	0.072	4477	1449495 at	0.031	7350	161642 f at	0.162	784	1449495 at	-0.035	7299	4977.5	3101.2933	FALSE	regenerating islet-derived 3 alpha	231661 at	-0.009	40293	8.860E-01	FALSE
93405 at	0.084	3584	1427462 at	-0.044	5819	93405 at	-0.013	7646	1434564 at	0.154	2864	4978.25	2178.5115	FALSE	E2F transcription factor 3	203692 s at	-0.131	9036	5.945E-03	FALSE
160422 at	0.063	5079	1422482 at	0.035	6805	160422 at	-0.066	4355	1422482 at	0.154	3674	4978.25	1346.189	FALSE	RuvB-like protein 2	201459 at	-0.022	36579	7.800E-01	FALSE
160749 at	-0.178	2312	1424192 at	0.036	7465.5	160749 at	0.031	7279	1424192 at	0.159	2859	4978.875	2773.6841	FALSE	RIKEN cDNA 1500011H22 gene	204521 at	-0.519	2164	5.140E-06	FALSE
93165 at	0.015	7833	1460438 at	0.081	5046.5	93165 at	0.052	5574	1460438 at	0.228	1464	4979.375	2636.8619	TRUE	LysM, putative peptidoglycan-binding, domain containing 1	232283 at	-0.170	7029	1.610E-03	FALSE
94420 f at	-0.126	4139	1433733 a at	-0.045	6211	94420 f at	0.257	2051	1433733 a at	0.037	7519	4980	2397.7909	FALSE	cryptochrome 1 (photolyase-like)	209674 at	0.112	22209	2.751E-01	FALSE
95653 at	-0.061	5574	1423764 s at	0.011	8000	95653 at	0.089	3944	1423764 s at	0.187	2403	4980.25	2393.565	FALSE	mitochondrial ribosomal protein L37	222993 at	-0.142	13126	3.872E-02	FALSE
92619 at	0.093	3110	1449441 a at	-0.052	5969.5	92619 at	-0.025	6705	1449441 a at	-0.125	4147	4982.875	1647.7754	FALSE	WW domain binding protein 1	223072 s at	-0.024	32241	6.398E-01	FALSE
102171 r at	0.202	1738	1425392 a at	0.040	6687	102171 r at	-0.076	4738	1425392 a at	-0.053	6771	4983.5	2358.715	FALSE	nuclear receptor subfamily 1, group I, member 3	207007 at	-0.042	24390	3.500E-01	FALSE
102826 at	0.163	1491	1423556 at	-0.017	7966	161918 at	0.059	5459	1423556 at	-0.108	5022	4984.5	2665.8608	FALSE	aldo-keto reductase family 1, member B7	NA	NA	NA	NA	
160815 at	0.047	6428	1433963 a at	0.085	3845.5	160815 at	0.003	8366	1433963 a at	-0.351	1300	4984.875	3076.3125	FALSE	cDNA sequence BC032204	223303 at	0.104	17770	1.341E-01	FALSE
161084 at	0.004	8400	1427104 at	-0.180	4069	161084 at	0.085	6972	1456824 at	0.336	499	4985	3491.5921	FALSE	zinc finger protein 612	213934 s at	0.196	6875	1.431E-03	FALSE
98298 at	0.066	4832	1450502 at	0.008	8209	98298 at	-0.067	4866	1458188 at	0.216	2034	4985.25	2525.8759	FALSE	dihydropyrimidinase-like 2	200762 at	0.272	6188	8.185E-04	FALSE
95509 at	0.058	5845	1451228 a at	0.175	951.5	95509 at	0.051	6496	1451228 a at	0.050	6649	4985.375	2711.7484	TRUE	syncollin	229995 at	-0.020	36552	7.787E-01	FALSE
102275 at	0.137	2303	1420943 at	0.077	5797	102275 at	-0.010	7874	1420944 at	-0.300	3968	4985.5	2396.7392	FALSE	zinc finger protein 185	203585 at	0.000	44632	9.987E-01	FALSE
160372 at	-0.025	7444	1418644 a at	-0.096	2597.5	160372 at	0.135	2550	1418644 a at	-0.035	7353	4986.125	2785.8859	FALSE	serine/threonine kinase 11	231019 x at	-0.137	9566	8.034E-03	FALSE
101136 at	0.072	4188	1450272 at	0.054	5925	101136 at	-0.049	4793	1450272 at	-0.090	5039	4986.25	720.78262	FALSE	tumor necrosis factor (ligand) superfamily, member 8	235735 at	-0.084	14257	5.724E-02	FALSE
96348 at	0.068	4049	1428591 at	0.093	4361.5	96348 at	0.045	5712	1428143 a at	-0.066	5823	4986.375	912.06975	FALSE	patatin-like phospholipase domain containing 2	39854 r at	-0.093	12788	3.462E-02	FALSE
92855 at	-0.176	3555	1423799 at	-0.029	7770	92855 at	0.195	2975	1423798 a at	-0.080	5653	4988.25	2182.3082	FALSE	eukaryotic translation initiation factor 1	202021 x at	-0.049	29471	5.376E-01	FALSE
160932 at	-0.060	4664	1421487 a at	0.130	3087	160932 at	0.022	7061	1447271 at	0.096	5152	4991	1637.3725	FALSE	non-catalytic region of tyrosine kinase adaptor protein 1	233274 at	0.124	7366	2.080E-03	FALSE
161400 f at	-0.072	4656	1456438 x at	-0.054	6633	94237 at	0.093	5745	1456438 x at	0.166	2935	4992.25	1592.0673	FALSE	ribophorin I	201011 at	0.165	14945	6.994E-02	FALSE
93855 at	-0.034	7022	1450159 at	0.144	2994	93855 at	0.051	6088	1450159 at	0.155	3868	4993	1877.7195	FALSE	rad and gem related GTP binding protein 1	210300 at	-0.025	34825	7.263E-01	FALSE
104383 at	-0.130	4079	1448289 at	-0.069	6474	104383 at	-0.226	3175	1448289 at	0.085	6247	4993.75	1623.4115	FALSE	collapsin response mediator protein 1	202517 at	-0.280	2428	8.462E-06	FALSE
94417 at	-0.089	4862	1452446 a at	0.059	6802	94417 at	0.142	1498	1452446 a at	0.057	6815	4994.25	2504.9514	FALSE	RIKEN cDNA 2010008E23 gene	218419 s at	0.072	14139	5.509E-02	FALSE
94067 at	0.061	5106	1424080 at	0.079	5147	94067 at	-0.046	5117	1459135 at	0.180	4607	4994.25	258.74746	FALSE	decapping enzyme, scavenger	218774 at	0.032	29470	5.376E-01	FALSE
97312 at	0.254	1339	1416440 at	-0.124	4684	97312 at	-0.018	7678	1416440 at	-0.065	6283	4996	2727.666	FALSE	CD164 antigen	208405 s at	0.376	6235	8.607E-04	FALSE
93392 at	0.040	6655	1420658 at	0.089	4675.5	93392 at	-0.075	5779	1420657 at	0.174	2877	4996.625	1628.7265	FALSE	uncoupling protein 3 (mitochondrial, proton carrier)	219827 at	-0.057	25348	3.847E-01	FALSE
160562 at	-0.143	3480	1415816 at	0.101	4581.5	160562 at	-0.098	4214	1415816 at	0.026	7711	4996.625	1866.6203	FALSE	chaperonin subunit 7 (eta)	200812 at	-0.040	33149	6.703E-01	FALSE
96858 at	-0.107	5793	1418127 a at	0.134	1718	96858 at	0.075	5769	1418127 a at	0.058	6710	4997.5	2229.7839	FALSE	programmed cell death 8	205512 s at	-0.090	15031	7.151E-02	FALSE
104179 at	0.164	3307	1434312 at	-0.098	4330	104179 at	-0.062	7637	1434312 at	-0.190	4718	4998	1857.2763	FALSE	expressed sequence AI788669	NA	NA	NA	NA	
102831 s at	0.135	2832	1449858 at	0.085	3992.5	102831 s at	0.028	6491	1420404 at	-0.086	6677	4998.125	1893.029	FALSE	CD86 antigen	210895 s at	0.166	11463	2.076E-02	FALSE
97471 at	0.285	2300	1415719 s at	0.017	7964	97471 at	-0.068	5424	1430472 at	-0.134	4309	4999.25	2361.6767	FALSE	armadillo repeat containing 1	218185 s at	-0.166	21996	2.680E-01	FALSE
100333 at	0.307	1662	1449326 x at	0.012	8036.5	103465 f at	-0.037	6829	1449326 x at	-0.168	3472	4999.875	2946.3311	FALSE	serum amyloid A 2	208607 s at	-0.093	24138	3.422E-01	FALSE
100462 at	0.029	7152	1418822 a at	-0.150	3418	100462 at	-0.089	3395	1418823 at	0.071	6043	5002	1897.1633	FALSE	ADP-ribosylation factor 6	203312 x at	0.185	8579	4.567E-03	FALSE
104432 at	-0.041	6924	1422670 at	-0.199	1239.5	104432 at	-0.009	8279	1422670 at	-0.200	3568	5002.625	3196.1213	TRUE	Rho family GTPase 2	214393 at	0.199	6802	1.330E-03	FALSE
95100 at	0.005	8366	1435177 a at	0.119	2919	95100 at	0.051	5747	1453307 a at	0.188	2981	5003.25	2600.9514	TRUE	anaphase-promoting complex subunit 5	235926 at	0.338	4710	1.997E-04	TRUE
93295 at	0.084	4660	1417258 at	-0.015	8108.5	93295 at	0.080	4410	1417258 at	0.146	2837	5003.875	2221.4846	FALSE	chaperonin subunit 5 (epsilon)	208696 at	-0.123	17147	1.181E-01	FALSE
102586 at	0.048	6244	1451014 at	0.024	7758	102586 at	0.051	5970.5	1429313 at	-0.699	45	5004.375	3398.427	FALSE	receptor tyrosine kinase-like orphan receptor 1	231142 at	0.075	10922	1.650E-02	FALSE
161305 r at	0.081	4459	1450892 a at	-0.101	3917	161305 r at	0.076	4396	1442319 at	-0.047	7246	5004.5	1513.8055	FALSE	ubiquitin specific peptidase 4 (proto-oncogene)	202682 s at	0.179	10272	1.182E-02	FALSE
160673 at	-0.016	7559	1424803 at	0.153	1567.5	160673 at	-0.063	4502	1424804 at	0.082	6391	5004.875	2614.9141	FALSE	cDNA sequence BC020002	209672 s at	0.026	20383	2.126E-01	FALSE
96239 at	-0.123	3888	1418121 at	0.103	3360	96239 at	-0.039	5890	1418121 at	-0.050	6882	5005	1659.324	FALSE	vaccinia related kinase 3	218022 at	0.091	11843	2.427E-02	FALSE
99013 f at	0.027	7322	1423089 at	-0.091	5341.5	99013 f at	0.058	6095	1423088 at	-0.320	1263	5005.375	2625.0324	FALSE	tropomodulin 3	220800 s at	-0.040	18366	1.513E-01	FALSE
92454 at	-0.010	8004	1422899 at	0.221	1636.5	92454 at	-0.048	5071	1422899 at	-0.093	5310	5005.375	2610.1196	FALSE	solute carrier family 6 (neurotransmitter transporter), member 20	NA	NA	NA	NA	
101184 at	0.058	5280	1421671 at	0.174	945.5	101184 at	0.038	6495	1421671 at	0.043	7306	5006.625	2832.5404	TRUE	hydroxysteroid (17-beta) dehydrogenase 3	206985 at	0.165	11833	2.410E-02	TRUE
98802 at	0.050	5539	1419431 at	0.130	2318.5	161158 f at	0.056	4964	1419431 at	-0.044	7205	5006.625	2028.473	FALSE	epiregulin	205767 at	-0.016	29473	5.377E-01	FALSE
162413 r at	-0.128	2083	1417760 at	0.004	8386	162413 r at	0.132	1652	1417760 at	-0.022	7909	5007.5	3635.2462	FALSE	nuclear receptor subfamily 0, group B, member 1	206644 at	-0.027	26193	4.111E-01	FALSE
95883 at	0.037	7165	1452179 at	-0.039	6607	95883 at	-0.134	3943	1452180 at	0.183	2316	5007.75	2279.6592	FALSE	PHD finger protein 17	218517 at	0.266	2373	7.712E-06	FALSE
93433 s at	0.092	4250	1421944 a at	0.031	7456.5	161566 r at	-0.204	625	1421944 a at	0.024	7702	5008.375	3318.5359	FALSE	asialoglycoprotein receptor 1	206743 s at	-0.041	27473	4.605E-01	FALSE
101684 r at	0.597	597	1460311 at	0.052	6053	101684 r at	0.107	5024	1460311 at	-0.006	8360	5008.5	3255.0015	FALSE	simple repeat sequence-containing transcript	NA	NA	NA	NA	
98837 at	0.218	468	1448074 at	-0.036	7461	98837 at	0.011	7950	1448074 at	-0.111	4156	5008.75	3464.5863	FALSE	relaxin 1	211753 s at	0.063	18322	1.495E-01	FALSE
104286 at	0.041	6435	1448889 at	0.147	2802.5	104286 at	-0.046	5966	1448889 at	0.141	4833	5009.125	1617.5025	FALSE	solute carrier family 38, member 4	220786 s at	-0.008	37699	8.111E-01	FALSE
92406 at	0.031	7108	1419711 at	0.104	3939	92406 at	0.038	6090	1419711 at	0.156	2900	5009.25	1929.3473	TRUE	CD7 antigen	214551 s at	0.074	14008	5.240E-02	FALSE
98824 at	0.017	7629	1423104 at	-0.139	3445	98824 at	-0.030	6823	1423104 at	0.255	2140	5009.25	2635.163	FALSE	insulin receptor substrate 1	204686 at	-0.083	17785	1.345E-01	FALSE
94233 at	-0.033	6544	1416885 at	0.153	1097.5	94233 at	-0.071	4300	1416885 at	-0.015	8096	5009.375	3037.9986	FALSE	RIKEN cDNA 1110038F14 gene	218187 s at	0.265	5057	2.824E-04	FALSE
160674 at	0.107	4069	1459994 x at	0.184	1689.5	160674 at	0.012	7834	1459994 x at	0.074	6446	5009.625	2704.8273	TRUE	transferrin receptor 2	210215 at	-0.091	15133	7.329E-02	FALSE
94644 at	-0.049	5825	1421218 at	0.098	3387.5	94644 at	0.046	5387	1421218 at	0.083	5439	5009.625	1098.9238	FALSE	butyrylcholinesterase	205433 at	-0.049	34323	7.087E-01	FALSE
99142 at	-0.119	1730	1460674 at	-0.011	8116	99142 at	-0.070	4941	1460674 at	0.157	5256	5010.75	2612.2092	FALSE	progestin and adipoQ receptor family member VII	242123 at	0.134	5564	4.679E-04	FALSE
96871 at	-0.035	7097	1448543 at	0.057	5674	96871 at	0.335	146	1448543 at	0.056	7127	5011	3313.4396	FALSE	RIKEN cDNA 2310042G06 gene	222441 x at	-0.194	10161	1.098E-02	FALSE
100072 at	-0.062	5335	1450953 at	-0.024	7868	100072 at	-0.156	1370	1450953 at	0.098	5473	5011.5	2691.824	FALSE	WD repeat domain 39	203536 s at	-0.158	6477	1.029E-03	FALSE
92456 at	-0.119	2824	1423483 s at	0.044	7134.5	92456 at	-0.091	2581	1423483 s at	-0.041	7507	5011.625	2672.5229	FALSE	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, C	203937 s at	0.088	9489	7.747E-03	FALSE
93275 at	-0.070	3928	1416338 at	0.033	7423	93275 at	-0.097	3746	1416338 at	-0.101	4950	5011.75	1692.5894	FALSE	SH3-domain GRB2-like 1	201851 at	0.001	44408	9.946E-01	FALSE
98027 at	0.006	8237	1450673 at	0.192	605	98027 at	0.007	8208	1450673 at	0.217	3000	5012.5	3833.3985	TRUE	procollagen, type IX, alpha 2	213622 at	0.332	7676	2.620E-03	TRUE
101531 at	0.266	726	1451194 at	0.031	7044	101532 g at	0.060	4346	1451194 at	-0.021	7934	5012.5	3239.3651	FALSE	aldolase 2, B isoform	204704 s at	-0.032	15826	8.663E-02	FALSE
100041 at	-0.021	7911	1439410 x at	-0.068	6032	100041 at	0.261	672	1453111 a at	-0.114	5437	5013	3080.0878	FALSE	DNA segment, Chr 11, ERATO Doi 333, expressed	223649 s at	0.065	22772	2.937E-01	FALSE
102138 at	-0.059	5955	1447276 at	-0.012	8070	102138 at	-0.141	2718	1447276 at	-0.145	3310	5013.25	2476.5464	TRUE	DNA segment, Chr 13, ERATO Doi 37, expressed	NA	NA	NA	NA	
160234 at	0.069	6660	1451080 at	-0.119	2666	160234 at	-0.066	6526	1423674 at	0.145	4202	5013.5	1929.4133	FALSE	ubiquitin specific peptdiase 1	202413 s at	0.281	8406	4.149E-03	FALSE
96426 at	-0.080	5775	1415906 at	0.246	1073.5	96426 at	0.077	5585	1415906 at	-0.027	7624	5014.375	2783.5709	FALSE	thymosin, beta 4, X chromosome	NA	NA	NA	NA	
96162 at	0.068	4811	1427238 at	0.096	4263	96162 at	0.099	2819	1427238 at	0.011	8169	5015.5	2264.012	TRUE	F-box protein 15	231472 at	0.192	15750	8.512E-02	FALSE
104164 at	0.108	2655	1428690 at	-0.125	2021.5	104164 at	0.015	7761	1441856 x at	0.026	7625	5015.625	3102.8619	FALSE	trypsin domain containing 1	NA	NA	NA	NA	
160344 at	0.010	8048	1416901 at	-0.108	4210	160344 at	0.061	4766	1455768 at	-0.139	3039	5015.75	2145.8245	FALSE	Niemann Pick type C2	200701 at	0.523	2013	3.914E-06	FALSE
160418 at	0.008	8203	1436730 at	0.186	2098	160418 at	-0.034	6016	1436390 a at	-0.136	3746	5015.75	2663.6186	FALSE	chloride channel CLIC-like 1	230002 at	0.395	4359	1.290E-04	FALSE
101178 at	0.025	7504	1420696 at	-0.197	548	101178 at	-0.045	5614	1420696 at	0.081	6402	5017	3078.515	FALSE	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	236947 at	-0.027	26721	4.327E-01	FALSE
92693 at	-0.068	4732	1419078 at	0.056	6308.5	92693 at	-0.088	3755	1419078 at	-0.094	5273	5017.125	1065.7356	FALSE	ninein	225921 at	0.168	11679	2.259E-02	FALSE
93820 at	-0.068	6425	1416970 a at	0.284	1817	93820 at	0.086	4716	1416970 a at	0.045	7112	5017.5	2359.526	FALSE	cytochrome c oxidase, subunit VIIa 2	201597 at	-0.321	6227	8.553E-04	FALSE
104638 at	0.054	5441	1422375 a at	0.168	2062	104638 at	-0.037	6291	1451372 a at	-0.069	6276	5017.5	2009.9716	FALSE	ADP-ribosyltransferase 1	207919 at	0.094	16457	1.007E-01	FALSE
94076 i at	-0.043	5890	1418896 a at	-0.084	4918.5	94076 i at	-0.212	4064	1418896 a at	-0.103	5198	5017.625	755.60124	TRUE	ribophorin II	213491 x at	0.238	6954	1.530E-03	FALSE
96271 at	0.115	4722	1417222 a at	-0.045	6234.5	96271 at	0.109	5375	1448623 at	-0.192	3744	5018.875	1051.667	FALSE	transmembrane protein 123	211967 at	0.591	4069	9.278E-05	FALSE
93540 at	-0.084	5230	1448333 at	0.102	3623	93540 at	0.005	8335	1448333 at	0.131	2891	5019.75	2416.4419	FALSE	ADP-ribosylarginine hydrolase	228042 at	0.129	5988	6.853E-04	FALSE
92515 at	-0.002	8424	1450723 at	0.189	1309.5	92515 at	0.132	3953	1450723 at	0.093	6398	5021.125	3076.3828	FALSE	ISL1 transcription factor, LIM/homeodomain	206104 at	-0.079	22458	2.836E-01	FALSE
104617 at	0.021	7536	1434906 at	0.135	1578	104617 at	0.090	4144	1434906 at	-0.060	6828	5021.5	2721.1426	FALSE	RIKEN cDNA 0610005C13 gene	NA	NA	NA	NA	
94429 at	-0.035	6363	1418062 at	-0.179	738	94429 at	0.040	5822	1418062 at	-0.057	7164	5021.75	2908.5564	FALSE	eukaryotic translation elongation factor 1 alpha 2	204540 at	-1.011	1624	1.849E-06	FALSE
103910 at	0.005	8330	1448784 at	0.102	4655.5	103910 at	0.089	3057	1448784 at	0.109	4045	5021.875	2301.6617	TRUE	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NA	NA	NA	NA	
96930 at	-0.040	6373	1416010 a at	0.058	5086	96929 at	-0.134	1991	1416012 at	-0.080	6642	5023	2132.3425	FALSE	EH-domain containing 1	208112 x at	0.196	1748	2.422E-06	FALSE
102049 at	-0.018	7595	1417273 at	-0.099	5647	102049 at	0.156	1904	1417273 at	-0.184	4948	5023.5	2362.0856	FALSE	pyruvate dehydrogenase kinase, isoenzyme 4	225207 at	0.849	3510	4.708E-05	FALSE
92199 at	0.025	7056	1422103 a at	0.038	6541.5	92199 at	-0.113	3757	1422103 a at	-0.154	2740	5023.625	2101.886	FALSE	signal transducer and activator of transcription 5B	212549 at	0.106	13720	4.722E-02	FALSE
97120 at	0.062	5932	1457905 at	0.158	2416	97120 at	0.026	6772	1457905 at	-0.121	4975	5023.75	1887.1524	FALSE	DNA segment, Chr 7, ERATO Doi 59, expressed	NA	NA	NA	NA	
103429 i at	0.166	4089	1449076 x at	-0.059	5834.5	103429 i at	-0.320	2352	1449076 x at	0.096	7820	5023.875	2344.3788	FALSE	acireductone dioxygenase 1	222400 s at	0.038	32782	6.573E-01	FALSE
101583 at	-0.018	7605	1416250 at	-0.070	6243.5	101583 at	0.104	2366	1448272 at	-0.162	3883	5024.375	2346.3152	FALSE	B-cell translocation gene 2, anti-proliferative	201236 s at	0.276	9359	7.171E-03	FALSE
97151 at	0.115	2753	1422154 at	-0.158	3435	97151 at	-0.021	7317	1422154 at	0.052	6593	5024.5	2265.831	FALSE	G protein-coupled receptor 27	221306 at	-0.093	15173	7.404E-02	FALSE
97134 at	0.182	2053	1419782 at	0.139	2663	97134 at	-0.013	7954	1419782 at	0.035	7428	5024.5	3096.5183	FALSE	expressed sequence AA517864	NA	NA	NA	NA	
102953 at	0.057	5565	1460238 at	0.023	7655	102953 at	0.131	2475	1460238 at	-0.107	4412	5026.75	2166.93	FALSE	mesothelin	204885 s at	0.002	43514	9.729E-01	FALSE
96171 at	0.058	5240	1448446 at	0.065	5676.5	96171 at	0.109	3987	1448446 at	0.122	5205	5027.125	725.83359	TRUE	deformed epidermal autoregulatory factor 1 (Drosophila)	209407 s at	-0.460	1536	1.512E-06	FALSE
92830 s at	0.045	6393	1452519 a at	0.092	4356	92830 s at	0.048	5528	1452519 a at	-0.183	3834	5027.75	1153.3205	FALSE	zinc finger protein 36	201531 at	0.192	23889	3.343E-01	FALSE
160596 at	0.019	7600	1417739 at	0.106	4779	160596 at	-0.049	6221	1417739 at	0.258	1514	5028.5	2610.7872	FALSE	mediator of RNA polymerase II transcription, subunit 11 homolog (S. cerevisiae)	226958 s at	0.151	6246	8.710E-04	FALSE
103332 at	-0.053	6122	1426782 at	0.035	7431	103332 at	0.073	3802	1426782 at	-0.173	2761	5029	2130.2274	FALSE	G protein-coupled receptor 125	210473 s at	0.630	2234	5.893E-06	FALSE
96123 at	0.068	5373	1448550 at	-0.076	6495	96123 at	0.121	2218	1448550 at	-0.530	6040	5031.5	1931.4338	FALSE	lipopolysaccharide binding protein	211652 s at	0.036	33143	6.697E-01	FALSE
160103 at	0.079	6139	1436893 a at	0.071	6283.5	160103 at	0.067	6961	1440966 at	0.426	743	5031.625	2881.45	TRUE	membrane-associated ring finger (C3HC4) 7	202654 x at	-0.193	11386	2.010E-02	FALSE
97373 at	0.053	5504	1437459 x at	0.116	2950	97373 at	-0.031	6786	1437459 x at	-0.113	4890	5032.5	1597.3089	FALSE	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19	223222 at	0.029	29028	5.213E-01	FALSE
101608 at	0.088	3303	1458041 at	0.009	8166.5	101608 at	-0.019	7091	1458041 at	0.236	1572	5033.125	3110.4987	FALSE	expressed sequence C80360	NA	NA	NA	NA	
101964 at	-0.063	6243	1439443 x at	-0.123	4109	101964 at	0.057	6178	1451015 at	0.232	3605	5033.75	1374.5403	FALSE	transketolase	228205 at	0.086	14419	6.023E-02	FALSE
160354 at	0.042	6718	1451999 at	0.116	2053	160354 at	-0.001	8484	1416752 at	0.275	2880	5033.75	3069.4426	FALSE	LIM domain binding 3	216887 s at	0.058	27841	4.746E-01	FALSE
99505 at	-0.065	5366	1451643 a at	0.047	6275.5	99505 at	-0.042	6392	1451643 a at	0.197	2104	5034.375	2006.7062	FALSE	RAB4B, member RAS oncogene family	237257 at	-0.135	12522	3.156E-02	FALSE
101211 at	-0.020	7364	1447494 at	0.085	4285.5	101211 at	0.130	1221	1447494 at	0.046	7269	5034.875	2916.8101	FALSE	DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed	NA	NA	NA	NA	
93963 at	-0.014	7779	1436212 at	0.085	5076	93963 at	0.101	2513	1436212 at	-0.179	4773	5035.25	2157.1853	FALSE	transmembrane protein 71	238429 at	0.026	30804	5.865E-01	FALSE

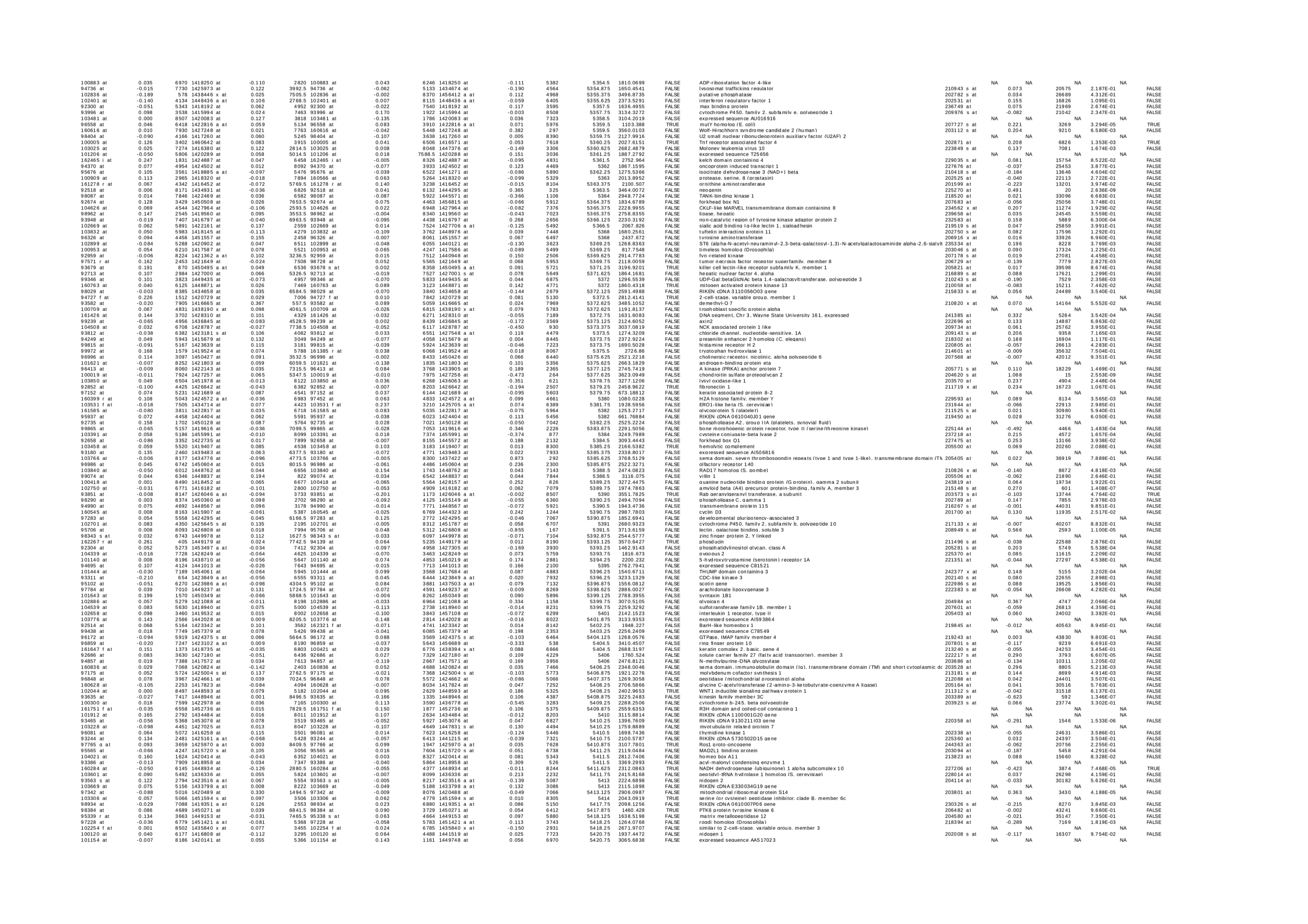
99033 at	0.073	3808	1426733 at	-0.091	3805.5	99033 at	-0.032	6368	1426733 at	-0.068	6160	5035.375	1421.2333	FALSE	inositol 1,3,4-triphosphate 5/6 kinase	210740 s at	0.174	4274	1.175E-04	FALSE
94152 at	0.227	890	1448168 a at	0.016	7848	94152 at	0.065	4098	1448168 a at	-0.040	7307	5035.75	3221.4875	FALSE	salivary protein 1	NA	NA	NA	NA	
99058 at	-0.017	7800	1450781 at	0.105	4515	99058 at	0.098	3533	1422851 at	-0.101	4297	5036.25	1889.9971	FALSE	high mobility group AT-hook 2	208025 s at	0.081	19639	1.886E-01	FALSE
95590 at	0.098	4676	1424160 at	0.045	6681	95590 at	0.173	1558	1424160 at	0.042	7231	5036.5	2565.8094	TRUE	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	222556 at	-0.059	24266	3.460E-01	FALSE
103538 at	0.006	8236	1439567 at	0.150	1694	103538 at	0.039	6186	1444594 at	0.139	4031	5036.75	2813.1528	TRUE	T-box 3	219682 s at	0.158	4003	8.624E-05	TRUE
100882 at	0.117	4086	1419492 s at	0.096	3020.5	100882 at	-0.037	6372	1419492 s at	-0.085	6669	5036.875	1771.6586	FALSE	defensin beta 1	NA	NA	NA	NA	
101302 at	0.070	4524	1421538 at	-0.005	8329	101302 at	-0.114	3160	1446556 at	-0.118	4135	5037	2268.4184	FALSE	potassium voltage-gated channel, Shal-related family, member 1	206842 at	0.170	6165	8.018E-04	FALSE
98130 at	-0.040	6133	1455640 a at	0.066	3790	98130 at	-0.020	7000	1455640 a at	-0.147	3227	5037.5	1815.2771	FALSE	thioredoxin 2	209077 at	0.056	20817	2.274E-01	FALSE
160892 at	-0.098	3439	1416918 at	0.126	1972	160892 at	0.017	7689	1416918 at	0.059	7051	5037.75	2771.1085	FALSE	discs, large homolog 3 (Drosophila)	212727 at	-0.307	3419	4.145E-05	FALSE
95019 at	0.070	4612	1418186 at	0.080	4670	95019 at	0.113	2588	1418186 at	-0.020	8281	5037.75	2368.9976	FALSE	glutathione S-transferase, theta 1	232193 at	0.009	42425	9.446E-01	FALSE
102556 at	-0.042	5885	1423022 at	0.015	7819	102556 at	0.115	3430	1433600 at	0.210	3021	5038.75	2243.9044	FALSE	adrenergic receptor, alpha 2a	209869 at	0.034	29617	5.429E-01	FALSE
94252 at	0.165	1950	1423744 x at	-0.090	5625	94252 at	0.113	4370	1423744 x at	0.027	8215	5040	2608.9493	FALSE	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	224935 at	-0.291	8372	4.092E-03	FALSE
99912 at	0.067	4848	1422116 at	0.049	6723	99912 at	0.012	7976	1422116 at	0.342	618	5041.25	3216.8062	TRUE	AF4/FMR2 family, member 2	210957 s at	0.119	11016	1.734E-02	TRUE
100738 at	0.022	7579	1426149 at	0.069	4693.5	100738 at	-0.019	7259	1426149 at	0.299	634	5041.375	3209.5365	FALSE	serine protease inhibitor 15	NA	NA	NA	NA	
103645 at	0.148	3199	1449223 at	0.088	3547.5	103645 at	0.046	6029	1449223 at	0.039	7391	5041.625	2010.1533	TRUE	DnaJ (Hsp40) homolog, subfamily B, member 8	237284 at	-0.016	37940	8.202E-01	FALSE
162164 f at	0.082	5305	1418677 at	0.107	3010	100879 at	0.067	4682	1418677 at	0.042	7170	5041.75	1718.1557	TRUE	actinin alpha 3	206891 at	-0.033	31401	6.094E-01	FALSE
92921 at	0.062	4769	1422253 at	0.076	4826	92921 at	0.012	7671	1422253 at	0.208	2903	5042.25	1967.0745	TRUE	procollagen, type X, alpha 1	205941 s at	-0.054	22497	2.846E-01	FALSE
96423 at	0.082	4303	1420555 at	0.064	5618.5	96423 at	-0.032	6712	1420555 at	0.135	3536	5042.375	1406.5808	FALSE	aristaless 3	228944 at	0.192	4043	8.976E-05	FALSE
96525 at	-0.012	8021	1448731 at	0.072	5464	96525 at	0.048	6248	1448731 at	-0.474	439	5043	3250.3623	FALSE	interleukin 10 receptor, alpha	204912 at	0.134	11283	1.938E-02	FALSE
92832 at	0.116	3016	1450446 a at	0.024	7325	92832 at	-0.017	7537	1450446 a at	-0.174	2294	5043	2774.4843	FALSE	suppressor of cytokine signaling 1	210000 s at	-0.008	39722	8.703E-01	FALSE
93448 at	-0.139	1594	1451970 at	-0.006	8302	93448 at	0.056	4672	1451970 at	-0.124	5605	5043.25	2767.0783	FALSE	RIKEN cDNA E330036I19 gene	225832 s at	-0.187	7556	2.409E-03	FALSE
160922 at	-0.160	1763	1429238 a at	0.044	6406	160922 at	0.012	8093	1429238 a at	0.137	3911	5043.25	2780.8927	FALSE	2-oxoglutarate and iron-dependent oxygenase domain containing 2	219245 s at	0.079	17553	1.280E-01	FALSE
96793 at	-0.089	4220	1417742 a at	0.089	3830.5	96793 at	0.041	5494	1417742 a at	0.087	6636	5045.125	1276.5209	FALSE	DNA methyltransferase 1-associated protein 1	224163 s at	-0.054	28702	5.094E-01	FALSE
95772 r at	-0.026	7145	1419301 at	0.049	6720	95772 r at	0.087	3551	1449416 at	-0.190	2765	5045.25	2209.5294	FALSE	frizzled homolog 4 (Drosophila)	218665 at	0.086	16347	9.843E-02	FALSE
93190 at	0.070	4597	1437970 at	0.056	6368.5	93190 at	0.074	4207	1447646 at	0.151	5009	5045.375	940.90306	TRUE	cDNA sequence BC053401	218460 at	0.248	2494	9.530E-06	TRUE
101815 at	0.057	5981	1421763 at	0.129	4243.5	101815 at	0.045	5724	1421763 at	0.164	4234	5045.625	937.59598	TRUE	bone morphogenetic protein 10	208292 at	-0.031	32625	6.514E-01	FALSE
99890 at	0.100	4009	1450413 at	-0.078	3854.5	99890 at	-0.030	7057	1450413 at	-0.108	5265	5046.375	1481.792	FALSE	platelet derived growth factor, B polypeptide	216061 x at	0.090	18336	1.501E-01	FALSE
101612 at	0.161	3040	1460264 at	0.017	7862	101612 at	-0.132	1729	1460264 at	-0.033	7555	5046.5	3122.577	FALSE	large tumor suppressor	219813 at	-0.007	39278	8.594E-01	FALSE
99151 at	0.036	6381	1448365 at	0.146	1505.5	99151 at	0.031	6654	1448365 at	0.094	5648	5047.125	2398.9879	TRUE	exosome component 7	213648 at	0.078	13168	3.939E-02	TRUE
102266 at	-0.081	3995	1422728 at	0.120	3014.5	102266 at	-0.011	7755	1422728 at	-0.110	5427	5047.875	2058.7554	FALSE	inhibin alpha	210141 s at	-0.173	9505	7.790E-03	FALSE
97094 at	0.003	8343	1425164 a at	-0.097	4528.5	97094 at	-0.135	2013	1422315 x at	-0.081	5311	5048.875	2608.1472	FALSE	phosphorylase kinase gamma 1	207312 at	0.251	3817	6.820E-05	FALSE
100745 r at	-0.058	5223	1459892 at	0.053	6193.5	100745 r at	0.115	1644	1459892 at	-0.039	7136	5049.125	2400.677	FALSE	expressed sequence AA408156	NA	NA	NA	NA	
99848 at	0.003	8377	1425376 at	0.142	2893.5	99848 at	-0.059	5986	1425376 at	-0.314	2943	5049.875	2647.9531	FALSE	arachidonate 8-lipoxygenase	206714 at	-0.004	43235	9.658E-01	FALSE
161887 r at	0.081	4691	1448537 at	0.058	6006	96921 at	0.076	3178	1448537 at	-0.083	6325	5050	1434.4367	FALSE	tetratricopeptide repeat domain 1	201434 at	-0.022	32800	6.580E-01	FALSE
95611 at	-0.364	117	1415904 at	0.014	8316	95611 at	-0.085	6458	1415904 at	-0.152	5316	5051.75	3514.4678	FALSE	lipoprotein lipase	203548 s at	-1.521	100	6.967E-09	FALSE
92279 at	0.013	7804	1460583 at	0.115	2011	92279 at	0.012	7749	1449859 at	0.208	2645	5052.25	3156.4032	TRUE	golgi transport 1 homolog B (S. cerevisiae)	222552 at	-0.135	18290	1.487E-01	FALSE
93198 at	0.033	7219	1418806 at	0.123	3226	93198 at	-0.007	8080	1418806 at	-0.200	1686	5052.75	3083.7695	FALSE	colony stimulating factor 3 receptor (granulocyte)	203591 s at	0.073	19838	1.956E-01	FALSE
95516 at	-0.161	3197	1448391 at	0.168	3802	95516 at	-0.125	4973	1448391 at	-0.010	8239	5052.75	2248.4612	FALSE	RAB9, member RAS oncogene family	221808 at	0.027	37825	8.157E-01	FALSE
100632 at	-0.071	4203	1417690 at	0.060	5712.5	100632 at	0.093	2723	1457803 at	-0.034	7578	5054.125	2078.6181	FALSE	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	201805 at	-0.072	16434	1.003E-01	FALSE
160832 at	-0.106	2452	1421821 at	-0.122	3812.5	160832 at	-0.040	6441	1459403 at	-0.032	7512	5054.375	2329.3246	TRUE	low density lipoprotein receptor	202068 s at	0.497	3726	6.129E-05	FALSE
162268 at	0.067	5674	1419141 at	0.136	2553	104171 f at	-0.036	6938	1419141 at	0.081	5054	5054.75	1842.9012	FALSE	crystallin, gamma D	NA	NA	NA	NA	
98054 at	-0.038	6976	1448613 at	0.051	5637.5	98054 at	0.138	1952	1448613 at	0.117	5654	5054.875	2161.5548	FALSE	extracellular matrix protein 1	209365 s at	0.058	23677	3.265E-01	FALSE
101917 at	0.025	7060	1420691 at	0.048	6447.5	101917 at	0.140	1544	1420691 at	-0.108	5168	5054.875	2469.7484	FALSE	interleukin 2 receptor, alpha chain	206341 at	0.036	25229	3.806E-01	FALSE
96001 at	0.141	2098	1460395 at	0.035	7041	96001 at	-0.018	7468	1442799 x at	0.141	3613	5055	2619.795	FALSE	NudC domain containing 3	201269 s at	-0.143	4524	1.608E-04	FALSE
102944 at	0.111	2758	1422801 at	-0.050	6110.5	102944 at	-0.029	6428	1455060 at	-0.096	4928	5056.125	1662.4823	FALSE	Ras-GTPase-activating protein SH3-domain binding protein	201503 at	0.360	6499	1.043E-03	FALSE
103959 at	0.078	3852	1455175 at	0.045	5887	103959 at	0.150	2748	1455175 at	0.024	7739	5056.5	2210.9974	TRUE	PHD finger protein 13	225005 at	0.096	13601	4.552E-02	TRUE
101555 at	-0.065	5622	1423734 at	-0.238	789.5	101555 at	-0.017	7551	1423734 at	-0.069	6269	5057.875	2956.3355	TRUE	RAS-related C3 botulinum substrate 1	208641 s at	0.165	10314	1.208E-02	FALSE
92476 at	0.201	2233	1449288 at	0.011	8211.5	161144 r at	0.115	4371	1460057 at	0.099	5416	5057.875	2484.9762	TRUE	growth differentiation factor 3	220053 at	-0.015	37717	8.117E-01	FALSE
101459 at	0.058	6191	1450077 at	0.090	3233	101459 at	0.076	5196	1450077 at	0.101	5613	5058.25	1283.4047	TRUE	chromodomain helicase DNA binding protein 1	235791 x at	0.213	6641	1.174E-03	TRUE
160397 at	0.075	6275	1451113 a at	0.105	4164	160397 at	0.181	4823	1435988 x at	-0.086	4973	5058.75	883.69919	FALSE	IK cytokine	200066 at	0.194	14087	5.404E-02	FALSE
99011 at	0.030	6906	1417588 at	0.089	3509	99011 at	0.082	3040	1417588 at	0.072	6782	5059.25	2070.3461	TRUE	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	203397 s at	0.247	7320	2.029E-03	TRUE
95054 at	-0.125	3042	1460323 at	0.041	7148	95054 at	0.083	4765	1460323 at	0.097	5285	5060	1690.1398	FALSE	threonyl-tRNA synthetase	240206 at	0.069	15558	8.106E-02	FALSE
94198 at	0.206	431	1425703 at	0.036	7458	94198 at	-0.009	8013	1425703 at	-0.123	4339	5060.25	3484.1591	FALSE	peroxisome proliferator activator receptor delta	37152 at	0.057	18104	1.433E-01	FALSE
92737 at	0.003	8394	1421174 at	-0.046	6158.5	92737 at	-0.172	526	1421173 at	0.098	5163	5060.375	3311.0936	FALSE	interferon regulatory factor 4	204562 at	0.045	28167	4.875E-01	FALSE
102638 at	-0.058	6513	1419202 at	0.030	7575	102638 at	0.080	2897	1419202 at	-0.255	3262	5061.75	2334.3661	FALSE	cystatin F (leukocystatin)	210140 at	0.036	28109	4.851E-01	FALSE
98860 at	0.001	8485	1421500 at	0.160	2246.5	98860 at	-0.104	2662	1421500 at	0.063	6854	5061.875	3088.4318	FALSE	steroid sulfatase	NA	NA	NA	NA	
104496 i at	0.109	3648	1449463 at	0.088	3958.5	104497 f at	0.090	4162	1449463 at	0.002	8482	5062.625	2289.3599	TRUE	kallikrein 1-related peptidase b8	NA	NA	NA	NA	
160294 at	-0.009	8110	1448726 at	-0.064	5035	160294 at	-0.031	6187	1448726 at	-0.254	919	5062.75	3039.7974	TRUE	small nuclear RNA activating complex, polypeptide 2	204104 at	-0.170	10605	1.403E-02	TRUE
96208 at	0.027	7398	1434009 at	-0.134	1956	96208 at	0.067	5744	1440675 at	-0.104	5154	5063	2278.7216	FALSE	glucocorticoid receptor DNA binding factor 1	229394 s at	0.193	12202	2.798E-02	FALSE
104434 at	-0.065	4404	1460733 at	-0.051	6185	104434 at	0.056	4671	1460733 at	-0.096	5000	5065	785.44722	FALSE	expressed sequence AA407659	202365 at	0.446	2553	1.047E-05	FALSE
99595 at	0.101	3036	1460561 x at	0.053	7120	99595 at	-0.144	2278	1416521 at	0.038	7829	5065.75	2813.4752	FALSE	selenoprotein W, muscle 1	201194 at	-0.025	36786	7.857E-01	FALSE
95760 at	-0.024	7515	1423820 at	0.126	2738.5	95760 at	0.047	4939	1423820 at	0.118	5074	5066.625	1952.0117	FALSE	elongation factor 1 homolog (ELF1, S. cerevisiae)	225156 at	0.139	6025	7.083E-04	FALSE
103459 at	-0.007	8304	1424674 at	0.079	6339	103459 at	0.147	4000	1424674 at	0.318	1625	5067	2891.4821	FALSE	solute carrier family 39 (metal ion transporter), member 6	202088 at	0.141	22584	2.876E-01	FALSE
162458 i at	0.054	6484	1455985 x at	0.215	341	162458 i at	0.027	7007	1455084 x at	0.090	6437	5067.25	3161.4061	TRUE	serine hydroxymethyl transferase 2 (mitochondrial)	214096 s at	0.131	10694	1.468E-02	TRUE
98448 at	0.129	3107	1416736 at	0.017	7774	98448 at	0.099	3842	1441274 at	-0.181	5547	5067.5	2073.6822	FALSE	cancer susceptibility candidate 3	207842 s at	0.531	128	1.152E-08	FALSE
103063 at	-0.100	5555	1425495 at	0.083	4269	103063 at	-0.150	4650	1425495 at	-0.125	5798	5068	726.45119	FALSE	zinc finger protein 62	227796 at	0.231	7409	2.146E-03	FALSE
101905 at	0.122	2038	1415769 at	0.004	8351	101905 at	0.035	5972	1459332 at	0.459	3915	5069	2714.5049	TRUE	itchy	242182 x at	0.128	8332	4.028E-03	TRUE
160074 at	0.015	7620	1426215 at	0.094	5482.5	160074 at	0.174	2136	1426215 at	0.199	5040	5069.625	2256.9826	TRUE	dopa decarboxylase	205311 at	-0.327	2873	1.792E-05	FALSE
102960 at	-0.063	5309	1448948 at	0.016	7879	102960 at	-0.115	3714	1448948 at	-0.121	3380	5070.5	2052.8384	FALSE	recombination activating gene 1 activating protein 1	219125 s at	0.032	33270	6.741E-01	FALSE
160494 at	-0.035	6471	1438317 a at	0.147	858.5	160494 at	0.003	8365	1421097 at	0.101	4588	5070.625	3203.5855	FALSE	endonuclease G	204824 at	0.011	41313	9.156E-01	FALSE
93097 at	0.163	2271	1419549 at	-0.054	5361	93097 at	0.023	6885	1419549 at	-0.078	5770	5071.75	1975.1198	FALSE	arginase 1, liver	231665 at	0.035	22347	2.802E-01	FALSE
101825 at	-0.019	7563	1422961 at	0.133	2593.5	101825 at	-0.068	4293	1422961 at	0.072	5845	5073.625	2125.4335	FALSE	N-acetyltransferase 3	NA	NA	NA	NA	
102799 at	-0.053	5675	1418037 at	0.127	3259	102799 at	0.072	4154	1418037 at	-0.052	7210	5074.5	1738.2291	FALSE	complement component 4 binding protein	NA	NA	NA	NA	
94987 at	0.184	1455	1450612 a at	0.017	7878	161893 i at	-0.084	4278	1450612 a at	-0.051	6690	5075.25	2840.4602	FALSE	phosphatidylethanolamine N-methyltransferase	207621 s at	-0.038	28204	4.893E-01	FALSE
104022 at	0.001	8468	1429080 at	0.184	1378	104022 at	-0.022	7221	1431388 at	0.218	3235	5075.5	3325.2154	FALSE	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	212885 at	0.048	23386	3.160E-01	FALSE
97098 at	-0.072	4521	1428780 at	0.110	2531.5	97098 at	0.042	6100	1428780 at	-0.090	7154	5076.625	2012.3919	FALSE	threonine aldolase 1	NA	NA	NA	NA	
103002 at	0.080	3644	1418014 a at	0.038	6903	103002 at	0.008	8044	1458773 at	-0.241	1718	5077.25	2913.9741	FALSE	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	201883 s at	0.126	11670	2.249E-02	FALSE
95352 at	-0.008	8054	1459932 at	0.071	5729	95352 at	0.113	1682	1459932 at	0.090	4851	5079	2637.2156	FALSE	DNA segment, Chr 8, ERATO Doi 28, expressed	NA	NA	NA	NA	
94187 at	0.129	3653	1421412 at	0.064	5259.5	94187 at	-0.097	3151	1421412 at	-0.013	8253	5079.125	2299.0952	FALSE	goosecoid	NA	NA	NA	NA	
97092 at	0.062	6032	1419629 at	0.106	3148	97092 at	-0.095	2625	1419629 at	0.001	8513	5079.5	2735.656	FALSE	mesoderm posterior 2	NA	NA	NA	NA	
99323 at	0.122	3516	1421623 at	0.093	4628	99323 at	0.013	7896	1421623 at	0.190	4281	5080.25	1933.7922	TRUE	interleukin 12 receptor, beta 2	206999 at	0.006	41000	9.073E-01	FALSE
104537 at	0.044	6481	1424505 at	0.040	6561.5	104537 at	-0.027	6831	1440281 at	0.641	448	5080.375	3091.8747	FALSE	RIKEN cDNA 0610042C05 gene	220329 s at	-0.033	25846	3.988E-01	FALSE
97159 at	0.122	2118	1419241 a at	0.053	6893	97159 at	0.084	4601	1419241 a at	-0.064	6712	5081	2232.5825	FALSE	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	208090 s at	0.004	42743	9.532E-01	FALSE
104270 at	0.081	4877	1451992 at	-0.195	3753.5	104270 at	-0.055	6031	1451992 at	0.105	5673	5083.625	1009.4237	FALSE	adrenergic receptor kinase, beta 1	201401 s at	-0.229	7463	2.228E-03	FALSE
102872 f at	0.196	1671	1424706 at	0.075	5023.5	102872 f at	0.048	6025	1424706 at	-0.054	7617	5084.125	2513.5499	FALSE	zinc finger protein 51	NA	NA	NA	NA	
94550 at	0.070	5673	1416260 a at	0.092	4889	94550 at	-0.168	1450	1416260 a at	-0.009	8326	5084.5	2834.3997	FALSE	sorting nexin 1	213364 s at	0.184	11824	2.405E-02	FALSE
94132 at	0.110	4098	1460671 at	-0.074	6204	94132 at	0.080	4675	1460671 at	-0.104	5363	5085	907.69194	FALSE	glutathione peroxidase 1	200736 s at	0.380	6389	9.712E-04	FALSE
161241 at	0.037	7103	1438095 x at	0.069	5005	97414 at	-0.064	3994	1443794 x at	-0.199	4239	5085.25	1412.4117	FALSE	Nucleolar complex associated 4 homolog (S. cerevisiae)	218860 at	0.035	27905	4.767E-01	FALSE
96515 at	0.202	602	1419192 at	0.062	5878.5	96515 at	-0.069	5525	1419192 at	0.009	8337	5085.625	3240.1663	FALSE	interleukin 4 induced 1	214935 at	-0.047	30884	5.899E-01	FALSE
161257 r at	0.180	3639	1455955 s at	0.081	4537	161257 r at	-0.060	6003	1455955 s at	0.078	6164	5085.75	1210.81	FALSE	sorting nexin 17	200991 s at	-0.023	34818	7.260E-01	FALSE
96619 at	-0.014	8037	1426747 at	0.090	2771.5	96619 at	-0.030	6523	1452177 at	-0.183	3017	5087.125	2608.3862	FALSE	ATP-binding cassette, sub-family F (GCN20), member 3	202394 s at	0.007	41031	9.084E-01	FALSE
94162 at	-0.008	8253	1427242 at	0.025	7460	94162 at	-0.102	4032	1427242 at	-0.521	606	5087.75	3504.6193	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	221630 s at	-0.010	38111	8.255E-01	FALSE
96321 at	-0.110	5535	1416663 at	0.167	2055	96321 at	0.068	6192	1416663 at	0.065	6570	5088	2066.7235	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	242620 at	-0.158	6097	7.608E-04	FALSE
98773 s at	-0.056	5924	1427381 at	0.144	3158	98774 at	-0.054	4753	1427381 at	-0.084	6517	5088	1480.7725	FALSE	immunoresponsive gene 1	NA	NA	NA	NA	
103887 at	0.111	2435	1448756 at	0.097	4119.5	103887 at	0.035	6410.5	1448756 at	-0.069	7390	5088.75	2237.9015	FALSE	S100 calcium binding protein A9 (calgranulin B)	203535 at	0.130	19389	1.808E-01	FALSE
103701 at	-0.021	7298	1427031 s at	0.050	6030	161266 r at	0.169	460	1427031 s at	-0.055	6569	5089.25	3129.6008	FALSE	coiled-coil domain containing 52	234995 at	0.200	8827	5.275E-03	FALSE
98977 at	0.115	2406	1451163 at	0.013	8202	162444 r at	0.120	4483	1451163 at	0.128	5266	5089.25	2400.5432	TRUE	Terf1 (TRF1)-interacting nuclear factor 2	224809 x at	0.104	11095	1.792E-02	TRUE
96783 at	0.031	6945	1426014 a at	0.079	4083	96783 at	0.030	7216	1426014 a at	0.185	2116	5090	2437.1859	TRUE	mucin and cadherin like	NA	NA	NA	NA	
95876 at	0.064	5506	1450162 at	0.129	3577	95876 at	0.004	8244	1442686 at	0.199	3034	5090.25	2354.9294	TRUE	D4, zinc and double PHD fingers, family 3	NA	NA	NA	NA	
93846 at	-0.036	6535	1422310 at	0.061	5528	93846 at	-0.081	4865	1452789 at	-0.312	3436	5091	1299.5135	FALSE	stannin	218033 s at	-0.660	185	1.800E-08	FALSE
98980 at	0.082	4516	1425736 at	0.098	3896	98980 at	-0.070	5019	1419206 at	-0.078	6933	5091	1311.0807	FALSE	CD37 antigen	204192 at	0.165	15128	7.320E-02	FALSE
161018 at	-0.041	6254	1439962 at	0.221	1093.5	161018 at	0.072	5551	1439962 at	0.040	7470	5092.125	2781.1156	FALSE	RIKEN cDNA 2310010J17 gene	NA	NA	NA	NA	
160242 at	0.072	5446	1438167 x at	0.076	5317	160242 at	0.050	6295	1438167 x at	0.156	3314	5093	1262.8579	TRUE	folliculin	235250 at	-0.101	14940	6.981E-02	FALSE
93324 at	0.049	6681	1450644 at	-0.123	3967	93324 at	0.073	5877	1450644 at	-0.203	3848	5093.25	1408.8176	FALSE	zinc finger protein 36, C3H type-like 1	211962 s at	0.773	3012	2.248E-05	FALSE
161972 r at	0.076	5321	1416464 at	0.079	4714	161972 r at	0.215	2833	1431743 a at	0.038	7505	5093.25	1925.3544	TRUE	solute carrier family 4 (anion exchanger), member 1	205592 at	0.013	40251	8.846E-01	FALSE
99490 at	0.038	7040	1423971 at	0.082	4523.5	99490 at	-0.074	4659	1423970 at	0.139	4155	5094.375	1314.4494	FALSE	THO complex 3	224623 at	-0.380	7126	1.756E-03	FALSE
104754 at	-0.084	4680	1448778 at	-0.079	4058	102093 f at	-0.057	5081	1448778 at	0.052	6559	5094.5	1063.1847	FALSE	splicing factor, arginine/serine-rich 4 (SRp75)	NA	NA	NA	NA	
100736 at	0.100	3649	1421761 a at	-0.002	8475	100736 at	0.122	2582	1421761 a at	0.112	5674	5095	2592.6644	FALSE	BarH-like homeobox 2	210419 at	0.048	27417	4.586E-01	FALSE
101791 f at	0.078	5134	1450614 x at	0.080	4183.5	101791 f at	-0.100	2933	1450614 x at	0.017	8130	5095.125	2214.9358	FALSE	interferon alpha family, gene 5	NA	NA	NA	NA	
160211 at	0.023	7173	1451284 at	-0.095	5077.5	160211 at	-0.152	674	1444012 at	-0.081	7457	5095.375	3132.7663	FALSE	Yip1 domain family, member 3	216338 s at	-0.087	17962	1.395E-01	FALSE
92295 at	-0.057	5182	1419717 at	-0.024	7770	92295 at	-0.124	1655	1425906 a at	0.137	5777	5096	2547.0188	FALSE	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	206941 x at	0.002	43189	9.651E-01	FALSE
160156 at	0.061	6954	1423829 at	0.047	6433	160156 at	-0.081	6486	1440461 at	1.014	512	5096.25	3065.1204	FALSE	RIKEN cDNA 0910001A06 gene	217916 s at	-0.198	5388	3.950E-04	FALSE
92399 at	0.048	6450	1452530 a at	0.130	2011	92399 at	-0.025	6640	1422864 at	-0.091	5286	5096.75	2142.4732	FALSE	runt related transcription factor 1	NA	NA	NA	NA	
98496 at	0.090	3108	1450196 s at	-0.132	2778	98496 at	-0.020	7183.5	1450196 s at	0.037	7322	5097.875	2492.5212	FALSE	glycogen synthase 1, muscle	201673 s at	0.231	4215	1.105E-04	FALSE
94171 at	0.037	6925	1449829 at	0.061	5150.5	94171 at	-0.137	3413	1449829 at	0.111	4903	5097.875	1439.6684	FALSE	integrin beta 2-like	NA	NA	NA	NA	
101053 at	0.055	5612	1454789 x at	0.219	1210	101053 at	-0.032	7372	1424036 at	0.057	6198	5098	2693.3137	FALSE	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	208880 s at	0.109	14506	6.145E-02	FALSE
96881 at	-0.013	8188	1435863 at	0.045	7278	96881 at	0.200	839	1435863 at	0.175	4090	5098.75	3339.4432	FALSE	COMM domain containing 6	225312 at	0.092	26274	4.147E-01	FALSE
94734 at	0.071	5258	1420438 at	0.102	3025	94734 at	-0.019	7018	1420438 at	0.114	5097	5099.5	1633.9442	FALSE	orosomucoid 2	205040 at	-0.070	21217	2.405E-01	FALSE
101413 at	0.144	1633	1452718 at	-0.016	8175	101413 at	0.078	5693	1444327 at	-0.125	4899	5100	2699.862	FALSE	E3 ubiquitin protein ligase, HECT domain containing, 1	232264 at	0.213	10514	1.334E-02	FALSE
99945 at	0.048	6880	1450570 a at	0.132	3110	99945 at	-0.076	3950	1450570 a at	0.071	6461	5100.25	1853.2243	FALSE	CD19 antigen	206398 s at	0.087	17840	1.365E-01	FALSE
97923 at	-0.026	7656	1434060 at	0.146	2077.5	97923 at	-0.067	6839	1440903 at	-0.154	3829	5100.375	2601.8073	FALSE	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NA	NA	NA	NA	
100285 at	-0.056	5517	1450224 at	0.073	5759	100285 at	0.086	3545	1450224 at	0.109	5581	5100.5	1042.0421	FALSE	procollagen, type IV, alpha 3	222073 at	0.256	5782	5.768E-04	FALSE
96483 at	0.261	1537	1442661 at	0.073	4203.5	96483 at	-0.017	7595	1442661 at	-0.042	7072	5101.875	2805.4991	FALSE	expressed sequence C80113	NA	NA	NA	NA	
93570 at	0.051	5966	1422856 at	0.163	2019	93570 at	0.034	7026	1446552 at	0.139	5397	5102	2163.3451	TRUE	solute carrier family 12, member 3	244477 at	-0.081	23078	3.044E-01	FALSE
92766 at	0.106	4095	1448750 at	0.026	7528	161468 f at	0.139	1806	1448750 at	0.069	6979	5102	2663.7236	TRUE	heart and neural crest derivatives expressed transcript 1	220138 at	0.019	38858	8.464E-01	FALSE
103941 at	-0.079	3609	1421278 s at	0.048	6305.5	103941 at	0.078	3404	1421278 s at	0.044	7091	5102.375	1872.3235	FALSE	similar to spectrin alpha 1	NA	NA	NA	NA	
100996 at	0.040	6232	1450776 at	-0.058	6228	100996 at	-0.025	6716	1436276 at	-0.289	1240	5104	2586.1683	FALSE	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	224776 at	0.179	6262	8.833E-04	FALSE
94667 at	0.072	5394	1459478 at	0.068	4848	94667 at	0.131	3362	1459478 at	0.049	6812	5104	1426.1211	TRUE	expressed sequence AA408396	NA	NA	NA	NA	

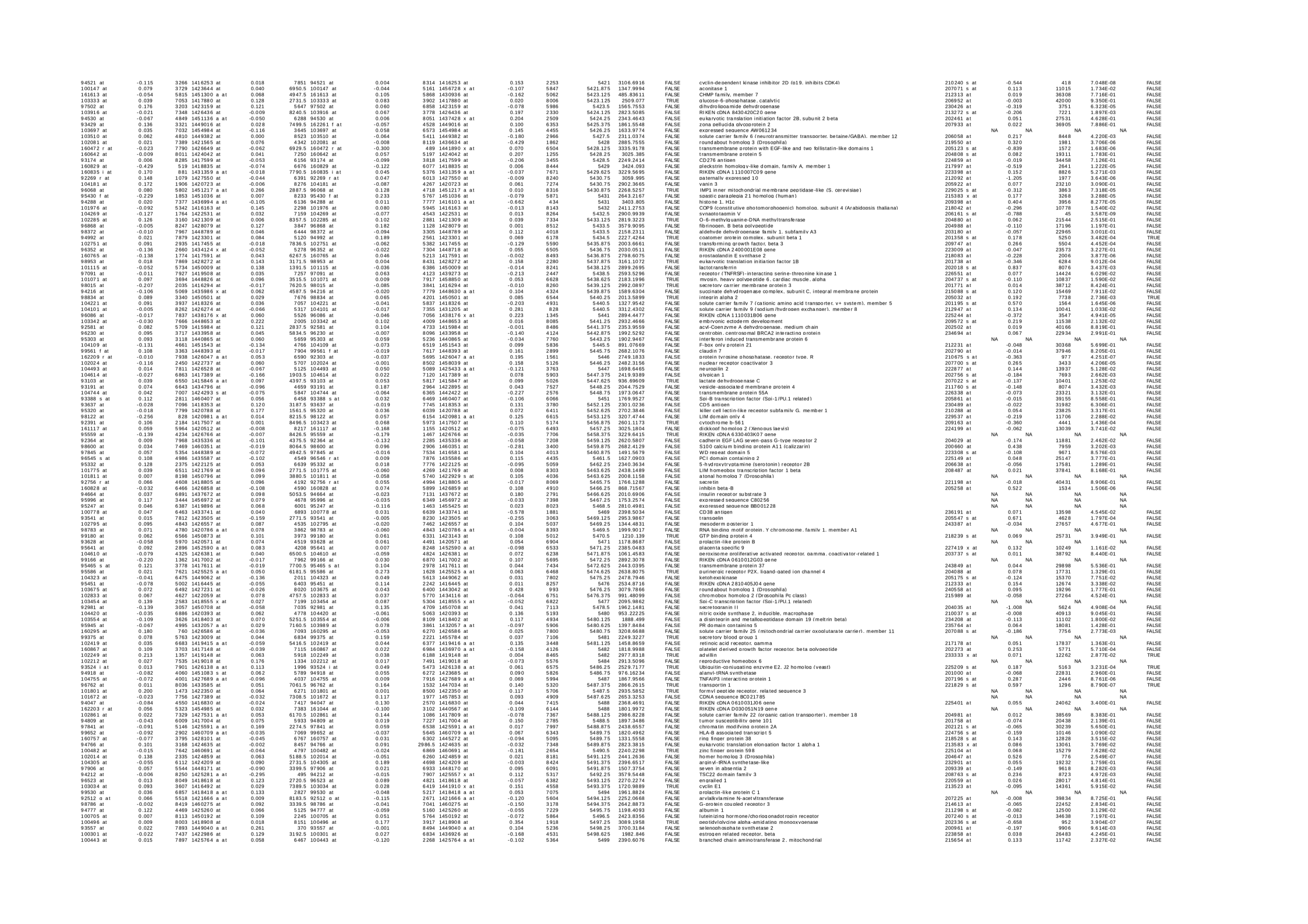
102782 at	-0.031	6796	1425358 at	0.197	953	102782 at	-0.029	6714	1459851 x at	0.095	5956	5104.75	2793.5441	FALSE	RIO kinase 1 (yeast)	224450 s at	0.025	34136	7.033E-01	FALSE
101067 at	-0.031	7340	1428709 a at	0.103	5226	101067 at	0.303	1368	1428709 a at	0.060	6488	5105.5	2638.669	FALSE	mitochondrial ribosomal protein L24	218270 at	-0.049	23533	3.213E-01	FALSE
97887 at	0.052	5824	1418069 at	0.133	2403	97887 at	-0.025	7236	1418069 at	-0.113	4961	5106	2031.3918	FALSE	apolipoprotein C-II	231561 s at	0.035	28708	5.099E-01	FALSE
103649 at	0.112	2981	1418654 at	-0.002	8455.5	103649 at	0.108	2759	1418654 at	0.071	6229	5106.125	2738.8753	FALSE	hydroxyacid oxidase (glycolate oxidase) 3	231156 at	0.015	35927	7.596E-01	FALSE
161898 i at	0.110	3682	1418522 at	0.027	6972	161898 i at	-0.049	6060	1447361 at	-0.109	3711	5106.25	1669.9174	FALSE	metaxin 1	213448 at	-0.182	8412	4.157E-03	FALSE
101729 at	0.160	1835	1423019 at	0.013	8052	101729 at	-0.066	6289	1423019 at	0.230	4249	5106.25	2677.8284	FALSE	gap junction membrane channel protein alpha 9	221407 at	-0.023	37493	8.048E-01	FALSE
93349 at	0.026	7098	1448433 a at	-0.045	5590	93349 at	0.070	3952	1437165 a at	-0.403	3796	5109	1554.5739	FALSE	procollagen C-endopeptidase enhancer protein	202465 at	0.043	26553	4.261E-01	FALSE
94229 at	-0.072	4379	1448412 a at	-0.007	8250	94229 at	-0.042	5265	1448412 a at	-0.218	2543	5109.25	2380.9993	TRUE	TSC22 domain family 4	208104 s at	0.307	4751	2.070E-04	FALSE
102263 at	-0.024	7503	1450681 at	-0.058	6541.5	102263 at	0.052	5023	1450681 at	-0.248	1371	5109.625	2693.4074	FALSE	zinc finger protein 143	221873 at	0.188	7545	2.387E-03	FALSE
97970 at	0.046	6542	1419755 at	0.044	6647.5	97970 at	-0.080	3615	1419755 at	0.185	3636	5110.125	1714.8597	FALSE	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	243629 x at	0.151	10454	1.295E-02	FALSE
96390 at	0.103	3711	1446572 at	0.069	5868.5	96390 at	0.061	5491	1458899 at	-0.096	5370	5110.125	956.60584	FALSE	Ubiquitin specific peptidase 53	216775 at	0.083	10643	1.434E-02	FALSE
93332 at	0.113	2782	1423166 at	0.043	6614.5	93332 at	0.047	5138	1450883 a at	-0.085	5908	5110.625	1665.4019	FALSE	CD36 antigen	209555 s at	0.266	12677	3.340E-02	FALSE
98971 at	0.080	4201	1423123 at	0.034	6847.5	98971 at	-0.049	4985	1453926 at	0.126	4409	5110.625	1204.4655	FALSE	RAD54 like (S. cerevisiae)	204558 at	0.003	43648	9.759E-01	FALSE
160396 at	-0.041	6695	1423955 a at	-0.063	5599	160396 at	0.197	2210	1423955 a at	-0.105	5939	5110.75	1987.342	FALSE	longevity assurance homolog 2 (S. cerevisiae)	222212 s at	0.316	5327	3.716E-04	FALSE
160531 at	-0.141	3155	1416393 at	0.127	1967	160531 at	-0.026	7019	1416393 at	0.009	6720	5111.25	3030.2027	FALSE	EMG1 nucleolar protein homolog (S. cerevisiae)	209233 at	0.110	15284	7.634E-02	FALSE
94638 at	-0.013	7898	1425868 at	0.100	4230	94638 at	0.093	3637	1425868 at	0.373	4682	5111.75	1906.1519	FALSE	histone 2, H2bb		NA	NA	NA	NA
93972 at	-0.276	1422	1451096 at	0.050	6724.5	93972 at	-0.115	5581	1451096 at	-0.049	8304	5111.875	2518.0602	FALSE	NADH dehydrogenase (ubiquinone) Fe-S protein 2	201966 at	-0.147	12698	3.357E-02	FALSE
96818 at	0.019	7470	1439429 x at	0.119	3102	96818 at	-0.011	8081	1439429 x at	0.219	1795	5112	3131.4381	FALSE	deltex 2 homolog (Drosophila)	215732 s at	0.042	30967	5.934E-01	FALSE
160382 at	-0.076	4753	1448141 at	-0.034	7009	160382 at	-0.019	7205	1456814 at	-0.236	1485	5113	2662.2837	TRUE	RIKEN cDNA 1110014J01 gene	202937 x at	-0.179	7875	3.016E-03	TRUE
103770 at	-0.059	6376	1435572 at	0.104	3635	103770 at	0.005	8290	1430715 at	-0.246	2156	5114.25	2745.7133	FALSE	RIKEN cDNA 2310014L17 gene		NA	NA	NA	NA
98308 at	0.001	8474	1427520 a at	0.107	3409	98308 at	-0.046	5663	1427867 at	0.130	2914	5115	2538.8988	FALSE	myosin, heavy polypeptide 1, skeletal muscle, adult	205951 at	-0.007	39133	8.551E-01	FALSE
94737 at	0.110	3378	1418754 at	-0.037	7448.5	94737 at	0.120	3126	1443704 at	-0.076	6513	5116.375	2188.8284	FALSE	adenylate cyclase 8	206811 at	0.331	4227	1.116E-04	FALSE
99904 at	0.225	784	1421511 at	0.069	5434	99904 at	-0.032	6576	1455257 at	0.038	7672	5116.5	3029.416	FALSE	integrin beta 3	216261 at	0.081	15200	7.445E-02	FALSE
100518 at	0.090	4218	1456473 x at	-0.153	1396.5	100518 at	-0.003	8400	1416458 at	-0.053	6452	5116.625	3011.6792	FALSE	ADP-ribosylation factor 2		NA	NA	NA	NA
104577 at	0.238	930	1417360 at	0.125	3311.5	104577 at	0.002	8469	1417360 at	-0.040	7758	5117.125	3605.6245	FALSE	mutL homolog 1 (E. coli)	202520 s at	0.056	28030	4.819E-01	FALSE
102294 at	0.049	6408	1421303 at	0.013	8072	102294 at	0.111	3182	1421303 at	-0.160	2807	5117.25	2548.1386	FALSE	zinc finger protein, subfamily 1A, 1 (Ikaros)	227346 at	0.095	20132	2.048E-01	FALSE
97480 f at	-0.147	1429	1423553 at	0.034	6893	97480 f at	0.097	3945	1423553 at	-0.014	8202	5117.25	3035.6948	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 3		NA	NA	NA	NA
101981 at	0.105	2687	1416353 at	0.078	4168.5	101981 at	-0.068	5647	1416353 at	0.018	7971	5118.375	2253.2022	FALSE	nuclear receptor subfamily 1, group H, member 2	218215 s at	0.049	28783	5.128E-01	FALSE
93562 at	-0.030	7140	1416547 at	0.314	802	93562 at	0.102	4459	1416547 at	0.018	8073	5118.5	3259.9921	FALSE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	203371 s at	-0.171	14557	6.237E-02	FALSE
100059 at	-0.083	4893	1454268 a at	0.038	6793	97013 f at	0.072	4345	1454268 a at	-0.243	4444	5118.75	1141.3519	FALSE	cytochrome b-245, alpha polypeptide	203028 s at	0.226	6662	1.195E-03	FALSE
96514 at	0.125	2636	1426103 a at	0.050	5734	96514 at	0.051	4916	1426103 a at	0.050	7191	5119.25	1904.1977	TRUE	estrogen receptor 2 (beta)	211119 at	0.026	27613	4.662E-01	FALSE
95232 at	-0.028	7126	1424101 at	-0.217	1353	95232 at	-0.085	6590	1445594 at	-0.105	5410	5119.75	2611.4699	TRUE	heterogeneous nuclear ribonucleoprotein L	221860 at	0.250	7361	2.073E-03	FALSE
96598 at	0.067	4659	1455653 at	-0.020	7674	96598 at	-0.119	2225	1455653 at	-0.089	5923	5120.25	2292.1075	FALSE	cyclin J	229091 s at	0.021	34882	7.272E-01	FALSE
161032 i at	0.161	2387	1419325 at	0.079	5174	161032 i at	0.064	5409	1419325 at	-0.036	7511	5120.25	2103.3788	FALSE	neuromedin U	206023 at	-0.015	36840	7.869E-01	FALSE
102106 at	0.073	5105	1459893 at	0.025	7711	102106 at	0.064	4202	1459893 at	0.185	3466	5121	1852.2007	TRUE	expressed sequence C76472		NA	NA	NA	NA
92769 at	-0.048	5731	1448479 at	0.063	4846	92769 at	-0.062	4451	1448479 at	0.137	5458	5121.5	580.28527	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	201388 at	-0.191	7800	2.865E-03	FALSE
93430 at	-0.143	3054	1417625 s at	-0.010	8240.5	93430 at	0.007	8189	1417625 s at	0.328	1004	5121.875	3668.1548	FALSE	chemokine orphan receptor 1	212977 at	0.777	4779	2.130E-04	FALSE
160384 at	-0.026	7657	1437984 x at	0.138	2536	160384 at	-0.092	5193	1437984 x at	-0.099	5104	5122.5	2091.1707	FALSE	HLA-B-associated transcript 1A	200041 s at	0.190	11404	2.026E-02	FALSE
94571 at	-0.084	4701	1450558 at	0.065	5625	94571 at	-0.054	6242	1450558 at	-0.132	3926	5123.5	1018.9957	FALSE	vomeronasal 1 receptor, A1		NA	NA	NA	NA
92879 at	0.110	2838	1416792 at	0.057	5736	92879 at	-0.021	7469	1416792 at	0.093	4453	5124	1962.1082	FALSE	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	200913 at	-0.001	44244	9.900E-01	FALSE
92733 at	0.083	4441	1427502 at	0.085	4947.5	92733 at	-0.084	2996	1427502 at	-0.015	8112	5124.125	2156.7081	FALSE	a disintegrin and metallopeptidase domain 4		NA	NA	NA	NA
99402 at	0.034	6775	1420794 at	0.096	4835.5	99402 at	0.014	7597	1420794 at	0.246	1289	5124.125	2806.658	TRUE	ADP-ribosyltransferase 2b		NA	NA	NA	NA
97423 at	-0.166	2156	1417474 at	0.024	7749	161949 at	-0.101	2253	1417474 at	-0.012	8339	5124.25	3380.2621	FALSE	RIKEN cDNA 1500035H01 gene	218483 s at	0.067	24102	3.413E-01	FALSE
98462 s at	0.035	6826	1425547 a at	0.042	6882	98461 at	0.066	4362	1425547 a at	0.210	2428	5124.5	2147.5899	TRUE	kinesin light chain 4	225596 at	0.031	26693	4.313E-01	FALSE
93780 at	-0.011	8055	1417316 at	0.284	599	93780 at	0.079	5600	1417316 at	0.078	6246	5125	3191.2298	FALSE	thioesterase superfamily member 2	204565 at	-0.135	13647	4.604E-02	FALSE
93302 at	0.084	3256	1422448 at	0.025	7302.5	93302 at	0.168	2297	1422448 at	-0.038	7645	5125.125	2743.6382	FALSE	trefoil factor 2 (spasmolytic protein 1)	214476 at	0.038	31489	6.123E-01	FALSE
162450 f at	-0.053	5904	1422826 at	0.058	5883	162450 f at	0.116	2721	1422826 at	0.075	5993	5125.25	1603.5424	FALSE	insulin-like growth factor binding protein, acid labile subunit	215712 s at	-0.127	17918	1.386E-01	FALSE
102147 at	0.135	2128	1450572 at	-0.039	7133	102147 at	-0.032	6787	1450572 at	-0.097	4454	5125.5	2325.6939	FALSE	alkaline phosphatase 3, intestine, not Mn requiring	207140 at	0.008	42107	9.377E-01	FALSE
104479 at	0.093	4358	1450318 a at	0.093	3982	104479 at	-0.093	4259	1450318 a at	-0.018	7904	5125.75	1858.9901	FALSE	purinergic receptor P2Y, G-protein coupled 2	206277 at	0.022	34855	7.268E-01	FALSE
97333 at	-0.171	2717	1416648 at	-0.017	8073	97333 at	-0.096	6577	1439950 at	0.233	3137	5126	2617.2258	FALSE	dynein cytoplasmic 1 heavy chain 1	211928 at	-0.086	21402	2.470E-01	FALSE
97086 i at	-0.111	4424	1451616 at	0.120	3594.5	97087 f at	0.056	4874	1451616 at	-0.039	7613	5126.375	1740.3993	FALSE	pregnancy specific glycoprotein pseudogene 1		NA	NA	NA	NA
103912 at	0.025	7416	1428265 at	0.062	5533	103912 at	-0.021	6949	1419871 at	-0.314	609	5126.75	3116.4277	FALSE	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	202883 s at	0.377	3204	3.024E-05	FALSE
98357 at	0.050	5969	1438297 at	0.131	2720.5	98357 at	0.086	4182	1438297 at	0.039	7639	5127.625	2137.2392	TRUE	EST AA545190		NA	NA	NA	NA
92950 at	-0.077	3969	1448257 at	0.104	4254	92950 at	-0.044	5348	1448257 at	0.056	6940	5127.75	1346.4646	FALSE	solute carrier family 29 (nucleoside transporters), member 2	204717 s at	0.025	32901	6.614E-01	FALSE
101209 at	-0.069	5249	1421775 at	0.178	1917	101209 at	-0.058	4915	1421775 at	0.007	8430	5127.75	2662.9392	FALSE	Fc receptor, IgE, high affinity I, alpha polypeptide	211734 s at	0.001	44081	9.863E-01	FALSE
102396 at	0.037	6258	1423068 at	0.053	6280	102396 at	0.073	3853	1423068 at	0.121	4122	5128.25	1321.8251	TRUE	intraflagellar transport 172 homolog (Chlamydomonas)	226324 s at	0.077	17267	1.212E-01	FALSE
162126 r at	-0.201	1122	1455206 at	-0.183	4546	162126 r at	0.005	8169	1455206 at	0.090	6676	5128.25	3056.7273	FALSE	Hypothetical protein C130006E23		NA	NA	NA	NA
96512 at	0.068	5620	1426825 at	-0.063	5062	96512 at	-0.061	4473	1426825 at	-0.130	5359	5128.5	492.88437	FALSE	formin-like 3	230850 at	0.178	6374	9.620E-04	FALSE
101637 at	-0.033	6798	1417074 at	0.144	2274.5	101637 at	0.068	6051	1417074 at	-0.103	5391	5128.625	1987.6669	FALSE	CEA-related cell adhesion molecule 10	210789 x at	0.029	31021	5.958E-01	FALSE
102344 s at	-0.064	5454	1424531 a at	0.155	1373.5	102344 s at	-0.070	5579	1424531 a at	-0.015	8110	5129.125	2786.7703	FALSE	transcription elongation factor A (SII), 3	226388 at	0.115	13806	4.906E-02	FALSE
94113 at	-0.068	4601	1459920 at	0.080	4888	94113 at	-0.024	7350	1439497 at	0.262	3679	5129.5	1567.6102	FALSE	RIKEN cDNA 4933415E08 gene		NA	NA	NA	NA
160078 at	-0.062	6027	1436716 at	0.105	4776.5	160078 at	0.008	8015	1450914 at	-0.182	1701	5129.875	2646.4339	FALSE	protein phosphatase 1, regulatory (inhibitor) subunit 14B	212680 x at	0.303	3307	3.532E-05	FALSE
101182 at	0.046	6313	1450525 at	0.031	7284	101182 at	-0.038	6605	1444043 at	-0.573	320	5130.5	3232.6939	FALSE	GLI-Kruppel family member GLI3	205201 at	0.062	28638	5.072E-01	FALSE
96615 at	-0.048	6473	1426624 a at	-0.052	6367	96615 at	-0.074	5305	1426624 a at	0.176	2378	5130.75	1909.4454	FALSE	yippee-like 3 (Drosophila)	232077 s at	0.186	3867	7.354E-05	FALSE
101821 at	0.069	4908	1450575 at	-0.070	5514	101821 at	-0.031	6760	1450575 at	-0.713	3344	5131.5	1419.3223	FALSE	cholinergic receptor, muscarinic 4	221357 at	-0.192	5990	6.861E-04	FALSE
94205 at	-0.061	6261	1449136 at	0.112	3781	94205 at	0.009	8179	1449136 at	0.169	2305	5131.5	2606.1452	FALSE	eosinophil peroxidase	214627 at	-0.006	42297	9.419E-01	FALSE
102079 at	0.133	2276	1426190 at	0.026	7450.5	102079 at	-0.080	2767	1426190 at	0.019	8035	5132.125	3030.5562	FALSE	activator of yeast meiotic promoters 1		NA	NA	NA	NA
94491 at	0.136	3741	1422472 at	-0.044	6992.5	94491 at	0.043	5567	1422472 at	-0.246	4230	5132.625	1460.4986	FALSE	peroxisomal biogenesis factor 13	205246 at	-0.012	38829	8.455E-01	FALSE
93633 at	0.030	6868	1419217 at	0.036	7108	93633 at	0.066	5192	1419217 at	0.258	1364	5133	2653.2805	TRUE	secretion regulating guanine nucleotide exchange factor	223483 at	-0.069	16388	9.933E-02	FALSE
103101 at	0.105	2878	1423616 at	0.114	1947	103101 at	-0.009	7986	1438952 x at	-0.024	7721	5133	3166.1214	FALSE	TAR (HIV) RNA binding protein 2	203677 s at	0.029	30385	5.706E-01	FALSE
102043 at	0.006	8258	1416689 at	-0.056	5496	102043 at	-0.133	1973	1444694 at	0.124	4806	5133.25	2581.3383	FALSE	tuftelin 1	205807 s at	-0.066	20018	2.008E-01	FALSE
103613 at	-0.034	6422	1423498 at	0.156	616.5	103613 at	0.042	5946	1423498 at	-0.031	7557	5135.375	3087.4486	FALSE	aldolase 1, A isoform, pseudogene 1		NA	NA	NA	NA
96679 at	0.229	3339	1417191 at	-0.065	7228.5	96679 at	-0.278	2403	1417191 at	-0.028	7572	5135.625	2646.4536	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 9	202843 at	-0.146	19924	1.981E-01	FALSE
98572 at	-0.308	2164	1423151 at	0.040	6877	98572 at	0.154	4380	1423151 at	0.049	7124	5136.25	2337.2024	FALSE	DnaJ (Hsp40) homolog, subfamily B, member 11	223054 at	0.026	37641	8.100E-01	FALSE
160611 at	0.028	7355	1417071 s at	0.154	1882	160611 at	-0.016	7621	1417070 at	-0.159	3691	5137.25	2815.1803	FALSE	cytochrome P450, family 4, subfamily v, polypeptide 3	228391 at	0.091	25046	3.744E-01	FALSE
97125 f at	-0.162	5116	1450534 x at	0.114	3218	97125 f at	0.040	5824	1450534 x at	0.099	6395	5138.25	1382.9351	FALSE	MHC (A.CA/J(H-2K-f) class I antigen		NA	NA	NA	NA
160363 at	0.025	7113	1418284 at	0.075	4198.5	160363 at	-0.213	834	1418284 at	-0.004	8409	5138.625	3366.8551	FALSE	vacuolar protein sorting 72 (yeast)	202261 at	0.015	36153	7.671E-01	FALSE
101575 i at	0.110	4413	1418282 x at	0.162	3640	101575 i at	0.117	4097	1418282 x at	0.004	8406	5139	2200.9945	TRUE	serine (or cysteine) preptidase inhibitor, clade A, member 1b	211429 s at	0.304	13283	4.099E-02	TRUE
100935 at	0.060	5352	1418437 a at	0.098	2946	100935 at	0.025	6735	1425930 a at	0.118	5529	5140.5	1586.8128	TRUE	MAX-like protein X	217909 s at	-0.171	6693	1.231E-03	FALSE
98345 at	0.066	4359	1419895 at	0.099	2818.5	98345 at	0.017	7593	1449658 at	0.068	5793	5140.875	2036.577	TRUE	expressed sequence AA536748		NA	NA	NA	NA
92505 g at	0.089	3273	1425366 a at	0.010	8173.5	92504 at	-0.138	1780	1425366 a at	-0.048	7338	5141.125	3098.8498	FALSE	Hus1 homolog (S. pombe)	204883 s at	0.139	5948	6.596E-04	FALSE
92450 at	0.117	2049	1417446 at	-0.054	5974.5	92450 at	0.063	5185	1417446 at	-0.038	7360	5142.125	2249.5243	FALSE	solute carrier family 12, member 4	209402 s at	0.149	5101	3.016E-04	FALSE
95065 at	-0.027	6802	1416373 at	0.093	4828.5	95065 at	-0.006	8175	1442017 at	0.833	765	5142.625	3225.4766	FALSE	nitrogen fixation gene 1 (S. cerevisiae)	218455 at	-0.072	21942	2.665E-01	FALSE
102426 at	0.161	3224	1422598 at	0.110	2795.5	102426 at	-0.007	8029	1422598 at	-0.077	6525	5143.375	2545.0761	FALSE	calsequestrin 1	219645 at	0.027	32345	6.432E-01	FALSE
98453 at	0.036	6405	1419300 at	-0.040	6956	98453 at	-0.033	6632	1454037 a at	-0.271	583	5144	3049.0616	FALSE	FMS-like tyrosine kinase 1	232809 s at	0.153	6386	9.704E-04	FALSE
102327 at	0.058	5783	1449396 at	0.022	7755.5	102327 at	0.058	4394	1449396 at	0.151	2647	5144.875	2162.2334	TRUE	amine oxidase, copper containing 3	204894 s at	-0.022	37653	8.104E-01	FALSE
103028 at	0.044	6818	1452518 a at	0.037	7323	103028 at	0.085	3259	1430833 at	-0.141	3182	5145.5	2232.5603	FALSE	IL2-inducible T-cell kinase	211339 s at	-0.041	21176	2.389E-01	FALSE
103059 at	0.048	5887	1418374 at	-0.032	6863.5	103059 at	0.116	1770	1418374 at	0.088	6063	5145.875	2290.3531	FALSE	FXYD domain-containing ion transport regulator 3		NA	NA	NA	NA
98401 at	0.111	4047	1427377 x at	0.413	29	98401 at	-0.002	8445	1427377 x at	-0.037	8064	5146.25	3949.2453	FALSE	hydroxysteroid dehydrogenase-3, delta<5>-3-beta		NA	NA	NA	NA
97473 at	0.062	5729	1448276 at	0.045	6043	97473 at	0.194	934	1448276 at	-0.055	7880	5146.5	2964.2423	FALSE	tetraspanin 4	209263 x at	0.217	4845	2.313E-04	FALSE
101145 at	0.032	6806	1421512 at	0.154	3038	101145 at	-0.030	6625	1421512 at	0.172	4117	5146.5	1865.9712	FALSE	centrosomal protein 250	209495 at	0.061	17317	1.223E-01	FALSE
101702 at	0.230	1243	1421084 at	0.037	6647.5	101702 at	0.095	4667	1421085 at	0.016	8030	5146.875	2945.8901	TRUE	retinoschisis 1 homolog (human)	207363 at	-0.054	15893	8.832E-02	FALSE
93063 at	0.010	7876	1420621 a at	-0.289	418.5	93063 at	0.005	8247	1420621 a at	0.107	4049	5147.625	3679.7534	FALSE	amyloid beta (A4) precursor protein	214953 s at	-0.288	5113	3.084E-04	FALSE
101111 at	0.031	6896	1437628 s at	-0.088	5012	101113 at	0.280	305	1437628 s at	-0.006	8378	5147.75	3510.0593	FALSE	ras homolog gene family, member A	200059 s at	0.135	22534	2.861E-01	FALSE
103594 at	-0.088	3396	1417855 at	-0.146	2444	103594 at	0.017	7710	1417855 at	-0.059	7044	5148.5	2616.5995	FALSE	F-box and leucine-rich repeat protein 15	218938 at	-0.367	3889	7.620E-05	FALSE
97208 at	0.036	6583	1420616 at	0.083	3736.5	97208 at	0.016	7248	1420615 at	0.212	3027	5148.625	2078.4767	TRUE	ash2 (absent, small, or homeotic)-like (Drosophila)	209517 s at	-0.093	11937	2.518E-02	FALSE
103394 at	-0.173	661	1418296 at	0.070	5765	103394 at	0.004	8284	1418296 at	-0.096	5887	5149.25	3209.074	FALSE	FXYD domain-containing ion transport regulator 5	218084 x at	0.197	8030	3.326E-03	FALSE
92891 f at	0.080	4052	1449867 at	0.100	2940	92891 f at	0.046	5838	1449867 at	-0.031	7769	5149.75	2115.1997	FALSE	homeo box C9	221350 at	-0.079	25613	3.915E-01	FALSE
97115 at	0.055	5624	1459931 a at	0.179	1275	97115 at	-0.046	6667	1459931 a at	-0.066	7037	5150.75	2652.1913	FALSE	Similar to zinc finger protein 709		NA	NA	NA	NA
92554 at	0.225	1947	1422887 a at	-0.057	6416.5	92554 at	0.017	7406	1439823 at	-0.096	4834	5150.875	2384.1574	FALSE	C-terminal binding protein 2	210835 s at	0.684	430	7.426E-08	FALSE
161656 r at	0.210	1681	1418845 at	0.024	7853	95585 at	0.065	4797	1444979 at	0.095	6274	5151.25	2628.5705	TRUE	protein C	206259 at	-0.044	30935	5.918E-01	FALSE
93167 f at	0.072	4591	1419534 at	0.070	5505.5	93167 f at	0.076	3332	1419534 at	-0.041	7179	5151.875	1618.725	FALSE	oxidized low density lipoprotein (lectin-like) receptor 1	210004 at	0.057	33542	6.841E-01	FALSE
94769 at	0.169	1443	1449366 at	0.058	6213	94769 at	-0.066	5065	1449366 at	0.026	7893	5153.5	2732.7058	FALSE	matrix metallopeptidase 8	207329 at	0.028	31591	6.161E-01	FALSE
92230 at	0.070	4121	1451555 at	0.262	764	92230 at	-0.002	8404	1424981 at	0.104	7327	5154	3445.9453	FALSE	neurolysin (metallopeptidase M3 family)	234762 x at	0.479	208	2.095E-08	FALSE
161355 f at	0.190	1021	1434104 at	-0.004	8386	161355 f at	-0.093	3031	1434104 at	-0.013	8180	5154.5	3705.4607	FALSE	hypothetical protein 6030458H05	220796 x at	0.351	2231	5.817E-06	FALSE
98107 at	-0.026	7560	1437721 at	0.306	748	98107 at	0.057	6770	1417752 at	0.140	5541	5154.75	3053.0255	FALSE	coronin, actin binding protein 1C	222409 at	0.548	930	3.716E-07	FALSE
94860 at	-0.114	5205	1426256 at	0.089	5413	94860 at	0.076	4424	1426256 at	0.082	5580	5155.5	511.2237	FALSE	translocase of inner mitochondrial membrane 17a	215171 s at	-0.298	5407	4.026E-04	FALSE
101288 at	0.022	7326	1422319 at	0.038	6493.5	101288 at	0.146	1510	1422319 at	0.097	5294	5155.875	2569.706	TRUE	Friend virus susceptibility 4		NA	NA	NA	NA
103356 at	-0.127	3760	1425315 at	0.044	6143	103356 at	0.075	5559	1448892 at	-0.106	5164	5156.5	1014.1428	FALSE	dedicator of cytokinesis 7	242611 at	0.460	2445	8.709E-06	FALSE
94732 at	-0.020	7354	1433210 at	0.165	1839	94732 at	0.025	6778	1433211 at	-0.098	4657	5157	2497.5704	FALSE	repetin		NA	NA	NA	NA
103563 at	-0.131	1635	1435226 at	0.069	4852	103563 at	-0.037	6041	1435226 at	-0.014	8102	5157.5	2705.0563	FALSE	IBR domain containing 3	36564 at	-0.080	15758	8.533E-02	FALSE
102784 at	0.025	7521	1426975 at	-0.212	3158	102784 at	-0.027	6633	1431696 at	-0.123	3320	5158	2246.3035	FALSE	RIKEN cDNA 4632413K17 gene	215399 s at	0.095	11892	2.477E-02	FALSE
100966 at	0.060	4976	1418680 at	-0.039	6536	100966 at	-0.190	873	1418680 at	-0.017	8247	5158	3153.5775	FALSE	serine (or cysteine) peptidase inhibitor, clade D, member 1	205576 at	-0.087	16462	1.008E-01	FALSE
95708 at	0.014	7875	1415828 a at	-0.159	2302	95708 at	-0.015	7961	1415827 a at	0.143	2495	5158.25	3187.8521	FALSE	DNA segment, Chr 3, University of California at Los Angeles 1	200971 s at	0.119	21844	2.627E-01	FALSE
161539 f at	-0.216	314	1434425 at	0.035	6385	160586 r at	0.034	6006	1434425 at	-0.024	7931	5159	3335.5906	FALSE	trichohyalin	213780 at	-0.117	12411	3.051E-02	FALSE
92575 at	0.027	7370	1423128 at	0.093	3368.5	92575 at	0.089	2692	1423128 at	0.044	7207	5159.375	2474.8605	TRUE	aryl-hydrocarbon receptor-interacting protein	201781 s at	-0.181	3459	4.333E-05	FALSE
100374 at	0.162	1586	1423582 at	0.055	5694.5	100374 at	-0.075	5405	1423582 at	-0.021	7956	5160.375	2641.7675	FALSE	doublesex and mab-3 related transcription factor 1	220493 at	-0.012	37454	8.038E-01	FALSE
93842 at	0.027	6984	1423790 at	-0.063	5884	93842 at	0.090	2532	1423790 at	-0.098	5242	5160.5	1894.2245	FALSE	death-associated protein	201095 at	0.049	27163	4.489E-01	FALSE
160968 at	0.109	2204	1434528 at	-0.007	8264.5	160968 at	-0.006	8134	1434528 at	-0.256	2043	5161.375	3508.8561	FALSE	alanine and arginine rich domain containing protein		NA	NA	NA	NA
160246 at	0.029	7183	1416950 at	0.073	5019	160246 at	0.033	6113	1442753 at	-0.166	2334	5162.25	2082.2163	FALSE	tumor necrosis factor, alpha-induced protein 8	210260 s at	0.209	4762	2.095E-04	FALSE
103671 at	-0.022	7207	1451814 a at	0.084	4087	103671 at	0.033	6899	1454227 at	0.165	2459	5163	2284.8066	FALSE	HIV-1 tat interactive protein 2, homolog (human)	209448 at	0.237	11259	1.917E-02	FALSE
93877 at	0.079	4148	1428500 at	0.033	7407	93877 at	0.057	5706	1428500 at	-0.183	3391	5163	1779.5687	FALSE	RIKEN cDNA 2210419D22 gene		NA	NA	NA	NA
101659 at	0.030	7889	1425127 at	0.168	2672	101659 at	-0.095	2764	1425127 at	0.038	7333	5164.5	2834.3282	FALSE	hydroxysteroid dehydrogenase-2, delta<5>-3-beta		NA	NA	NA	NA
161831 at	0.049	6378	1422217 a at	0.146	2880.5	94715 at	-0.066	3556	1422217 a at	0.031	7845	5164.875	2342.4766	FALSE	cytochrome P450, family 1, subfamily a, polypeptide 1	205749 at	-0.016	38669	8.411E-01	FALSE
162110 f at	-0.077	3980	1418143 at	0.096	3353	162110 f at	0.029	6328	1418143 at	0.046	7000	5165.25	1770.8155	FALSE	vacuolar protein sorting 45 (yeast)	207967 at	0.022	38606	8.393E-01	FALSE
92322 at	0.130	2198	1419691 at	0.019	7983	92322 at	0.093	3080	1419691 at	-0.038	7401	5165.5	2949.0752	FALSE	cathelicidin antimicrobial peptide	210244 at	-0.027	32724	6.550E-01	FALSE
160131 at	0.186	1157	1452387 a at	0.064	5585	160131 at	0.028	6385	1452387 a at	-0.045	7538	5166.25	2790.4591	FALSE	angiomotin like 2	203002 at	0.509	1667	2.035E-06	FALSE
101407 at	-0.074	4600	1427282 a at	0.123	2489	101407 at	0.042	5408	1427282 a at	-0.015	8174	5167.75	2351.8291	FALSE	frataxin	205565 s at	-0.027	29034	5.220E-01	FALSE

104214 at	-0.111	2634	1417929 at	0.039	7032	104214 at	-0.140	3257	1417929 at	-0.041	7750	5168.25	2595.7848	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	202752 x at	-0.190	5208	3.379E-04	FALSE
100967 at	0.071	5794	1416316 at	0.053	6346	100967 at	0.132	1779	1416316 at	0.064	6756	5168.75	2293.9502	TRUE	solute carrier family 27 (fatty acid transporter), member 2	205769 at	-0.049	21008	2.336E-01	FALSE
103277 s at	-0.049	6918	1425585 at	0.145	1667	103277 s at	-0.019	7386	1425585 at	-0.114	4705	5169	2611.0911	FALSE	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	203506 s at	0.212	3822	6.841E-05	FALSE
95518 at	-0.005	8378	1424683 at	-0.145	4275	95518 at	0.122	5772	1450505 a at	-0.168	2254	5169.75	2579.2601	FALSE	RIKEN cDNA 1810015C04 gene	218510 x at	0.214	13386	4.237E-02	FALSE
104544 at	0.121	3853	1423327 at	0.030	7270	104544 at	0.060	4976	1423327 at	-0.115	4583	5170.5	1474.9794	FALSE	RIKEN cDNA 4930517K11 gene		NA	NA	NA	NA
99925 f at	-0.198	1196	1449318 at	0.035	7170	99925 f at	0.033	6692	1420248 at	-0.076	5625	5170.75	2727.4031	FALSE	tubulin, gamma 2	203894 at	-0.145	14202	5.615E-02	FALSE
103420 at	-0.033	6455	1417357 at	0.025	7623	103420 at	0.102	3628	1417357 at	0.154	2979	5171.25	2224.6103	FALSE	emerin	209477 at	0.039	30989	5.945E-01	FALSE
94753 at	-0.081	4181	1421302 a at	0.029	7302.5	94753 at	0.076	3454	1421302 a at	-0.122	5748	5171.375	1713.1267	FALSE	guanine nucleotide binding protein, alpha 15	205349 at	0.112	12787	3.460E-02	FALSE
99981 at	0.048	6102	1450115 at	-0.016	7999	99981 at	-0.039	5975	1446688 at	0.366	611	5171.75	3178.2783	FALSE	guanine nucleotide binding protein, alpha q polypeptide	211426 x at	-0.180	4793	2.155E-04	FALSE
101103 at	0.017	7888	1423257 at	0.137	2466	101103 at	0.101	2737	1423257 at	0.030	7597	5172	2972.5938	TRUE	cytochrome P450, family 4, subfamily a, polypeptide 14		NA	NA	NA	NA
99556 s at	0.206	4132	1450579 x at	0.116	2562	99556 s at	0.045	6729	1450578 at	0.039	7270	5173.25	2215.0656	TRUE	sex determining region of Chr Y		NA	NA	NA	NA
102612 at	0.100	4028	1450946 at	-0.010	8116	102612 at	0.024	7190	1450946 at	0.302	1361	5173.75	3086.0927	FALSE	neural retina leucine zipper gene	242993 at	0.018	32987	6.650E-01	FALSE
94134 at	0.143	2886	1425377 at	0.003	8458	94134 at	0.135	2464	1425377 at	-0.049	6892	5175	2961.7123	FALSE	wingless-related MMTV integration site 1	208570 at	-0.055	25169	3.785E-01	FALSE
103654 at	0.293	680	1418152 at	0.078	4951	103654 at	-0.013	7695	1418152 at	0.040	7375	5175.25	3237.5711	FALSE	nucleosome binding protein 1	221606 s at	0.213	6903	1.467E-03	FALSE
161865 r at	0.149	3167	1452592 at	0.070	4775	161865 r at	-0.139	6160	1452592 at	-0.086	6602	5176	1549.0442	FALSE	microsomal glutathione S-transferase 2		NA	NA	NA	NA
97857 at	0.065	6094	1423647 a at	-0.069	6200	97857 at	0.099	4116	1423647 a at	0.125	4295	5176.25	1124.1383	FALSE	zinc finger, DHHC domain containing 3	218077 s at	0.040	22850	2.964E-01	FALSE
101855 at	0.043	6199	1422550 a at	-0.048	5997	101855 at	-0.023	7143	1457316 at	0.566	1367	5176.5	2588.316	FALSE	microtubule-associated protein 6	228943 at	-0.198	3016	2.270E-05	FALSE
95344 at	0.079	4686	1422177 at	0.177	1699	95344 at	-0.035	5954	1422177 at	-0.007	8369	5177	2776.6982	FALSE	interleukin 13 receptor, alpha 2	206172 at	-0.252	14247	5.708E-02	FALSE
98597 at	-0.019	7684	1417172 at	0.123	1703.5	98597 at	-0.062	4838	1417172 at	-0.055	6484	5177.375	2593.159	FALSE	ubiquitin-conjugating enzyme E2L 6	201649 at	0.189	11294	1.945E-02	FALSE
102950 at	-0.066	5474	1422400 a at	0.028	7473	102950 at	0.152	2355	1422400 a at	0.093	5408	5177.5	2111.6241	FALSE	hematopoietic cell transcript 1		NA	NA	NA	NA
103932 at	0.014	7908	1435442 at	0.124	1835	103932 at	-0.068	7099	1435442 at	-0.116	3870	5178	2830.174	FALSE	WD repeats and SOF domain containing 1	225676 s at	-0.137	16502	1.019E-01	FALSE
101762 at	0.076	5144	1422401 at	0.065	5465	101762 at	0.051	6313	1422401 at	-0.179	3795	5179.25	1046.3321	FALSE	small proline-rich protein 3	232082 x at	0.002	43769	9.789E-01	FALSE
97252 at	0.103	2569	1423823 at	0.105	3133.5	97252 at	-0.012	7613	1423823 at	0.039	7403	5179.625	2699.7963	FALSE	RIKEN cDNA 2610012O22 gene	220688 s at	-0.182	5106	3.055E-04	FALSE
94115 at	0.119	2070	1449312 at	0.046	6622	94115 at	-0.058	5086	1449312 at	-0.078	6942	5180	2225.9787	FALSE	neuropeptide Y receptor Y5	207400 at	-0.304	2436	8.601E-06	FALSE
98777 at	0.121	2937	1423004 at	-0.108	3799	98777 at	-0.025	6694	1423004 at	-0.054	7292	5180.5	2136.27	FALSE	vasoactive intestinal peptide receptor 1	205019 s at	-0.163	11412	2.029E-02	FALSE
102666 at	0.114	3693	1417717 a at	0.161	2990	102666 at	-0.008	7946	1448821 at	-0.069	6093	5180.5	2272.4138	FALSE	tyrosinase	206630 at	-0.014	38414	8.345E-01	FALSE
94973 at	-0.095	4793	1428320 at	-0.047	6122.5	94973 at	-0.028	7416	1438508 at	0.214	2391	5180.625	2146.0266	FALSE	jumonji domain containing 1B	210878 s at	0.119	14222	5.670E-02	FALSE
94399 at	-0.116	3763	1451330 a at	0.016	7965	94399 at	-0.123	2339	1451330 a at	-0.054	6656	5180.75	2582.8904	FALSE	inositol polyphosphate-5-phosphatase B	213804 at	0.172	4612	1.749E-04	FALSE
160198 at	0.123	3752	1433442 at	0.047	6963.5	160198 at	0.082	4934	1433442 at	0.105	5075	5181.125	1328.1054	TRUE	Kelch-like 9 (Drosophila)	213233 s at	0.176	9872	9.428E-03	TRUE
100876 at	-0.221	1744	1454674 at	-0.017	8045.5	100876 at	-0.138	2730	1454674 at	0.011	8206	5181.375	3424.2447	FALSE	fasciculation and elongation protein zeta 1 (zygin I)	205973 at	-0.157	8645	4.745E-03	FALSE
96318 at	-0.086	4910	1448439 at	0.055	5761.5	96318 at	0.021	7392	1448440 x at	-0.232	2662	5181.375	1970.1356	FALSE	DNA segment, Chr 17, Wayne State University 104, expressed	221739 at	0.024	32706	6.544E-01	FALSE
96675 at	-0.059	6006	1435811 a at	0.019	7761	96675 at	0.077	4691	1435812 at	-0.184	2268	5181.5	2313.9211	FALSE	unc-50 homolog (C. elegans)	239505 at	-0.018	33099	6.684E-01	FALSE
101932 at	0.105	3981	1418539 a at	-0.098	4388.5	101932 at	0.056	6387	1418540 a at	0.107	5973	5182.375	1176.1163	FALSE	protein tyrosine phosphatase, receptor type, E	221840 at	-0.120	21814	2.618E-01	FALSE
160742 at	-0.126	2966	1415901 at	0.000	8513.5	95009 at	0.174	1329	1415901 at	-0.019	7924	5183.125	3576.4841	FALSE	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	202185 at	0.233	7023	1.606E-03	FALSE
100928 at	0.017	7701	1423407 a at	0.074	5273	100928 at	0.137	1167	1423407 a at	0.117	6592	5183.25	2855.5187	TRUE	fibulin 2	203886 s at	0.029	34712	7.228E-01	FALSE
162034 r at	-0.042	6576	1426708 at	0.022	7560.5	162034 r at	0.087	4115	1426708 at	-0.208	2482	5183.375	2311.4916	FALSE	Anthrax toxin receptor 2	225524 at	0.535	830	2.946E-07	FALSE
100495 at	0.015	7603	1448616 at	-0.097	5198.5	100495 at	-0.077	3876	1417207 at	-0.144	4056	5183.375	1716.1019	FALSE	dishevelled 2, dsh homolog (Drosophila)	57532 at	0.189	3116	2.665E-05	FALSE
95661 at	0.110	5123	1416066 at	-0.031	7757	95661 at	0.175	3822	1416066 at	-0.225	4034	5184	1807.5392	FALSE	CD9 antigen	233317 at	0.206	6948	1.523E-03	FALSE
160748 at	-0.009	8023	1438182 x at	0.118	3569	160748 at	-0.114	2873	1448431 at	-0.069	6272	5184.25	2393.9236	FALSE	ankyrin repeat and SOCS box-containing protein 6	221657 s at	-0.137	8484	4.307E-03	FALSE
98435 at	-0.073	5873	1449383 at	-0.104	3919.5	98435 at	0.331	3093	1449383 at	0.037	7852	5184.375	2126.3573	FALSE	adenylosuccinate synthetase like 1	226325 at	0.099	24000	3.382E-01	FALSE
94871 r at	-0.093	4716	1428163 at	0.177	2764.5	94871 r at	-0.115	5484	1428163 at	-0.024	7774	5184.625	2071.3202	FALSE	SAR1 gene homolog B (S. cerevisiae)	223512 at	0.122	3215	3.089E-05	FALSE
93328 at	-0.023	7225	1454713 s at	0.097	3532.5	93328 at	0.135	3248	1454713 s at	-0.184	6733	5184.625	2084.9164	FALSE	histidine decarboxylase	207067 s at	-0.007	41871	9.312E-01	FALSE
99381 at	0.156	2444	1450359 at	-0.084	5647	99381 at	-0.035	6470	1450359 at	-0.063	6180	5185.25	1859.0118	FALSE	fucosyltransferase 1	225776 at	0.280	4254	1.149E-04	FALSE
100759 at	0.049	6098	1421045 at	0.083	5461.5	100759 at	-0.049	5773	1421045 at	-0.145	3411	5185.875	1211.4507	FALSE	mannose receptor, C type 2	37408 at	0.195	3392	3.947E-05	FALSE
96943 at	-0.193	2694	1415699 a at	-0.024	7567	96943 at	-0.151	2043	1415699 a at	0.004	8441	5186.25	3283.9356	FALSE	G protein pathway suppressor 1	217782 s at	-0.050	27447	4.595E-01	FALSE
104730 at	-0.045	5976	1417675 a at	0.066	4725.5	104730 at	0.011	7708	1439585 at	0.164	2342	5187.875	2257.2082	FALSE	midasin homolog (yeast)	242839 at	-0.055	19285	1.773E-01	FALSE
95994 at	0.043	6459	1447965 at	0.116	3841.5	95994 at	-0.014	7576	1447965 at	0.149	2875	5187.875	2197.0447	FALSE	expressed sequence C80012		NA	NA	NA	NA
101714 at	0.075	5126	1421508 at	0.046	7101.5	101714 at	0.000	8522	1421508 at	0.856	5	5188.625	3725.7827	TRUE	odd Oz/ten-m homolog 1 (Drosophila)		NA	NA	NA	NA
161460 r at	0.138	2817	1418093 a at	0.029	6946.5	102774 at	0.059	4216	1418093 a at	-0.065	6776	5188.875	2014.9845	FALSE	epidermal growth factor	206254 at	0.035	20019	2.008E-01	FALSE
104271 at	0.074	5524	1418554 at	0.053	5793.5	162449 f at	0.267	1318	1418554 at	-0.015	8121	5189.125	2831.8963	FALSE	adrenomedullin receptor	214506 at	-0.003	43852	9.810E-01	FALSE
98031 at	-0.107	2449	1417040 a at	0.047	6169	98031 at	0.005	8222	1417040 a at	-0.141	3917	5189.25	2535.4206	FALSE	Bcl-2-related ovarian killer protein	223349 s at	0.500	6057	7.309E-04	FALSE
101397 at	-0.038	6545	1450628 at	0.039	6286	161555 f at	0.162	1363	1450628 at	-0.061	6563	5189.25	2553.9706	FALSE	solute carrier family 2, (facilitated glucose transporter), member 8	218985 at	0.049	27185	4.494E-01	FALSE
102061 at	0.063	5591	1418589 a at	0.090	4440	102061 at	0.070	4074	1418589 a at	-0.193	6652	5189.25	1169.9286	FALSE	myeloid leukemia factor 1	204784 s at	-0.070	33388	6.782E-01	FALSE
94264 at	-0.065	5897	1425419 a at	-0.082	5719	94264 at	0.079	5041	1425419 a at	0.108	4101	5189.5	814.00471	FALSE	v-raf-leukemia viral oncogene 1	201244 s at	0.235	6482	1.032E-03	FALSE
96491 at	0.189	1058	1447947 at	0.022	7799	96491 at	0.091	3776	1447947 at	0.016	8125	5189.5	3390.8664	TRUE	zinc finger, FYVE domain containing 16	203651 at	0.224	19787	1.939E-01	FALSE
98305 at	0.075	4760	1437138 at	0.104	3616.5	98306 g at	0.011	7837	1448834 at	0.116	4548	5190.375	1832.9916	TRUE	forkhead box M1	202580 x at	0.005	42580	9.494E-01	FALSE
93843 at	0.052	5291	1415677 at	0.090	3246	93843 at	0.034	6217	1415677 at	0.090	6013	5191.75	1356.6359	TRUE	dehydrogenase/reductase (SDR family) member 1	213279 at	0.056	21589	2.534E-01	FALSE
102708 at	0.136	3960	1425754 a at	0.031	7244	102708 at	-0.030	6493	1419175 a at	0.149	3071	5192	1993.303	FALSE	butyrophilin, subfamily 1, member A1	207395 at	0.040	33311	6.758E-01	FALSE
100334 f at	0.045	6127	1421788 x at	0.104	2940	100334 f at	-0.042	5761	1421788 x at	-0.081	5944	5193	1509.4138	FALSE	epidermal growth factor binding protein type B		NA	NA	NA	NA
93808 at	0.071	4322	1418509 at	0.152	929	93808 at	-0.004	8287	1418509 at	-0.047	7235	5193.25	3300.6533	FALSE	carbonyl reductase 2		NA	NA	NA	NA
101439 at	0.012	8128	1417331 a at	0.163	3279	101439 at	0.211	2194	1417331 a at	0.040	7178	5194.75	2898.9558	TRUE	ADP-ribosylation factor-like 6	235320 at	-0.706	501	1.059E-07	FALSE
92574 at	0.058	6386	1437489 x at	0.056	5922	92574 at	0.092	4186	1428235 at	0.134	4290	5196	1123.1076	TRUE	succinate dehydrogenase complex, subunit D, integral membrane protein	202026 at	-0.095	21898	2.650E-01	FALSE
98127 at	-0.206	3870	1423058 at	-0.045	7414	98127 at	-0.099	5079	1423058 at	0.102	4426	5197.25	1558.245	FALSE	capping protein (actin filament) muscle Z-line, alpha 2	240146 at	0.310	6539	1.082E-03	FALSE
98770 at	0.006	8243	1420441 at	0.136	3246	98770 at	-0.144	872	1420441 at	-0.004	8428	5197.25	3751.8663	FALSE	centromere autoantigen C1	204739 at	0.053	19804	1.945E-01	FALSE
160613 at	0.080	5416	1417109 at	0.075	5744.5	160613 at	-0.027	7200	1417109 at	-0.181	2429	5197.375	2001.795	FALSE	tubulointerstitial nephritis antigen-like	219058 x at	0.076	19800	1.944E-01	FALSE
93452 at	0.051	5468	1450257 at	0.073	4650.5	93452 at	0.113	2965	1450256 at	0.034	7709	5198.125	1971.8068	TRUE	cerberus 1 homolog (Xenopus laevis)	221378 at	0.041	33354	6.770E-01	FALSE
97573 at	0.118	1824	1417306 at	0.095	3681	97573 at	-0.003	8362	1417306 at	-0.046	6926	5198.25	2982.2835	FALSE	tyrosine kinase 2	205546 s at	0.201	4139	1.016E-04	FALSE
95442 at	0.009	8001	1430421 a at	0.099	3176	95442 at	-0.074	3719	1430421 a at	-0.088	5897	5198.25	2207.6635	FALSE	cDNA sequence BC010787	225003 at	-0.136	14538	6.206E-02	FALSE
92210 at	0.083	4004	1448831 at	0.047	6218	92210 at	0.013	7853	1448831 at	-0.304	2718	5198.25	2285.1302	FALSE	angiopoietin 2	205572 at	0.077	27828	4.740E-01	FALSE
160239 at	-0.042	7368	1423697 at	0.169	3496.5	160239 at	0.095	4696	1423697 at	0.081	5233	5198.375	1618.3562	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	202753 at	-0.180	12913	3.600E-02	FALSE
160186 at	0.080	4679	1432435 s at	0.124	2069	160186 at	0.007	8056	1454236 a at	0.084	5992	5199	2507.2294	TRUE	RIKEN cDNA C030004A17 gene	223386 at	-0.118	13730	4.736E-02	FALSE
104487 at	-0.040	6685	1440252 at	0.243	1285.5	104487 at	0.034	6024	1440252 at	-0.172	6802	5199.125	2631.4706	FALSE	H2A histone family, member J	228213 at	-0.130	6715	1.245E-03	FALSE
93015 at	0.024	7293	1423436 at	0.087	3904.5	93015 at	0.061	4093	1423437 at	-0.089	5507	5199.375	1568.2969	FALSE	glutathione S-transferase, alpha 3	222102 at	0.050	26744	4.336E-01	FALSE
96999 at	0.012	7942	1422343 at	0.163	2993	96999 at	0.072	5029	1422343 at	0.141	4835	5199.75	2045.4729	TRUE	olfactory receptor 155		NA	NA	NA	NA
100034 at	0.098	2968	1424623 at	0.081	4700	100034 at	0.027	7438	1438856 x at	0.103	5696	5200.5	1869.6241	TRUE	serine (or cysteine) peptidase inhibitor, clade B, member 5	204855 at	0.015	36641	7.818E-01	FALSE
96597 at	0.107	2427	1421566 at	-0.021	7856	96597 at	0.082	2995	1421566 at	-0.032	7529	5201.75	2888.4897	FALSE	plasmacytoma expressed transcript 2		NA	NA	NA	NA
100943 at	-0.026	7093	1456003 a at	0.245	587	100943 at	0.027	6980	1456003 a at	-0.095	6149	5202.25	3105.4897	FALSE	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	209611 s at	-0.243	4366	1.302E-04	FALSE
160592 at	0.048	6073	1423770 at	0.069	5282.5	160592 at	0.118	2901	1423770 at	0.067	6554	5202.625	1621.4833	TRUE	transmembrane channel-like gene family 6	204328 at	0.238	5664	5.092E-04	TRUE
94147 at	0.008	8053	1419149 at	0.054	5625	94147 at	0.089	4781	1419149 at	-0.180	2354	5203.25	2351.9828	FALSE	serine (or cysteine) peptidase inhibitor, clade E, member 1	202628 s at	-0.010	40647	8.967E-01	FALSE
101337 at	0.056	5159	1426077 at	0.147	2901.5	101337 at	0.014	7598	1426077 at	0.130	5157	5203.875	1918.0699	TRUE	monooxygenase, DBH-like 2		NA	NA	NA	NA
99631 f at	-0.120	3247	1417417 a at	0.039	6770	99631 f at	0.080	3725	1417417 a at	0.039	7078	5205	1998.4592	FALSE	cytochrome c oxidase, subunit VI a, polypeptide 1	200925 at	-0.296	823	2.919E-07	FALSE
103693 at	-0.014	7870	1418685 at	0.110	3229	103693 at	0.114	2342	1418685 at	-0.036	7379	5205	2824.2902	FALSE	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	239796 x at	-0.062	13908	5.077E-02	FALSE
160701 at	0.074	3745	1426966 at	0.035	6922.5	160701 at	-0.051	4988	1426967 at	0.091	5167	5205.625	1307.6617	FALSE	axin 1	212849 at	0.076	15416	7.816E-02	FALSE
94897 at	-0.061	5576	1451695 a at	0.099	4655.5	94897 at	0.176	2529	1451695 a at	-0.018	8063	5205.875	2292.6497	FALSE	glutathione peroxidase 4	201106 at	-0.243	6945	1.521E-03	FALSE
103871 at	0.037	6966	1433627 at	0.078	4460.5	103871 at	0.025	7096	1433627 at	0.176	2304	5206.625	2283.7887	TRUE	Sec23 interacting protein	216392 s at	-0.048	22537	2.863E-01	FALSE
98891 at	0.079	4977	1428218 a at	-0.096	2782	98891 at	-0.032	6484	1428217 at	-0.065	6585	5207	1776.0572	FALSE	RIKEN cDNA 1600012H06 gene	221787 at	-0.153	10399	1.252E-02	FALSE
95595 at	0.066	5650	1452714 at	-0.192	3213	95595 at	-0.067	3871	1446029 at	-0.028	8095	5207.25	2183.096	FALSE	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	234039 at	0.160	8321	3.985E-03	FALSE
93245 at	0.015	7933	1439810 s at	0.157	2252	93245 at	0.093	3468	1439809 at	-0.037	7177	5207.5	2772.972	FALSE	preferentially expressed antigen in melanoma like 7		NA	NA	NA	NA
104002 at	-0.041	6703	1418397 at	0.069	5029.5	104002 at	0.098	2741	1418397 at	0.063	6359	5208.125	1796.0862	FALSE	zinc finger protein 275	225383 at	0.198	7318	2.020E-03	FALSE
94357 at	0.071	3989	1419057 at	-0.041	6911	94357 at	0.063	5358	1419057 at	0.101	4576	5208.5	1265.977	FALSE	solute carrier family 5 (sodium/glucose cotransporter), member 1	242773 at	-0.030	30161	5.618E-01	FALSE
104489 at	0.001	8443	1420371 at	0.101	3305	104489 at	0.036	6139	1420372 at	0.329	2950	5209.25	2585.3403	TRUE	syntrophin, basic 2	205315 s at	0.162	12096	2.689E-02	TRUE
94164 at	0.151	1791	1419695 at	0.104	4439	94164 at	0.039	6635	1419694 at	0.019	7972	5209.25	2704.519	TRUE	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	210073 at	0.157	12968	3.662E-02	TRUE
101058 at	-0.019	8087	1417765 a at	0.149	4413	101058 at	-0.175	4680	1417765 a at	-0.168	3658	5209.5	1966.5487	FALSE	amylase 1, salivary	208498 s at	-0.174	18597	1.579E-01	FALSE
99426 at	-0.074	4920	1419126 at	0.074	4940	99426 at	-0.036	6851	1419126 at	0.159	4127	5209.5	1157.9823	FALSE	homeo box D9	229493 at	-0.064	21953	2.670E-01	FALSE
160924 at	-0.184	2302	1436896 at	-0.028	7579.5	160924 at	0.073	3319	1436896 at	-0.030	7638	5209.625	2801.3127	FALSE	DNA segment, Chr 14, ERATO Doi 231, expressed	203941 at	0.103	9847	9.254E-03	FALSE
97237 at	-0.187	2841	1450735 at	0.036	7098	97237 at	0.143	4023	1450735 at	0.057	6877	5209.75	2110.6526	FALSE	RIKEN cDNA 1810003N24 gene	203622 s at	-0.337	3125	2.687E-05	FALSE
95679 at	0.027	7133	1417161 at	0.092	2672	95679 at	-0.055	4914	1456490 at	0.067	6120	5209.75	1919.6431	FALSE	CDK2-associated protein 2	203252 at	0.318	6986	1.565E-03	FALSE
103038 at	0.079	4511	1421061 at	0.035	7381	103038 at	-0.012	7884	1421061 at	-0.290	1065	5210.25	3137.5756	FALSE	guanylate cyclase activator 1a (retina)	1255 g at	-0.424	1131	6.269E-07	FALSE
101717 at	0.069	4938	1422281 at	0.147	2197	101717 at	-0.009	8033	1422281 at	-0.103	5675	5210.75	2404.0039	FALSE	somatostatin receptor 4	214556 at	0.029	35587	7.490E-01	FALSE
92858 at	-0.154	1320	1448377 at	0.053	6357	162329 r at	0.053	4739	1448377 at	-0.004	8433	5212.25	3003.1794	FALSE	secretory leukocyte peptidase inhibitor	203021 at	0.029	33312	6.758E-01	FALSE
100606 at	-0.002	8412	1416130 at	-0.087	4645	100606 at	0.028	6805	1416130 at	0.278	988	5212.5	3211.506	FALSE	prion protein	215707 s at	-0.471	6077	7.471E-04	FALSE
93069 at	0.135	4280	1416477 at	-0.045	7056	93069 at	0.138	4598	1439655 at	0.127	4919	5213.25	1255.8926	FALSE	ubiquitin-conjugating enzyme E2D 2	215604 x at	0.308	2777	1.545E-05	FALSE
98112 r at	-0.014	7937	1450860 at	-0.124	3486	98112 r at	-0.068	4075	1450860 at	-0.113	5355	5213.25	1976.3529	TRUE	leucine aminopeptidase 3	217933 s at	0.277	16642	1.047E-01	FALSE
103548 at	-0.048	5974	1419411 at	-0.029	7930	103548 at	0.199	509	1419411 at	-0.449	6442	5213.75	3245.472	FALSE	tachykinin 2	219992 at	-0.057	26591	4.278E-01	FALSE
100509 at	-0.077	5195	1417508 at	0.072	5480	161814 f at	0.086	3610	1417508 at	0.059	6572	5214.25	1223.124	FALSE	ring finger protein (C3HC4 type) 19	223085 at	0.797	1483	1.345E-06	FALSE
102054 at	-0.029	6803	1417685 at	0.051	6087.5	102054 at	0.083	5202	1443654 at	0.235	2767	5214.875	1758.3964	FALSE	ankyrin repeat and FYVE domain containing 1	224900 at	0.297	4544	1.621E-04	FALSE
94119 at	0.141	2060	1450228 a at	0.030	7691.5	94119 at	-0.128	3271	1450228 a at	-0.046	7837	5214.875	2985.5819	FALSE	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	212518 at	-0.196	8534	4.439E-03	FALSE
94445 at	-0.006	8292	1423725 at	-0.030	7380	94445 at	-0.262	3338	1423725 at	0.187	1851	5215.25	3108.8465	FALSE	plastin 3 (T-isoform)	201215 at	0.464	6923	1.498E-03	FALSE
93305 f at	0.049	5800	1420624 a at	0.086	5070.5	93305 f at	0.145	1761	1420624 a at	-0.026	8235	5216.625	2671.6793	FALSE	vesicle-associated membrane protein 8	202546 at	0.253	11307	1.955E-02	FALSE
94107 at	0.041	6697	1421057 at	0.054	5892	94107 at	0.263	278	1421057 at	-0.027	8000	5216.75	3405.1351	FALSE	deoxyribonuclease 1-like 3	205554 s at	-0.009	41265	9.144E-01	FALSE
102816 at	0.006	8273	1421921 at	0.166	1677	102816 at	0.085	2941	1421921 at	-0.018	7986	5219.25	3401.8746	FALSE	serine (or cysteine) peptidase inhibitor, clade A, member 3M		NA	NA	NA	NA
99980 at	0.081	5813	1427454 at	0.060	5138.5	99980 at	0.038	5919	1427362 x at	0.112	4011	5220.375	877.2253	TRUE	homeo box C6	206858 s at	0.231	3625	5.468E-05	TRUE
95066 at	-0.234	2869	1425129 a at	-0.116	3091.5	95066 at	-0.064	6875	1425129 a at	-0.018	8046	5220.375	2632.047	TRUE	transaldolase 1	201463 s at	0.153	19760	1.931E-01	FALSE
97179 at	0.053	5481	1460713 at	0.072	4300.5	97179 at	-0.086	3280	1460713 at	0.034	7822	5220.875	1953.4245	FALSE	cDNA sequence BC048355	213871 s at	-0.063	21322	2.441E-01	FALSE
99321 at	0.100	2732	1421729 a at	0.095	4154	99321 at	-0.023	6848	1421729 a at	0.044	7150	5221	2137.1149	FALSE	fer (fms/fps related) protein kinase, testis specific 2	206412 at	0.012	39396	8.615E-01	FALSE
100091 at	-0.067	5902	1448769 at	0.006	8339	100091 at	0.091	3981	1448769 at	0.167	2664	5221.5	2467.2206	FALSE	solute carrier family 35, member B1	202433 at	-0.196	11202	1.873E-02	FALSE
161835 at	0.041	6648	1448964 at	0.066	5145	160918 at	-0.079	3434	1448964 at	0.072	5661	5222	1345.2472	FALSE	S100 calcium binding protein G	207885 at	0.025	35681	7.520E-01	FALSE
103468 at	0.046	5757	1419402 at	0.069	5387	103468 at	0.099	2162	1419402 at	-0.075	7585	5222.75	2255.4243	FALSE	meiosis-specific nuclear structural protein 1	219703 at	0.482	8865	5.369E-03	FALSE
92731 at	0.054	6155	1418666 at	0.095	3553.5	92731 at	0.079	4425	1456903 at	0.075	6758	5222.875	1488.7224	TRUE	pentraxin related gene	206157 at	0.037	28394	4.972E-01	FALSE
97884 at	-0.015	7709	1455233 at	0.075	4875.5	97884 at	-0.036	6033	1460195 at	0.199	2275	5223.125	2283.8386	FALSE	mitochondrial ribosomal protein S11	211595 s at	-0.113	12916	3.603E-02	FALSE
95103 at	0.045	6580	1417243 at	0.090	4135	95103 at	0.174	2035	1417243 at	-0.018	8145	5223.75	2691.1348	FALSE	RIKEN cDNA 2310065K24 gene	217896 s at	0.079	13306	4.117E-02	FALSE
100549 at	0.088	4702	1448716 at	0.064	4660.5	100549 at	0.088	4165	1448716 at	0.054	7369	5224.125	1450.5771	TRUE	hemoglobin X, alpha-like embryonic chain in Hba complex	206647 at	0.057	21246	2.416E-01	FALSE
99085 at	0.047	6026	1425023 at	0.054	6934	99085 at	-0.080	4054	1446886 at	0.135	3888	5225.5	1496.7844	FALSE	ubiquitin specific peptidase 3	221654 s at	0.224	7275	1.960E-03	FALSE
103897 r at	0.136	2146	1418918 at	0.066	6120	103897 r at	0.082	4435	1418918 at	0.023	8201	5225.5	2566.5763	TRUE	insulin-like growth factor binding protein 1	237989 at	-0.055	17273	1.212E-01	FALSE
95060 at	0.004	8295	1448502 at	0.040	7002	95060 at	-0.224	655	1448502 at	0.089	4952	5226	3343.7531	FALSE	solute carrier family 16 (monocarboxylic acid transporters), member 7	210807 s at	-0.066	18204	1.459E-01	FALSE
160951 at	-0.033	6572	1421092 at	0.145	1872.5	160951 at	0.037	5923	1421091 at	-0.054	6538	5226.375	2255.7209	FALSE	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12		NA	NA	NA	NA
161785 f at	0.119	3511	1420140 at	0.060	5647	161785 f at	0.058	5406	1424288 at	-0.062	6342	5226.5	1210.5537	FALSE	bin3, bicoid-interacting 3, homolog (Drosophila)	219798 s at	0.060	20309	2.100E-01	FALSE
95372 at	0.060	5745	1419847 at	0.050	6038	95372 at	0.097	4376	1433522 at	-0.104	4749	5227	791.35538	FALSE	Protein serine kinase H1	213141 at	0.035	30107	5.597E-01	FALSE

100454 at	-0.079	4206	1416674 at	0.044	6234.5	100454 at	-0.047	6201	1416674 at	0.175	4267	5227.125	1144.228	FALSE	protein tyrosine phosphatase, receptor type, U	211320 s at	-0.003	43203	9.653E-01	FALSE
97734 at	0.102	3248	1449569 at	-0.003	8412.5	97734 at	0.004	8286	1449569 at	-0.242	965	5227.875	3723.1695	FALSE	thrombopoietin	211155 s at	-0.030	27487	4.611E-01	FALSE
94258 at	-0.026	7223	1426454 at	0.017	7840	94258 at	-0.070	5078	1426454 at	-0.324	771	5228	3198.4328	FALSE	Rho, GDP dissociation inhibitor (GDI) beta	201288 at	0.296	12020	2.617E-02	FALSE
101213 at	-0.179	3035	1419441 at	-0.081	5983	101213 at	0.078	4311	1419441 at	-0.035	7583	5228	1980.4198	FALSE	acidic ribosomal phosphoprotein P0	211720 x at	0.171	12223	2.828E-02	FALSE
160335 at	-0.119	4733	1418627 at	-0.084	5489	160335 at	-0.005	8302	1418627 at	0.209	2388	5228	2437.7737	FALSE	glutamate-cysteine ligase , modifier subunit	203925 at	0.070	33378	6.776E-01	FALSE
94120 s at	0.153	3557	1449833 at	-0.060	6087.5	94120 s at	0.051	5554	1449833 at	0.118	5718	5229.125	1136.86	FALSE	small proline-rich protein 2F	NA	NA	NA	NA	
102258 at	0.053	5545	1422723 at	-0.016	7846	102258 at	-0.082	3097	1422723 at	0.193	4429	5229.25	2011.1331	FALSE	stimulated by retinoic acid gene 6	221701 s at	-0.020	37202	7.968E-01	FALSE
94815 at	-0.219	2972	1415865 s at	0.074	4568	94815 at	0.051	6637	1415864 at	0.048	6741	5229.5	1807.3532	FALSE	2,3-bisphosphoglycerate mutase	238724 at	0.105	12133	2.726E-02	FALSE
161780 f at	0.169	1622	1427264 at	0.069	4696	93457 at	-0.022	7281	1427264 at	-0.035	7320	5229.75	2700.4642	FALSE	crystallin, gamma B	207715 at	-0.034	29119	5.250E-01	FALSE
99839 at	0.050	5634	1420735 at	0.018	7910	99839 at	0.041	5821	1420735 at	-0.222	1557	5230.5	2657.4314	FALSE	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	208217 at	-0.054	24327	3.482E-01	FALSE
93692 f at	0.010	8058	1449417 at	0.121	4045	93692 f at	0.112	2327	1449417 at	-0.067	6496	5231.5	2545.0583	FALSE	ameloblastin	221114 at	-0.344	2364	7.576E-06	FALSE
95058 f at	-0.269	2378	1423833 a at	-0.047	6299	95058 f at	0.122	6094	1423833 a at	0.102	6157	5232	1904.5974	FALSE	brain protein 44	227669 at	-0.698	775	2.543E-07	FALSE
93586 at	-0.015	7696	1417081 a at	-0.072	5558	93586 at	0.090	2444	1448577 x at	-0.129	5230	5232	2156.4261	FALSE	synaptogyrin 2	201079 at	0.163	14109	5.449E-02	FALSE
99847 at	0.092	4883	1418946 at	0.128	3502	99847 at	-0.068	4726	1418946 at	-0.032	7817	5232	1830.5702	FALSE	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	215874 at	0.067	21010	2.336E-01	FALSE
160348 at	-0.064	4478	1452673 at	-0.002	8452	160348 at	0.058	5258	1457711 at	0.256	2742	5232.5	2390.097	FALSE	RAN binding protein 3	202640 s at	0.115	13493	4.389E-02	FALSE
96937 at	-0.071	4566	1417026 at	0.100	5848	96937 at	0.081	3654	1417026 at	0.066	6864	5233	1411.4432	FALSE	prefoldin 1	201507 at	-0.161	5032	2.768E-04	FALSE
104050 at	0.155	2087	1449552 at	0.013	8160	104050 at	-0.006	8186	1444096 at	0.253	2500	5233.25	3398.7323	FALSE	zinc finger RNA binding protein	242797 x at	0.174	14372	5.938E-02	FALSE
93859 at	-0.258	1472	1415685 at	-0.044	7535	93859 at	0.061	6404	1415685 at	0.083	5532	5235.75	2639.7561	FALSE	mitochondrial translational initiation factor 2	203095 at	0.071	25673	3.936E-01	FALSE
100491 at	0.034	6555	1418446 at	-0.104	3025	100491 at	-0.023	6722	1418446 at	-0.328	4642	5236	1750.1728	FALSE	solute carrier family 16 (monocarboxylic acid transporters), member 2	204462 s at	-0.087	14705	6.522E-02	FALSE
102311 at	0.021	7587	1419720 at	0.116	3875	102311 at	0.095	4514	1419720 at	-0.113	4970	5236.5	1630.088	FALSE	glycoprotein 9 (platelet)	206883 x at	0.071	21198	2.398E-01	FALSE
162190 r at	0.104	2741	1451165 at	0.014	7909	104722 at	0.025	6670	1457792 at	0.147	3628	5237	2450.3041	TRUE	limb region 1 like	220036 s at	0.023	36116	7.662E-01	FALSE
97229 at	0.116	2635	1453816 at	0.110	2970.5	97229 at	0.026	7059	1453816 at	0.009	8287	5237.875	2859.4642	TRUE	RIKEN cDNA 5730427N09 gene	201922 at	-0.335	4196	1.081E-04	FALSE
104349 at	0.169	882	1428133 at	0.067	4626	104349 at	0.005	8216	1459773 x at	0.064	7228	5238	3275.0503	TRUE	Smad nuclear interacting protein 1	219409 at	-0.002	43397	9.698E-01	FALSE
95633 r at	0.096	3758	1418052 at	-0.102	3764.5	95633 r at	0.005	8309	1418052 at	0.084	5124	5238.875	2145.199	FALSE	mevalonate kinase	36907 at	0.085	11166	1.843E-02	FALSE
102209 at	0.076	5018	1417621 at	0.033	7213.5	102209 at	0.054	5244	1447085 s at	-0.162	3487	5240.625	1529.38	FALSE	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	211105 s at	0.343	1805	2.677E-06	FALSE
97998 at	-0.003	8381	1421149 a at	0.147	4225	97998 at	0.103	4292	1421149 a at	-0.262	4071	5242.25	2094.5446	FALSE	atrophin 1	236961 at	0.223	3825	6.854E-05	FALSE
162144 at	0.115	3902	1428181 at	0.065	5086	96947 at	0.113	4306	1428181 at	0.043	7680	5243.5	1697.0432	TRUE	electron transferring flavoprotein, beta polypeptide	202942 at	-0.102	17546	1.278E-01	FALSE
160402 at	-0.264	1163	1428263 a at	0.141	5317	160402 at	0.035	6687	1428263 a at	0.023	7807	5243.5	2904.6576	FALSE	transcription elongation factor B (SIII), polypeptide 2	200085 s at	-0.065	28312	4.939E-01	FALSE
102763 at	0.170	883	1418595 at	0.057	6346	102763 at	0.052	5762	1418595 at	0.020	7983	5243.5	3055.2233	TRUE	plasma membrane associated protein, S3-12	NA	NA	NA	NA	
103573 at	0.068	6099	1421834 at	0.080	4447	103573 at	-0.194	3172	1450389 s at	0.049	7258	5244	1799.5938	FALSE	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	205632 s at	-0.147	19511	1.851E-01	FALSE
96487 at	0.034	7115	1442976 at	0.136	3748	96487 at	0.109	2695	1442976 at	-0.038	7418	5244	2377.8375	FALSE	expressed sequence C81072	NA	NA	NA	NA	
103006 at	0.105	2466	1425927 a at	-0.026	7401	103006 at	-0.071	4839	1425927 a at	-0.066	6273	5244.75	2128.5987	FALSE	activating transcription factor 5	204998 s at	-0.035	31817	6.256E-01	FALSE
104042 at	0.027	6823	1423927 at	-0.081	3600	104042 at	-0.112	3143	1423927 at	-0.047	7416	5245.5	2185.3873	FALSE	solute carrier family 35, member B2	NA	NA	NA	NA	
94948 at	0.024	7134	1449041 a at	-0.047	6702.5	94948 at	0.045	6298	1449041 a at	-0.318	852	5246.625	2949.5692	FALSE	thyroid hormone receptor interactor 6	209129 at	0.480	1541	1.525E-06	FALSE
94932 at	0.077	4559	1449187 at	-0.085	4006	94932 at	0.091	5098	1418711 at	0.045	7324	5246.75	1454.8258	FALSE	platelet derived growth factor, alpha	205463 s at	0.358	4398	1.358E-04	FALSE
101385 at	-0.080	3481	1417728 at	0.015	8060.5	101385 at	-0.051	4677	1417728 at	0.171	4769	5246.875	1965.3602	FALSE	methyl-CpG binding domain protein 3	241680 at	0.101	13939	5.130E-02	FALSE
99351 at	0.223	866	1441146 at	0.028	7397	99351 at	-0.011	7906	1441146 at	0.147	4820	5247.25	3218.088	FALSE	expressed sequence C76132	NA	NA	NA	NA	
99158 at	-0.158	1144	1452246 at	-0.032	7425	99158 at	-0.007	8079	1446023 at	0.137	4345	5248.25	3183.9239	FALSE	osteoclast stimulating factor 1	204479 at	-0.093	20412	2.134E-01	FALSE
98503 at	0.009	8122	1417513 at	0.071	5808	98503 at	-0.040	6607	1417513 at	0.608	457	5248.5	3335.3679	FALSE	ecotropic viral integration site 5	209717 at	0.365	2257	6.109E-06	FALSE
160420 r at	0.151	3368	1438611 at	0.049	6746	160420 r at	0.070	5962	1438611 at	0.140	4918	5248.5	1460.2624	TRUE	tubulin, alpha 3	NA	NA	NA	NA	
96270 at	-0.120	3474	1426745 at	0.000	8526	96270 at	-0.134	3929	1426745 at	0.084	5070	5249.75	2285.0086	FALSE	DNA segment, Chr 11, Brigham & Women's Genetics 0434 expressed	224573 at	-0.241	7291	1.984E-03	FALSE
100020 at	0.140	2391	1416637 at	-0.039	7550	100020 at	0.048	4991	1416637 at	-0.199	6070	5250.5	2175.88	FALSE	solute carrier family 4 (anion exchanger), member 2	202111 at	0.134	9262	6.813E-03	FALSE
95692 at	-0.088	4823	1433708 at	-0.005	8316	95692 at	-0.228	1738	1433708 at	0.075	6126	5250.75	2749.8002	FALSE	signal recognition particle 68	224607 s at	-0.075	22072	2.707E-01	FALSE
104310 at	0.050	5500	1428245 at	0.098	3610	104310 at	-0.006	8142	1428245 at	0.218	3753	5251.25	2110.0369	FALSE	glucose 6 phosphatase, catalytic, 3	44654 at	0.225	1257	8.163E-07	FALSE
96841 at	-0.007	8131	1437100 x at	-0.168	2112	96841 at	0.036	5729	1451069 at	-0.085	5034	5251.5	2478.1238	FALSE	proviral integration site 3	224739 at	0.111	21193	2.395E-01	FALSE
103060 at	-0.009	8024	1434121 at	-0.073	5262.5	103060 at	0.022	6981	1434121 at	-0.284	740	5251.875	3216.1923	FALSE	leucine-rich repeat LGI family, member 4	227821 at	0.286	4515	1.599E-04	FALSE
93213 at	-0.068	4904	1425871 a at	0.141	3984	93213 at	0.011	7991	1427792 at	0.110	4132	5252.75	1869.5317	FALSE	Similar to immunoglobulin light chain variable region	NA	NA	NA	NA	
104134 at	0.050	5782	1424057 at	0.124	2011	104134 at	0.032	6282	1424057 at	0.055	6937	5253	2212.4724	TRUE	ganglioside-induced differentiation-associated-protein 2	219473 at	-0.005	42554	9.486E-01	FALSE
161971 r at	-0.067	4616	1422755 at	0.021	7718	161971 r at	-0.057	4908	1422755 at	-0.137	3773	5253.75	1711.8622	FALSE	Bruton agammaglobulinemia tyrosine kinase	205504 at	0.023	37785	8.146E-01	FALSE
104335 at	0.007	8101	1416199 at	-0.075	3888	104335 at	-0.107	3510	1416199 at	0.100	5518	5254.25	2088.2686	FALSE	kinesin family member C3	209661 at	-0.055	25002	3.724E-01	FALSE
98543 at	-0.323	4056	1448591 at	0.033	7698	98543 at	0.129	5629	1448591 at	-0.431	3635	5254.5	1841.2066	FALSE	cathepsin S	237104 at	0.136	10449	1.291E-02	FALSE
99442 at	0.150	4901	1417988 at	-0.085	7833	99442 at	0.287	676	1417988 at	-0.109	7610	5255	3330.8991	FALSE	regulated endocrine-specific protein 18	NA	NA	NA	NA	
101679 at	0.106	3410	1419723 at	0.074	5273	101679 at	0.060	5036	1419723 at	-0.041	7304	5255.75	1596.9459	FALSE	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)	221327 s at	0.012	37804	8.150E-01	FALSE
101139 r at	0.390	1874	1449587 a at	0.090	3880.5	101139 r at	0.015	8100	1449587 a at	0.055	7171	5256.375	2891.6826	TRUE	mucin 10, submandibular gland salivary mucin	NA	NA	NA	NA	
103485 at	0.150	1549	1439064 at	0.047	6632	103485 at	0.055	5881	1439064 at	0.047	6964	5256.5	2512.8412	TRUE	cDNA sequence BC030046	220911 s at	0.079	13294	4.105E-02	TRUE
98839 at	0.126	3831	1427436 at	0.031	7525	98839 at	0.003	8303	1427436 at	-0.234	1368	5256.75	3244.469	FALSE	sine oculis-related homeobox 2 homolog (Drosophila)	206511 s at	0.047	23397	3.166E-01	FALSE
98040 at	0.050	5713	1427764 a at	-0.068	5574	98040 at	-0.046	5830	1452542 x at	0.150	3913	5257.5	902.42063	FALSE	transcription factor E2a	209153 s at	0.200	2919	1.901E-05	FALSE
93898 at	0.117	3790	1419667 at	0.025	7411	93898 at	-0.101	4072	1419668 at	0.083	5757	5257.5	1677.8984	FALSE	sarcoglycan, beta (dystrophin-associated glycoprotein)	205121 at	-0.104	9205	6.561E-03	FALSE
97997 at	-0.010	7969	1438620 x at	0.131	2221	97997 at	0.052	5030	1428136 at	-0.153	5815	5258.75	2375.9293	FALSE	secreted frizzled-related sequence protein 1	202035 s at	0.064	17104	1.171E-01	FALSE
98324 at	-0.021	7807	1431900 a at	-0.096	3573.5	98324 at	0.034	7012	1431900 a at	0.151	2646	5259.625	2532.0605	FALSE	forkhead box A3	228463 at	0.010	39127	8.549E-01	FALSE
102376 r at	0.062	4806	1419084 a at	0.075	5723.5	162452 at	0.055	5562	1419085 at	-0.167	4951	5260.625	450.04877	FALSE	Purkinje cell protein 2 (L7)	244751 at	-0.002	43602	9.751E-01	FALSE
161544 r at	-0.170	934	1449360 at	-0.026	7587	103210 at	0.063	4496	1449360 at	-0.024	8027	5261	3284.7722	FALSE	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	205159 at	0.068	23314	3.128E-01	FALSE
98289 at	0.109	4646	1421337 at	0.075	5875	98289 at	0.034	6679	1421337 at	-0.145	3845	5261.25	1261.0843	FALSE	E74-like factor 4 (ets domain transcription factor)	31845 at	0.170	1224	7.580E-07	FALSE
100424 at	0.077	4633	1417328 at	0.088	3332.5	100424 at	-0.028	6821	1437447 s at	-0.068	6262	5262.125	1586.3052	FALSE	excision repair cross-complementing rodent repair deficiency, complementation group 1	228131 at	0.145	7948	3.178E-03	FALSE
162436 at	0.019	7400	1449004 at	0.187	995.5	162436 at	0.061	4381	1449004 at	0.009	8276	5263.125	3298.2024	TRUE	mitochondrial ribosomal protein L46	219244 s at	0.016	39114	8.548E-01	FALSE
103817 at	0.053	6184	1448592 at	0.040	6954	103817 at	0.083	3171	1448592 at	-0.178	4744	5263.25	1668.6868	FALSE	cartilage associated protein	226656 at	0.507	26	2.825E-09	FALSE
104220 at	0.094	3082	1422771 at	0.038	7315.5	104220 at	-0.044	5847	1422771 at	-0.125	4811	5263.875	1780.9056	FALSE	similar to Mothers against decapentaplegic homolog 6 (SMAD 6) (Mothers against DPP homolog 6) (Smad6) (Mad hor	NA	NA	NA	NA	
93042 at	0.017	7623	1438948 x at	0.265	1285.5	93042 at	-0.023	6791	1456251 x at	-0.183	5357	5264.125	2812.6927	FALSE	benzodiazepine receptor, peripheral	202096 s at	0.395	2288	6.595E-06	FALSE
99818 at	0.229	2336	1442597 at	0.071	5634	99818 at	-0.081	4760	1442597 at	-0.009	8327	5264.25	2472.9246	FALSE	expressed sequence C79122	NA	NA	NA	NA	
160195 at	-0.188	1540	1415721 a at	-0.053	6474	160195 at	0.023	7654	1415721 a at	0.089	5392	5265	2649.5758	FALSE	RIKEN cDNA 1200013P24 gene	218661 at	-0.051	25422	3.873E-01	FALSE
92846 at	0.250	1533	1416385 a at	0.018	7919	92846 at	0.071	3713	1416386 a at	0.023	7896	5265.25	3178.1758	TRUE	mannose-6-phosphate receptor, cation dependent	200900 s at	-0.184	11245	1.906E-02	FALSE
160118 at	0.038	6846	1448383 at	-0.088	3779.5	160118 at	-0.092	3113	1416572 at	0.044	7325	5265.875	2127.6726	FALSE	matrix metallopeptidase 14 (membrane-inserted)	202827 s at	0.094	19300	1.778E-01	FALSE
97719 at	0.161	2352	1420461 at	0.133	2785.5	97719 at	0.002	8391	1420461 at	0.037	7536	5266.125	3139.1507	TRUE	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	205455 at	-0.001	44485	9.959E-01	FALSE
103516 at	0.054	5921	1418925 at	-0.007	8213	103516 at	0.057	4467	1418925 at	-0.336	2464	5266.25	2422.3569	FALSE	cadherin EGF LAG seven-pass G-type receptor 1	41660 at	0.041	23682	3.266E-01	FALSE
99387 at	0.122	2051	1450808 at	0.084	3808	99387 at	0.020	7208	1450808 at	0.025	8003	5267.5	2812.147	TRUE	formyl peptide receptor 1	205119 s at	0.228	17579	1.289E-01	FALSE
92692 at	-0.076	5597	1427291 at	0.107	2451	92692 at	0.089	4673	1427291 at	0.008	8352	5268.25	2443.2772	FALSE	synaptonemal complex protein 1	206740 x at	-0.037	26491	4.246E-01	FALSE
101235 f at	0.098	4863	1457833 at	0.163	2153	101235 f at	0.006	8200	1457833 at	-0.068	5858	5268.5	2504.1281	FALSE	Expressed sequence AI450241	NA	NA	NA	NA	
95037 at	-0.238	631	1417269 at	-0.001	8509	95037 at	0.038	6862	1457240 at	-0.142	5073	5268.75	3395.3256	FALSE	cyclin-dependent kinase 9 (CDC2-related kinase)	203198 at	0.144	13076	3.797E-02	FALSE
103970 at	-0.090	5097	1423526 at	-0.073	4814	103970 at	-0.078	4326	1423526 a at	-0.174	6839	5269	1094.0381	TRUE	AT rich interactive domain 3B (Bright like)	218964 at	-0.012	39015	8.511E-01	FALSE
96155 at	-0.074	4357	1423067 at	0.022	7813	96155 at	-0.093	2808	1423067 at	-0.088	6102	5270	2164.4157	FALSE	CDK5 regulatory subunit associated protein 3	218740 s at	0.135	13089	3.818E-02	FALSE
100527 at	-0.009	8266	1423840 at	0.127	4838	100527 at	-0.075	3247	1423840 at	0.124	4729	5270	2125.0765	FALSE	coiled-coil domain containing 56	NA	NA	NA	NA	
95248 at	0.071	5699	1420169 at	0.124	2582	95248 at	-0.049	5394	1420168 at	0.033	7408	5270.75	1999.6502	FALSE	expressed sequence AA517841	NA	NA	NA	NA	
97562 r at	0.240	817	1422932 a at	0.027	7669	96511 s at	-0.023	6863	1422932 a at	-0.099	5737	5271.5	3073.5506	FALSE	vav 1 oncogene	206219 s at	-0.040	26126	4.086E-01	FALSE
92927 at	-0.015	8175	1422607 at	-0.113	4133	92927 at	-0.035	7420	1422607 at	0.304	1360	5272	3143.3728	FALSE	ets variant gene 1	217061 s at	-0.253	2760	1.513E-05	FALSE
160302 at	0.060	5604	1424106 at	0.089	4026	160302 at	0.029	6448	1424106 at	0.128	5010	5272	1018.8817	TRUE	RIKEN cDNA 1200003C05 gene	223547 at	0.037	35657	7.510E-01	FALSE
160823 at	0.073	3971	1423196 at	0.084	5032.5	160823 at	-0.019	7237	1423196 at	0.114	4849	5272.375	1389.2582	FALSE	neural precursor cell expressed, developmentally down-regulated gene 1	234984 at	0.251	5058	2.824E-04	FALSE
101161 at	0.052	5234	1422069 at	0.105	3158	101161 at	0.009	8053	1422069 at	0.110	4645	5272.5	2049.1892	TRUE	melanocortin 1 receptor	205458 at	-0.029	35306	7.403E-01	FALSE
98561 at	0.063	5833	1450813 a at	0.031	7242	98561 at	0.025	6720	1450813 a at	-0.310	1304	5274.75	2710.3086	FALSE	troponin I, skeletal, slow 1	205177 at	0.002	43379	9.688E-01	FALSE
160663 at	0.011	7913	1423814 at	-0.040	6454	160663 at	-0.151	1788	1423814 at	0.091	4946	5275.25	2621.4814	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	217840 at	-0.219	6152	7.937E-04	FALSE
103980 at	0.125	2432	1421151 a at	0.050	6256	103980 at	0.074	4662.5	1421151 a at	0.033	7751	5275.375	2276.7478	TRUE	Eph receptor A2	203499 at	0.080	16744	1.072E-01	FALSE
103245 at	0.256	2489	1424479 at	0.051	5938	103245 at	0.049	4724	1424479 at	0.021	7952	5275.75	2285.5556	TRUE	cystatin 8 (cystatin-related epididymal spermatogenic)	220627 at	0.026	34887	7.273E-01	FALSE
93594 r at	0.095	4725	1417104 at	0.003	8426.5	93594 r at	0.037	5703	1417104 at	-0.198	2249	5275.875	2554.3629	FALSE	epithelial membrane protein 3	203729 at	0.588	2109	4.610E-06	FALSE
95857 at	0.055	5878	1444866 at	0.182	922	95857 at	0.058	5905	1444866 at	0.006	8400	5276.25	3134.4716	TRUE	RIKEN cDNA E230006M18 gene	NA	NA	NA	NA	
100634 at	0.051	5975	1448723 at	0.153	1186.5	100634 at	0.019	7465	1448723 at	-0.059	6479	5276.375	2795.9221	FALSE	retinol dehydrogenase 7	NA	NA	NA	NA	
160331 at	0.038	6773	1420663 at	0.097	4591.5	160331 at	0.096	4546	1455071 at	-0.079	5197	5276.875	1040.6228	FALSE	Vzinc finger and BTB domain containing 7B	205853 at	-0.035	33488	6.814E-01	FALSE
101153 at	-0.029	6722	1427814 at	0.108	2944.5	101153 at	0.061	4382	1427814 at	-0.049	7062	5277.625	1959.2371	FALSE	oncofetal antigen	NA	NA	NA	NA	
101450 at	0.013	7778	1425155 x at	0.133	2698	101450 at	0.034	6035	1425154 a at	-0.092	4605	5279	2155.0231	FALSE	colony stimulating factor 1 (macrophage)	209716 at	0.186	3106	2.630E-05	FALSE
94274 at	0.089	4215	1416726 s at	0.173	1519.5	94274 at	0.034	7034	1416726 s at	-0.017	8349	5279.375	3042.5242	FALSE	ubiquitin-conjugating enzyme E2S	202779 s at	-0.301	7088	1.687E-03	FALSE
99817 at	0.031	6792	1450303 at	0.094	4546	99817 at	-0.083	3052	1450303 at	0.061	6730	5280	1815.7995	FALSE	ventral anterior homeobox containing gene 2	220443 s at	0.011	39871	8.741E-01	FALSE
96524 at	0.048	5838	1459911 at	0.077	4474	96524 at	0.091	2908	1459911 at	0.022	7901	5280.25	2117.9412	TRUE	cerebellar degeneration-related protein 2-like	213230 at	0.214	7620	2.502E-03	TRUE
161716 at	0.186	3170	1423100 at	0.017	8143	160901 at	0.311	3621	1423100 at	-0.175	6189	5280.75	2325.7564	FALSE	FBJ osteosarcoma oncogene	209189 at	0.367	20301	2.099E-01	FALSE
93748 at	0.024	7497	1431390 a at	-0.028	7516	93748 at	0.098	2398	1431390 a at	0.122	3713	5281	2625.2742	FALSE	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	212244 at	0.381	513	1.080E-07	FALSE
99844 at	0.107	3486	1427529 at	0.007	8260	99844 at	0.100	2852	1427529 at	0.087	6527	5281.25	2552.7125	TRUE	frizzled homolog 9 (Drosophila)	207639 at	0.032	34033	6.997E-01	FALSE
94772 at	0.178	698	1450296 at	0.097	5177.5	94772 at	-0.018	7616	1450296 at	0.028	7634	5281.375	3266.1616	FALSE	killer cell lectin-like receptor subfamily B member 1A	NA	NA	NA	NA	
95932 at	0.095	4080	1450306 at	0.016	7981.5	95932 at	0.047	6240	1450306 at	-0.224	2826	5281.875	2286.322	FALSE	zona pellucida glycoprotein 1	237335 at	0.062	21644	2.554E-01	FALSE
94372 at	0.030	6923	1449349 at	0.100	2365	94372 at	0.012	7832	1449349 at	0.218	4009	5282.25	2538.0307	TRUE	nudix (nucleoside diphosphate linked moiety X)-type motif 1	204766 s at	-0.215	6772	1.304E-03	FALSE
99179 at	-0.130	4120	1431145 a at	0.083	4830	99179 at	0.037	7040	1431145 a at	0.112	5140	5282.5	1247.0331	FALSE	CUE domain containing 2	218097 s at	-0.062	23163	3.074E-01	FALSE
99607 at	0.096	5618	1423149 at	0.102	6296	99607 at	0.037	7415	1423148 at	0.193	1803	5283	2435.4478	TRUE	S-phase kinase-associated protein 1A	200711 s at	-0.115	14836	6.744E-02	FALSE
160860 at	-0.001	8487	1424007 at	-0.041	7246	160860 at	0.137	1611	1424007 at	-0.204	3789	5283.25	3153.5485	FALSE	growth differentiation factor 10	206159 at	0.251	8089	3.465E-03	FALSE
102628 at	0.012	8018	1425893 a at	0.188	1510.5	102628 at	0.088	4056	1425893 a at	-0.051	7550	5283.625	3074.4538	FALSE	fragile histidine triad gene	206492 at	-0.050	26114	4.082E-01	FALSE
161482 f at	-0.045	6240	1422530 at	0.073	5769.5	161482 f at	0.132	2572	1422530 at	-0.061	6556	5284.375	1836.8972	FALSE	similar to peripherin 1	NA	NA	NA	NA	
97147 at	0.070	5391	1441421 at	0.073	4250	97147 at	0.104	3159	1441421 at	0.009	8344	5286	2233.0707	TRUE	RIKEN cDNA C530030P08 gene	NA	NA	NA	NA	
96148 at	-0.061	6148	1427984 at	0.042	6939.5	96148 at	0.045	5748	1452627 at	0.175	2312	5286.875	2044.1154	FALSE	SUMO/sentrin specific peptidase 6	243768 at	0.407	1578	1.696E-06	FALSE
104484 at	-0.041	6569	1419528 at	0.025	7120	104484 at	0.110	1613	1419528 at	-0.067	5846	5287	2504.2743	FALSE	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 2	206293 at	0.041	24341	3.486E-01	FALSE
97686 r at	0.078	4604	1449250 at	-0.040	7182	92250 s at	0.134	3527	1449250 at	-0.085	5835	5287	1576.4325	FALSE	papillary renal cell carcinoma (translocation-associated)	208938 at	-0.042	30739	5.840E-01	FALSE
94559 at	0.076	4640	1427027 a at	0.058	6302	94558 g at	-0.035	5987	1427027 a at	-0.110	4225	5288.5	1011.0504	FALSE	general transcription factor III A	NA	NA	NA	NA	
92556 at	0.087	5387	1417085 at	0.080	4674	92556 at	-0.012	7802	1417085 at	-0.148	3293	5289	1887.4157	FALSE	aldo-keto reductase family 1, member C6	210558 at	-0.004	42723	9.530E-01	FALSE
92933 at	0.087	3979	1450507 at	0.135	2135	92933 at	0.037	6569	1450507 at	0.002	8474	5289.25	2795.618	TRUE	POU domain, class 2, transcription factor 3	215355 at	-0.010	37072	7.928E-01	FALSE
92754 at	0.100	4170	1416806 at	0.001	8494.5	162122 f at	-0.025	6763	1416806 at	-0.211	1735	5290.625	2962.5987	FALSE	ferredoxin reductase	207813 s at	0.196	4819	2.226E-04	FALSE
100510 at	-0.090	4611	1418053 at	0.045	6881	100510 at	-0.021	7459	1418053 at	0.167	2212	5290.75	2392.4161	FALSE	synuclein, beta	207853 s at	-0.435	2478	9.209E-06	FALSE
101009 at	0.147	1494	1423691 x at	-0.063	5800	101009 at	0.010	8171	1423691 x at	-0.155	5698	5290.75	2777.0691	FALSE	keratin complex 2, basic, gene 8	209008 x at	0.157	6127	7.752E-04	FALSE
93939 at	0.035	6720	1450183 a at	-0.013	7946	93939 at	-0.054	6265	1433455 at	-0.364	232	5290.75	3446.4099	FALSE	linker of T-cell receptor pathways	203320 at	-0.011	40886	9.040E-01	FALSE
101934 at	0.018	7855	1434348 at	0.036	7614	101934 at	0.214	1079	1434348 at	0.136	4615	5290.75	3171.1378	TRUE	fasciculation and elongation protein zeta 2 (zygin II)	NA	NA	NA	NA	
96520 at	-0.004	8335	1457776 at	-0.051	6092	96520 at	0.126	2014	1457776 at	0.112	4724	5291.25	2643.7193	FALSE	DNA segment, Chr 9, ERATO Doi 720, expressed	NA	NA	NA	NA	
96431 at	0.054	6132	1444959 at	0.097	2315.5	96431 at	0.058	4357	1444959 at	0.007	8363	5291.875	2573.6108	TRUE	DNA segment, Chr 1, ERATO Doi 83, expressed	NA	NA	NA	NA	
93867 at	-0.081	4347	1427829 at	0.051	6428.5	93867 at	0.009	7968	1419572 a at	-0.230	2425	5292.125	2419.7329	FALSE	ATP-binding cassette, sub-family D (ALD), member 4	203981 s at	0.124	11585	2.176E-02	FALSE
103679 at	0.052	5431	1433430 s at	-0.019	8005.5	104090 at	-0.061	4576	1460549 a at	0.208	3158	5292.625	2037.0742	FALSE	CDC23 (cell division cycle 23, yeast, homolog)	223651 x at	-0.252	6560	1.103E-03	FALSE
93941 at	-0.091	4936	1419304 at	-0.057	5505.5	93941 at	0.058	4529	1419304 at	0.074	6200	5292.625	725.47678	FALSE	brachyury	206524 at	0.036	28827	5.143E-01	FALSE

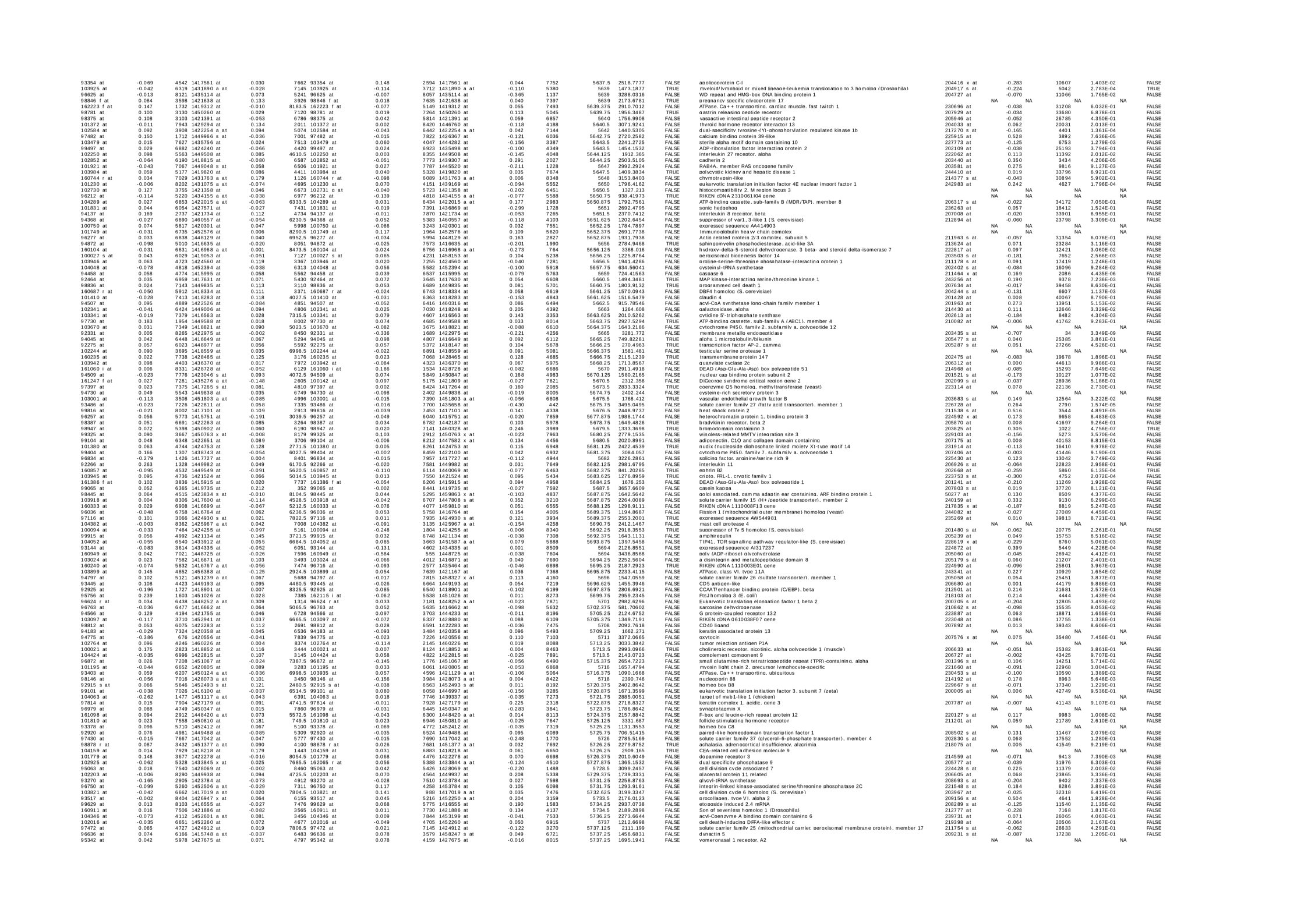
96672 at	-0.044	6490	1428662 a at	0.057	5961.5	96672 at	-0.260	2871	1444266 at	-0.095	5849	5292.875	1638.5889	FALSE	homeobox only domain	211597 s at	-0.376	8657	4.789E-03	FALSE
99129 at	-0.073	5326	1448212 at	0.122	3028	99129 at	-0.037	7302	1448212 at	-0.082	5516	5293	1752.8191	FALSE	tumor necrosis factor superfamily, member 5-induced protein 1	218467 at	0.028	35563	7.484E-01	FALSE
93490 at	-0.037	6604	1451126 at	0.085	3429	93490 at	0.026	7179	1451126 at	0.102	3963	5293.75	1872.5304	FALSE	MAF1 homolog (S. cerevisiae)	222998 at	0.192	2351	7.389E-06	FALSE
103655 at	0.065	4499	1426437 s at	-0.023	7188	103655 at	0.065	4558	1426437 s at	0.098	4930	5293.75	1277.1652	FALSE	histone deacetylase 3	216326 s at	-0.010	38071	8.240E-01	FALSE
103220 at	-0.055	5861	1422554 at	0.063	4875.5	103220 at	-0.152	3695	1422554 at	0.054	6744	5293.875	1310.9707	FALSE	necdin-like 2	226008 at	-0.158	6595	1.128E-03	FALSE
101185 at	0.165	1694	1423027 at	0.055	6136	101185 at	-0.004	8277	1423027 at	0.158	5071	5294.5	2745.7228	FALSE	forkhead box L1	216572 at	-0.043	32000	6.316E-01	FALSE
97709 at	-0.053	5275	1422080 at	0.122	1948	97709 at	-0.002	8411	1422080 at	-0.111	5545	5294.75	2644.1612	FALSE	interleukin 7	206693 at	0.019	27008	4.429E-01	FALSE
96158 at	0.054	6305	1451125 at	0.018	7900	96158 at	0.121	4241	1451125 at	-0.147	2735	5295.25	2270.8765	FALSE	cDNA sequence BC017133	221868 at	0.543	2803	1.624E-05	FALSE
93951 at	0.052	5384	1419160 at	0.068	4469	93951 at	-0.047	4959	1419159 at	-0.060	6369	5295.25	807.58256	FALSE	golgi autoantigen, golgin subfamily a, 3	226949 at	0.117	10304	1.200E-02	FALSE
98055 at	0.110	5191	1420631 a at	0.075	6125	98055 at	0.132	1396	1420631 a at	0.002	8470	5295.5	2942.9317	TRUE	bladder cancer associated protein homolog (human)	201032 at	-0.506	2756	1.505E-05	FALSE
92745 at	-0.037	6669	1421579 at	0.170	1171	92745 at	0.015	7488	1421579 at	0.077	5857	5296.25	2829.6253	FALSE	homeo box A9	209905 at	-0.039	31247	6.047E-01	FALSE
96544 at	0.069	6181	1419797 at	0.110	3065.5	96544 at	-0.037	6783	1419797 at	0.097	5156	5296.375	1631.8827	FALSE	expressed sequence AA672641		NA	NA	NA	NA
99059 at	0.055	6311	1416916 at	0.100	3943	99059 at	0.070	4499	1416916 at	0.073	6434	5296.75	1263.7358	TRUE	E74-like factor 3	201510 at	0.053	23374	3.155E-01	FALSE
93241 r at	0.121	1800	1434842 s at	0.017	8097.5	93241 r at	0.153	3811	1434842 s at	-0.033	7479	5296.875	3002.2841	FALSE	UPF3 regulator of nonsense transcripts homolog B (yeast)	218757 s at	0.036	35061	7.321E-01	FALSE
94387 at	0.064	4442	1448639 a at	0.102	3457.5	94387 at	-0.006	8265	1446292 at	0.105	5023	5296.875	2081.5767	FALSE	spermatogenesis associated 5	241546 at	0.005	41505	9.207E-01	FALSE
161112 at	0.136	3166	1426950 at	0.132	2064	161112 at	-0.001	8475	1426950 at	-0.053	7484	5297.25	3155.7409	FALSE	poly (ADP-ribose) polymerase family, member 16	219034 at	0.093	15453	7.883E-02	FALSE
93242 at	0.081	6426	1422913 at	0.039	7127	93242 at	0.084	3063	1422913 at	0.133	4573	5297.25	1838.3392	TRUE	protamine 3	231758 at	-0.046	25267	3.819E-01	FALSE
99952 at	-0.247	274	1451537 at	0.031	7139	99952 at	0.027	7476	1451537 at	-0.064	6303	5298	3385.4377	FALSE	chitinase 3-like 1	209395 at	1.067	10061	1.041E-02	FALSE
100413 at	-0.022	7519	1424532 at	-0.008	8188.5	100413 at	-0.052	4918	1457514 at	0.305	569	5298.625	3454.2568	FALSE	YLP motif containing 1		NA	NA	NA	NA
95011 at	0.093	4227	1427905 at	0.015	7975.5	95011 at	0.014	7480	1442200 at	0.204	1520	5300.625	3019.4054	TRUE	RIKEN cDNA 1810063B07 gene	232992 at	0.029	28641	5.073E-01	FALSE
162362 f at	0.060	5047	1416342 at	0.007	8215.5	162362 f at	0.167	1925	1456344 at	-0.106	6018	5301.375	2612.1696	FALSE	tenascin C	201645 at	0.870	3763	6.418E-05	FALSE
97004 at	0.072	5031	1422373 at	-0.002	8485.5	97004 at	-0.069	3481	1422373 at	0.181	4212	5302.375	2214.5168	FALSE	olfactory receptor 71		NA	NA	NA	NA
102971 at	0.132	3161	1422105 at	0.028	7156	102971 at	0.009	7929	1445748 at	-0.156	2967	5303.25	2606.0535	FALSE	CD3 antigen, epsilon polypeptide	205456 at	-0.022	37287	7.995E-01	FALSE
161516 r at	0.069	5491	1416465 a at	-0.106	6222	161516 r at	0.144	3039	1416465 a at	0.071	6466	5304.5	1566.1163	FALSE	vesicle-associated membrane protein, associated protein A	228480 at	-0.297	3856	7.196E-05	FALSE
101514 at	-0.041	7249	1416771 at	0.094	3835.5	101514 at	0.087	4460	1416771 at	0.228	5676	5305.125	1504.4636	FALSE	trafficking protein particle complex 3	203511 s at	-0.209	8961	5.642E-03	FALSE
96998 at	0.083	3873	1427424 at	0.035	7047	96998 at	-0.104	3236	1434399 at	-0.087	7070	5306.5	2039.703	FALSE	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	219956 at	0.097	25594	3.912E-01	FALSE
103392 at	0.087	4737	1456307 s at	-0.071	5135	103392 at	-0.012	7648	1456307 s at	-0.451	3707	5306.75	1672.7985	FALSE	adenylate cyclase 7	203741 s at	0.219	10079	1.051E-02	FALSE
98128 at	-0.041	7002	1416143 at	0.276	1466	98128 at	0.056	5167	1416143 at	0.032	7595	5307.5	2761.6933	FALSE	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	229127 at	0.303	7874	3.016E-03	FALSE
96394 at	0.079	4410	1446378 at	0.006	8377	96394 at	0.112	3274	1446378 at	0.095	5172	5308.25	2189.4304	TRUE	DNA segment, Chr 2, ERATO Doi 357, expressed		NA	NA	NA	NA
94970 at	-0.014	7806	1433851 at	0.023	7627.5	94970 at	-0.166	528	1442834 at	0.093	5274	5308.875	3389.6724	FALSE	protein phosphatase 4, regulatory subunit 2	226317 at	0.495	3638	5.605E-05	FALSE
100743 at	0.077	4798	1433859 at	0.037	6813.5	100743 at	0.058	4497	1433859 at	-0.098	5128	5309.125	1035.4944	FALSE	RIKEN cDNA D030070L09 gene	229582 at	-0.189	8073	3.432E-03	FALSE
97832 at	0.048	6064	1418394 a at	-0.035	7014	97832 at	-0.059	5280	1418394 a at	-0.194	2879	5309.25	1768.5013	FALSE	CD97 antigen	202910 s at	0.108	15840	8.688E-02	FALSE
102690 at	0.120	3073	1419731 at	0.071	5176	102690 at	0.059	4827	1419731 at	0.017	8162	5309.5	2112.6064	TRUE	cytochrome P450, family 2, subfamily b, polypeptide 19		NA	NA	NA	NA
161858 f at	-0.063	5593	1417850 at	0.054	7174	161858 f at	-0.078	5345	1441494 at	0.189	3128	5310	1665.0259	FALSE	retinoblastoma 1	203132 at	0.230	14127	5.482E-02	FALSE
103239 at	-0.017	7496	1422074 at	0.086	3694	103239 at	-0.064	4832	1422074 at	0.099	5219	5310.25	1594.4505	FALSE	caudal type homeo box 2	206387 at	-0.109	19121	1.724E-01	FALSE
92884 at	-0.245	1330	1435638 at	0.009	8161	92884 at	-0.079	5828	1435638 at	-0.071	5926	5311.25	2864.5171	FALSE	glycogen synthase kinase 3 alpha	632 at	-0.100	12457	3.099E-02	FALSE
101316 at	-0.015	7589	1423367 at	-0.082	3873	101316 at	-0.033	6616	1458334 at	-0.125	3168	5311.5	2125.4491	TRUE	wingless-related MMTV integration site 7A	210248 at	-0.001	44158	9.882E-01	FALSE
160619 at	-0.007	8139	1427270 a at	0.185	761	160619 at	0.013	7716	1427270 a at	0.089	4631	5311.75	3413.0391	FALSE	BSD domain containing 1	218004 at	0.116	18785	1.633E-01	FALSE
100752 at	0.264	1258	1450280 a at	0.005	8372.5	100752 at	-0.098	3550	1450280 a at	-0.018	8068	5312.125	3488.1588	FALSE	retinal pigment epithelium derived rhodopsin homolog	208314 at	-0.061	22662	2.902E-01	FALSE
95854 at	-0.067	4764	1447990 at	0.011	8204	95854 at	-0.061	5094	1447990 at	0.142	3187	5312.25	2099.7712	FALSE	expressed sequence C76332		NA	NA	NA	NA
95719 at	0.091	3540	1448542 at	0.112	3550	95719 at	0.038	6357	1448542 at	-0.023	7803	5312.5	2124.5967	FALSE	BRCA2 and CDKN1A interacting protein	227322 s at	-0.183	8379	4.101E-03	FALSE
101572 f at	0.039	6509	1420553 x at	-0.052	5544.5	101572 f at	0.084	3635	1420553 x at	0.081	5562	5312.625	1205.7767	FALSE	serine (or cysteine) peptidase inhibitor, clade A, member 1a		NA	NA	NA	NA
100680 at	0.176	3310	1420773 at	0.081	5814	100680 at	0.036	6345	1420773 at	0.109	5784	5313.25	1360.1317	TRUE	deubiquitinating enzyme 1		NA	NA	NA	NA
98281 at	0.037	6290	1427794 at	0.153	2163	98281 at	-0.038	6539	1427794 at	-0.068	6263	5313.75	2104.1707	FALSE	hypothetical protein, P4(21)n gene		NA	NA	NA	NA
97531 at	0.156	2369	1448700 at	0.024	7615	97531 at	0.087	3249	1448700 at	-0.038	8026	5314.75	2920.4333	FALSE	G0/G1 switch gene 2	213524 s at	0.367	6303	9.159E-04	FALSE
96864 at	-0.099	2944	1433878 at	0.026	7810	96864 at	0.116	4256	1433878 at	0.072	6249	5314.75	2147.9062	FALSE	mitochondrial ribosomal protein S26	225196 s at	-0.103	12282	2.894E-02	FALSE
98854 at	-0.058	5017	1450499 at	0.030	7283	98854 at	-0.040	5656	1457605 at	0.377	3305	5315.25	1645.0136	FALSE	ataxin 1	203232 s at	-0.320	3846	7.141E-05	FALSE
92817 at	-0.027	7569	1416210 at	0.100	3896	92817 at	0.081	3826	1416210 at	0.063	5970	5315.25	1801.8715	FALSE	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	221688 s at	-0.192	8377	4.099E-03	FALSE
160404 at	-0.116	3205	1448512 at	0.049	6588.5	160404 at	-0.072	4188	1448512 at	0.050	7280	5315.375	1932.6369	FALSE	histone H1-like protein in spermatids 1	231229 at	-0.103	16965	1.133E-01	FALSE
103344 at	0.040	6547	1420500 at	-0.031	7808	103344 at	-0.034	6555	1459791 at	0.503	356	5316.5	3359.6699	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 1	222620 s at	0.320	1221	7.535E-07	FALSE
161048 at	0.191	2254	1422873 at	0.054	5282.5	161048 at	0.020	7747	1422873 at	0.075	5983	5316.625	2289.9501	TRUE	proteoglycan 2, bone marrow	211743 s at	-0.030	29054	5.226E-01	FALSE
92595 r at	0.030	7167	1427696 at	0.083	4498	92595 r at	0.032	6983	1427696 at	0.186	2623	5317.75	2169.9809	TRUE	ferrochelatase	203115 at	0.056	28233	4.904E-01	FALSE
93136 at	-0.013	7988	1421114 a at	-0.036	6968.5	93136 at	-0.051	5100	1421114 a at	-0.283	1221	5319.375	2982.5032	TRUE	dermatan sulphate proteoglycan 3	206439 at	-0.006	39675	8.693E-01	FALSE
97391 at	-0.009	8052	1451103 at	0.105	3424	97391 at	0.027	7306	1451103 at	-0.183	2502	5321	2765.4991	FALSE	DNA segment, Chr 14, ERATO Doi 500, expressed	218383 at	0.231	2643	1.224E-05	FALSE
160969 at	0.081	4449	1421759 a at	0.099	5287	160969 at	0.021	7592	1434655 at	-0.261	3959	5321.75	1609.7642	FALSE	forkhead box K1		NA	NA	NA	NA
95616 at	-0.004	8427	1452064 at	0.121	2132	95616 at	-0.062	6258	1452064 at	-0.103	4471	5322	2671.917	FALSE	cofactor required for Sp1 transcriptional activation, subunit 3	218846 at	0.109	12536	3.177E-02	FALSE
97691 at	0.002	8416	1437729 at	0.020	8275	97691 at	0.092	3710	1437729 at	0.353	890	5322.75	3675.7861	TRUE	Ribosomal protein L27a	212044 s at	0.090	13557	4.478E-02	TRUE
94285 at	-0.388	3288	1417025 at	0.028	7342.5	94285 at	0.015	7436	1417025 at	-0.432	3226	5323.125	2386.1952	FALSE	histocompatibility 2, class II antigen E beta		NA	NA	NA	NA
99674 at	-0.066	5218	1415681 at	-0.027	7716	99674 at	0.082	4938	1415681 at	0.144	3421	5323.25	1779.8223	FALSE	mitochondrial ribosomal protein L43	224332 s at	0.086	21554	2.519E-01	FALSE
102651 at	0.080	4506	1425303 at	0.053	6100.5	102651 at	-0.103	3642	1425303 at	0.059	7046	5323.625	1534.7621	FALSE	glucokinase	211167 s at	0.113	14445	6.050E-02	FALSE
93774 at	0.017	7973	1431419 at	0.062	5317	93774 at	-0.031	6350	1431419 at	0.197	1657	5324.25	2678.1097	FALSE	RIKEN cDNA 2610524G07 gene	224232 s at	-0.137	12264	2.877E-02	FALSE
94839 at	-0.059	5994	1416903 at	-0.146	2736.5	94839 at	-0.058	5742	1416903 at	-0.051	6825	5324.375	1786.2233	TRUE	nucleobindin 1	200649 at	0.129	12311	2.932E-02	FALSE
104642 at	0.087	4005	1449905 at	0.100	3540.5	104642 at	-0.044	6354	1449905 at	0.033	7399	5324.625	1851.77	FALSE	C-type lectin domain family 4, member f		NA	NA	NA	NA
102220 at	0.029	6933	1416899 at	0.105	4475	102220 at	-0.092	3041	1416899 at	-0.045	6850	5324.75	1901.7926	FALSE	undifferentiated embryonic cell transcription factor 1	208275 x at	0.010	40447	8.910E-01	FALSE
94527 at	0.019	7475	1438983 x at	0.127	1656	94527 at	-0.057	4606	1416096 at	-0.030	7563	5325	2805.3322	FALSE	expressed sequence AI413782	233140 s at	-0.116	8719	4.965E-03	FALSE
94503 at	-0.051	6300	1418692 at	-0.010	8074.5	94503 at	0.049	5205	1418692 at	0.248	1723	5325.625	2677.0119	FALSE	RAB8A, member RAS oncogene family	208819 at	0.286	3033	2.366E-05	FALSE
160612 at	0.020	7347	1423570 at	-0.040	6584.5	160612 at	0.068	3444	1423570 at	0.141	3927	5325.625	1929.3684	FALSE	ATP-binding cassette, sub-family G (WHITE), member 1	211113 s at	-0.024	33105	6.684E-01	FALSE
93369 at	0.026	7156	1418745 at	0.217	770	93369 at	-0.029	6202	1418745 at	-0.043	7175	5325.75	3070.9506	FALSE	osteomodulin	205908 s at	-0.026	35985	7.614E-01	FALSE
99546 at	-0.149	2956	1450694 at	-0.112	5007.5	99546 at	-0.055	6157	1450694 at	-0.053	7183	5325.875	1812.6732	TRUE	FK506 binding protein 2	203391 at	-0.086	18449	1.535E-01	FALSE
103013 at	-0.050	5822	1460228 at	0.118	3119	103013 at	-0.028	6659	1460228 at	-0.102	5704	5326	1531.5175	FALSE	upstream transcription factor 2	215737 x at	0.108	12878	3.555E-02	FALSE
97366 at	0.063	4631	1424326 at	0.004	8379	97366 at	-0.040	5492	1424326 at	-0.177	2803	5326.25	2323.569	FALSE	LEM domain containing 2	224980 at	-0.024	33715	6.891E-01	FALSE
94790 at	0.205	375	1431033 x at	-0.094	6290.5	94790 at	0.005	8173	1431032 at	-0.132	6467	5326.375	3408.3207	FALSE	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	203566 s at	0.004	43785	9.791E-01	FALSE
93502 r at	0.047	6117	1452206 at	-0.081	5380	93502 r at	0.111	4468	1430402 at	0.087	5341	5326.5	674.53317	FALSE	succinate-Coenzyme A ligase, ADP-forming, beta subunit	202930 s at	-0.466	4063	9.221E-05	FALSE
100702 at	0.070	5846	1421602 at	0.051	6800	100702 at	0.082	4792	1421602 at	0.169	3871	5327.25	1270.8594	TRUE	sex hormone binding globulin	215689 s at	0.000	44518	9.970E-01	FALSE
104011 at	0.020	7441	1419435 at	0.020	7888	104011 at	0.046	5294	1419435 at	-0.401	687	5327.5	3294.3591	FALSE	aldehyde oxidase 1	205083 at	-0.026	35467	7.453E-01	FALSE
100373 at	0.024	7604	1424424 at	0.110	3324.5	96832 at	0.086	3893	1424424 at	0.083	6498	5329.875	2051.2028	TRUE	solute carrier family 39 (zinc transporter), member 1	217778 at	0.160	5060	2.833E-04	TRUE
103557 at	-0.101	4415	1426227 s at	-0.036	6921	103557 at	0.080	4199	1426227 s at	-0.145	5788	5330.75	1272.4555	FALSE	vacuolar protein sorting 37C (yeast)	219053 s at	-0.025	35432	7.442E-01	FALSE
93029 at	0.199	2039	1416788 a at	0.070	5502.5	93029 at	-0.053	6056	1416789 at	0.031	7728	5331.375	2390.1122	FALSE	isocitrate dehydrogenase 3 (NAD+), gamma	202471 s at	-0.381	6534	1.075E-03	FALSE
96097 at	0.069	4730	1433684 at	0.071	5048.5	96097 at	-0.006	8082	1433684 at	0.145	3465	5331.375	1957.1206	FALSE	chromatin modifying protein 6	216107 at	-0.073	27013	4.433E-01	FALSE
93381 at	-0.209	4017	1450794 at	-0.016	8388.5	93381 at	-0.148	1289	1450794 at	0.125	7633	5331.875	3302.1138	FALSE	arginine vasopressin	207848 at	0.086	33494	6.816E-01	FALSE
160212 at	-0.009	8162	1451192 a at	-0.294	891	160212 at	0.034	6323	1451193 x at	-0.114	5952	5332	3114.3679	FALSE	tetratricopeptide repeat domain 4	218442 at	0.174	7688	2.645E-03	FALSE
94690 at	0.128	3775	1449595 at	0.115	3727.5	94690 at	-0.056	6348	1449595 at	-0.044	7481	5332.875	1884.0668	FALSE	expressed sequence C79490		NA	NA	NA	NA
104142 at	-0.085	3448	1435250 at	0.070	6474	104142 at	0.005	8193	1435250 at	0.185	3217	5333	2416.0686	FALSE	integrator complex subunit 8	211784 s at	0.226	9062	6.042E-03	FALSE
98627 at	0.385	1026	1454159 a at	-0.077	6960.5	98627 at	0.079	6277	1454159 a at	-0.217	7069	5333.125	2892.7402	FALSE	insulin-like growth factor binding protein 2	202718 at	0.162	18034	1.417E-01	FALSE
97325 at	-0.021	7731	1451253 at	-0.149	3360	97325 at	0.114	3592	1451253 at	0.056	6651	5333.5	2191.7525	FALSE	PX domain containing serine/threonine kinase	238223 at	0.158	9349	7.130E-03	FALSE
102728 f at	0.123	4464	1450171 x at	0.052	5936	102728 f at	-0.054	5791	1421227 at	0.079	5147	5334.5	674.07245	FALSE	granzyme E		NA	NA	NA	NA
92968 at	-0.108	3271	1422807 at	-0.059	6757.5	92968 at	-0.049	5359	1422807 at	0.124	5954	5335.375	1490.7871	FALSE	ADP-ribosylation factor 5	201526 at	-0.342	2751	1.493E-05	FALSE
104131 at	0.030	6658	1460276 a at	-0.105	4143.5	104131 at	-0.109	3203	1460276 a at	-0.042	7337	5335.375	1976.818	FALSE	G protein-coupled receptor 175	218855 at	0.146	6382	9.699E-04	FALSE
95522 i at	0.062	6419	1448760 at	0.053	7111	95522 i at	-0.191	2120	1457571 at	0.142	5692	5335.5	2220.5784	FALSE	zinc finger protein 68		NA	NA	NA	NA
102968 at	0.012	7994	1455747 at	0.118	2215	102968 at	-0.049	6036	1455747 at	0.171	5098	5335.75	2405.012	FALSE	gamma-glutamyltransferase-like activity 1	205582 s at	0.202	8209	3.725E-03	FALSE
96837 at	-0.058	5265	1427109 at	0.051	5458	96837 at	-0.091	3120	1427109 at	-0.032	7503	5336.5	1791.3188	FALSE	open reading frame 61	212575 at	-0.179	10744	1.505E-02	FALSE
101868 i at	0.130	3096	1419744 at	-0.027	7369.5	101868 i at	-0.097	3854	1419744 at	-0.049	7027	5336.625	2176.2755	FALSE	histocompatibility 2, class II, locus Mb2	203932 at	0.083	24103	3.413E-01	FALSE
98502 at	0.002	8417	1418038 s at	-0.007	8262	98502 at	-0.319	385	1448922 at	-0.209	4286	5337.5	3815.2732	FALSE	dual specificity phosphatase 19		NA	NA	NA	NA
99444 at	0.024	7357	1418187 at	-0.022	7632.5	99444 at	-0.242	1901	1418187 at	-0.128	4460	5337.625	2703.3895	FALSE	receptor (calcitonin) activity modifying protein 2	205779 at	0.225	6927	1.502E-03	FALSE
160577 at	-0.047	6357	1427604 a at	-0.140	2542	160577 at	0.015	7546	1427604 a at	0.126	4908	5338.25	2153.7673	FALSE	ATPase, class II, type 9A	212062 at	-0.292	7828	2.928E-03	FALSE
101133 at	0.047	5816	1422306 at	0.059	5999.5	101133 at	0.135	1843	1422306 at	-0.030	7695	5338.375	2479.0146	FALSE	lipocalin 3		NA	NA	NA	NA
101755 f at	0.165	1765	1450811 at	0.015	7868	101755 f at	0.066	4324	1450811 at	0.037	7402	5339.75	2855.1421	TRUE	small proline-rich protein 2J		NA	NA	NA	NA
100994 at	0.021	7578	1416936 at	-0.185	1743	100994 at	0.083	5064	1416936 at	-0.055	6978	5340.75	2627.1829	FALSE	apoptosis-associated tyrosine kinase		NA	NA	NA	NA
104263 at	-0.068	6480	1438685 at	-0.002	8468	104263 at	-0.114	5690	1438685 at	-0.298	726	5341	3291.1739	TRUE	zinc finger, MYM-type 6		NA	NA	NA	NA
96003 at	0.175	1087	1423165 a at	-0.006	8322	96003 at	0.006	8120	1423165 a at	0.150	3836	5341.25	3510.4958	FALSE	metastasis-associated gene family, member 2	203444 s at	0.004	42981	9.597E-01	FALSE
98831 at	0.143	1558	1425291 at	0.017	7744	98831 at	0.029	7102	1425291 at	-0.255	4963	5341.75	2788.6377	FALSE	forkhead box J1	205906 at	0.168	14092	5.427E-02	FALSE
104297 at	-0.104	3678	1428096 at	0.114	2473	104297 at	-0.006	8064	1428096 at	-0.046	7152	5341.75	2688.5833	FALSE	importin 11	222659 at	0.048	22140	2.730E-01	FALSE
96684 at	0.072	6200	1439366 at	0.094	3756	161453 r at	-0.030	6309	1439366 at	-0.138	5102	5341.75	1189.4325	FALSE	G-rich RNA sequence binding factor 1	215030 at	-0.052	28107	4.850E-01	FALSE
99802 at	0.140	1365	1450003 at	0.070	5886	99802 at	0.018	7428	1450003 at	0.107	6688	5341.75	2724.9206	TRUE	adrenergic receptor, alpha 2b	208544 at	-0.016	39142	8.554E-01	FALSE
99134 at	0.034	6900	1421682 a at	0.071	4768	99134 at	0.065	4541	1421682 a at	0.154	5170	5344.75	1068.9551	TRUE	t-complex-associated testis expressed 3	232258 at	-0.053	20579	2.188E-01	FALSE
99413 at	0.000	8521	1419609 at	0.125	3788.5	99413 at	-0.068	4623	1419610 at	-0.123	4449	5345.375	2147.3835	FALSE	chemokine (C-C motif) receptor 1	205099 s at	0.093	16499	1.018E-01	FALSE
100690 at	-0.009	8089	1420546 at	0.062	5749	100690 at	-0.047	5803	1420546 at	-0.309	1741	5345.5	2638.8969	FALSE	tyrosine hydroxylase	208291 s at	-0.256	4453	1.455E-04	FALSE
92578 at	0.009	8278	1416486 at	0.146	2985	92578 at	0.199	1799	1416486 at	-0.007	8321	5345.75	3444.9373	FALSE	small inducible cytokine subfamily E, member 1	235594 at	0.055	20010	2.007E-01	FALSE
160203 at	0.010	8180	1426473 at	0.190	1402	160203 at	-0.115	3816	1426473 at	0.017	7988	5346.5	3311.9861	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 9	213088 s at	0.034	29797	5.496E-01	FALSE
103781 at	-0.208	1754	1451573 a at	-0.084	5050.5	103781 at	-0.018	7889	1451573 a at	-0.072	6696	5347.375	2663.2765	TRUE	syntaxin 4A (placental)	203530 s at	0.108	20965	2.323E-01	FALSE
102568 at	0.053	5435	1425759 at	0.135	2518	102568 at	-0.024	7325	1425759 at	0.074	6113	5347.75	2042.076	FALSE	NOBOX oogenesis homeobox		NA	NA	NA	NA
103882 at	0.046	6548	1417745 at	0.031	7421	103882 at	0.050	5624	1440576 at	0.190	1799	5348	2477.156	TRUE	carboxypeptidase N, polypeptide 1	206256 at	-0.020	36392	7.744E-01	FALSE
103295 at	-0.064	5761	1455066 s at	0.083	4902.5	103295 at	-0.037	7166	1455066 s at	0.130	3566	5348.875	1511.0354	FALSE	RIKEN cDNA 9130229H14 gene		NA	NA	NA	NA
102688 f at	0.064	5654	1420344 x at	0.092	3709	102688 f at	-0.005	8194	1420343 at	0.115	3840	5349.25	2093.9381	FALSE	granzyme D		NA	NA	NA	NA
96320 at	-0.199	1737	1424038 a at	0.022	7755.5	96320 at	-0.055	6002	1424038 a at	-0.076	5904	5349.625	2554.2265	FALSE	RIKEN cDNA 2310044H10 gene	224727 at	0.019	35038	7.314E-01	FALSE
93675 at	-0.035	6446	1422725 at	-0.011	8147.5	93675 at	-0.069	5052	1422724 at	0.248	1754	5349.875	2710.9188	FALSE	male germ cell-associated kinase	220302 at	0.293	9593	8.168E-03	FALSE
92453 at	0.027	7024	1456647 a at	-0.024	7685.5	92453 at	-0.038	5575	1432461 at	-0.270	1118	5350.625	2956.196	FALSE	eyes absent 4 homolog (Drosophila)	207327 at	0.084	18958	1.677E-01	FALSE
97912 at	-0.116	4311	1416009 at	0.016	7759	97912 at	0.190	3358	1442841 at	0.077	5977	5351.25	1935.9742	FALSE	tetraspanin 3	200972 at	0.167	13944	5.142E-02	FALSE
100508 at	0.122	3961	1416992 at	-0.031	6853	100508 at	-0.080	4645	1416992 at	-0.106	5948	5351.75	1296.527	FALSE	manic fringe homolog (Drosophila)	204153 s at	0.119	17173	1.192E-01	FALSE
93832 at	-0.059	5772	1433940 at	0.080	6440.5	93832 at	0.068	3631	1433940 at	0.103	5564	5351.875	1206.6506	FALSE	sperm associated antigen 7	200053 at	-0.041	26046	4.058E-01	FALSE
95885 at	0.108	2840	1429219 at	0.092	4561	95885 at	0.058	6052	1429219 at	0.028	7955	5352	2175.7324	TRUE	RIKEN cDNA 1200009F10 gene	227295 at	-0.304	891	3.418E-07	FALSE
102654 at	0.004	8301	1449232 at	0.167	1349.5	102654 at	0.012	7748	1449232 at	0.115	4010	5352.125	3279.1456	TRUE	GATA binding protein 1	210446 at	0.027	34900	7.275E-01	FALSE
104706 at	-0.056	6759	1418988 at	0.079	4215.5	104706 at	-0.080	5699	1418988 at	0.115	4736	5352.375	1121.1818	FALSE	peroxisome biogenesis factor 7	205420 at	0.028	33390	6.782E-01	FALSE
95577 at	0.083	4803	1452122 at	0.072	4993	95577 at	0.028	7519	1452122 at	0.117	4096	5352.75	1494.8472	TRUE	expressed sequence AI314180		NA	NA	NA	NA
104128 at	0.099	3017	1416747 at	-0.014	7950	104128 at	-0.060	4095	1416747 at	0.059	6350	5353	2219.4502	FALSE	DNA Segment, Chr 15, Mouse Genome Informatics 27	212861 at	0.117	15170	7.399E-02	FALSE
103719 at	0.069	5908	1449537 at	0.127	3721.5	103719 at	-0.041	6845	1449537 at	-0.119	4939	5353.375	1337.5695	FALSE	mutS homolog 5 (E. coli)	221406 s at	0.058	16996	1.144E-01	FALSE
97528 at	0.138	2568	1423727 at	0.138	3271.5	97528 at	0.032	7446	1423727 at	-0.013	8129	5353.625	2838.7609	FALSE	cornichon homolog (Drosophila)	201653 at	-0.109	24213	3.447E-01	FALSE
96285 at	-0.010	7991	1439389 s at	0.025	7354	96285 at	0.106	3054	1423321 at	0.283	3018	5354.25	2689.5269	FALSE	myeloid-associated differentiation marker	225673 at	-0.100	23240	3.101E-01	FALSE

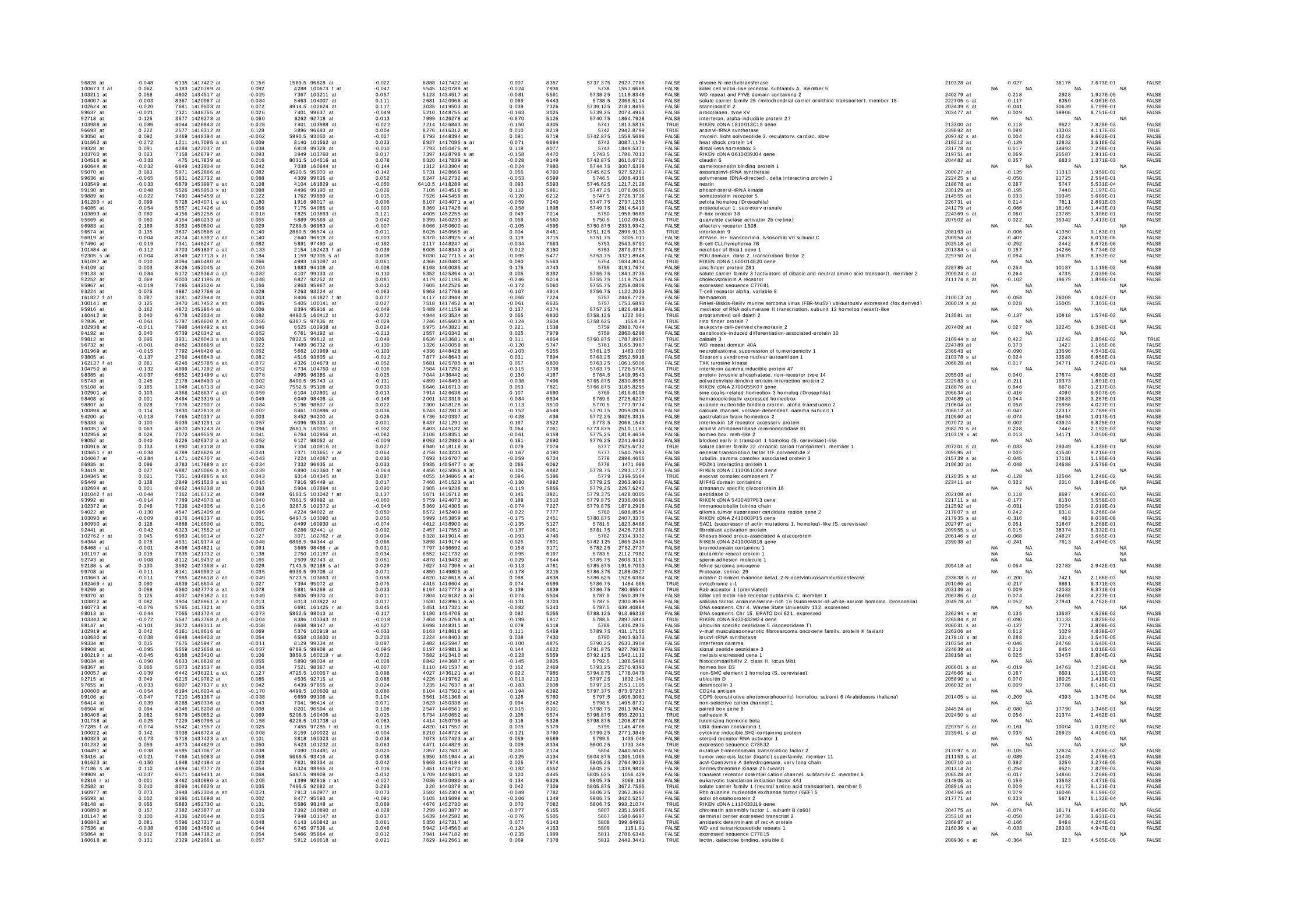


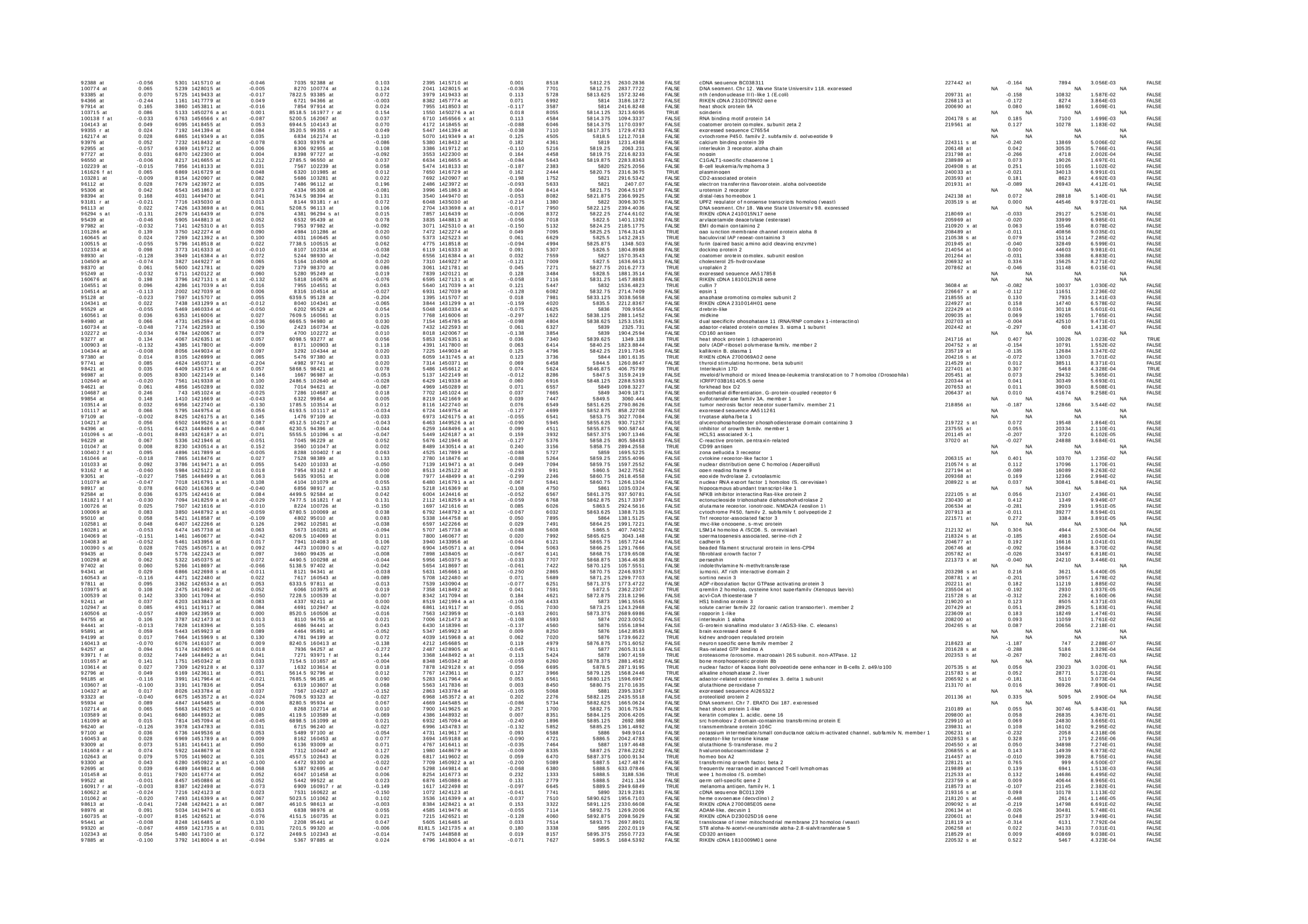


100968 at	0.019	7445	1424723 s at	-0.056	5971	100968 at	-0.110	2121	1424723 s at	-0.060	6459	5499	2333.9654	FALSE	cleavage stimulation factor, 3' pre-RNA, subunit 3	203947 at	-0.086	15959	9.015E-02	FALSE
162147 f at	0.046	6645	1416825 at	0.062	5630	102890 at	0.036	5968	1416825 at	-0.157	3758	5500.25	1235.7876	FALSE	syntrophin, acidic 1	203516 at	0.211	10843	1.601E-02	FALSE
93470 at	0.075	3987	1419750 at	0.041	6607	93470 at	0.057	4400	1419749 at	-0.054	7007	5500.25	1527.0524	FALSE	DNA methyltransferase 2	243504 at	-0.040	28479	4.998E-01	FALSE
98859 at	0.052	5374	1431609 a at	0.200	1285.5	98859 at	0.029	7204	1431609 a at	-0.015	8140	5500.875	3035.9567	FALSE	acid phosphatase 5, tartrate resistant	204638 at	0.048	25752	3.953E-01	FALSE
94166 g at	-0.020	7767	1421688 a at	0.111	3640	94166 g at	0.033	6383	1421688 a at	-0.136	4215	5501.25	1917.4459	FALSE	chemokine (C-C motif) ligand 1	NA	NA	NA	NA	
161985 f at	-0.067	5135	1455434 a at	0.021	8015.5	161985 f at	0.052	5103	1459429 at	0.127	3752	5501.375	1795.7423	FALSE	kinectin 1	200914 x at	0.488	3133	2.742E-05	FALSE
101739 at	0.105	3258	1422426 at	0.097	3391	101739 at	-0.003	8414	1422426 at	0.070	6949	5503	2586.2074	FALSE	cell matrix adhesion regulator	NA	NA	NA	NA	
97965 at	0.026	6889	1422147 a at	-0.068	5121.5	97965 at	-0.093	3087	1431278 s at	-0.090	6919	5504.125	1817.3832	FALSE	phospholipase A2, group VI	204691 x at	0.054	21603	2.539E-01	FALSE
100338 s at	0.099	4825	1421692 at	-0.052	6934	100337 at	-0.120	3632	1421692 at	-0.071	6627	5504.5	1556.8615	FALSE	calcium channel, voltage-dependent, R type, alpha 1E subunit	242410 s at	-1.393	546	1.180E-07	FALSE
101128 at	0.102	3464	1420442 at	-0.032	7053.5	101128 at	-0.040	5880	1420442 at	0.121	5621	5504.625	1496.3972	FALSE	calcium channel, voltage-dependent, L type, alpha 1S subunit	217515 s at	0.010	40105	8.805E-01	FALSE
100292 at	0.082	4466	1449105 at	0.109	3544	100292 at	-0.037	6193	1449105 at	-0.027	7816	5504.75	1892.0101	FALSE	SH2 domain protein 2A	207351 s at	0.023	35544	7.477E-01	FALSE
94041 at	0.038	7206	1454692 x at	0.111	2746.5	94041 at	0.021	8215	1448176 a at	-0.130	3852	5504.875	2619.1113	FALSE	heterogeneous nuclear ribonucleoprotein K	200097 s at	-0.282	10626	1.417E-02	FALSE
98880 at	-0.044	6359	1456056 a at	0.067	5379	98880 at	0.006	8307	1433589 at	0.190	1977	5505.5	2648.4699	FALSE	DNA segment, Chr 6, Wayne State University 116, expressed	211068 x at	0.140	10663	1.456E-02	FALSE
101806 at	0.017	7857	1450581 at	-0.101	4373	101806 at	-0.068	4206	1450581 at	0.077	5587	5505.75	1683.9884	FALSE	galanin receptor 3	33579 i at	0.026	34423	7.111E-01	FALSE
104559 at	0.107	2752	1460690 at	-0.072	4649	104559 at	-0.007	8017	1460690 at	0.082	6607	5506.25	2297.5557	FALSE	cDNA sequence BC003940	NA	NA	NA	NA	
98853 at	-0.069	4273	1450144 at	0.089	3844	98853 at	-0.045	6021	1454145 at	-0.034	7890	5507	1846.7277	FALSE	phospholipase A2 receptor 1	240039 at	0.055	21657	2.561E-01	FALSE
95929 at	-0.037	6840	1419533 at	0.129	3271.5	95929 at	0.042	5903	1419533 at	0.087	6017	5507.875	1548.253	FALSE	nescient helix loop helix 1	214628 at	-0.138	10685	1.464E-02	FALSE
93444 at	0.093	4526	1419410 at	0.083	4782.5	93444 at	-0.062	5511	1419410 at	0.040	7215	5508.625	1211.6835	FALSE	basic leucine zipper transcription factor, ATF-like	205965 at	-0.146	9885	9.494E-03	FALSE
92239 at	0.081	6534	1452524 a at	-0.029	7679.5	92239 at	-0.072	4333	1452524 a at	0.187	3488	5508.625	1934.6931	FALSE	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	206338 at	-0.068	27966	4.792E-01	FALSE
100779 at	0.037	6730	1419530 at	-0.040	6558	100779 at	0.048	5685	1449497 at	0.143	3064	5509.25	1693.1472	FALSE	interleukin 12b	207901 at	0.003	41810	9.295E-01	FALSE
96867 at	0.198	3217	1417776 at	0.112	3257	96867 at	-0.003	8319	1417776 at	-0.046	7245	5509.5	2660.4864	FALSE	alpha-2-glycoprotein 1, zinc	209309 at	0.627	5047	2.789E-04	FALSE
94900 at	-0.053	5657	1438290 x at	0.059	6489	94900 at	-0.003	8360	1438290 x at	0.213	1536	5510.5	2880.6958	FALSE	surfactant associated protein C	38691 s at	0.052	21393	2.467E-01	FALSE
94128 at	0.082	4057	1420594 at	0.148	2944.5	94128 at	-0.009	7969	1420594 at	0.044	7076	5511.625	2393.8829	FALSE	BRCA1 associated RING domain 1	205345 at	0.415	1007	4.587E-07	FALSE
160560 at	0.019	7374	1427866 x at	-0.069	5571	160560 at	0.119	1939	1427866 x at	-0.069	7165	5512.25	2514.575	FALSE	Hemoglobin, beta adult major chain	206834 at	-0.021	38793	8.440E-01	FALSE
95690 at	-0.087	5735	1428068 at	0.092	3435	95690 at	-0.113	5143	1428068 at	0.026	7740	5513.25	1776.1191	FALSE	sorting and assembly machinery component 50 homolog (S. cerevisiae)	201570 at	-0.113	11136	1.826E-02	FALSE
94163 at	0.091	5137	1421286 a at	-0.026	7648.5	94163 at	0.041	5879	1421286 a at	0.166	3393	5514.375	1763.5272	FALSE	ATPase, H+/K+ exchanging, gastric, alpha polypeptide	207139 at	-0.004	42964	9.593E-01	FALSE
93298 at	-0.060	6091	1415890 at	-0.166	851.5	93298 at	-0.028	6991	1415890 at	-0.014	8128	5515.375	3219.0243	TRUE	3'-phosphoadenosine 5'-phosphosulfate synthase 1	209043 at	-0.153	10545	1.358E-02	TRUE
95316 at	0.173	1198	1449545 at	0.040	6719	95316 at	0.045	6340	1449545 at	-0.026	7809	5516.5	2945.5705	FALSE	fibroblast growth factor 18	231382 at	-0.090	17777	1.342E-01	FALSE
94635 at	0.097	4231	1422282 at	0.063	6257	94635 at	-0.088	3956	1422282 at	0.034	7623	5516.75	1739.0949	FALSE	tachykinin receptor 1	210637 at	-0.102	19251	1.763E-01	FALSE
101597 at	-0.058	6050	1446829 at	0.139	3110	101597 at	-0.052	5166	1446829 at	-0.024	7743	5517.25	1928.3857	FALSE	DNA segment, Chr 12, ERATO Doi 216, expressed	NA	NA	NA	NA	
94537 at	0.014	7700	1428608 at	0.083	4918.5	94537 at	0.106	2260	1428608 at	0.041	7193	5517.875	2486.0084	TRUE	myosin light chain, regulatory B	221474 at	-0.043	24526	3.551E-01	FALSE
161910 at	0.041	6757	1448811 at	0.079	5267	161910 at	0.106	2593	1448811 at	0.039	7455	5518	2152.9604	TRUE	mitochondrial ribosomal protein L2	229884 s at	-0.115	16797	1.090E-01	FALSE
99382 at	0.021	7485	1421393 at	0.041	7439	99382 at	-0.139	1731	1421393 at	0.081	5417	5518	2702.5235	FALSE	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	229883 at	0.037	30652	5.805E-01	FALSE
96192 at	0.095	6345	1431804 a at	-0.106	5608.5	96192 at	-0.140	5016	1459360 at	0.114	5103	5518.125	610.01317	FALSE	trans-acting transcription factor 3	213168 at	0.414	6618	1.153E-03	FALSE
103990 at	0.069	5445	1422134 at	-0.070	4610.5	103990 at	-0.036	6543	1422134 at	-0.142	5476	5518.625	791.89071	FALSE	FBJ osteosarcoma oncogene B	202768 at	-0.270	4372	1.315E-04	FALSE
92339 at	0.064	4399	1419702 at	0.108	3332.5	92339 at	0.003	8318	1419702 at	0.089	6025	5518.625	2169.9169	TRUE	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	NA	NA	NA	NA	
96804 at	0.003	8369	1424019 at	0.175	799	96804 at	-0.018	7089	1424019 at	0.079	5827	5521	3314.6467	FALSE	nucleolar protein 1	214427 at	0.054	27649	4.676E-01	FALSE
99238 at	0.097	3419	1449159 at	-0.002	8465.5	99238 at	0.032	6449.5	1449159 at	-0.149	3750	5521	2386.5622	FALSE	guanine nucleotide binding protein, beta 3	206047 at	0.024	33215	6.726E-01	FALSE
99823 r at	0.151	3596	1441115 at	0.015	7975.5	99823 r at	-0.087	4894	1441115 at	0.071	5619	5521.125	1837.8364	FALSE	DNA segment, Chr 18, ERATO Doi 232, expressed	NA	NA	NA	NA	
97894 at	0.026	6835	1448472 at	0.031	6979	97894 at	-0.062	4804	1448472 at	-0.158	3467	5521.25	1691.6821	FALSE	valyl-tRNA synthetase 2	201797 s at	-0.068	21829	2.623E-01	FALSE
160946 at	0.007	8134	1427478 at	-0.257	450	160946 at	-0.010	7758	1425805 a at	0.297	5745	5521.75	3540.1108	FALSE	ubiquitin specific peptidase 12	236975 at	-0.078	19698	1.907E-01	FALSE
93347 at	-0.149	4507	1421873 s at	0.029	7526	93347 at	0.025	7683	1421873 s at	0.160	2373	5522.25	2558.1479	FALSE	RAB24, member RAS oncogene family	225251 at	-0.026	36148	7.671E-01	FALSE
102921 s at	0.120	2829	1460251 at	-0.005	8354	AFFX-MurFAS at	0.087	2690	1460251 at	0.015	8218	5522.75	3191.7138	FALSE	Fas (TNF receptor superfamily member)	204780 s at	0.167	12838	3.520E-02	FALSE
98609 at	0.015	7610	1417038 at	-0.083	4966.5	98609 at	-0.174	2211	1417038 at	0.067	7305	5523.125	2504.0054	FALSE	septin 9	41220 at	0.271	2095	4.520E-06	FALSE
104695 at	0.047	6554	1429536 at	0.145	2293	104695 at	0.039	6510	1453184 at	0.051	6736	5523.25	2155.721	TRUE	RIKEN cDNA 2310040C09 gene	NA	NA	NA	NA	
98892 at	0.050	6248	1418288 at	-0.203	209	98892 at	0.005	8252	1426516 a at	0.052	7387	5524	3637.1305	FALSE	lipin 1	212274 at	0.117	15000	7.103E-02	FALSE
102905 at	-0.084	4267	1449591 at	0.023	7660.5	102905 at	-0.046	5953	1449591 at	-0.161	4221	5525.375	1635.698	FALSE	caspase 4, apoptosis-related cysteine peptidase	213596 at	0.084	18743	1.623E-01	FALSE
98135 r at	-0.115	2316	1428277 at	0.038	7260.5	98135 r at	-0.073	4108	1428277 at	-0.004	8420	5526.125	2810.6079	FALSE	OTU domain containing 6B	222825 at	0.074	28464	4.992E-01	FALSE
96559 at	-0.034	6615	1424813 at	0.028	7091.5	96559 at	0.089	3593	1435686 at	0.112	4808	5526.875	1621.596	FALSE	Expressed sequence AA536717	NA	NA	NA	NA	
94220 at	-0.022	7454	1416528 at	-0.099	5455	94220 at	0.038	7541	1416528 at	-0.214	1661	5527.75	2752.0091	FALSE	SH3 domain binding glutamic acid-rich protein-like 3	221269 s at	-0.023	37163	7.957E-01	FALSE
96346 at	-0.007	8359	1448842 at	0.058	5763	96346 at	0.282	1990	1448842 at	0.077	6001	5528.25	2633.8159	FALSE	cysteine dioxygenase 1, cytosolic	204154 at	-0.418	2584	1.094E-05	FALSE
100586 i at	0.062	5127	1448193 at	0.050	5916	100586 i at	-0.075	5363	1447951 at	-0.073	5710	5529	351.98958	FALSE	RIKEN cDNA 5730403B10 gene	218183 at	0.346	6617	1.153E-03	FALSE
99109 at	-0.164	1105	1416442 at	-0.075	5381	99109 at	0.002	8425	1416442 at	-0.075	7206	5529.25	3203.7907	FALSE	immediate early response 2	202081 at	0.268	12037	2.633E-02	FALSE
97800 at	-0.056	5148	1460635 at	-0.062	5828	97800 at	-0.089	4025	1460635 at	-0.061	7117	5529.5	1293.3575	TRUE	Fas-activated serine/threonine kinase	210975 x at	-0.096	10130	1.080E-02	TRUE
162091 f at	0.034	6563	1438637 x at	-0.162	4327	162091 f at	0.060	6194	1429362 a at	0.112	5036	5530	1032.6713	FALSE	Splicing factor 3b, subunit 2	200619 at	-0.021	37347	8.007E-01	FALSE
162004 i at	0.131	3749	1416641 at	0.005	8351	92551 at	0.017	7424	1416641 at	0.205	2597	5530.25	2788.0535	TRUE	Ligase I, DNA, ATP-dependent	202726 at	0.092	13436	4.301E-02	TRUE
95770 s at	0.166	2078	1421661 at	0.018	7913	95770 s at	-0.092	4590	1421661 at	0.035	7542	5530.75	2740.2393	FALSE	formyl peptide receptor-like 1	214560 at	-0.076	22178	2.743E-01	FALSE
160361 at	0.028	7556	1429632 at	0.097	4371	160361 at	0.178	3168	1429632 at	0.059	7029	5531	2103.489	TRUE	trafficking protein particle complex 4	217959 s at	-0.108	25011	3.726E-01	FALSE
100013 at	0.090	4238	1424617 at	0.044	6780.5	100013 at	0.063	4372	1424617 at	-0.153	6734	5531.125	1416.9908	FALSE	interferon-induced protein 35	209417 s at	0.292	5710	5.300E-04	FALSE
97915 at	-0.011	8064	1460341 at	-0.157	1760	97915 at	-0.016	7575	1460341 at	-0.094	4728	5531.75	2913.1468	TRUE	pleckstrin homology domain containing, family B (evectins) member 2	201410 at	-0.438	3118	2.673E-05	TRUE
94037 at	0.041	6526	1448281 a at	0.138	2261	94037 at	0.054	4884	1448281 a at	0.003	8456	5531.75	2624.0653	TRUE	elastase 2A	206446 s at	0.056	12327	2.946E-02	TRUE
93772 i at	0.116	4397	1454652 at	0.039	6811	93773 f at	0.291	3053	1454652 at	0.023	7868	5532.25	2200.485	TRUE	zinc finger protein 265	241345 at	-0.045	18973	1.681E-01	FALSE
100308 at	0.055	6272	1418441 at	-0.027	7695	100308 at	0.145	1641	1447819 x at	-0.128	6523	5532.75	2667.5912	FALSE	procollagen, type VIII, alpha 1	226237 at	0.508	10194	1.122E-02	FALSE
92787 at	-0.007	8229	1448199 at	-0.057	5661	92787 at	-0.071	4770	1429304 at	-0.151	3474	5533.5	2008.8512	TRUE	ankyrin repeat domain 10	223251 s at	0.395	4613	1.751E-04	FALSE
96760 at	-0.004	8313	1449886 a at	0.095	2493	96760 at	0.020	7125	1428010 at	-0.183	4204	5533.75	2662.7494	FALSE	translocase of inner mitochondrial membrane 9 homolog (yeast)	218316 at	-0.193	3560	4.984E-05	FALSE
97121 at	0.054	6682	1427582 at	0.095	3536	97121 at	-0.090	4063	1427582 at	0.022	7858	5534.75	2071.6115	FALSE	fibroblast growth factor 6	208417 at	-0.076	17734	1.330E-01	FALSE
95540 r at	0.045	5892	1424161 at	0.065	5107.5	95540 r at	0.068	4997	1424161 at	-0.094	6145	5535.375	569.13639	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	215693 x at	0.106	7526	2.353E-03	FALSE
102902 at	-0.010	8144	1421753 a at	0.085	4195	102902 at	0.088	4560	1421753 a at	0.117	5244	5535.75	1792.3713	FALSE	LIM homeobox protein 3	221670 s at	0.002	43863	9.811E-01	FALSE
92191 at	0.028	7654	1460519 a at	0.072	4741.5	92191 at	0.127	4652	1460519 a at	0.120	5096	5535.875	1425.0392	TRUE	methyltransferase like 5	NA	NA	NA	NA	
102887 at	0.087	4682	1449033 at	-0.056	4786.5	102887 at	-0.031	6492	1449033 at	0.073	6188	5537.125	936.32281	FALSE	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	204932 at	0.150	10867	1.616E-02	FALSE
96585 at	0.150	3445	1450277 at	0.007	8258.5	96585 at	-0.106	3282	1450277 at	-0.039	7168	5538.375	2551.3529	FALSE	arginine vasopressin receptor 2	208108 s at	0.041	22492	2.845E-01	FALSE
93931 at	0.134	2401	1451862 a at	0.012	8168	93931 at	-0.009	8041	1451862 a at	0.188	3544	5538.5	2999.9285	FALSE	perforin 1 (pore forming protein)	214617 at	0.062	19861	1.965E-01	FALSE
94876 f at	-0.013	8135	1460460 a at	-0.257	1372	94876 f at	0.065	6311	1460460 a at	0.086	6337	5538.75	2906.0794	FALSE	golgi reassembly stacking protein 2	208842 s at	-0.137	15552	8.092E-02	FALSE
95004 at	0.034	7009	1431181 a at	0.045	6734	95004 at	0.017	7383	1452708 a at	0.337	1036	5540.5	3014.756	TRUE	Luc7 homolog (S. cerevisiae)-like	223295 s at	0.210	5367	3.877E-04	TRUE
161297 f at	0.074	6176	1449869 at	-0.006	8258.5	161297 f at	0.123	1457	1449869 at	-0.086	6271	5540.625	2886.7506	FALSE	pre-B lymphocyte gene 1	221349 at	-0.010	36256	7.696E-01	FALSE
102940 at	0.045	6895	1419135 at	0.150	2970.5	102940 at	0.069	5050	1419135 at	0.034	7247	5540.625	1965.7316	TRUE	lymphotoxin B	207339 s at	0.002	44147	9.879E-01	FALSE
92488 at	0.041	6294	1418981 at	0.082	5050.5	92488 at	-0.029	6742	1418981 at	-0.147	4076	5540.625	1210.5405	FALSE	caspase 12	NA	NA	NA	NA	
102917 at	-0.081	5000	1421211 a at	0.028	7560.5	102917 at	0.007	8098	1421210 at	-0.207	1507	5541.375	3010.1199	FALSE	class II transactivator	205101 at	0.118	7691	2.657E-03	FALSE
93274 at	0.140	4402	1426124 a at	0.177	3339.5	93274 at	0.035	6950	1426124 a at	-0.042	7477	5542.125	1989.7483	FALSE	CDC-like kinase 1	NA	NA	NA	NA	
102228 at	0.199	1239	1460651 at	0.076	4408	102228 at	-0.006	8233	1460651 at	-0.012	8290	5542.5	3395.8185	FALSE	linker for activation of T cells	209881 s at	0.059	19208	1.750E-01	FALSE
100117 at	0.089	3510	1417683 at	-0.042	6079	100117 at	-0.023	7134	1417683 at	0.095	5452	5543.75	1523.1486	FALSE	diablo homolog (Drosophila)	219350 s at	0.141	10050	1.037E-02	FALSE
101367 at	-0.141	3872	1422521 at	-0.098	4595	101367 at	-0.050	6498	1422521 at	-0.040	7211	5544	1568.9901	TRUE	dynactin 1	211780 x at	-0.220	5272	3.567E-04	TRUE
161336 r at	0.154	2284	1417931 at	0.076	4243.5	161336 r at	-0.046	7138	1417931 at	0.001	8511	5544.125	2808.4886	FALSE	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	214867 at	0.126	10078	1.051E-02	FALSE
97149 at	-0.074	4145	1418558 at	0.092	4488	97149 at	-0.039	5982	1418558 at	-0.034	7566	5545.25	1565.5307	FALSE	retina and anterior neural fold homeobox	208242 at	-0.053	30474	5.747E-01	FALSE
102841 at	-0.072	5099	1435782 at	0.063	5741	102841 at	0.025	7043	1435782 at	0.121	4299	5545.5	1159.5762	FALSE	similar to ubiquitin A-52 residue ribosomal protein fusion product 1	NA	NA	NA	NA	
100891 at	0.012	7906	1418358 at	0.090	3478	100891 at	-0.116	2526	1418358 at	-0.011	8272	5545.5	2966.3501	FALSE	sperm mitochondria-associated cysteine-rich protein	NA	NA	NA	NA	
98792 at	0.083	4772	1448067 at	0.020	7863	98792 at	-0.034	6557	1448067 at	0.238	2997	5547.25	2120.3051	FALSE	expressed sequence AW011956	NA	NA	NA	NA	
102321 at	-0.101	3292	1418128 at	0.023	7873	102321 at	0.004	8353	1418128 at	0.157	2677	5548.75	2978.0209	FALSE	adenylate cyclase 6	209195 s at	0.132	6214	8.424E-04	FALSE
101793 at	0.066	6252	1417876 at	0.033	6872	102879 s at	0.023	7069	1436625 at	-0.358	2002	5548.75	2389.9893	FALSE	Fc receptor, IgG, high affinity I	216950 s at	0.253	18209	1.461E-01	FALSE
97387 at	-0.044	6016	1454023 a at	-0.035	6728	97387 at	-0.141	1705	1454023 a at	-0.027	7748	5549.25	2659.5781	TRUE	DNA segment, Chr 1, Brigham & Women's Genetics 1363 expressed	202175 at	-0.070	17159	1.185E-01	FALSE
99395 at	0.119	3651	1418552 at	0.072	5081	99395 at	0.033	6653	1418552 at	-0.053	6814	5549.75	1487.7799	FALSE	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	229549 at	-0.261	6311	9.220E-04	FALSE
98810 at	0.068	5554	1422196 at	0.030	7724.5	98810 at	-0.194	996	1422196 at	0.020	7928	5550.625	3220.8831	FALSE	5-hydroxytryptamine (serotonin) receptor 5B	NA	NA	NA	NA	
102691 at	0.076	4792	1418865 at	-0.048	6619	102691 at	-0.009	8111	1418865 at	-0.159	2681	5550.75	2345.7198	FALSE	zinc finger protein 385	226111 s at	0.138	11516	2.116E-02	FALSE
102880 at	0.015	7598	1427341 at	0.113	2448	102881 at	-0.080	4320	1427341 at	-0.036	7840	5551.5	2618.7592	FALSE	RIKEN cDNA E130103I17 gene	37549 g at	0.108	12891	3.572E-02	FALSE
104104 at	0.074	4655	1439973 at	0.080	4480.5	95353 at	0.041	5831	1460605 at	-0.046	7242	5552.125	1276.2787	FALSE	Crx opposite strand transcript 1	NA	NA	NA	NA	
93608 at	0.069	5081	1449222 at	0.100	4486.5	162357 at	0.039	6425	1449222 at	-0.105	6219	5552.875	924.50819	FALSE	Epstein-Barr virus induced gene 3	219424 at	0.166	11487	2.092E-02	FALSE
94401 s at	0.086	4903	1418199 at	-0.007	8284	94401 s at	0.111	2669	1418199 at	0.063	6358	5553.5	2369.6934	FALSE	hemogen	223670 s at	-0.116	14018	5.262E-02	FALSE
161856 f at	0.123	5060	1449207 a at	0.028	7523.5	161856 f at	0.207	1583	1449207 a at	-0.020	8051	5554.375	2951.0911	FALSE	kinesin family member 20A	218755 at	0.005	42179	9.392E-01	FALSE
101046 at	-0.017	7718	1456292 a at	0.089	6315.5	101046 at	0.079	4289	1450641 at	-0.215	3897	5554.875	1789.66	FALSE	vimentin	201426 s at	0.557	4814	2.210E-04	FALSE
102792 at	0.107	3735	1425753 a at	-0.006	8360.5	162227 r at	-0.146	3888	1425753 a at	0.084	6240	5555.875	2193.2731	FALSE	uracil DNA glycosylase	202330 s at	0.391	5288	3.619E-04	FALSE
101552 at	0.016	7634	1423279 at	0.113	2832	101552 at	0.017	7508	1427627 at	0.155	4250	5556	2398.2077	TRUE	solute carrier family 34 (sodium phosphate), member 1	208177 at	0.106	11161	1.839E-02	TRUE
92439 at	0.055	5982	1452403 a at	0.125	2753	92439 at	-0.042	5445	1452403 a at	-0.023	8044	5556	2178.742	FALSE	otoconin 90	NA	NA	NA	NA	
161969 f at	0.085	5307	1450355 a at	0.033	7190	161969 f at	0.062	5412	1450355 a at	-0.188	4316	5556.25	1195.8669	FALSE	capping protein (actin filament), gelsolin-like	201850 at	0.364	5834	6.013E-04	FALSE
98519 r at	0.137	2121	1453092 at	0.095	4761	98519 r at	0.028	6999	1453092 at	-0.011	8346	5556.75	2726.2671	FALSE	RIKEN cDNA 2300002G24 gene	220620 at	-0.036	29328	5.325E-01	FALSE
101229 at	0.206	1305	1448088 at	0.040	6838	101229 at	0.046	5929	1448088 at	0.015	8166	5559.5	2981.3702	TRUE	expressed sequence C78228	NA	NA	NA	NA	
96267 at	-0.063	5989	1415967 at	-0.019	7770	96267 at	-0.143	1563	1415966 a at	0.045	6918	5560	2762.1437	FALSE	NADH dehydrogenase (ubiquinone) flavoprotein 1	208714 at	-0.184	17736	1.330E-01	FALSE
102958 at	0.107	4724	1449102 at	0.103	3968	102958 at	0.022	7417	1418494 at	-0.154	6131	5560	1528.3815	FALSE	early B-cell factor 2	220392 at	-0.039	28516	5.022E-01	FALSE
102713 at	0.046	6172	1418863 at	0.058	5321	102713 at	-0.072	4383	1418863 at	0.065	6368	5561	907.35035	FALSE	GATA binding protein 4	230855 at	0.081	14493	6.125E-02	FALSE
104719 at	-0.030	7111	1449011 at	-0.020	7804.5	104719 at	-0.037	6087	1418257 at	-0.485	1242	5561.125	2964.5814	TRUE	solute carrier family 12, member 7	218066 at	0.301	3066	2.506E-05	FALSE
99147 at	0.016	7766	1425531 at	0.161	2469.5	99147 at	0.062	5178	1425531 at	0.060	6831	5561.125	2322.2824	TRUE	zinc finger, HIT domain containing 1	201541 s at	0.028	35047	7.317E-01	FALSE
162036 r at	0.127	4582	1448599 s at	0.076	4391.5	162028 f at	0.039	6124	1417120 at	-0.051	7151	5562.125	1312.9147	FALSE	DNA segment, Chr 4, Wayne State University 114, expressed	218551 at	0.092	17090	1.169E-01	FALSE
103407 at	-0.054	6522	1424722 at	0.020	7928	103407 at	0.187	328	1424722 at	0.043	7473	5562.75	3538.6547	FALSE	RIKEN cDNA 1300017J02 gene	NA	NA	NA	NA	
101171 at	0.151	2469	1420457 at	0.030	7694	101171 at	-0.096	3823	1420457 at	0.011	8266	5563	2854.6924	FALSE	dishevelled 3, dsh homolog (Drosophila)	201908 at	0.122	12212	2.807E-02	FALSE
94173 at	0.087	3955	1449925 at	-0.045	6411	94173 at	-0.037	6422	1449925 at	-0.089	5464	5563	1162.2464	FALSE	chemokine (C-X-C motif) receptor 3	217119 s at	-0.033	32908	6.616E-01	FALSE
94101 at	0.017	7596	1420738 at	-0.074	4887	94101 at	-0.030	6768	1420738 at	-0.176	3003	5563.5	2049.0395	FALSE	zinc finger protein 98	222097 at	0.063	15049	7.187E-02	FALSE
101188 at	0.066	4975	1421468 at	0.001	8499	101188 at	0.021	7217	1421468 at	0.188	1563	5563.5	3038.7253	TRUE	potassium inwardly-rectifying channel, subfamily J, member 3	207142 at	0.030	22166	2.738E-01	FALSE
94175 at	0.125	4318	1421558 at	0.102	3063	94175 at	-0.022	7622	1421558 at	0.080	7251	5563.5	2227.7679	FALSE	brachyury 2	NA	NA	NA	NA	
94408 at	0.112	3119	1417624 at	-0.094	4197	94408 at	-0.003	8395	1448781 at	-0.133	6545	5564	2368.096	FALSE	Ngfi-A binding protein 1	209272 at	0.542	822	2.908E-07	FALSE
98516 at	-0.031	6769	1424117 at	0.079	5502.5	98516 at	-0.126	1624	1424117 at	0.008	8362	5564.375	2875.6571	FALSE	cDNA sequence BC056474	217780 at	-0.014	39879	8.744E-01	FALSE
103237 at	-0.001	8499	1448878 at	0.081	4897	103237 at	-0.039	6329	1448878 at	-0.159	2533	5564.5	2505.4141	FALSE	Max dimerization protein 3	221250 s at	-0.037	31517	6.136E-01	FALSE
99399 at	-0.006	8257	1421690 s at	0.130	2139	99399 at	-0.012	7631	1421690 s at	0.118	4233	5565	2888.3052	FALSE	agouti related protein	207193 at	0.042	24534	3.553E-01	FALSE
101620 at	-0.071	4980	1422316 at	0.089	4679	101620 at	-0.102	4446	1422316 at	-0.015	8156	5565.25	1740.9445	FALSE	glycoprotein 1b, alpha polypeptide	207389 at	0.045	24795	3.652E-01	FALSE
98813 at	0.067	4420	1420710 at	0.120	2521	98813 at	0.017	7516	1420710 at	0.028	7805	5565.5	2543.0271	TRUE	reticuloendotheliosis oncogene	206036 s at	0.021	33647	6.865E-01	FALSE
99400 at	-0.013	7751	1420278 at	0.099	4444	99400 at	-0.028	6780	1420279 at	-0.180	3290	5566.25	2056.4598	FALSE	cDNA sequence BC048599	NA	NA	NA	NA	
92889 r at	0.005	8249	1422210 at	0.107	3626.5	92889 r at	0.092	3266	1422210 at	0.045	7129	5567.625	2496.2043	TRUE	forkhead box D3	208500 x at	-0.059	18522	1.558E-01	FALSE
101127 at	0.138	1877	1419628 at	0.005	8341	161711 f at	0.051	5141	1419628 at	0.061	6912	5567.75	2786.9742	TRUE	C. elegans ceh-10 homeo domain containing homolog	NA	NA	NA	NA	
100985 at	0.036	6411	1449733 s at	0.041	6379.5	100985 at	0.047	5961	1423390 at	0.140	3520	5567.875	1380.5716	TRUE	seven in absentia 1A	202980 s at	0.098	9838	9.216E-03	TRUE
94393 r at	0.104	4536	1416444 at	0.067	6104	94393 r at	-0.012	8065	1416444 at	-0.180	3567	5568	1965.6492	FALSE	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	220029 at	-0.211	5422	4.088E-04	FALSE

161542 r at	0.083	5297	1415715 at	-0.003	8431	97392 at	-0.114	2240	1415715 at	-0.070	6305	5568.25	2574.8115	FALSE	transmembrane protein 129	225588 s at	0.098	18932	1.667E-01	FALSE
101802 at	-0.027	6977	1422358 at	0.025	8015.5	101802 at	0.060	4935	1422358 at	0.182	2348	5568.875	2499.6415	FALSE	formyl peptide receptor, related sequence 4		NA	NA	NA	NA
103730 at	0.047	5810	1429280 at	0.052	5845	103730 at	-0.009	8047	1453084 s at	-0.170	2574	5569	2254.2379	FALSE	collagen, type XXII, alpha 1	243301 at	-0.078	13163	3.933E-02	FALSE
93658 at	0.018	7544	1418759 at	0.151	3694	93658 at	-0.054	5164	1418759 at	0.112	5878	5570	1599.5574	FALSE	protein tyrosine phosphatase, non-receptor type 20	215172 at	-0.138	5399	3.989E-04	FALSE
96537 at	-0.022	7278	1420562 at	0.092	3353	96537 at	0.064	4979	1420562 at	0.064	6670	5570	1769.3345	FALSE	secreted Ly6/Plaur domain containing 1	214536 at	0.013	39781	8.717E-01	FALSE
94520 at	0.018	7987	1424743 at	0.023	7456.5	94520 at	0.117	1553	1424743 at	0.083	5287	5570.875	2922.1651	TRUE	RIKEN cDNA 2610003J06 gene	224886 at	0.002	43787	9.791E-01	FALSE
104616 g at	-0.264	1406	1450187 a at	-0.024	7264	104615 at	-0.037	6143	1450187 a at	0.035	7474	5571.75	2837.9608	FALSE	galactose-1-phosphate uridyl transferase	203179 at	-0.097	12910	3.597E-02	FALSE
102192 r at	0.054	5527	1425559 a at	0.151	1055	102192 r at	0.015	7511	1425559 a at	-0.010	8194	5571.75	3216.6193	FALSE	acyl-CoA synthetase medium-chain family member 3	205942 s at	-0.054	29568	5.409E-01	FALSE
96840 at	0.059	5872	1423187 at	0.012	8208	96840 at	0.044	6505	1441376 at	-0.226	1705	5572.5	2760.5961	FALSE	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	209046 s at	-0.172	14513	6.153E-02	FALSE
97122 at	0.102	3886	1427560 at	0.021	7618	97122 at	0.083	4522	1427560 at	0.062	6267	5573.25	1694.5236	TRUE	sine oculis-related homeobox 5 homolog (Drosophila)	229009 at	0.180	8320	3.985E-03	TRUE
92347 at	0.077	4008	1421981 at	-0.032	6800	92347 at	-0.016	7461	1421980 at	0.185	4025	5573.5	1818.021	FALSE	potassium voltage gated channel, Shaw-related subfamily, member 3	230531 at	-0.218	8641	4.743E-03	FALSE
98315 at	0.146	2296	1419632 at	0.025	7732	98315 at	-0.042	5936	1419632 at	0.077	6332	5574	2317.1718	FALSE	tectorin alpha	236904 x at	-0.142	9314	7.017E-03	FALSE
92429 at	0.074	5909	1422926 at	0.076	5816	92429 at	-0.023	7273	1422926 at	-0.145	3299	5574.25	1656.6044	FALSE	melanocortin 2 receptor	217425 at	-0.060	23039	3.025E-01	FALSE
102411 at	-0.084	4244	1416586 at	0.098	3298.5	102411 at	-0.056	6283	1416586 at	0.002	8473	5574.625	2298.8171	FALSE	zinc finger protein 239	206261 at	-0.035	31784	6.239E-01	FALSE
95153 at	-0.233	1136	1435220 s at	-0.058	5557	95153 at	0.032	7587	1435220 s at	0.021	8019	5574.75	3147.8207	FALSE	CDC42 small effector 2	215846 at	0.059	13868	5.006E-02	FALSE
103622 at	-0.008	8071	1449964 a at	0.081	4953	103622 at	-0.065	3678	1449964 a at	0.091	5599	5575.25	1845.3622	FALSE	malonyl-CoA decarboxylase	218869 at	0.139	8329	4.021E-03	FALSE
162405 at	0.115	4171	1419876 at	0.041	6874	162405 at	0.061	4213	1419876 at	0.063	7047	5576.25	1600.0457	TRUE	RIKEN cDNA 2810449G22 gene		NA	NA	NA	NA
98467 at	0.004	8255	1431808 a at	0.216	383.5	98467 at	0.017	7665	1431808 a at	-0.089	6002	5576.375	3590.9374	FALSE	inter alpha-trypsin inhibitor, heavy chain 4	206287 s at	-0.069	15580	8.167E-02	FALSE
93636 at	0.036	6955	1436588 at	0.143	2080	93636 at	-0.045	5920	1431919 at	-0.037	7354	5577.25	2408.5453	FALSE	rotatin	227072 at	-0.195	7716	2.695E-03	FALSE
160651 at	0.143	4324	1423323 at	0.051	6152	160651 at	0.102	3602	1423323 at	-0.010	8234	5578	2070.4995	FALSE	tumor-associated calcium signal transducer 2	227128 s at	0.042	28057	4.829E-01	FALSE
160405 at	0.067	6107	1434004 at	0.100	4856	160405 at	0.042	6324	1434004 at	0.110	5028	5578.75	743.89487	TRUE	deoxyhypusine synthase	202802 at	-0.279	4680	1.926E-04	FALSE
104646 at	-0.044	6380	1418949 at	0.149	2229	104646 at	-0.056	5535	1418949 at	-0.011	8171	5578.75	2488.9423	FALSE	growth differentiation factor 15	221576 at	0.037	24046	3.396E-01	FALSE
160505 at	0.156	1901	1455808 at	0.051	5849	160505 at	-0.035	6162	1455808 at	-0.004	8407	5579.75	2704.1976	FALSE	RIKEN cDNA 4922502D21 gene		NA	NA	NA	NA
95304 at	0.010	8174	1421785 at	0.149	2449	95304 at	-0.001	8453	1421785 at	-0.145	3244	5580	3175.0602	FALSE	signaling molecule ATTP	220775 s at	0.028	31941	6.289E-01	FALSE
103780 at	0.005	8303	1421019 at	0.119	2708.5	103780 at	0.069	5310	1421019 at	0.091	5999	5580.125	2302.8028	TRUE	RIKEN cDNA 1700021F05 gene	223576 at	0.014	39907	8.751E-01	FALSE
99887 at	0.044	6312	1421796 a at	0.118	5227	99887 at	0.003	8321	1436866 at	0.251	2461	5580.25	2442.7904	TRUE	ephrin A5	207301 at	-0.002	43824	9.802E-01	FALSE
94817 at	-0.010	8161	1450843 a at	-0.111	4394.5	94817 at	0.033	6675	1450843 a at	-0.223	3092	5580.625	2269.8119	FALSE	serine (or cysteine) peptidase inhibitor, clade H, member 1	207714 s at	0.231	13834	4.952E-02	FALSE
92648 at	-0.116	5589	1416653 at	-0.086	4710	92648 at	0.090	6585	1416653 at	-0.115	5443	5581.75	771.52722	FALSE	syntaxin binding protein 3A	203310 at	0.346	6558	1.101E-03	FALSE
92634 at	-0.031	7334	1441342 at	0.062	5038.5	92634 at	-0.014	7835	1441242 at	0.161	2120	5581.875	2609.3645	FALSE	dipeptidylpeptidase 4	203717 at	0.046	20369	2.121E-01	FALSE
97128 at	-0.044	6079	1421620 at	0.154	1903.5	97128 at	-0.032	6304	1421620 at	0.018	8041	5581.875	2604.2488	FALSE	interleukin 5 receptor, alpha	211517 s at	0.048	20441	2.140E-01	FALSE
98338 at	0.061	6136	1418868 at	-0.014	8019	98338 at	0.102	2602	1418868 at	-0.081	5571	5582	2245.47	FALSE	engrailed 2	207060 at	0.030	30417	5.727E-01	FALSE
94015 at	0.021	7383	1416198 at	0.046	6807.5	94015 at	0.066	5132	1416198 at	0.173	3008	5582.625	1964.1305	TRUE	TH1-like homolog (Drosophila)	225865 x at	0.180	3468	4.418E-05	TRUE
101623 at	0.058	5684	1420445 at	0.051	6222	101623 at	0.036	6424	1420445 at	-0.150	4002	5583	1099.2974	FALSE	solute carrier family 16 (monocarboxylic acid transporters), member 8	220455 at	-0.080	14061	5.363E-02	FALSE
95147 at	0.010	7926	1417722 at	0.015	7949	95147 at	0.038	6256	1457728 at	-0.362	202	5583.25	3674.0393	FALSE	6-phosphogluconolactonase	218387 s at	0.369	2979	2.134E-05	FALSE
99876 at	0.178	3520	1420819 at	0.047	6561.5	99876 at	-0.013	7859	1420818 at	-0.172	4398	5584.625	1983.0802	FALSE	src-like adaptor	203760 s at	0.236	8438	4.206E-03	FALSE
93071 at	0.023	7456	1415869 a at	-0.052	6126	93071 at	-0.244	2109	1415869 a at	-0.064	6648	5584.75	2380.8869	FALSE	tripartite motif protein 28	200990 at	0.162	9724	8.761E-03	FALSE
97085 at	0.014	8075	1457476 at	0.143	1558	97085 at	-0.001	8480	1457476 at	-0.101	4226	5584.75	3298.7237	FALSE	DNA segment, Chr 8, ERATO Doi 362, expressed		NA	NA	NA	NA
99055 at	0.073	4851	1417616 at	0.040	7028.5	99055 at	0.080	4059	1417617 at	0.055	6410	5587.125	1370.1254	TRUE	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyl	204542 at	0.148	16727	1.068E-01	FALSE
93488 at	-0.017	8000	1433502 s at	0.132	2108	93488 at	0.015	8086	1455643 s at	0.134	4157	5587.75	2956.1184	FALSE	TSR1, 20S rRNA accumulation, homolog (yeast)	218155 x at	0.229	6192	8.265E-04	FALSE
99831 at	-0.101	2945	1449820 at	0.043	6428.5	99831 at	0.025	7341	1449820 at	-0.094	5637	5587.875	1894.4919	FALSE	cortistatin	210182 at	-0.313	6228	8.555E-04	FALSE
104600 at	-0.024	7301	1421222 at	0.096	4749.5	104600 at	-0.171	2248	1452720 a at	0.014	8061	5589.875	2639.9979	FALSE	FIP1 like 1 (S. cerevisiae)	233405 at	0.107	15781	8.565E-02	FALSE
93760 at	0.066	6704	1423486 at	0.049	7656	93760 at	0.059	4945	1423487 at	-0.161	3059	5591	2027.4232	FALSE	RIKEN cDNA 1200020A08 gene	222702 x at	-0.108	24807	3.658E-01	FALSE
98529 at	-0.015	7783	1448608 at	0.026	7401	98529 at	-0.049	5704	1448608 at	0.180	1478	5591.5	2887.3576	FALSE	decidual/trophoblast prolactin-related protein		NA	NA	NA	NA
94210 at	-0.092	3762	1455211 a at	0.114	3262	94210 at	0.019	7473	1455211 a at	0.025	7872	5592.25	2416.2202	FALSE	translocase of inner mitochondrial membrane 13 homolog (yeast)	231749 at	-0.034	27937	4.779E-01	FALSE
161992 at	0.056	5232	1428351 at	0.029	7806.5	161992 at	-0.136	1841	1428351 at	-0.072	7490	5592.375	2751.1219	FALSE	protein phosphatase 1M		NA	NA	NA	NA
96498 at	0.015	7802	1420335 at	-0.073	5467	96498 at	0.021	7050	1449819 at	-0.210	2058	5594.25	2550.4656	FALSE	disrupted meiotic cDNA 1 homolog	208386 x at	0.087	7050	1.642E-03	FALSE
94528 at	0.058	5744	1418906 at	0.064	5541	94528 at	-0.008	7981	1430778 a at	0.157	3113	5594.75	1989.8439	FALSE	nucleotide binding protein 1	203978 at	0.087	16874	1.107E-01	FALSE
101146 at	0.066	6126	1450002 at	0.052	5930	101146 at	-0.008	8001	1450002 at	-0.185	2324	5595.25	2372.2326	FALSE	genomic screened homeo box 1	234791 at	-0.085	15524	8.026E-02	FALSE
94284 at	-0.045	6575	1422185 a at	0.051	6288	94284 at	-0.050	5832	1422185 a at	-0.134	3692	5596.75	1306.1668	FALSE	cytochrome b5 reductase 3	201885 s at	0.211	5286	3.617E-04	FALSE
95740 at	0.085	4290	1452732 at	0.052	6089.5	95740 at	-0.072	3779	1452732 at	0.013	8229	5596.875	2015.2215	FALSE	RIKEN cDNA 2300003P22 gene	235514 at	0.066	12957	3.648E-02	FALSE
93151 at	-0.061	6138	1449921 s at	-0.006	8290.5	93151 at	-0.301	3447	1449921 s at	0.139	4512	5596.875	2109.2928	FALSE	copine VI	210408 s at	-0.214	14134	5.503E-02	FALSE
102279 at	0.020	7662	1426971 at	0.024	7534	102279 at	0.053	5139	1426971 at	-0.531	2053	5597	2632.2293	FALSE	ubiquitin-activating enzyme E1-like	1294 at	0.149	5659	5.051E-04	FALSE
102030 at	0.119	2498	1420948 s at	-0.028	7427.5	102030 at	-0.117	4579	1420948 s at	-0.030	7885	5597.375	2531.5212	FALSE	RIKEN cDNA 4833408C14 gene		NA	NA	NA	NA
160243 r at	0.239	3277	1426650 at	0.077	4704.5	160243 r at	-0.059	6471	1426650 at	0.022	7940	5598.125	2035.7207	FALSE	myosin, heavy polypeptide 8, skeletal muscle, perinatal	206717 at	0.042	19962	1.995E-01	FALSE
102238 at	0.110	3425	1450164 at	0.006	8294.5	102238 at	0.065	5673	1437086 at	0.129	5001	5598.375	2029.3739	TRUE	achaete-scute complex homolog-like 1 (Drosophila)	209988 s at	1.197	262	2.983E-08	TRUE
101736 at	0.013	7912	1422271 at	0.171	791.5	101736 at	0.022	7182	1422271 at	0.078	6508	5598.375	3255.4669	TRUE	pancreatic polypeptide receptor 1	210956 at	0.042	22879	2.973E-01	FALSE
93655 at	0.064	5094	1426164 a at	0.139	3659	93656 g at	0.005	8207	1426164 a at	0.099	5435	5598.75	1901.5068	TRUE	upstream transcription factor 1	231768 at	-0.006	41562	9.225E-01	FALSE
102116 f at	-0.166	1270	1417708 at	-0.005	8399	102116 f at	-0.030	6866	1417708 at	0.071	5863	5599.5	3068.9425	FALSE	synaptotagmin III	223901 at	-0.349	2089	4.468E-06	FALSE
92517 at	0.014	7748	1423540 at	0.050	6220	92517 at	0.085	5209	1423540 at	0.161	3222	5599.75	1897.8996	TRUE	RNA binding motif, single stranded interacting protein 2	34187 at	0.029	24899	3.686E-01	FALSE
97693 at	0.071	4619	1443414 at	0.080	4254	97693 at	-0.035	6325	1443414 at	-0.053	7201	5599.75	1397.9631	FALSE	EST C78513		NA	NA	NA	NA
94741 at	0.020	7478	1432486 a at	0.082	5317	94741 at	0.077	4036	1432486 a at	-0.082	5570	5600.25	1420.5596	FALSE	testicular serine protease 2		NA	NA	NA	NA
99388 at	0.057	5130	1450918 s at	-0.031	7672	99388 at	0.023	7458	1450918 s at	-0.336	2142	5600.5	2577.0792	FALSE	Rous sarcoma oncogene	237103 at	-0.121	9485	7.731E-03	FALSE
103805 at	0.051	6198	1448746 at	0.072	4977.5	103805 at	-0.110	2752	1448746 at	0.002	8475	5600.625	2388.9913	FALSE	nibrin	202905 x at	0.039	32861	6.604E-01	FALSE
99139 at	-0.050	6021	1428247 at	-0.111	3169	99139 at	0.001	8458	1428247 at	-0.139	4767	5603.75	2232.2633	FALSE	vacuolar protein sorting 26 homolog B (yeast)	225483 at	-0.291	3955	8.275E-05	FALSE
93800 f at	0.120	2518	1449378 at	0.078	5335.5	93800 f at	0.031	6224	1449378 at	0.008	8342	5604.875	2413.6093	TRUE	keratin complex-1, acidic, gene C29	240388 at	-0.092	12551	3.192E-02	FALSE
96262 at	-0.154	2948	1424684 at	-0.059	6983	96262 at	-0.038	7625	1424684 at	-0.510	4864	5605	2128.2241	TRUE	RAB5C, member RAS oncogene family	201156 s at	-0.203	9563	8.017E-03	TRUE
102770 at	-0.023	7554	1423016 a at	0.083	4150	102770 at	-0.021	7178	1425643 at	-0.123	3538	5605	2054.4621	FALSE	glycophorin A		NA	NA	NA	NA
97377 at	-0.046	6276	1416692 at	0.045	5908	97377 at	-0.082	3251.5	1416692 at	-0.049	6988	5605.875	1632.3499	FALSE	coilin	203653 s at	0.076	17819	1.358E-01	FALSE
160292 at	0.094	3190	1432181 s at	0.082	5510	160292 at	0.050	6507	1432181 s at	0.045	7221	5607	1757.4882	TRUE	endothelial cell growth factor 1 (platelet-derived)	204858 s at	0.225	10351	1.231E-02	TRUE
93705 at	0.078	4389	1420682 at	0.154	2500	93705 at	0.024	7401	1420682 at	-0.017	8141	5607.75	2631.6384	FALSE	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	206703 at	0.003	43757	9.787E-01	FALSE
160658 at	-0.009	8117	1451741 a at	0.117	2850	160658 at	0.005	8192	1458987 at	-0.194	3274	5608.25	2945.4064	FALSE	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	211297 s at	-0.251	8709	4.949E-03	FALSE
98108 at	-0.069	4629	1448326 a at	0.075	5595	98108 at	0.068	5546	1448326 a at	-0.077	6664	5608.5	832.18367	FALSE	cellular retinoic acid binding protein I	205350 at	-0.159	21650	2.557E-01	FALSE
99094 at	0.003	8358	1424260 at	0.170	2513.5	99094 at	-0.028	6355	1421390 at	0.094	5208	5608.625	2439.702	FALSE	solute carrier family 12, member 1	220281 at	-0.027	23443	3.184E-01	FALSE
160515 at	0.052	6260	1437334 x at	-0.024	7219.5	160515 at	-0.098	3225	1425422 a at	0.090	5731	5608.875	1704.4893	FALSE	poly(A)-specific ribonuclease (deadenylation nuclease)	203905 at	0.066	20487	2.156E-01	FALSE
96691 at	0.005	8322	1451995 at	0.213	590	96691 at	0.007	8141	1446161 at	0.082	5384	5609.25	3606.1234	TRUE	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	209358 at	0.016	39610	8.678E-01	FALSE
94645 at	0.033	7452	1421263 at	0.059	6487.5	94645 at	0.021	7740	1421263 at	0.307	760	5609.875	3277.3145	TRUE	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	207210 at	-0.051	31421	6.099E-01	FALSE
93961 at	0.174	1287	1449216 at	-0.004	8341	161730 f at	-0.048	5988	1447541 s at	0.055	6824	5610	3042.1138	FALSE	integrin, alpha E, epithelial-associated	205055 at	-0.353	2885	1.803E-05	FALSE
101632 at	0.095	4745	1430259 at	0.114	2870	101632 at	-0.037	7092	1430259 at	0.026	7733	5610	2233.0307	FALSE	tumor necrosis factor receptor superfamily, member 11a	238846 at	-0.097	13361	4.204E-02	FALSE
102930 at	-0.046	6326	1422523 at	0.045	6702.5	102930 at	-0.150	1322	1422523 at	0.021	8090	5610.125	2957.6768	FALSE	silver	209848 s at	-0.020	34512	7.140E-01	FALSE
99073 at	0.000	8515	1422513 at	0.043	6809	99073 at	-0.085	3298	1443807 x at	0.196	3820	5610.5	2478.3105	FALSE	cyclin F	241551 at	-0.015	35712	7.529E-01	FALSE
101995 at	0.032	7415	1450957 a at	-0.031	7409	101995 at	0.098	5101	1450957 a at	0.167	2520	5611.25	2331.0656	FALSE	sequestosome 1	244804 at	0.422	3668	5.728E-05	FALSE
95747 at	-0.019	7625	1425560 a at	-0.056	5512	95747 at	0.037	5909	1425560 a at	-0.208	3399	5611.25	1736.639	FALSE	S100 calcium binding protein A16	227998 at	0.224	9606	8.200E-03	FALSE
98493 at	0.034	6854	1424328 s at	0.092	4031	98493 at	0.008	8156	1428734 at	0.172	3404	5611.25	2264.9005	TRUE	RIKEN cDNA 3200002M19 gene		NA	NA	NA	NA
92296 at	0.113	3381	1425997 a at	-0.036	6989	92296 at	-0.021	7020	1421284 at	-0.106	5058	5612	1747.6527	FALSE	phosphatidylinositol glycan, class N	232101 s at	-0.013	38408	8.342E-01	FALSE
101282 at	0.042	6676	1422275 at	0.065	4765	101282 at	-0.116	3223	1422275 at	0.026	7786	5612.5	2023.4542	FALSE	G protein-coupled receptor 44	206361 at	0.073	21016	2.339E-01	FALSE
160461 f at	-0.025	6958	1416431 at	0.083	3812.5	160461 f at	-0.071	4534	1416431 at	0.089	7147	5612.875	1689.9923	FALSE	tubulin, beta 6	209191 at	0.250	14369	5.934E-02	FALSE
160601 at	-0.005	8286	1449943 at	-0.102	2420.5	160601 at	0.012	8028	1420643 at	-0.160	3721	5613.875	2986.0158	FALSE	lunatic fringe gene homolog (Drosophila)	228762 at	0.229	3548	4.941E-05	FALSE
98865 at	0.107	4183	1418678 at	0.078	5455	98865 at	0.003	8280	1449169 at	-0.099	4539	5614.25	1856.1809	FALSE	hyaluronan synthase 2	206432 at	-0.003	42742	9.532E-01	FALSE
98526 r at	0.033	6740	1452406 x at	0.275	5355	98525 f at	0.277	4401	1452406 x at	-0.166	5961	5614.25	987.71365	FALSE	Erythroid differentiation regulator 1		NA	NA	NA	NA
102995 s at	0.035	6787	1417898 a at	0.109	3039.5	102995 s at	-0.043	6753	1417898 a at	0.079	5879	5614.625	1767.4392	FALSE	granzyme A	205488 at	0.008	41287	9.152E-01	FALSE
93217 at	-0.069	5285	1428742 at	0.006	8318	93217 at	0.048	6011	1440824 at	-0.276	2848	5615.5	2253.0138	FALSE	F-box protein 45	225099 at	0.131	20790	2.265E-01	FALSE
101636 at	0.014	7769	1420466 at	0.078	4436	101636 at	0.171	2305	1420466 at	-0.020	7953	5615.75	2735.6961	FALSE	salivary protein 2		NA	NA	NA	NA
97320 at	0.135	3230	1451139 at	0.065	5771.5	162284 r at	0.033	6560	1451139 at	0.063	6902	5615.875	1659.5289	TRUE	solute carrier family 39 (zinc transporter), member 4	219215 s at	0.022	36922	7.890E-01	FALSE
99846 at	0.052	5348	1418220 at	0.054	6652	99846 at	0.019	7686	1418220 at	-0.156	2780	5616.5	2119.1913	FALSE	forkhead box F2	206377 at	0.192	11492	2.095E-02	FALSE
93603 at	0.090	4315	1448849 at	0.054	6596.5	93603 at	0.018	7319	1448849 at	-0.105	4238	5617.125	1576.1841	FALSE	mitochondrial ribosomal protein L40	203152 at	0.086	26216	4.122E-01	FALSE
92623 at	0.010	8167	1427396 a at	-0.040	7099.5	92623 at	0.149	2508	1423997 at	-0.087	4697	5617.875	2530.651	FALSE	cold shock domain containing E1, RNA binding	202646 s at	0.078	22397	2.816E-01	FALSE
160705 at	0.019	7488	1449031 at	0.116	2818.5	160705 at	0.052	4786	1449031 at	-0.083	7381	5618.375	2246.0701	FALSE	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	207144 s at	-0.063	28302	4.934E-01	FALSE
101652 i at	0.063	5418	1422405 at	0.103	2777	101653 f at	-0.078	5870	1422405 at	-0.005	8411	5619	2307.6417	FALSE	histocompatibility 2, D region locus 4		NA	NA	NA	NA
95584 at	0.016	7863	1453223 s at	0.079	5801.5	95584 at	0.074	4923	1429654 at	-0.139	3893	5620.125	1686.4489	FALSE	developmental pluripotency associated 2	240301 at	0.012	38053	8.235E-01	FALSE
101160 at	0.079	4427	1449984 at	0.080	6015.5	101160 at	0.018	7688	1449984 at	-0.110	4352	5620.625	1577.3518	FALSE	chemokine (C-X-C motif) ligand 2	207850 at	0.083	13935	5.126E-02	FALSE
96268 at	-0.154	2915	1415891 at	0.085	4581.5	96268 at	-0.022	7790	1415891 at	-0.040	7198	5621.125	2279.9478	FALSE	succinate-CoA ligase, GDP-forming, alpha subunit	217874 at	-0.019	38434	8.350E-01	FALSE
96327 at	0.006	8159	1422551 at	-0.152	2032	96327 at	0.045	6521	1422551 at	0.097	5778	5622.5	2592.1037	FALSE	zinc finger protein 306	211773 s at	-0.081	20663	2.220E-01	FALSE
92365 at	-0.045	6726	1449528 at	0.101	4553.5	92365 at	0.114	2758	1449528 at	0.006	8453	5622.625	2488.4777	FALSE	c-fos induced growth factor	206742 at	0.017	37740	8.125E-01	FALSE
98282 at	0.091	5269	1421930 at	-0.029	7638	98282 at	0.100	2902	1421930 at	0.071	6683	5623	2058.5579	FALSE	inducible T-cell co-stimulator	210439 at	0.045	22391	2.814E-01	FALSE
104532 at	0.093	3074	1448345 at	0.068	5118	104532 at	0.025	6733	1448345 at	-0.033	7571	5624	1981.5168	FALSE	translocase of outer mitochondrial membrane 34	201870 at	-0.431	1181	6.972E-07	FALSE
104723 at	0.090	4158	1423912 at	-0.023	7630	104723 at	0.083	4712	1458570 at	-0.090	5996	5624	1543.0835	FALSE	Alveolar soft part sarcoma chromosome region, candidate 1 (human)	218908 at	0.014	38327	8.315E-01	FALSE
98624 at	0.100	3801	1421265 a at	0.047	6260	98624 at	-0.038	5995	1421265 a at	0.072	6441	5624.25	1229.2213	FALSE	RNA-binding region (RNP1, RRM) containing 1	212430 at	0.309	1532	1.505E-06	FALSE
100564 at	-0.160	2786	1417103 at	0.113	4359.5	100564 at	0.028	7191	1417103 at	-0.023	8161	5624.375	2486.2999	FALSE	D-dopachrome tautomerase	202929 s at	-0.119	18428	1.531E-01	FALSE
93146 at	0.064	6344	1449091 at	0.175	2003	93146 at	-0.015	7764	1449091 at	-0.089	6388	5624.75	2502.8873	FALSE	claudin 8	214598 at	0.032	26395	4.206E-01	FALSE
99492 at	0.021	7543	1417567 at	-0.098	5194	99492 at	-0.030	6669	1431694 a at	0.200	3095	5625.25	1945.5351	FALSE	catenin beta interacting protein 1	203081 at	0.035	27422	4.588E-01	FALSE
95502 at	0.201	2308	1423507 a at	-0.088	4563	95502 at	0.013	7596	1423507 a at	0.018	8036	5625.75	2697.4119	FALSE	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	220605 s at	0.095	18396	1.520E-01	FALSE
104372 at	-0.104	3976	1416863 at	-0.060	6487.5	161243 f at	0.093	3702	1416863 at	0.010	8341	5626.625	2201.3391	FALSE	abhydrolase domain containing 8	219101 x at	-0.203	6793	1.326E-03	FALSE
160537 at	0.149	1935	1418138 at	0.042	6767	160537 at	0.015	7433	1448973 at	0.058	6372	5626.75	2499.8083	TRUE	sulfotransferase family 1D, member 1		NA	NA	NA	NA
93440 at	0.079	5685	1415766 at	0.057	6093.5	93440 at	0.140	3085	1449063 at	0.029	7650	5628.375	1895.1932	TRUE	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	243902 at	0.102	9956	9.882E-03	TRUE
100428 at	-0.019	7796	1452505 at	0.015	8112	100428 at	0.120	2163	1452505 at	-0.098	4447	5629.5	2844.3779	FALSE	laminin, gamma 2	202267 at	-0.121	14702	6.520E-02	FALSE
160190 at	-0.090	5868	1415844 at	0.129	4891	160190 at	0.065	7522	1415845 at	0.178	4241	5630.5	1427.3226	FALSE	synaptotagmin IV	223529 at	-0.975	2249	6.074E-06	FALSE
96917 at	-0.108	2904	1420058 s at	0.087	3740	96917 at	0.010	7915	1420059 at	-0.020	7964	5630.75	2687.7472	FALSE	RIKEN cDNA 2410166I05 gene	224280 s at	-0.088	15837	8.687E-02	FALSE
102961 at	0.033	6910	1449242 s at	0.051	6903	102961 at	0.180	3756	1449242 s at	-0.103	4957	5631.5	1551.7436	FALSE	histidine-rich glycoprotein	206226 at	-0.084	25070	3.752E-01	FALSE
97157 at	0.075	5171	1449998 at	0.039	7163.5	97157 at	-0.076	3072	1449998 at	0.054	7120	5631.625	1943.0008	FALSE	NK-3 transcription factor, locus 1 (Drosophila)	209706 at	0.101	11315	1.961E-02	FALSE
102911 at	0.049	5790	1419076 a at	0.054	6413	102911 at	0.116	2564	1419076 a at	0.038	7762	5632.25	2204.8771	TRUE	breast cancer 2	214727 at	-0.011	36856	7.876E-01	FALSE
103452 at	0.216	426	1432099 a at	0.014	8166.5	103452 at	-0.020	7494	1432099 a at	-0.058	6444	5632.625	3542.7161	FALSE	proline dehydrogenase (oxidase) 2	243614 s at	0.078	21088	2.366E-01	FALSE
93809 at	0.022	7214	1415742 at	-0.056	5761.5	93809 at	-0.169	1305	1415742 at	-0.012	8252	5633.125	3060.8723	FALSE	ancient ubiquitous protein	220525 s at	0.209	6487	1.035E-03	FALSE
93578 at	0.057	5678	1449255 a at	0.196	1677	93578 at	0.030	7296	1434328 at	0.032	7882	5633.25	2797.3518	TRUE	Ribosomal protein L15	221476 s at	-0.248	2168	5.159E-06	FALSE
103735 at	-0.015	7780	1419708 at	0.143	2977	103735 at	0.066	5291	1435980 x at	-0.059	6486	5633.5	2041.9367	FALSE	wingless-related MMTV integration site 6	221609 s at	-0.209	4698	1.965E-04	FALSE
101335 at	0.004	8337	1450465 at	-0.196	2509	101335 at	-0.106	4720	1450465 at	-0.054	6973	5634.75	2562.5605	FALSE	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	205852 at	-0.640	904	3.564E-07	FALSE
93531 at	0.005	8317	1423692 at	-0.023	7609.5	93531 at	0.220	1066	1423692 at	0.087	5551	5635.875	3264.6893	FALSE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	218160 at	-0.417	1910	3.314E-06	FALSE
161744 f at	0.141	1660	1418316 a at	0.023	7514.5	98933 at	-0.052	5435	1418316 a at	0.024	7938	5636.875	2868.0388	FALSE	MAP/microtubule affinity-regulating kinase 3	239166 at	0.158	6594	1.128E-03	FALSE
104045 at	0.575	52	1424029 at	0.028	7727.5	104045 at	0.044	6802	1424029 at	-0.017	7968	5637.375	3757.3573	FALSE	TSPY-like 4	212928 at	-0.536	2484	9.411E-06	FALSE

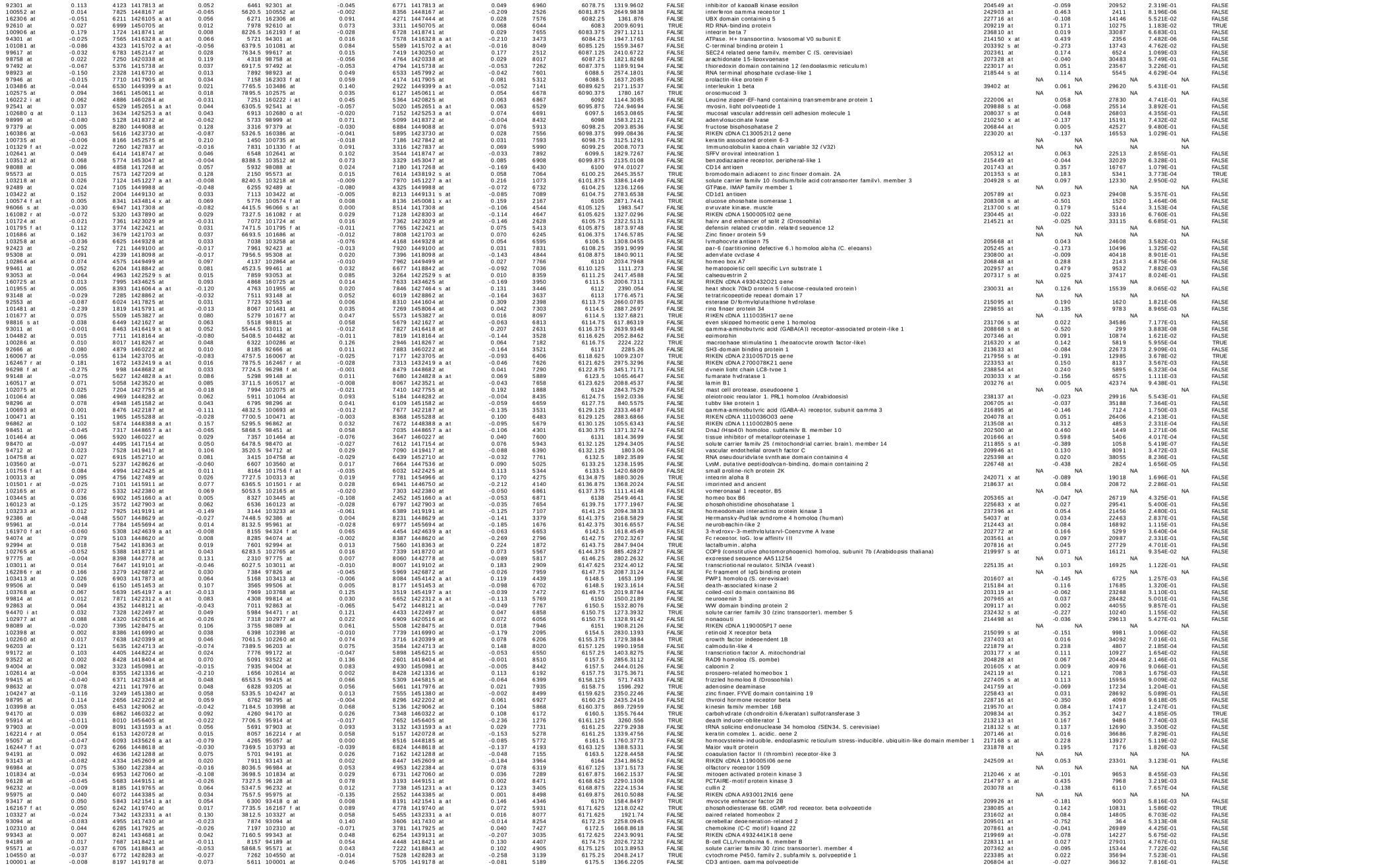






101859 at	0.090	3766	1418848 at	0.082	5671.5	101859 at	0.040	6189	1418848 at	-0.021	7957	5895.875	1724.4197	FALSE	aquaporin 7	206955 at	-0.046	25606	3.913E-01	FALSE
102908 at	0.046	6068	1417338 at	0.039	6484	161151 at	0.056	5004	1417338 at	0.083	6030	5896.5	629.53607	TRUE	erythrocyte protein band 4.2	240274 at	-0.023	31212	6.032E-01	FALSE
101039 at	0.022	7295	1424051 at	-0.099	4610.5	101039 at	0.004	8240	1424051 at	-0.129	3441	5896.625	2245.8162	FALSE	procollagen, type IV, alpha 2	237624 at	0.168	6676	1.214E-03	FALSE
101682 f at	0.023	7275	1420793 at	0.036	6755.5	101682 f at	-0.160	1388	1420793 at	-0.013	8168	5896.625	3061.831	FALSE	major urinary protein 4		NA	NA	NA	NA
95628 at	0.038	6180	1422944 a at	0.041	6463	95628 at	0.035	7228	1443445 at	0.151	3717	5897	1519.2549	TRUE	diaphanous homolog 3 (Drosophila)	229097 at	0.257	12386	3.012E-02	TRUE
102755 at	0.056	6364	1418165 at	0.152	2583	102755 at	0.009	8003	1418165 at	-0.082	6639	5897.25	2322.8205	FALSE	intelectin a		NA	NA	NA	NA
101473 at	0.102	4383	1432517 a at	0.111	3495	101473 at	0.027	7193	1432517 a at	0.000	8527	5899.5	2356.4303	FALSE	nicotinamide N-methyltransferase	202237 at	0.170	8346	4.058E-03	FALSE
94976 at	0.018	7386	1423974 at	-0.030	7324	94976 at	0.070	4559	1444577 x at	0.147	4331	5900	1682.8561	FALSE	nuclear mitotic apparatus protein 1	200747 s at	0.274	389	5.864E-08	FALSE
160902 at	0.104	2667	1417412 at	-0.011	8103	160902 at	0.026	6812	1447530 at	-0.070	6019	5900.25	2320.3019	FALSE	factor 8-associated gene A	203274 at	-0.522	82	5.455E-09	FALSE
160606 r at	0.013	7772	1450716 at	-0.137	3691	160606 r at	0.053	4795	1450716 at	-0.049	7344	5900.5	1974.0166	FALSE	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	222162 s at	0.395	12160	2.756E-02	FALSE
101899 at	0.049	6147	1418897 at	0.209	978.5	101899 at	0.004	8293	1418897 at	-0.014	8184	5900.625	3426.6249	FALSE	coagulation factor II	205754 at	-0.065	23946	3.366E-01	FALSE
102421 at	-0.015	7722	1424259 at	-0.064	5224.5	102421 at	-0.049	5292	1424259 at	-0.170	5365	5900.875	1215.4382	TRUE	RIKEN cDNA 2400010G15 gene	46142 at	0.114	6687	1.227E-03	FALSE
98928 at	-0.100	4455	1448351 at	0.016	7745.5	98928 at	-0.042	5407	1448351 at	-0.084	5997	5901.125	1383.9976	FALSE	coronin, actin binding protein 1B	64486 at	0.163	3894	7.640E-05	FALSE
104308 at	0.003	8415	1419128 at	0.060	6275.5	104308 at	0.036	6280	1419128 at	-0.284	2634	5901.125	2399.8178	FALSE	integrin alpha X	210184 at	-0.044	30460	5.740E-01	FALSE
97137 at	0.041	6668	1442941 at	0.003	8412.5	97137 at	0.127	1903	1442941 at	0.052	6634	5904.375	2793.8724	TRUE	expressed sequence C77027		NA	NA	NA	NA
160974 at	-0.032	6585	1434239 at	0.038	6292	160974 at	0.083	2999	1434239 at	0.050	7746	5905.5	2036.8509	FALSE	expressed sequence AA408556	216913 s at	-0.136	8392	4.129E-03	FALSE
94099 at	0.028	7128	1420720 at	-0.253	771	94099 at	-0.005	8197	1420720 at	-0.077	7526	5905.5	3451.3084	FALSE	neuronal pentraxin 2	213479 at	0.199	28673	5.081E-01	FALSE
92814 at	0.003	8370	1417531 at	0.214	450	92814 at	-0.003	8394	1445086 at	0.055	6409	5905.75	3754.2147	FALSE	cytochrome P450, family 2, subfamily i, polypeptide 5		NA	NA	NA	NA
101356 at	0.006	8245	1426100 a at	0.055	6198.5	101356 at	0.079	3971	1426100 a at	0.096	5209	5905.875	1806.1479	TRUE	thymidine kinase 2, mitochondrial	204227 s at	0.082	12558	3.209E-02	TRUE
103949 at	0.072	5592	1450704 at	0.064	5995.5	103949 at	0.045	5102	1450704 at	0.050	6936	5906.375	777.58637	TRUE	Indian hedgehog	239689 at	0.075	16947	1.126E-01	FALSE
104697 at	0.003	8376	1418892 at	0.006	8384	104697 at	0.231	700	1418892 at	-0.203	6166	5906.5	3624.5192	FALSE	ras homolog gene family, member J	238905 at	0.113	10872	1.619E-02	FALSE
103083 at	0.027	6816	1422820 at	-0.024	7889	103083 at	0.118	2184	1422820 at	0.055	6740	5907.25	2537.0076	FALSE	lipase, hormone sensitive	213855 s at	-0.150	12976	3.668E-02	FALSE
101406 at	-0.040	6100	1417335 at	0.123	2530	101406 at	-0.005	8164	1417335 at	0.042	6836	5907.5	2408.2128	FALSE	sulfotransferase family, cytosolic, 2B, member 1	205759 s at	-0.028	34742	7.233E-01	FALSE
98354 at	0.026	7408	1421760 at	0.023	7688.5	98354 at	-0.145	1089	1421760 at	0.042	7446	5907.875	3214.985	FALSE	pre T-cell antigen receptor alpha	211837 s at	-0.029	36489	7.772E-01	FALSE
92682 at	0.050	5680	1450800 at	0.116	2285.5	92682 at	0.011	7840	1450800 at	-0.023	7830	5908.875	2620.5086	FALSE	synaptotagmin VIII	232802 at	0.026	32159	6.371E-01	FALSE
98065 at	-0.047	6152	1419450 at	0.065	5588	98065 at	0.002	8446	1419450 at	-0.125	3451	5909.25	2052.6587	FALSE	ORM1-like 3 (S. cerevisiae)	240701 at	0.046	24043	3.396E-01	FALSE
92605 at	0.039	6429	1456306 a at	0.061	5744.5	92605 at	-0.050	5293	1456306 a at	-0.070	6173	5909.875	498.86845	FALSE	uromodulin	206716 at	-0.013	39590	8.674E-01	FALSE
104182 at	0.065	5770	1418405 at	0.081	4932	104182 at	0.048	5900.5	1418405 at	0.052	7039	5910.375	866.18218	TRUE	hepatocyte growth factor activator	207027 at	-0.052	26212	4.119E-01	FALSE
160593 at	0.044	6372	1423077 at	0.031	7368	160593 at	0.081	3241	1423076 at	-0.064	6663	5911	1828.4578	FALSE	sorting nexin 9	223028 s at	0.300	4574	1.657E-04	FALSE
98284 f at	0.116	2676	1460418 x at	0.041	6458	98284 f at	0.020	7257	1460418 x at	-0.038	7254	5911.25	2189.3529	FALSE	histocompatibility 2, T region locus 18		NA	NA	NA	NA
161068 at	0.066	6020	1434739 at	0.042	6748	161068 at	0.007	8165	1434739 at	0.190	2712	5911.25	2311.3176	TRUE	fragile X mental retardation 1 neighbor		NA	NA	NA	NA
94711 at	0.149	2979	1420601 at	0.084	4801	94711 at	0.002	8383	1420601 at	-0.037	7483	5911.5	2477.2761	FALSE	glial cells missing homolog 1 (Drosophila)	206269 at	-0.009	40775	9.013E-01	FALSE
94782 at	0.011	7892	1449596 at	0.145	3466	94782 at	-0.012	7701	1449596 at	-0.105	4587	5911.5	2225.5682	FALSE	expressed sequence C78142		NA	NA	NA	NA
94447 at	-0.114	3309	1433923 at	0.016	7881.5	94447 at	-0.093	4244	1433923 at	0.016	8214	5912.125	2499.0643	FALSE	RIKEN cDNA 4732484G22 gene	237120 at	0.025	31739	6.222E-01	FALSE
92486 at	0.013	7848	1449215 at	-0.155	1303	92486 at	-0.037	6261	1449215 at	-0.009	8242	5913.5	3190.6984	FALSE	solute carrier family 22 (organic cation transporter), member 21		NA	NA	NA	NA
93255 at	-0.020	7669	1448634 at	0.025	7508	93255 at	-0.003	8393	1417248 at	0.594	92	5915.5	3901.3663	FALSE	ralA binding protein 1	202844 s at	0.251	4185	1.070E-04	FALSE
101765 at	0.011	8031	1450573 at	0.067	5057	101765 at	-0.091	3701	1450573 at	-0.062	6874	5915.75	1917.9064	FALSE	anti-Mullerian hormone	206516 at	-0.070	22698	2.915E-01	FALSE
94407 at	-0.097	3139	1431219 at	0.030	6821	94407 at	-0.003	8323	1416960 at	0.080	5383	5916.5	2206.6937	FALSE	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	35179 at	-0.057	19507	1.851E-01	FALSE
93526 at	0.073	5272	1416553 at	0.167	1894.5	93526 at	0.010	8075	1416553 at	0.006	8425	5916.625	3030.0472	TRUE	stimulated by retinoic acid 13		NA	NA	NA	NA
102089 at	0.033	6786	1422148 at	-0.083	5091	102089 at	0.054	4681	1422148 at	0.061	7109	5916.75	1209.1315	FALSE	matrilin 3	206091 at	0.038	16148	9.422E-02	FALSE
161889 f at	-0.025	6928	1416921 x at	-0.093	4618	160090 f at	0.045	5576	1433604 x at	-0.060	6547	5917.25	1036.4527	FALSE	Aldolase 1, A isoform	200966 x at	-0.271	6673	1.212E-03	FALSE
95910 f at	-0.041	6282	1451392 at	0.073	4623	95910 f at	0.003	8385	1436695 x at	0.107	4382	5918	1848.8651	TRUE	RNA binding motif and ELMO domain 1	226286 at	0.059	17445	1.253E-01	FALSE
103076 at	0.052	6565	1432270 a at	0.102	4749.5	103076 at	0.144	4505	1458572 at	0.025	7855	5918.625	1584.5649	TRUE	chromatin modifying protein 5	219356 s at	-0.158	19529	1.857E-01	FALSE
95877 at	-0.003	8395	1420101 at	0.031	7153	95877 at	0.021	7331	1436673 at	0.288	796	5918.75	3458.9114	FALSE	RIKEN cDNA 2610020H08 gene		NA	NA	NA	NA
94086 at	-0.028	6859	1450566 at	0.089	5878.5	94086 at	0.150	2676	1450566 at	0.015	8271	5921.125	2375.863	FALSE	interleukin 3		NA	NA	NA	NA
94146 at	-0.040	6993	1421578 at	0.048	5739	94146 at	-0.027	6661	1421578 at	0.170	4293	5921.5	1208.3447	FALSE	chemokine (C-C motif) ligand 4	234223 at	0.096	18416	1.525E-01	FALSE
160599 r at	0.134	2909	1417643 at	0.049	7302.5	160599 r at	-0.077	5732	1417643 at	0.045	7745	5922.125	2186.5786	FALSE	testis specific gene A2	230093 at	0.112	30548	5.770E-01	FALSE
92872 at	0.218	3854	1448106 at	0.036	7021	92872 at	-0.023	7603	1448106 at	0.088	5213	5922.75	1713.9491	FALSE	NECAP endocytosis associated 1	209300 s at	-0.666	1842	2.921E-06	FALSE
160808 at	-0.092	3275	1424119 at	0.059	5450	160808 at	0.016	7818	1452457 a at	0.076	7148	5922.75	2027.0901	FALSE	protein kinase, AMP-activated, beta 1 non-catalytic subunit	201834 at	0.126	10524	1.340E-02	FALSE
98022 at	-0.088	2992	1417180 at	0.091	4138	98022 at	-0.003	8330	1417180 at	-0.010	8237	5924.25	2764.37	FALSE	proprotein convertase subtilisin/kexin type 7	232521 at	0.050	21417	2.474E-01	FALSE
97003 at	0.023	7333	1450590 at	0.084	4776.5	97003 at	0.033	6767	1450590 at	-0.095	4821	5924.375	1320.2645	FALSE	olfactory receptor 159		NA	NA	NA	NA
160730 at	0.062	4874	1420165 s at	0.056	6012	160730 at	0.011	7784	1449756 at	-0.112	5029	5924.75	1338.0168	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 17	219861 at	0.060	19971	1.997E-01	FALSE
99406 at	0.038	6336	1450834 at	-0.054	6815	99406 at	0.054	5700	1455843 at	-0.124	4853	5926	848.69036	FALSE	fucosyltransferase 4	209892 at	-0.034	28698	5.093E-01	FALSE
100765 at	0.052	6451	1448055 at	0.024	7592.5	100765 at	-0.025	6947	1444367 at	-0.179	2714	5926.125	2191.8206	FALSE	fibronectin type III domain containing 7		NA	NA	NA	NA
101898 s at	0.107	3926	1425137 a at	-0.042	6415	101898 s at	-0.040	5823	1425137 a at	0.031	7541	5926.25	1511.9474	FALSE	histocompatibility 2, O region locus 10	211529 x at	0.223	11439	2.046E-02	FALSE
95389 at	-0.005	8261	1451763 at	0.018	8004	95389 at	0.054	5199	1451763 at	-0.174	2242	5926.5	2820.7973	FALSE	cyclic nucleotide gated channel alpha 1	206417 at	0.009	41209	9.133E-01	FALSE
160715 at	-0.051	7166	1451127 at	0.116	3870	160715 at	0.002	8492	1423812 s at	0.199	4181	5927.25	2265.2528	FALSE	expressed sequence AW146242	208091 s at	0.355	2181	5.341E-06	FALSE
96204 at	0.069	4626	1422644 at	0.020	8124.5	96205 at	0.065	5684	1422644 at	0.214	5277	5927.875	1527.8692	TRUE	SH3-binding domain glutamic acid-rich protein	204979 s at	0.022	37046	7.922E-01	FALSE
103956 at	0.006	8168	1419216 at	0.114	3128	103956 at	0.073	4670	1419216 at	-0.036	7747	5928.25	2432.3462	FALSE	5-azacytidine induced gene 1	214742 at	0.065	16057	9.223E-02	FALSE
95154 at	-0.023	7399	1448868 at	0.137	4835.5	95154 at	0.072	3828	1448868 at	-0.048	7652	5928.625	1892.0511	FALSE	SCAN domain-containing 1	218206 x at	0.040	33372	6.775E-01	FALSE
96278 at	0.150	1827	1423686 a at	0.040	7377	96278 at	0.006	8135	1423686 a at	0.079	6378	5929.25	2827.9053	TRUE	proline rich 13	217794 at	0.160	11553	2.152E-02	TRUE
96907 at	0.067	4914	1451896 a at	-0.036	6564.5	96907 at	-0.002	8415	1451896 a at	-0.232	3827	5930.125	2002.7215	FALSE	calcium homeostasis endoplasmic reticulum protein	202230 s at	0.173	7422	2.167E-03	FALSE
98020 at	0.134	4026	1434688 x at	0.098	5165	98020 at	0.022	7003	1448336 at	0.029	7531	5931.25	1625.3169	TRUE	developmentally regulated GTP binding protein 1	202810 at	-0.102	9811	9.110E-03	FALSE
160751 i at	0.091	3351	1420849 at	0.063	5216	160751 i at	-0.006	8073	1420850 at	0.049	7090	5932.5	2089.5822	FALSE	Crn, crooked neck-like 1 (Drosophila)	219913 s at	-0.240	9785	8.980E-03	FALSE
101045 at	-0.035	6592	1438391 x at	0.121	3394.5	101045 at	0.000	8515	1438391 x at	-0.141	5229	5932.625	2163.3772	FALSE	hydroxyacyl-Coenzyme A dehydrogenase type II	202282 at	0.165	8131	3.560E-03	FALSE
97429 at	0.031	7622	1425678 a at	-0.241	2338.5	97429 at	0.007	8306	1425678 a at	-0.092	5465	5932.875	2684.7287	FALSE	SNF related kinase	237942 at	-0.054	22131	2.728E-01	FALSE
160863 at	0.101	2827	1417276 at	0.061	5193	160863 at	0.025	7792	1417276 at	0.027	7922	5933.5	2422.5907	TRUE	tubby-like protein 2	206733 at	-0.004	42984	9.598E-01	FALSE
103036 at	-0.011	8042	1417437 at	0.101	2899	103036 at	0.114	5073	1442250 at	-0.027	7722	5934	2421.6492	FALSE	X-ray repair complementing defective repair in Chinese hamster cells 6	215308 at	0.064	10734	1.497E-02	FALSE
92281 at	0.025	7499	1457675 at	-0.036	7172	92281 at	-0.041	6398	1457675 at	-0.221	2670	5934.75	2224.9239	FALSE	RIKEN cDNA 2510002D24 gene		NA	NA	NA	NA
97123 at	0.050	5957	1449854 at	0.080	4902.5	97123 at	-0.053	6233	1449854 at	-0.066	6647	5934.875	744.37629	FALSE	nuclear receptor subfamily 0, group B, member 2	206410 at	0.005	42380	9.438E-01	FALSE
100547 at	0.175	841	1430032 at	0.021	7902	100547 at	-0.004	8292	1444314 at	-0.054	6711	5936.5	3462.9246	FALSE	RIKEN cDNA 4921506I22 gene	235511 at	0.193	2708	1.394E-05	FALSE
97469 at	-0.019	7690	1452957 at	0.056	5804	97469 at	0.015	7525	1452957 at	0.143	2728	5936.75	2302.9056	FALSE	keratin associated protein 3-3		NA	NA	NA	NA
160588 at	-0.080	4820	1428616 at	0.073	5580	160588 at	-0.066	6451	1428616 at	-0.069	6901	5938	925.31544	FALSE	zinc finger protein 131		NA	NA	NA	NA
99157 at	-0.043	6089	1427895 at	0.086	4119.5	99157 at	0.007	8008	1427895 at	0.097	5536	5938.125	1609.9945	FALSE	RIKEN cDNA 2310004N24 gene		NA	NA	NA	NA
95506 at	-0.033	6988	1419649 s at	0.039	6339	95506 at	0.040	6433	1419649 s at	0.116	3997	5939.25	1326.1223	FALSE	myosin IC	214656 x at	0.243	6370	9.607E-04	FALSE
103987 at	0.225	1808	1448768 at	-0.056	6888	103987 at	-0.042	7699	1448768 at	0.067	7364	5939.75	2774.5261	FALSE	myelin oligodendrocyte glycoprotein	205989 s at	0.125	32589	6.500E-01	FALSE
100382 at	0.056	5758	1421517 at	0.075	5012	100382 at	0.065	4963	1421517 at	-0.021	8031	5941	1440.0363	FALSE	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialylt	227725 at	0.071	20986	2.330E-01	FALSE
101371 at	-0.091	3899	1424469 a at	-0.027	7007	101371 at	0.031	6171	1424469 a at	-0.054	6689	5941.5	1404.5786	FALSE	cleavage and polyadenylation specific factor 4	206688 s at	0.128	5695	5.250E-04	FALSE
99095 at	-0.102	5095	1423501 at	0.042	7471.5	99095 at	0.134	3421	1423501 at	0.062	7779	5941.625	2064.5249	FALSE	Max protein	209332 s at	0.378	1227	7.591E-07	FALSE
101902 at	-0.008	8130	1448957 at	-0.060	5077.5	101902 at	0.000	8521	1438848 at	-0.236	2040	5942.125	3022.7774	TRUE	recombining binding protein suppressor of hairless (Drosophila)	211974 x at	0.427	344	4.855E-08	FALSE
104147 at	0.026	6972	1417773 at	0.081	3750	104147 at	0.015	7628	1417773 at	0.214	5420	5942.5	1730.2064	TRUE	N-acetylneuraminic acid synthase (sialic acid synthase)	241923 x at	-0.056	23984	3.376E-01	FALSE
94508 at	0.025	7801	1451000 at	0.227	1999.5	94508 at	-0.001	8449	1451000 at	0.073	5526	5943.875	2913.0327	FALSE	transmembrane protein 126A	223334 at	-0.216	12377	3.005E-02	FALSE
96703 at	0.109	4519	1450062 a at	-0.072	6045	96703 at	0.029	7326	1450062 a at	0.080	5886	5944	1148.0584	FALSE	melanoma antigen, family D, 1	209014 at	-0.241	9434	7.466E-03	FALSE
104623 at	-0.096	3397	1419655 at	-0.031	7053.5	104623 at	-0.016	7735	1419654 at	-0.087	5594	5944.875	1919.0603	TRUE	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	228340 at	0.264	3457	4.326E-05	FALSE
160407 at	-0.070	4693	1415873 a at	-0.041	6174.5	160407 at	-0.026	6816	1415873 a at	-0.084	6099	5945.625	894.89845	TRUE	ARP1 actin-related protein 1 homolog A (yeast)	200720 s at	-0.302	7761	2.783E-03	TRUE
94552 at	-0.100	4881	1448642 at	-0.081	5357	94552 at	-0.039	7117	1448642 at	0.059	6428	5945.75	1014.0202	FALSE	poly(rC) binding protein 1	208620 at	-0.020	39825	8.723E-01	FALSE
94135 at	0.068	5319	1418159 at	0.048	6581	94135 at	-0.098	3549	1418159 at	0.008	8336	5946.25	2021.061	FALSE	transcription factor CP2	242859 at	0.237	5251	3.483E-04	FALSE
99555 at	0.067	5743	1449742 at	-0.094	3835.5	99555 at	0.018	7457	1420126 at	-0.049	6750	5946.375	1573.2086	FALSE	expressed sequence AA522020		NA	NA	NA	NA
99371 at	0.033	7179	1426070 a at	0.082	4620.5	99371 at	0.025	7171	1426070 a at	0.164	4817	5946.875	1420.3875	TRUE	potassium voltage-gated channel, Shal-related family, member 3	211827 s at	-0.064	21094	2.366E-01	FALSE
99403 at	-0.073	4115	1423008 at	0.000	8524.5	99403 at	-0.053	5805	1423008 at	0.075	5347	5947.875	1860.0978	FALSE	ADP-ribosyltransferase 2a		NA	NA	NA	NA
95905 at	0.067	4437	1436112 at	0.055	6023	95905 at	0.063	4897	1436112 at	-0.004	8438	5948.75	1788.2435	FALSE	expressed sequence AI118078		NA	NA	NA	NA
162085 r at	0.044	5851	1435788 at	0.058	6547	161057 at	0.125	2960	1435788 at	0.007	8440	5949.5	2273.5002	TRUE	RIKEN cDNA 2900086B20 gene		NA	NA	NA	NA
95319 at	0.038	6436	1420799 at	0.040	6867	95319 at	0.058	6009	1420799 at	-0.107	4495	5951.75	1032.4048	FALSE	neurotensin receptor 1	207360 s at	-0.010	40395	8.897E-01	FALSE
99057 at	-0.159	1714	1423135 at	-0.006	8344.5	99057 at	0.011	8206	1423135 at	0.125	5544	5952.125	3105.4619	FALSE	thymus cell antigen 1, theta	213869 x at	-0.807	1184	6.998E-07	FALSE
92924 at	0.021	7252	1419594 at	0.028	7729	92924 at	0.093	3441	1419594 at	-0.088	5390	5953	1955.2229	FALSE	cathepsin G	205653 at	0.025	32751	6.559E-01	FALSE
101891 at	0.051	5907	1418352 at	-0.028	7427.5	101891 at	-0.185	3163	1418352 at	0.042	7316	5953.375	1984.7867	FALSE	hydroxysteroid (17-beta) dehydrogenase 2	204818 at	-0.048	24676	3.606E-01	FALSE
95984 at	0.075	4018	1459900 at	0.071	4377	95984 at	-0.016	7565	1459900 at	-0.041	7854	5953.5	2036.3648	FALSE	expressed sequence C79468		NA	NA	NA	NA
104483 at	-0.007	8219	1421381 a at	0.069	5820	104483 at	-0.110	2227	1428571 at	-0.057	7552	5954.5	2682.8041	FALSE	procollagen, type IX, alpha 1	222008 at	-0.028	33786	6.917E-01	FALSE
94704 at	0.045	5688	1419015 at	0.106	4093	94704 at	0.031	6608	1419015 at	-0.046	7429	5954.5	1430.3166	FALSE	WNT1 inducible signaling pathway protein 2	205792 at	0.022	35686	7.521E-01	FALSE
100913 at	0.109	3169	1417443 at	0.045	6285	100913 at	-0.047	5976	1417443 at	0.005	8388	5954.5	2144.0324	FALSE	cDNA sequence BC026682		NA	NA	NA	NA
94157 i at	0.069	4097	1427871 at	0.026	7282	94157 i at	-0.036	6230	1427872 at	0.070	6214	5955.75	1336.1383	FALSE	platelet-activating factor receptor	206278 at	-0.098	26081	4.069E-01	FALSE
93431 at	0.005	8275	1434944 at	-0.026	7764	93431 at	-0.031	6929	1434944 at	-0.542	862	5957.5	3442.0043	FALSE	dystrophia myotonica-protein kinase	37996 s at	0.093	18146	1.440E-01	FALSE
104715 at	0.022	7146	1424281 at	-0.049	5878.5	104715 at	-0.042	5871	1458088 at	-0.095	4936	5957.875	907.32522	FALSE	ubiquitin-associated protein 2	219192 at	0.235	8616	4.681E-03	FALSE
97381 s at	0.062	5747	1420730 a at	0.033	7187	97382 at	0.058	4729	1420730 a at	0.086	6169	5958	1018.1558	TRUE	t-complex protein 11	220378 at	0.037	28357	4.960E-01	FALSE
101506 at	-0.048	6461	1417351 a at	0.153	4485	101506 at	0.077	5325	1417353 x at	0.055	7562	5958.25	1341.174	FALSE	small nuclear ribonucleoprotein polypeptide A'	216977 x at	-0.145	14489	6.123E-02	FALSE
98018 at	-0.103	3106	1420664 s at	-0.021	7801	98018 at	0.000	8518	1420664 s at	-0.249	4408	5958.25	2613.2134	TRUE	protein C receptor, endothelial	234340 at	0.056	16503	1.020E-01	FALSE
95069 at	0.038	6670	1426788 a at	0.110	1574.5	95069 at	0.006	8228	1426788 a at	-0.037	7362	5958.625	2991.4395	FALSE	structure specific recognition protein 1	200957 s at	0.153	5737	5.445E-04	FALSE
101345 at	0.141	3431	1447953 at	0.039	6895.5	101345 at	-0.032	6601	1447953 at	-0.072	6909	5959.125	1691.3979	FALSE	EGF-like domain 8	208469 s at	0.080	14824	6.724E-02	FALSE
104238 at	-0.042	6036	1427759 a at	-0.009	8194	104238 at	-0.060	4743	1427759 a at	0.116	4868	5960.25	1598.9668	FALSE	ADP-ribosyltransferase 5		NA	NA	NA	NA
94211 at	0.017	7864	1452073 at	0.088	4430.5	94211 at	0.056	5326	1452073 at	0.107	6221	5960.375	1464.5435	TRUE	RIKEN cDNA 6720460F02 gene	221591 s at	-0.020	37506	8.052E-01	FALSE
104677 at	-0.003	8436	1452235 at	0.100	5038.5	104677 at	0.198	2492	1452235 at	0.025	7881	5961.875	2750.575	FALSE	mannosidase, alpha, class 1B, member 1	218636 s at	0.115	8727	4.981E-03	FALSE
99671 at	0.010	8019	1417867 at	0.234	1693	99671 at	0.044	5816	1417867 at	-0.009	8320	5962	3057.0732	FALSE	complement factor D (adipsin)	205382 s at	-0.042	29279	5.307E-01	FALSE
104555 at	0.066	4699	1460202 at	0.041	7105	104555 at	-0.007	8016	1448636 at	0.120	4032	5963	1901.353	FALSE	myozenin 1	219509 at	-0.028	34215	7.060E-01	FALSE
95023 at	0.004	8279	1426940 at	-0.050	6664	95023 at	-0.012	7873	1426940 at	-0.223	1037	5963.25	3355.0376	FALSE	SID1 transmembrane family, member 2	218765 at	0.076	15809	8.627E-02	FALSE
98139 at	0.079	4663	1436992 x at	-0.048	6701	98139 at	-0.021	7814	1437452 x at	-0.092	4678	5964	1561.2032	FALSE	voltage-dependent anion channel 1	212038 s at	-0.527	4202	1.087E-04	FALSE
93572 at	0.093	5880	1425143 a at	0.010	8264.5	93572 at	-0.012	7949	1453354 at	0.180	1763	5964.125	2993.7703	FALSE	NADH dehydrogenase (ubiquinone) Fe-S protein 1	236356 at	-0.217	10223	1.140E-02	FALSE
96781 at	-0.007	8311	1415725 at	0.031	7216	96781 at	0.126	4042	1415725 at	-0.110	4288	5964.25	2127.516	FALSE	RRN3 RNA polymerase I transcription factor homolog (yeast)	216902 s at	-0.098	21311	2.438E-01	FALSE
160997 at	0.058	5201	1434981 at	0.048	6630	160997 at	-0.088	3908	1434981 at	0.022	8119	5964.5	1816.3044	FALSE	RIKEN cDNA E130303B06 gene	223407 at	0.244	4642	1.829E-04	FALSE
101449 at	-0.190	1898	1424275 s at	-0.018	7790.5	101449 at	0.005	8272	1440268 at	0.094	5900	5965.125	2898.2416	FALSE	tripartite motif-containing 41	226445 s at	0.249	3502	4.675E-05	FALSE
95310 at	-0.043	6019	1421161 at	0.096	3449	95310 at	0.007	8160	1435541 at	0.101	6236	5966	1934.3073	FALSE	betacellulin, epidermal growth factor family member	241412 at	0.181	13844	4.981E-02	FALSE
96981 at	0.147	4082	1422371 at	0.112	4457	96981 at	-0.010	8128	1422371 at	0.050	7199	5966.5	2001.755	FALSE	olfactory receptor 1507		NA	NA	NA	NA
101920 at	0.041	6074	1427094 at	0.101	5881.5	101920 at	-0.021	7429	1431440 at	0.103	4482	5966.625	1205.7401	FALSE	polymerase (DNA directed), epsilon 2 (p59 subunit)	205909 at	-0.009	40543	8.939E-01	FALSE
93173 at	0.023	7376	1417881 at	-0.082	3784	93173 at	-0.002	8405	1417881 at	-0.151	4302	5966.75	2270.5975	FALSE	solute carrier family 39 (zinc transporter), member 3	223917 s at	0.067	18171	1.446E-01	FALSE
96507 at	-0.011	7923	1421577 at	0.160	1737	96507 at	-0.031	7015	1421577 at	-0.049	7194	5967.25	2847.3771	FALSE	even skipped homeotic gene 2 homolog		NA	NA	NA	NA
98856 at	0.112	3064	1422171 at	0.088	4865.5	98856 at	-0.015	7778	1422171 at	0.013	8163	5967.625	2431.9297	FALSE	prostaglandin D receptor	234165 at	-0.062	19441	1.828E-01	FALSE
98426 at	0.041	6196	1418302 at	-0.008	8147.5	98426 at	-0.073	3774	1418302 at	-0.071	5765	5970.625	1794.1592	FALSE	palmitoyl-protein thioesterase 2	209490 s at	-0.052	23638	3.251E-01	FALSE
160298 at	-0.010	7972	1424187 at	0.149	1294	160298 at	-0.018	7679	1424187 at	0.050	6944	5972.25	3148.6673	FALSE	coiled-coil domain containing 80	225242 s at	0.321	5989	6.858E-04	FALSE
93824 at	0.160	3264	1455540 at	0.077	5061	93824 at	-0.015	7775	1455540 at	-0.036	7791	5972.75	2215.3068	FALSE	carbamoyl-phosphate synthetase 1	204920 at	0.104	15390	7.786E-02	FALSE

160907 at	-0.030	7014	1454622 at	0.041	6055	160907 at	0.079	3798	1454622 at	-0.067	7024	5972.75	1519.3892	FALSE	solute carrier family 38, member 5	234973 at	0.142	16543	1.027E-01	FALSE
92750 s at	-0.117	3753	1426091 a at	0.053	6263	92750 s at	-0.061	5609	1426091 a at	-0.012	8267	5973	1862.5638	FALSE	wingless related MMTV integration site 10b	206213 at	-0.232	7387	2.114E-03	FALSE
96535 at	0.026	7203	1435802 at	0.176	1494.5	96535 at	0.022	6898	1435802 at	-0.011	8299	5973.625	3046.0774	FALSE	zinc finger protein 499	240551 at	-0.188	7406	2.141E-03	FALSE
104458 at	0.089	3844	1436207 at	0.040	6974	104458 at	0.047	5488	1450117 at	0.030	7589	5973.75	1671.4585	TRUE	transcription factor 3	221016 s at	0.193	7256	1.937E-03	TRUE
98098 at	0.008	8222	1416193 at	0.042	6525	98098 at	0.095	3634	1416193 at	0.087	5517	5974.5	1918.4675	TRUE	carbonic anhydrase 1	205950 s at	0.052	26090	4.070E-01	FALSE
99044 at	0.046	5701	1456151 at	0.097	3669	99044 at	-0.008	8113	1456151 at	0.065	6416	5974.75	1840.1301	FALSE	zinc finger protein 358	219379 x at	0.090	21479	2.489E-01	FALSE
94978 at	-0.076	4429	1416171 at	0.083	3988.5	94978 at	-0.002	8435	1416171 at	0.045	7048	5975.125	2124.4001	FALSE	RIKEN cDNA 2310037I24 gene	221821 s at	0.147	9138	6.319E-03	FALSE
100272 at	0.131	4245	1424903 at	0.106	4984	100272 at	0.007	8151	1452562 at	0.065	6522	5975.5	1732.9325	TRUE	jumonji, AT rich interactive domain 1D (Rbp2 like)	206700 s at	0.035	39018	8.511E-01	FALSE
162228 f at	-0.085	5601	1417405 at	-0.085	3438	95607 at	-0.015	7720	1417405 at	0.039	7145	5976	1913.9981	FALSE	START domain containing 3	202991 at	0.072	23243	3.102E-01	FALSE
102798 at	0.043	6030	1416077 at	-0.001	8505	102798 at	0.081	3641	1416077 at	-0.109	5736	5978	1992.3659	FALSE	adrenomedullin	202912 at	0.410	19839	1.956E-01	FALSE
102665 at	0.067	4675	1418756 at	0.118	4095	102665 at	-0.026	7065	1418756 at	0.040	8079	5978.5	1900.8127	FALSE	thyrotropin releasing hormone	206622 at	-0.017	38207	8.277E-01	FALSE
102876 at	-0.082	4870	1422867 at	0.049	6477	102876 at	-0.100	4413	1422867 at	-0.016	8158	5979.5	1700.8117	FALSE	granzyme G	210321 at	-0.032	33428	6.791E-01	FALSE
103825 at	-0.019	7523	1422268 a at	0.054	7225	103825 at	-0.159	886	1422268 a at	0.015	8285	5979.75	3425.0418	FALSE	ribosomal protein S6 kinase, polypeptide 2	203777 s at	-0.036	32115	6.356E-01	FALSE
161005 at	0.014	8061	1427050 at	0.004	8382	161005 at	0.157	3331	1427050 at	-0.107	4151	5981.25	2611.6789	FALSE	RIKEN cDNA 5730420B22 gene	226747 at	-0.315	9115	6.202E-03	FALSE
102807 at	0.103	2379	1434138 at	-0.041	6728	102807 at	-0.009	8027	1433281 at	-0.091	6793	5981.75	2475.0671	FALSE	prune homolog (Drosophila)	209586 s at	0.180	5168	3.264E-04	FALSE
97780 at	-0.045	6005	1459934 at	0.097	4394.5	97780 at	-0.035	6112	1434782 at	0.046	7423	5983.625	1240.1688	FALSE	ubiquitin specific peptidase 42	NA	NA	NA	NA	
103967 at	0.064	4782	1450537 at	0.039	6638	103968 at	-0.068	5410	1450537 at	0.059	7105	5983.75	1073.722	FALSE	Midline 2	208384 s at	-0.026	33040	6.664E-01	FALSE
103231 at	-0.014	7817	1429319 at	0.119	3916	103231 at	-0.034	6820	1441385 at	0.094	5387	5985	1702.1373	FALSE	ras homolog gene family, member H	204951 at	-0.035	30833	5.879E-01	FALSE
95407 at	-0.051	5493	1454638 a at	0.123	3380.5	95407 at	0.012	7591	1454638 a at	-0.035	7478	5985.625	1986.099	FALSE	phenylalanine hydroxylase	205719 s at	0.193	4834	2.294E-04	FALSE
101190 at	-0.008	8189	1450352 at	0.029	7512	101190 at	0.088	2885	1450352 at	-0.092	5360	5986.5	2393.7391	FALSE	melatonin receptor 1A	221369 at	0.046	20513	2.169E-01	FALSE
162350 at	-0.035	6646	1433808 at	-0.010	8220	162350 at	0.017	7148	1433808 at	0.202	1933	5986.75	2781.0913	FALSE	RIKEN cDNA D330001F17 gene	NA	NA	NA	NA	
103863 at	-0.090	2803	1460656 a at	0.059	6427	103863 at	-0.003	8291	1460656 a at	-0.075	6429	5987.5	2297.4794	FALSE	RIKEN cDNA 5630401J11 gene	238292 at	0.082	14333	5.847E-02	FALSE
92887 at	0.020	7303	1416457 at	-0.072	4821	92887 at	0.061	5001	1416457 at	0.052	6826	5987.75	1260.6251	FALSE	dimethylarginine dimethylaminohydrolase 2	202262 x at	0.336	994	4.374E-07	FALSE
96773 at	0.005	8315	1423246 at	0.048	5979	96773 at	0.076	4364	1423247 at	0.084	5293	5987.75	1686.7534	TRUE	thioredoxin domain containing 4 (endoplasmic reticulum)	208959 s at	0.070	20222	2.076E-01	FALSE
95981 at	0.025	7570	1441401 at	0.133	3621	95981 at	-0.056	4238	1441401 at	0.000	8523	5988	2421.7169	FALSE	expressed sequence C79329	NA	NA	NA	NA	
104439 at	0.059	5089	1419213 at	0.058	5515	104439 at	0.025	6629	1419213 at	-0.053	6727	5990	814.23093	FALSE	N-acetyltransferase 6	210874 s at	-0.157	10144	1.089E-02	FALSE
100106 at	0.059	5769	1417370 at	0.012	8138	100106 at	0.040	5475	1417370 at	0.141	4578	5990	1518.9595	TRUE	trefoil factor 3, intestinal	NA	NA	NA	NA	
101485 at	0.051	5216	1417242 at	0.049	6063	101485 at	0.061	4907	1417242 at	0.025	7785	5992.75	1290.9026	TRUE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	201303 at	-0.014	39612	8.679E-01	FALSE
102623 at	-0.014	8005	1425840 a at	-0.014	8071	102623 at	0.041	6099	1438947 x at	-0.196	1800	5993.75	2941.5818	FALSE	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F	35666 at	0.056	22528	2.860E-01	FALSE
103388 at	0.001	8480	1451592 at	-0.128	1527.5	103388 at	-0.035	6150	1451592 at	-0.035	7824	5995.375	3135.9765	FALSE	Myb protein P42POP	227937 at	-0.255	1833	2.853E-06	FALSE
101609 at	0.044	6341	1428752 at	0.116	2192.5	101609 at	0.015	7318	1428752 at	0.017	8137	5997.125	2640.5301	TRUE	solute carrier family 5 (sodium/glucose cotransporter), member 11	237254 at	0.230	12417	3.057E-02	TRUE
93990 at	-0.119	4812	1437267 x at	0.042	6966	93990 at	-0.036	7466	1415872 at	-0.137	4747	5997.75	1421.6944	FALSE	heterogeneous nuclear ribonucleoprotein H1	201031 s at	0.266	9374	7.207E-03	FALSE
99993 at	0.042	6809	1421424 a at	0.062	5212.5	99993 at	0.070	4619	1421424 a at	0.039	7351	5997.875	1291.8954	TRUE	alanyl (membrane) aminopeptidase	234458 at	0.027	32258	6.403E-01	FALSE
103414 at	0.016	7831	1422584 at	-0.130	3700	103414 at	0.114	4621	1422584 at	-0.029	7842	5998.5	2155.393	FALSE	superkiller viralicidic activity 2-like (S. cerevisiae)	203727 at	0.047	23570	3.227E-01	FALSE
96143 at	0.069	4421	1418294 at	0.060	5901.5	96143 at	0.007	8246	1418294 at	0.086	5429	5999.375	1620.0307	TRUE	erythrocyte protein band 4.1-like 4b	NA	NA	NA	NA	
94762 at	0.035	7116	1421407 at	0.071	4808	94762 at	-0.020	7431	1445680 x at	-0.102	4643	5999.5	1478.2342	FALSE	coagulation factor II (thrombin) receptor-like 2	206795 at	0.034	25664	3.934E-01	FALSE
100712 at	0.006	8299	1420801 at	-0.053	6986	100712 at	0.156	2323	1420801 at	-0.126	6394	6000.5	2577.6708	FALSE	neuronal PAS domain protein 1	216975 x at	-0.041	30381	5.705E-01	FALSE
103477 at	0.111	2152	1449582 at	-0.010	8180	103477 at	0.018	7393	1449582 at	-0.060	6282	6001.75	2682.0058	FALSE	caudal type homeo box 1	206430 at	0.014	39006	8.508E-01	FALSE
102636 at	-0.001	8495	1431487 at	0.113	3635	102636 at	-0.075	4707	1418214 at	0.049	7172	6002.25	2225.8828	FALSE	kinesin light chain 2	218906 x at	-0.296	3121	2.675E-05	FALSE
99908 at	0.112	3822	1451598 at	-0.038	6602	99908 at	-0.056	5386	1451598 at	-0.014	8199	6002.25	1854.6037	FALSE	paired box gene 4	207867 at	-0.058	20649	2.216E-01	FALSE
102974 at	0.052	6263	1449498 at	0.061	6258	102974 at	0.091	4462	1449498 at	-0.058	7028	6002.75	1089.0257	FALSE	macrophage receptor with collagenous structure	205819 at	0.002	43573	9.743E-01	FALSE
104538 at	0.113	3251	1448816 at	0.007	8293	104538 at	0.004	8234	1445044 at	0.106	4237	6003.75	2640.3105	TRUE	prostaglandin I2 (prostacyclin) synthase	208131 s at	-0.221	4507	1.587E-04	FALSE
97359 at	0.002	8422	1418198 a at	0.010	8188.5	97359 at	-0.043	5204	1442908 at	0.191	2214	6007.125	2922.489	FALSE	transmembrane 9 superfamily member 1	209150 s at	0.199	10526	1.341E-02	FALSE
96342 at	0.047	5937	1419287 at	0.095	3713	96342 at	0.026	7155	1419287 at	0.059	7225	6007.5	1639.9962	TRUE	HSPC171 protein	NA	NA	NA	NA	
160389 r at	-0.026	7546	1435429 x at	0.349	1588.5	160389 r at	-0.060	7173	1435429 x at	-0.038	7727	6008.625	2955.7632	FALSE	ribosomal protein S27-like	218007 s at	0.185	12901	3.584E-02	FALSE
99365 at	0.016	7699	1437364 at	0.081	4797	99365 at	-0.044	5819	1436351 at	0.140	5724	6009.75	1216.8767	FALSE	coenzyme Q3 homolog, methyltransferase (yeast)	223515 s at	-0.337	3339	3.675E-05	FALSE
92606 at	0.056	5614	1422604 at	0.048	7030.5	92606 at	0.119	3367	1422604 at	-0.017	8029	6010.125	2021.5544	FALSE	urate oxidase	NA	NA	NA	NA	
94081 at	-0.078	4255	1452691 at	0.033	7079	94081 at	0.080	5799	1452691 at	-0.055	6921	6013.5	1303.4798	FALSE	RNA binding motif protein 17	224780 at	0.453	875	3.337E-07	FALSE
161392 f at	0.087	4805	1432083 a at	0.069	5179	161392 f at	0.038	6168	1432083 a at	-0.050	7906	6014.5	1385.9155	FALSE	leucine rich repeat containing 23	206076 at	0.229	12085	2.680E-02	FALSE
98954 f at	-0.024	7545	1427976 at	0.101	4310	98954 f at	0.052	5536	1427976 at	-0.060	6668	6014.75	1402.8275	FALSE	oogenesin 1	NA	NA	NA	NA	
93923 at	-0.293	819	1435019 at	0.018	7836.5	93923 at	-0.030	7280	1435019 at	-0.014	8124	6014.875	3481.5889	FALSE	ataxin 7-like 3	NA	NA	NA	NA	
95315 at	-0.004	8328	1456770 at	0.005	8355	95315 at	-0.050	6490	1456770 at	-0.335	887	6015	3528.3413	FALSE	zinc finger protein 14	232911 at	0.020	33443	6.798E-01	FALSE
95752 at	-0.073	5257	1426480 at	0.025	7501	95752 at	-0.045	5541	1426480 at	0.093	5766	6016.25	1011.5056	FALSE	Shwachman-Bodian-Diamond syndrome homolog (human)	222669 s at	0.057	33725	6.892E-01	FALSE
104058 at	-0.016	7810	1428655 at	0.013	8025	104058 at	-0.113	4282	1428655 at	-0.112	3953	6017.5	2199.7904	FALSE	RIKEN cDNA 1110018J12 gene	241351 at	0.158	4144	1.021E-04	FALSE
93612 at	0.011	7997	1422597 at	0.025	7545	93612 at	-0.022	7278	1422597 at	-0.242	1257	6019.25	3188.6719	FALSE	matrix metallopeptidase 15	243883 at	-0.044	19243	1.762E-01	FALSE
104313 at	0.006	8223	1451149 at	-0.113	2822	104313 at	0.024	7463	1437240 at	-0.090	5573	6020.25	2405.7203	FALSE	phosphoglucomutase 2	201968 s at	0.265	8112	3.515E-03	FALSE
96718 at	0.008	8098	1416914 s at	0.040	6418.5	96718 at	-0.070	4928	1416914 s at	0.106	4644	6022.125	1587.7351	FALSE	mammary tumor virus receptor 2	32209 at	-0.187	1732	2.343E-06	FALSE
98444 g at	0.155	2236	1422582 at	0.026	6897	98443 at	0.036	6651	1422582 at	0.008	8309	6023.25	2628.3978	TRUE	leptin	207092 at	0.026	30993	5.946E-01	FALSE
96028 at	0.036	6702	1453651 a at	0.192	3302.5	96028 at	0.015	7673	1456886 at	-0.059	6419	6024.125	1892.2185	FALSE	brain protein 44-like	218024 at	-0.072	23295	3.122E-01	FALSE
94697 at	0.085	4882	1419526 at	0.053	6129	94697 at	0.035	6478	1442804 at	-0.053	6612	6025.25	788.8901	FALSE	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	208438 s at	0.242	4473	1.500E-04	FALSE
95123 at	-0.053	5287	1426889 at	-0.005	8344.5	95123 at	0.167	2310	1426889 at	0.015	8160	6025.375	2845.1229	FALSE	RIKEN cDNA 4930566A11 gene	205494 at	-0.018	35479	7.456E-01	FALSE
160355 at	0.032	6790	1427099 at	0.115	4693.5	160355 at	0.007	8122	1427099 at	0.149	4497	6025.625	1740.7191	TRUE	MYC-associated zinc finger protein (purine-binding transcription factor)	207824 s at	-0.146	9498	7.777E-03	FALSE
95144 at	-0.092	5306	1416079 a at	0.004	8393	95144 at	-0.141	3146	1416079 a at	-0.043	7267	6028	2306.1912	FALSE	actin related protein 2/3 complex, subunit 1A	200950 at	-0.249	8568	4.531E-03	FALSE
160300 at	0.097	4585	1448156 at	-0.024	7382	160300 at	-0.048	5311	1448156 at	0.061	6846	6031	1303.6797	FALSE	trefoil factor 1	205009 at	0.099	16692	1.061E-01	FALSE
95662 at	-0.023	7861	1417241 at	0.005	8357.5	95662 at	0.148	2714	1417241 at	0.102	5192	6031.125	2612.0179	FALSE	EST X83328	243915 at	0.657	1161	6.617E-07	FALSE
96566 at	0.083	4454	1421355 at	0.021	7792.5	96566 at	0.019	7342	1421355 at	0.122	4536	6031.125	1783.5879	TRUE	transglutaminase 3, E polypeptide	206004 at	0.050	25176	3.786E-01	FALSE
98346 at	0.080	5311	1440230 at	0.005	8376	98346 at	0.081	4554.5	1440230 at	-0.076	5884	6031.375	1655.2025	FALSE	leucine rich repeat containing 54	218245 at	0.054	23632	3.247E-01	FALSE
160125 at	-0.069	4180	1452200 at	0.030	7334	160125 at	0.057	4905	1452200 at	-0.030	7708	6031.75	1751.591	FALSE	DNA segment, Chr 11, ERATO Doi 497, expressed	235006 at	-0.189	5856	6.113E-04	FALSE
104624 at	0.028	6797	1426814 at	-0.034	6863.5	104624 at	0.072	4834	1426815 s at	-0.085	5634	6032.125	978.13175	FALSE	expressed sequence AU024582	215696 s at	0.084	22032	2.693E-01	FALSE
101061 at	0.048	6628	1449930 a at	0.050	6865	101061 at	0.040	5947	1449930 a at	0.103	4693	6033.25	974.55028	TRUE	signal sequence receptor, beta	200652 at	-0.104	11791	2.374E-02	FALSE
161167 r at	0.129	4054	1424399 at	0.037	7043	161167 r at	0.040	6455	1424399 at	-0.068	6583	6033.75	1343.7662	FALSE	uridine-cytidine kinase 1	223141 at	0.141	5465	4.310E-04	FALSE
93048 at	0.040	7082	1416616 s at	0.219	1119	93048 at	-0.024	7731	1416615 at	0.018	8205	6034.25	3309.0068	FALSE	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	202799 at	0.023	32719	6.548E-01	FALSE
100017 at	0.053	6001	1419487 at	0.087	3684.5	100017 at	-0.028	7239	1419487 at	-0.036	7213	6034.375	1669.6611	FALSE	myosin binding protein H	206304 at	-0.028	36932	7.892E-01	FALSE
101730 at	0.004	8272	1450288 at	-0.028	7502.5	101730 at	-0.055	5884	1450288 at	0.159	2480	6034.625	2570.2497	FALSE	cadherin 6	205533 s at	-0.098	8483	4.305E-03	FALSE
98847 at	0.028	7177	1436482 a at	-0.103	3657	98847 at	-0.020	7594	1420853 at	0.072	5719	6036.75	1778.5174	FALSE	syndecan 3	202898 at	0.154	23540	3.214E-01	FALSE
101200 at	0.014	7721	1449920 at	0.032	7406	101200 at	0.163	1416	1449920 at	-0.029	7616	6039.75	3085.2806	FALSE	cytochrome P450, family 19, subfamily a, polypeptide 1	240705 at	0.062	21727	2.594E-01	FALSE
97205 at	0.044	6912	1426394 at	0.079	4272	97205 at	0.011	8271	1452052 s at	0.092	4704	6039.75	1884.0086	TRUE	eukaryotic translation initiation factor 3, subunit 1 alpha	208985 s at	0.064	26674	4.310E-01	FALSE
100730 at	0.005	8213	1421547 at	0.049	6661.5	100730 at	0.039	6252	1421547 at	-0.163	3033	6039.875	2175.2536	FALSE	CD180 antigen	206206 at	0.068	19503	1.850E-01	FALSE
102699 at	-0.031	6975	1419676 at	0.024	7730.5	102699 at	-0.047	5802	1419676 at	-0.211	3654	6040.375	1777.794	FALSE	myxovirus (influenza virus) resistance 2	202086 at	0.157	15387	7.783E-02	FALSE
101368 at	0.049	6141	1423429 at	0.042	6395	101368 at	-0.026	6892	1423429 at	0.158	4734	6040.5	925.16035	FALSE	reproductive homeobox 5	NA	NA	NA	NA	
97293 at	-0.130	3276	1423741 at	0.032	7486	97293 at	-0.030	6570	1423741 at	-0.058	6833	6041.25	1883.291	FALSE	RNA binding motif protein 10	215089 s at	0.128	10885	1.630E-02	FALSE
99641 at	-0.086	5814	1451431 a at	-0.144	2132	99641 at	-0.022	7766	1451431 a at	-0.004	8457	6042.25	2836.9282	TRUE	dysbindin (dystrobrevin binding protein 1) domain containing 2	NA	NA	NA	NA	
93625 at	0.083	5227	1418833 at	0.024	7646.5	93625 at	0.146	3862	1418833 at	0.043	7435	6042.625	1819.4773	TRUE	alanine-glyoxylate aminotransferase	210326 at	-0.058	29098	5.242E-01	FALSE
160144 at	0.045	5881	1426905 a at	-0.044	6955	160144 at	0.030	7532	1426904 s at	-0.129	3806	6043.5	1641.0644	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 10	229588 at	0.181	9835	9.216E-03	FALSE
103289 at	-0.014	7694	1419017 at	0.038	6783	103289 at	0.131	1400	1419017 at	-0.008	8297	6043.5	3157.6027	FALSE	corin	220356 at	-0.044	19415	1.818E-01	FALSE
98582 at	-0.066	5107	1452986 at	0.085	5831.5	98582 at	0.068	4814	1452986 at	0.004	8423	6043.875	1642.728	FALSE	homogentisate 1, 2-dioxygenase	205221 at	0.031	24136	3.422E-01	FALSE
97427 at	0.076	4371	1418787 at	0.099	4708	97427 at	0.022	7075	1418787 at	0.019	8025	6044.75	1786.1639	TRUE	mannose binding lectin (C)	NA	NA	NA	NA	
102932 at	0.011	7878	1449706 s at	0.086	4707	102932 at	-0.066	4604	1449707 at	0.045	6997	6046.5	1646.5023	FALSE	nuclear receptor subfamily 5, group A, member 2	210174 at	-0.011	37090	7.937E-01	FALSE
98064 at	0.073	5662	1454754 a at	0.056	6024.5	98064 at	-0.015	7533	1454754 a at	0.094	4967	6046.625	1083.7169	FALSE	angio-associated migratory protein	201511 at	-0.051	22168	2.738E-01	FALSE
95755 at	0.068	5262	1435800 a at	-0.084	5302	95755 at	0.021	7157	1435800 a at	-0.069	6469	6047.5	927.61935	FALSE	cold shock domain protein A	201160 s at	0.685	8834	5.291E-03	FALSE
101389 at	-0.037	6717	1454704 at	-0.093	4528.5	101389 at	0.075	5069	1460235 at	0.024	7876	6047.625	1533.6738	FALSE	scavenger receptor class B, member 2	215754 at	0.169	7718	2.696E-03	FALSE
99937 at	-0.042	6295	1424234 s at	0.031	6834	99937 at	0.036	5885	1424234 s at	-0.090	5181	6048.75	696.91242	FALSE	mesenchyme homeobox 2	206201 s at	0.013	30066	5.586E-01	FALSE
104200 at	0.069	4599	1435860 at	0.024	7340	104200 at	-0.063	3966	1435860 at	0.012	8295	6050	2093.8467	FALSE	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	204087 s at	0.042	31003	5.952E-01	FALSE
96422 at	-0.021	7567	1422284 at	0.040	6817	96422 at	-0.104	3176	1422284 at	0.063	6643	6050.75	1957.9837	FALSE	NK2 transcription factor related, locus 9 (Drosophila)	207451 at	0.006	42108	9.378E-01	FALSE
99119 at	-0.128	2989	1448346 at	0.028	7360	99119 at	-0.022	6992	1448346 at	-0.104	6865	6051.5	2052.4295	FALSE	cofilin 1, non-muscle	NA	NA	NA	NA	
102267 at	-0.001	8451	1419138 at	0.023	7169	102267 at	-0.140	1756	1419138 at	0.077	6832	6052	2947.7057	FALSE	UDP-Gal:betaGalNAc beta 1,3-galactosyltransferase, polypeptide 4	210205 at	0.043	25833	3.980E-01	FALSE
103579 at	0.015	7945	1417620 at	0.069	4406	103579 at	0.046	5930	1417620 at	-0.108	5929	6052.5	1451.7549	FALSE	RAS-related C3 botulinum substrate 2	213603 s at	0.112	13766	4.801E-02	FALSE
102084 f at	0.030	7023	1452501 at	0.177	2024	102084 f at	0.015	7674	1452501 at	0.047	7501	6055.5	2701.7316	TRUE	cytochrome P450, family 2, subfamily c, polypeptide 38	NA	NA	NA	NA	
101557 at	0.009	8096	1460644 at	0.060	5541	101557 at	-0.053	5047	1443813 x at	-0.105	5539	6055.75	1379.8786	FALSE	branched chain ketoacid dehydrogenase kinase	202030 at	0.065	17807	1.355E-01	FALSE
103336 r at	0.046	6296	1449211 at	-0.037	7437	103336 r at	-0.007	8059	1418764 a at	-0.163	2432	6056	2523.8955	FALSE	bisphosphate 3'-nucleotidase 1	232103 at	-0.162	5571	4.699E-04	FALSE
161055 r at	0.033	6732	1429723 at	0.064	5855.5	161055 r at	0.108	3133	1429723 at	-0.001	8504	6056.125	2238.5865	FALSE	RIKEN cDNA 6330409N04 gene	230151 at	-0.256	5178	3.312E-04	FALSE
95485 at	0.000	8519	1455972 x at	0.066	5330.5	95485 at	0.092	4061	1460184 at	-0.081	6317	6056.875	1883.3359	FALSE	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	201036 s at	0.207	11321	1.964E-02	FALSE
99552 at	0.169	2806	1418673 at	0.049	5448	99552 at	-0.002	8406	1418673 at	0.026	7569	6057.25	2499.5884	FALSE	snail homolog 2 (Drosophila)	213139 at	0.058	16392	9.950E-02	FALSE
102064 at	-0.009	8165	1449265 at	0.008	8253.5	102064 at	-0.039	6775	1449265 at	-0.266	1042	6058.875	3412.4288	FALSE	caspase 1	206011 at	0.113	9792	9.002E-03	FALSE
104232 at	0.040	6318	1416715 at	0.035	7253	104232 at	0.083	3139	1416715 at	0.028	7532	6060.5	2015.675	TRUE	gap junction membrane channel protein beta 3	205490 x at	0.072	19301	1.778E-01	FALSE
95951 at	0.052	6443	1420804 s at	0.073	5604.5	95951 at	0.028	6699	1420804 s at	0.083	5497	6060.875	599.84892	TRUE	C-type lectin domain family 4, member d	NA	NA	NA	NA	
160982 at	-0.075	5444	1428762 at	-0.005	8363	160982 at	-0.143	2951	1428762 at	-0.033	7489	6061.75	2407.7081	TRUE	RIKEN cDNA 4921526G09 gene	227357 at	-0.051	28022	4.816E-01	FALSE
98852 at	-0.034	6579	1452386 at	0.095	2344.5	98852 at	-0.024	6934	1441186 at	0.005	8396	6063.375	2600.9631	FALSE	sal-like 3 (Drosophila)	230785 at	0.223	8364	4.072E-03	FALSE
94462 at	-0.076	5610	1460730 at	0.156	2161	94462 at	0.005	8299	1460730 at	0.012	8185	6063.75	2882.9031	FALSE	eukaryotic translation initiation factor 2B, subunit 1 (alpha)	201632 at	-0.002	44013	9.849E-01	FALSE
160544 at	-0.068	4418	1416022 at	0.030	7997	160544 at	-0.079	3649	1416022 at	-0.016	8193	6064.25	2367.1833	FALSE	fatty acid binding protein 5, epidermal	202345 s at	0.658	7349	2.059E-03	FALSE
104526 at	0.035	6525	1422566 at	0.045	6816	104526 at	-0.035	6903	1422566 at	-0.128	4014	6064.5	1376.5228	FALSE	transcription factor EB	50221 at	0.461	80	5.381E-09	FALSE
96153 at	0.097	3374	1418722 at	0.121	4066.5	96153 at	0.003	8337	1418722 at	0.002	8481	6064.625	2722.4084	TRUE	neutrophilic granule protein	NA	NA	NA	NA	
93585 at	0.009	8073	1417651 at	0.062	6669.5	93585 at	-0.111	1507	1417651 at	0.023	8011	6065.125	3106.9687	FALSE	cytochrome P450, family 2, subfamily c, polypeptide 29	216025 x at	-0.033	32999	6.654E-01	FALSE
92257 at	0.159	2721	1418659 at	-0.004	8431	92257 at	0.015	7828	1439314 at	-0.109	5282	6065.5	2614.1633	FALSE	circadian locomoter output cycles kaput	230657 at	0.096	21289	2.430E-01	FALSE
92826 at	-0.039	6832	1427173 a at	0.240	2689.5	92826 at	-0.032	6930	1427173 a at	-0.023	7811	6065.625	2293.3984	FALSE	mitochondrial ribosomal protein S33	218654 s at	-0.311	2823	1.656E-05	FALSE
94002 at	0.172	3111	1448174 at	0.000	8520.5	94002 at	0.047	5431	1448174 at	0.041	7209	6067.875	2342.8085	TRUE	cullin 1	243286 at	0.150	5678	5.149E-04	TRUE
103236 at	0.110	2260	1422647 at	-0.017	7939	103236 at	-0.037	5651	1422647 at	-0.006	8426	6069	2812.8013	FALSE	ring finger protein 1	35685 at	0.075	14923	6.941E-02	FALSE
99417 at	0.020	7614	1421667 at	0.049	5894	99417 at	-0.076	5085	1421667 at	0.076	5683	6069	1085.4956	FALSE	neuromedin U receptor 1	221383 at	0.029	33343	6.768E-01	FALSE
99837 at	0.017	7683	1427704 a at	0.065	5401.5	99837 at	0.044	6102	1441329 at	-0.088	5094	6070.125	1155.0269	FALSE	galanin receptor 1	220821 at	0.012	38141	8.262E-01	FALSE
102041 at	0.011	7873	1450917 at	-0.062	6022	102041 at	-0.001	8470	1438175 x at	0.177	1920	6071.25	2957.2288	FALSE	myomesin 2	243913 at	0.075	23451	3.187E-01	FALSE
100085 at	0.179	1729	1448485 at	0.030	7295.5	100085 at	-0.023	7049	1448485 at	0.017	8223	6074.125	2940.5166	FALSE	gamma-glutamyltransferase 1	215603 x at	0.066	22520	2.856E-01	FALSE
92758 at	0.068	5026	1450698 at	0.041	6249	92758 at	-0.044	5603	1450698 at	0.043	7425	6075.75	1028.9086	FALSE	dual specificity phosphatase 2	204794 at	-0.207	5217	3.408E-04	FALSE
97685 at	0.126	4436	1448030 at	0.078	4630	97685 at	-0.019	7421	1448030 at	-0.040	7818	6076.25	1791.0988	FALSE	RIKEN cDNA 1700023D09 gene	NA	NA	NA	NA	
160587 at	-0.032	6751	1436955 at	0.062	4259	160587 at	-0.025	7062	1445308 at	-0.073	6234	6076.5	1258.8716	FALSE	tumor suppressing subtransferable candidate 1	217968 at	-0.314	3712	6.028E-05	FALSE
103537 at	0.049	6921	1430371 x at	0.052	6260	103537 at	0.047	4870	1453505 a at	0.097	6258	6077.25	863.21777	TRUE	eukaryotic translation initiation factor 2 alpha kinase 3	218696 at	0.155	14897	6.884E-02	FALSE
101448 at	0.120	2502	1416540 at	-0.027	7479.5	101448 at	0.017	7194	1416540 at	-0.040	7134	6077.375	2388.3445	FALSE	HGF-regulated tyrosine kinase substrate	232627 at	0.074	18190	1.454E-01	FALSE
103040 at	0.055	6553	1416111 at	-0.025	7991	103040 at	0.074	3612	1416111 at	-0.245	6154	6077.5	1823.1955	FALSE	CD83 antigen	204440 at	-0.019	36807	7.861E-01	FALSE
102982 at	0.090	4855	1454872 at	-0.057	6359.5	102982 at	0.055	5815	1454872 at	-0.044	7285	6078.625	1016.692	FALSE	RIKEN cDNA B230308N11 gene	NA	NA	NA	NA	



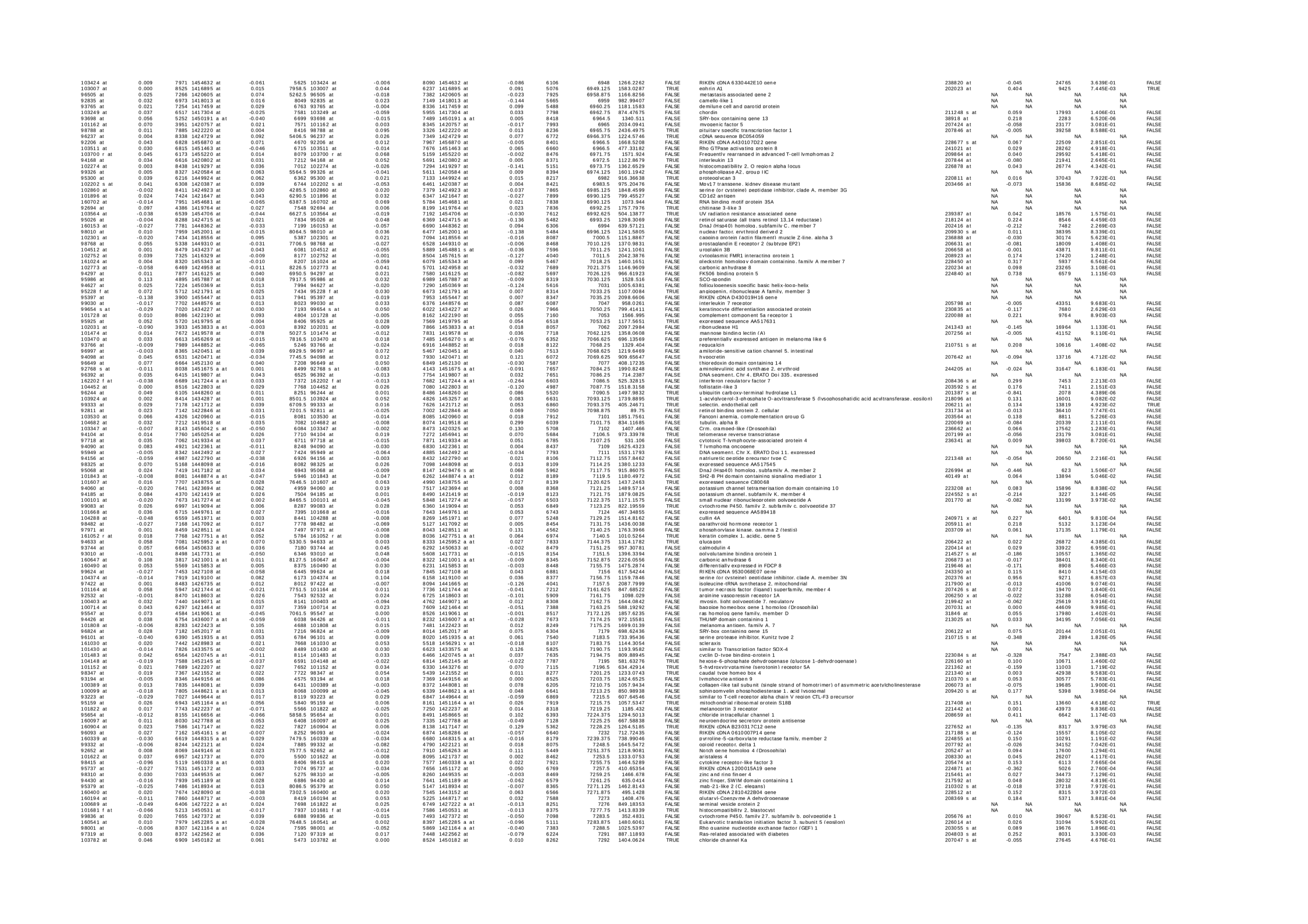
92487 at	0.018	7646	1416564 at	0.029	7266.5	92487 at	-0.079	3895	1432495 at	-0.070	5898	6176.375	1696.1068	FALSE	SRY-box containing gene 7	228698 at	0.138	21430	2.476E-01	FALSE
92246 at	0.029	7205	1419707 at	0.046	6624	92246 at	0.041	6896	1419707 at	0.121	3981	6176.5	1482.7867	TRUE	keratin associated protein 14	NA	NA	NA	NA	
100359 at	0.041	6483	1427421 at	0.065	5666	100359 at	0.049	5440	1427421 at	0.047	7123	6178	773.05412	TRUE	t-complex protein 10b	NA	NA	NA	NA	
96050 at	-0.005	8263	1416045 a at	0.033	7091.5	96050 at	0.097	5296	1416045 a at	-0.112	4063	6178.375	1864.8374	FALSE	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member	231324 at	0.120	8620	4.689E-03	FALSE
98936 at	-0.073	5551	1426257 a at	-0.027	7231	98936 at	0.056	4695	1426257 a at	0.048	7244	6180.25	1269.8507	FALSE	seryl-aminoacyl-tRNA synthetase	200802 at	-0.173	12641	3.304E-02	FALSE
94248 at	0.030	6746	1416307 at	-0.061	5309	94248 at	-0.066	4264	1416307 at	0.004	8404	6180.75	1797.7974	FALSE	adaptor-related protein complex AP-1, mu subunit 1	223025 s at	-0.072	19496	1.848E-01	FALSE
93888 at	0.077	4355	1453501 at	-0.016	7835	93888 at	0.083	4776	1453501 at	0.036	7757	6180.75	1873.303	FALSE	homeo box B1	208224 at	-0.009	42081	9.371E-01	FALSE
95382 at	-0.047	5665	1459922 at	-0.004	8419	95382 at	0.075	3482	1459922 at	-0.055	7166	6183	2123.6533	FALSE	expressed sequence AI646383	NA	NA	NA	NA	
97371 at	0.052	5842	1452715 at	0.083	5029.5	97371 at	-0.036	6135	1452715 at	0.032	7726	6183.125	1129.8962	FALSE	RIKEN cDNA 2310022K01 gene	213053 at	0.029	35311	7.405E-01	FALSE
162188 f at	-0.016	7613	1417149 at	-0.040	6403	98983 at	-0.053	5227	1417149 at	-0.103	5495	6184.5	1077.1213	TRUE	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	202733 at	0.439	5316	3.690E-04	FALSE
103993 at	0.036	6306	1422106 a at	0.098	4047	103993 at	-0.039	6746	1422106 a at	-0.026	7641	6185	1529.7431	FALSE	splA/ryanodine receptor domain and SOCS box containing 2	223580 at	0.211	4981	2.641E-04	FALSE
92645 at	0.050	5599	1415831 at	-0.058	6198.5	92645 at	0.041	6423	1415831 at	0.069	6520	6185.125	413.2986	FALSE	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	200830 at	-0.126	14727	6.558E-02	FALSE
104692 at	0.041	7110	1420558 at	0.053	6440.5	104692 at	0.048	5425	1449906 at	0.150	5767	6185.625	746.82164	TRUE	selectin, platelet	206049 at	0.014	39811	8.720E-01	FALSE
97287 at	0.119	4685	1431701 a at	-0.008	8278.5	97288 at	-0.010	8019	1431701 a at	-0.175	3764	6186.625	2299.0961	FALSE	PDZ domain containing 1	205380 at	-0.039	19865	1.967E-01	FALSE
97418 at	-0.030	7222	1418914 s at	-0.023	7505.5	97418 at	0.060	4715	1418913 at	-0.101	5313	6188.875	1383.2707	FALSE	betaine-homocysteine methyltransferase 2	219902 at	0.153	9230	6.634E-03	FALSE
92917 at	0.050	6644	1449478 at	0.067	5088	92917 at	0.046	6148	1449478 at	0.055	6876	6189	794.32907	TRUE	matrix metallopeptidase 7	204259 at	0.005	41797	9.288E-01	FALSE
103895 at	0.191	3022	1426459 s at	0.005	8360.5	103895 at	0.076	5697	1426459 s at	-0.026	7681	6190.125	2395.3722	FALSE	expressed sequence AW549877	226159 at	0.199	6094	7.577E-04	FALSE
98419 at	0.069	5229	1417595 at	0.020	7868	98419 at	-0.069	3692	1417595 at	-0.028	7973	6190.5	2094.3016	FALSE	mesenchyme homeobox 1	205619 s at	0.016	31102	5.998E-01	FALSE
160157 at	0.044	6304	1417935 at	0.011	7991	160157 at	0.094	4404	1417935 at	-0.067	6064	6190.75	1467.6815	FALSE	makorin, ring finger protein, 2	222510 s at	-0.160	11591	2.179E-02	FALSE
99860 at	-0.013	7822	1460212 at	-0.036	7061.5	99860 at	0.072	4517	1460212 at	-0.082	5368	6192.125	1516.3038	FALSE	guanine nucleotide binding protein, alpha transducing 1	214286 at	-0.055	22194	2.747E-01	FALSE
97316 at	0.028	7363	1448382 at	-0.021	7536	97316 at	0.077	3166	1448382 at	-0.073	6704	6192.25	2049.0971	FALSE	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	205222 at	0.074	12362	2.988E-02	FALSE
102336 at	-0.078	5378	1448396 at	-0.086	4493.5	102336 at	-0.038	7769	1448396 at	-0.049	7130	6192.625	1518.1425	TRUE	transmembrane protein 131	212507 at	-0.135	18320	1.495E-01	FALSE
99899 at	0.057	5702	1450357 a at	0.062	6529	99899 at	-0.058	5297	1450357 a at	0.060	7248	6194	869.83025	FALSE	chemokine (C-C motif) receptor 6	206983 at	-0.017	30340	5.688E-01	FALSE
96890 at	-0.031	7315	1460178 at	0.040	6862	96890 at	-0.125	5308	1460178 at	-0.088	5306	6197.75	1045.0437	FALSE	RIKEN cDNA 1300002A08 gene	229663 at	-0.058	20851	2.280E-01	FALSE
101916 at	0.025	7169	1423938 at	0.141	1494.5	101916 at	-0.008	8118	1423938 at	-0.016	8010	6197.875	3164.148	FALSE	lethal giant larvae homolog 2 (Drosophila)	203713 s at	0.140	7841	2.941E-03	FALSE
96481 at	0.048	6358	1439995 at	0.082	4009.5	96481 at	0.009	7932	1439995 at	-0.072	6495	6198.625	1623.7914	FALSE	expressed sequence C80638	237648 x at	-0.038	18809	1.640E-01	FALSE
94138 s at	0.046	6368	1420756 at	0.043	6271	94138 s at	-0.046	6185	1420756 at	0.107	5971	6198.75	169.23824	FALSE	fucosyltransferase 7	210506 at	-0.052	25013	3.728E-01	FALSE
102793 at	-0.008	8088	1427211 at	0.059	6172	102793 at	0.115	2427	1427211 at	-0.024	8108	6198.75	2673.407	FALSE	keratin associated protein 8-1	NA	NA	NA	NA	
95970 at	0.063	4964	1442665 at	0.004	8433	95970 at	-0.047	6191	1442665 at	0.080	5214	6200.5	1579.6899	FALSE	expressed sequence C77874	NA	NA	NA	NA	
102915 at	0.025	7387	1448931 at	-0.033	6885	102915 at	0.093	2480	1448931 at	0.019	8060	6203	2528.2509	FALSE	coagulation factor II (thrombin) receptor-like 1	213506 at	0.331	4846	2.319E-04	FALSE
102712 at	-0.055	7061	1450826 a at	0.032	6903	102712 at	-0.065	4518	1450826 a at	-0.073	6333	6203.75	1166.5171	FALSE	serum amyloid A 3	208607 s at	-0.093	24138	3.422E-01	FALSE
93351 at	-0.001	8461	1419906 at	0.078	4394.5	93351 at	0.076	4428	1419906 at	-0.061	7535	6204.625	2105.0792	FALSE	hydroxyprostaglandin dehydrogenase 15 (NAD)	211548 s at	-0.027	28276	4.926E-01	FALSE
102298 at	-0.007	8205	1419675 at	0.052	6179	102298 at	-0.009	8152	1419675 at	-0.189	2286	6205.5	2777.8916	FALSE	nerve growth factor, beta	206814 at	-0.051	31314	6.060E-01	FALSE
102783 at	-0.024	7461	1452799 at	0.073	4339	102783 at	-0.063	4569	1452799 at	-0.004	8459	6207	2066.9211	FALSE	RIKEN cDNA 2310009E04 gene	NA	NA	NA	NA	
160847 at	0.095	4738	1425562 s at	0.066	6359.5	160847 at	0.058	7142	1425562 s at	0.085	6590	6207.375	1033.1393	TRUE	tRNA nucleotidyl transferase, CCA-adding, 1	222754 at	-0.203	15130	7.322E-02	FALSE
101101 at	-0.034	7552	1421823 a at	-0.104	3921.5	101101 at	0.041	7536	1421822 at	-0.070	5820	6207.375	1727.0924	FALSE	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	201375 s at	0.126	17567	1.285E-01	FALSE
93443 at	-0.015	7874	1453321 at	0.033	7240	93443 at	-0.049	5606	1453321 at	-0.129	4111	6207.75	1693.162	FALSE	fibronectin type III domain containing 1	226930 at	0.134	21683	2.572E-01	FALSE
101218 at	-0.006	8194	1420001 at	0.083	4902.5	101218 at	0.015	7795	1420001 at	0.191	3942	6208.375	2105.6947	FALSE	DNA segment, Chr 7, ERATO Doi 1, expressed	NA	NA	NA	NA	
95295 s at	0.010	7953	1419538 at	0.019	7734	95295 s at	0.109	2861	1419538 at	-0.116	6288	6209	2351.064	FALSE	FMS-like tyrosine kinase 3	206674 at	-0.043	27119	4.474E-01	FALSE
92395 r at	0.045	5888	1417173 at	-0.022	7702	92394 f at	-0.096	2763	1417173 at	-0.004	8485	6209.5	2542.1238	FALSE	cAMP responsive element binding protein-like 1	216208 s at	-0.048	24233	3.452E-01	FALSE
94746 at	0.063	4570	1422160 at	0.040	6859	94746 at	0.067	5233	1422160 at	-0.031	8178	6210	1626.6893	FALSE	histocompatibility 2, T region locus 24	NA	NA	NA	NA	
98418 at	-0.030	7139	1450978 at	-0.041	6447.5	98418 at	0.021	7642	1450978 at	-0.130	3617	6211.375	1797.5643	FALSE	dishevelled, dsh homolog 1 (Drosophila)	203230 at	-0.051	31593	6.161E-01	FALSE
103214 at	-0.007	8140	1429888 a at	-0.021	7467.5	103215 g at	0.049	5402	1429888 a at	0.114	3839	6212.125	1964.7471	FALSE	heat shock protein 2	205824 at	0.261	4781	2.132E-04	FALSE
97755 at	-0.060	5448	1422829 at	0.080	5944	97755 at	-0.035	6402	1422829 at	0.055	7059	6213.25	685.32784	FALSE	dopamine receptor 4	208215 x at	-0.038	29610	5.427E-01	FALSE
162062 r at	0.014	7808	1460374 at	0.041	6197	162062 r at	0.050	5056	1460374 at	-0.082	5797	6214.5	1162.7521	FALSE	A disintegrin and metallopeptidase domain 2	207664 at	-0.026	24890	3.684E-01	FALSE
98109 at	0.044	5895	1429453 a at	0.060	6453	98109 at	0.011	7905	1429453 a at	0.121	4606	6214.75	1366.751	TRUE	mitochondrial ribosomal protein L55	225719 s at	-0.101	13391	4.245E-02	FALSE
103928 at	0.032	7001	1418919 at	-0.015	7887	103928 at	0.071	3656	1439510 at	0.061	6315	6214.75	1823.1713	FALSE	shugoshin-like 1 (S. pombe)	231938 at	0.013	37353	8.008E-01	FALSE
100302 at	-0.042	5925	1418936 at	0.036	7140.5	100302 at	-0.100	3680	1418936 at	0.020	8118	6215.875	1913.834	FALSE	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	36711 at	0.981	10664	1.456E-02	FALSE
97579 f at	0.071	4802	1429948 x at	0.088	4977.5	97579 f at	0.024	7028	1429948 x at	0.019	8056	6215.875	1589.3628	TRUE	crystallin, gamma F	207532 at	-0.038	30390	5.710E-01	FALSE
104064 at	-0.002	8409	1431208 a at	-0.052	6096	104064 at	-0.077	5570	1431208 a at	0.097	4799	6218.5	1554.4376	FALSE	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	209830 s at	-0.006	42353	9.434E-01	FALSE
98042 at	0.008	8109	1426555 at	-0.094	3324.5	98042 at	0.008	8154	1426555 at	-0.098	5289	6219.125	2349.4223	FALSE	serine carboxypeptidase 1	218217 at	0.315	3876	7.490E-05	FALSE
101850 at	-0.006	8210	1417635 at	0.054	7111	101850 at	-0.005	8349	1417635 at	-0.460	1208	6219.5	3386.5796	FALSE	sperm autoantigenic protein 17	239515 at	0.224	9973	9.994E-03	FALSE
100346 at	0.026	6979	1420795 at	-0.047	6447.5	100346 at	-0.059	4977	1445258 at	0.065	6476	6219.875	863.79438	FALSE	fibroblast growth factor 9	206404 at	-0.512	991	4.354E-07	FALSE
97328 at	-0.017	7538	1456618 at	-0.015	8147.5	97328 at	-0.172	2025	1456618 at	0.043	7169	6219.875	2825.5387	FALSE	MAP/microtubule affinity-regulating kinase 4	55065 at	-0.425	1804	2.677E-06	FALSE
102663 at	0.093	5074	1452521 a at	0.073	5625	102663 at	-0.026	6750	1452521 a at	0.042	7441	6222.5	1070.6784	FALSE	plasminogen activator, urokinase receptor	214866 at	-0.023	37227	7.975E-01	FALSE
95446 at	0.026	7608	1425194 a at	-0.019	8031.5	95446 at	-0.214	1293	1425194 a at	-0.016	7958	6222.625	3291.6066	FALSE	RIKEN cDNA 6330577E15 gene	236027 at	0.204	11305	1.953E-02	FALSE
160119 at	-0.058	5586	1452754 at	-0.026	7967	160119 at	-0.045	5462	1452754 at	0.073	5883	6224.5	1175.0201	FALSE	cysteine-rich with EGF-like domains 2	218358 at	0.113	19137	1.730E-01	FALSE
103588 at	0.064	5346	1454206 a at	0.059	6166.5	103588 at	-0.012	7864	1425170 a at	-0.159	5524	6225.125	1148.0106	FALSE	a disintegrin and metallopeptidase domain 15 (metargidin)	217007 s at	0.045	25276	3.822E-01	FALSE
94176 at	0.021	7458	1422262 a at	-0.060	6071	94176 at	-0.079	4358	1422262 a at	-0.096	7015	6225.5	1372.8065	FALSE	LIM homeobox protein 6	219884 at	0.072	22221	2.759E-01	FALSE
94150 at	0.013	8045	1419025 at	-0.011	8101	94150 at	0.023	7121	1419025 at	0.189	1638	6226.25	3091.6638	FALSE	retinal S-antigen	206671 at	-0.132	11564	2.160E-02	FALSE
104120 at	-0.004	8282	1452603 at	0.145	2906	104120 at	0.028	6739	1452603 at	0.061	6983	6227.5	2315.5809	FALSE	RIKEN cDNA 5330431N19 gene	226009 at	-0.171	5207	3.374E-04	FALSE
94639 at	-0.028	6986	1422427 a at	0.055	5435	94639 at	0.026	7218	1456188 at	-0.108	5272	6227.75	1016.1117	FALSE	seminal vesicle protein, secretion 2	NA	NA	NA	NA	
103199 at	0.136	2731	1419412 at	-0.025	7523.5	103199 at	-0.035	6396	1419412 at	0.012	8261	6227.875	2454.1558	FALSE	chemokine (C motif) ligand 1	206365 at	-0.026	26718	4.325E-01	FALSE
94626 at	-0.015	7678	1421580 at	-0.042	7941	94626 at	-0.220	1085	1421580 at	0.019	8209	6228.25	3435.6794	FALSE	contactin associated protein 1	219400 at	-0.337	883	3.372E-07	FALSE
100610 at	-0.091	5071	1426400 a at	0.030	7046	100610 at	0.010	7937	1426400 a at	0.115	4860	6228.5	1505.5317	FALSE	calpain, small subunit 1	200001 at	-0.133	14853	6.785E-02	FALSE
102926 at	0.023	7489	1418880 at	0.034	7131	102926 at	-0.007	8146	1418880 at	0.182	2157	6230.75	2748.1669	FALSE	glial cell line derived neurotrophic factor family receptor alpha 3	214479 at	-0.012	39472	8.636E-01	FALSE
101402 at	-0.016	7676	1431282 at	-0.037	6920	101402 at	-0.090	4100	1431282 at	0.073	6228	6231	1538.8216	FALSE	thyroid hormone receptor associated protein 4	215337 at	-0.016	36558	7.789E-01	FALSE
99414 at	-0.039	6342	1450789 at	0.049	6847.5	99414 at	0.002	8442	1450789 at	-0.184	3294	6231.375	2153.0508	FALSE	rhophilin, Rho GTPase binding protein 1	235998 at	0.113	7254	1.936E-03	FALSE
161081 at	0.130	5063	1434272 at	0.030	7795	161081 at	0.201	5176	1443017 at	0.081	6897	6232.75	1337.5212	TRUE	cytoplasmic polyadenylation element binding protein 2	243605 at	-0.108	13636	4.588E-02	FALSE
102087 at	0.100	4523	1427433 s at	0.052	6089.5	102087 at	0.009	8078	1427433 s at	0.064	6243	6233.375	1454.7413	TRUE	homeo box A3	235521 at	0.020	31865	6.267E-01	FALSE
100007 at	0.088	3506	1451252 at	0.011	8077	100007 at	0.004	8267	1451252 at	0.126	5084	6233.5	2330.5379	TRUE	interferon regulatory factor 2 binding protein 1	213771 at	-0.068	12678	3.342E-02	FALSE
96670 at	-0.002	8447	1452823 at	0.028	7789	96670 at	0.226	583	1452823 at	0.030	8116	6233.75	3776.7322	FALSE	glutathione S-transferase kappa 1	217751 at	0.262	1548	1.557E-06	FALSE
98056 at	0.000	8517	1449002 at	-0.009	8214	98056 at	0.116	1714	1449002 at	-0.122	6491	6234	3142.6601	FALSE	pleckstrin homology-like domain, family A, member 3	218634 at	0.226	2863	1.764E-05	FALSE
160891 at	0.068	4785	1437028 at	0.058	5727	160891 at	0.052	5939	1437028 at	0.001	8502	6238.25	1590.3277	TRUE	surfactant associated protein B	213936 x at	0.173	7234	1.908E-03	TRUE
98969 at	0.082	3560	1418838 at	-0.006	8370	98969 at	0.005	8285	1418838 at	-0.121	4745	6240	2458.7497	FALSE	ATP-binding cassette, sub-family D (ALD), member 1	216418 at	-0.021	34966	7.286E-01	FALSE
102085 at	0.102	2735	1421399 at	0.076	6114	102085 at	-0.001	8488	1421399 at	0.049	7629	6241.5	2535.3315	FALSE	insulinoma-associated 1	206502 s at	-0.594	2250	6.080E-06	FALSE
101639 r at	-0.020	7381	1421741 at	0.025	7219.5	101639 r at	0.059	5231	1421741 at	-0.087	5145	6244.125	1221.7937	FALSE	cytochrome P450, family 3, subfamily a, polypeptide 16	NA	NA	NA	NA	
100436 at	-0.029	6842	1451054 at	0.037	6264	100436 at	0.039	6204	1451054 at	-0.078	5670	6245	479.26193	FALSE	orosomucoid 1	205041 s at	-0.021	31044	5.967E-01	FALSE
103086 at	-0.003	8429	1448926 at	0.068	6181.5	103086 at	-0.048	5497	1448926 at	0.092	4874	6245.375	1550.5948	FALSE	homeo box A5	213844 at	0.028	34415	7.110E-01	FALSE
99913 at	-0.020	7624	1420569 at	0.166	2762.5	99913 at	-0.019	7185	1420569 at	-0.053	7421	6248.125	2330.664	FALSE	chondroadherin	206869 at	-0.137	7271	1.952E-03	FALSE
96168 at	-0.011	7915	1453748 a at	0.068	4566.5	96168 at	0.083	4744	1450827 at	-0.023	7771	6249.125	1842.8123	FALSE	kinesin family member 23	204709 s at	-0.019	28217	4.899E-01	FALSE
103570 at	-0.050	6197	1422606 at	0.088	3573.5	103570 at	0.009	7821	1422606 at	0.031	7409	6250.125	1912.9195	FALSE	C1q and tumor necrosis factor related protein 3	220988 s at	0.144	6099	7.621E-04	FALSE
100992 at	-0.016	7706	1423212 at	-0.100	2909	100992 at	-0.009	8102	1423212 at	-0.093	6284	6250.25	2360.3161	TRUE	polyhomeotic-like 1 (Drosophila)	225958 at	0.105	9579	8.101E-03	FALSE
93158 at	-0.043	6059	1434992 at	0.027	7195	93158 at	0.057	4589	1434992 at	-0.040	7159	6250.5	1226.7446	FALSE	RIKEN cDNA 9130206N08 gene	NA	NA	NA	NA	
102877 at	0.014	7829	1419060 at	0.097	4097	102877 at	0.007	8024	1419060 at	0.113	5053	6250.75	1975.5618	TRUE	granzyme B	210164 at	-0.016	35180	7.360E-01	FALSE
160983 at	-0.029	7239	1457964 at	0.049	6020	160983 at	0.019	7305	1457964 at	-0.161	4442	6251.5	1343.2425	FALSE	RIKEN cDNA 1810044D09 gene	NA	NA	NA	NA	
104363 at	-0.024	7516	1435191 at	0.105	4119.5	104363 at	0.044	6092	1444607 at	0.034	7282	6252.375	1552.6055	FALSE	corneodesmosin	206192 at	-0.011	41416	9.182E-01	FALSE
160077 at	0.042	6058	1431411 a at	0.030	7410	160077 at	-0.002	8398	1444136 at	-0.193	3148	6253.5	2281.7189	FALSE	retinoic acid induced 12	223286 at	-0.097	7385	2.112E-03	FALSE
93862 i at	0.186	1782	1422422 at	-0.029	7247.5	93862 i at	0.004	8367	1422422 at	-0.034	7630	6256.625	3019.0475	FALSE	Defensin related cryptdin 4	NA	NA	NA	NA	
94167 at	-0.002	8418	1422622 at	0.021	7562.5	94167 at	-0.019	7284	1422622 at	0.205	1765	6257.375	3033.5372	FALSE	nitric oxide synthase 3, endothelial cell	205581 s at	0.117	18762	1.627E-01	FALSE
99982 at	0.022	7209	1421266 s at	0.082	4860	99982 at	-0.011	7926	1446718 at	0.150	5038	6258.25	1541.5824	FALSE	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	228388 at	0.148	6469	1.027E-03	FALSE
161638 f at	0.041	6392	1419384 at	0.080	5172.5	97684 at	-0.038	5514	1419384 at	-0.026	7962	6260.125	1245.4451	FALSE	protein interacting with C kinase 1	204746 s at	0.091	17412	1.245E-01	FALSE
162502 f at	0.023	7643	1418549 at	-0.736	4780	162502 f at	-0.048	5223.5	1418549 at	-0.051	7394	6260.125	1467.8076	FALSE	glycoprotein hormones, alpha subunit	204637 at	0.079	23062	3.031E-01	FALSE
101281 at	0.089	4257	1422370 at	0.051	6952.5	101281 at	-0.012	7606	1422370 at	-0.153	6227	6260.625	1449.64	FALSE	olfactory receptor 49	NA	NA	NA	NA	
98288 at	0.001	8486	1420763 at	0.034	7218	98288 at	-0.027	6906	1420763 at	0.257	2443	6263.25	2636.8923	FALSE	kallikrein 4 (prostase, enamel matrix, prostate)	224062 x at	-0.101	13768	4.802E-02	FALSE
92649 at	0.011	8195	1419516 at	0.028	7272	92649 at	0.256	1974	1419516 at	-0.032	7615	6264	2885.2571	FALSE	DNA segment, human DXS9928E	203262 s at	0.329	1784	2.576E-06	FALSE
101737 at	0.092	3998	1450996 at	-0.176	6870	101737 at	-0.016	7558	1450996 at	0.073	6633	6264.75	1561.2588	FALSE	follicle stimulating hormone beta	214489 at	-0.036	34543	7.156E-01	FALSE
103490 at	0.027	7564	1450772 at	0.082	5647	103490 at	0.054	6318.5	1450772 at	0.090	5533	6265.625	932.3822	TRUE	wingless-related MMTV integration site 11	206737 at	-0.037	30440	5.734E-01	FALSE
103830 at	0.018	7685	1448742 at	0.069	5195	103830 at	0.002	8361	1448742 at	0.146	3824	6266.25	2122.3407	TRUE	snail homolog 1 (Drosophila)	219480 at	0.041	28259	4.917E-01	FALSE
101156 at	0.009	8059	1452552 at	0.030	7274	101156 at	0.007	8211	1452552 at	0.185	1525	6267.25	3188.0513	TRUE	neoplastic progression 2	NA	NA	NA	NA	
97940 at	0.002	8449	1439002 s at	-0.058	5630	97940 at	0.005	8221	1415848 at	-0.139	2769	6267.25	2659.6374	FALSE	chorionic somatomammotropin hormone 1	NA	NA	NA	NA	
93715 at	-0.005	8270	1423253 at	0.102	4405	93715 at	0.014	7570	1423253 at	-0.106	4827	6268	1936.5311	FALSE	myelin protein zero	210280 at	-0.048	29329	5.326E-01	FALSE
97425 at	-0.097	2890	1433645 at	-0.029	7405	97425 at	-0.004	8324	1433645 at	-0.079	6453	6268	2378.0254	TRUE	RIKEN cDNA 2210409B22 gene	NA	NA	NA	NA	
98937 at	0.016	8028	1452648 at	0.016	8154	98937 at	-0.084	3655	1452648 at	0.123	5240	6269.25	2201.4497	FALSE	transforming growth factor beta regulated gene 1	240955 at	-0.040	24983	3.716E-01	FALSE
94687 at	-0.024	7289	1420705 at	0.082	4423	94687 at	0.039	5980	1420705 at	0.039	7385	6269.25	1387.6951	FALSE	forkhead box B1	208513 at	-0.021	36928	7.891E-01	FALSE
99929 at	0.004	8329	1460170 at	0.020	7584.5	99929 at	0.004	8256	1447743 x at	0.245	908	6269.375	3589.9225	TRUE	exostoses (multiple) 2	202013 s at	0.079	18184	1.451E-01	FALSE
93840 at	0.044	6334	1419095 a at	-0.049	5580	93840 at	-0.061	5593	1419096 at	0.028	7573	6270	937.4316	FALSE	apolipoprotein M	214910 s at	0.115	14414	6.015E-02	FALSE
96845 at	-0.009	8231	1426668 at	-0.109	4881	96845 at	0.126	4875	1426668 at	0.043	7102	6272.25	1674.6214	FALSE	solute carrier family 30 (zinc transporter), member 9	202614 at	-0.208	14970	7.057E-02	FALSE
104464 s at	0.127	3879	1418538 at	0.029	7494	104464 s at	0.056	5454	1418538 at	0.009	8263	6272.5	1987.707	TRUE	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	207265 s at	0.055	21723	2.593E-01	FALSE
100982 at	0.039	6692	1418399 at	0.028	7142	100982 at	-0.005	8137	1418399 at	-0.376	3121	6273	2186.3457	FALSE	potassium channel tetramerisation domain containing 9	218823 s at	0.192	10353	1.232E-02	FALSE
101002 at	0.057	6716	1422702 at	-0.090	5351.5	101002 at	0.013	8140	1422702 at	0.106	4888	6273.875	1466.2108	FALSE	antizyme inhibitor 1	240231 at	0.200	8217	3.749E-03	FALSE
104693 at	0.057	5455	1429126 at	0.135	2846.5	104693 at	0.003	8352	1429126 at	-0.004	8443	6274.125	2673.3975	FALSE	RIKEN cDNA 2600001M11 gene	NA	NA	NA	NA	
96722 at	0.030	7149	1434511 at	-0.038	7698	96722 at	0.028	7001	1434511 at	-0.198	3252	6275	2037.5156	FALSE	phosphorylase kinase beta	242643 x at	0.055	13941	5.133E-02	FALSE
104636 at	0.121	2809	1422072 a at	0.021	7735.5	104637 at	-0.042	6518	1422072 a at	-0.058	8038	6275.125	2402.3207	FALSE	glutathione S-transferase, mu 6	NA	NA	NA	NA	
162397 r at	-0.099	6143	1424874 a at	-0.041	7088	162397 r at	0.122	6367	1424874 a at	-0.077	5503	6275.25	653.9217	FALSE	polypyrimidine tract binding protein 1	202189 x at	0.486	573	1.272E-07	FALSE
101707 at	0.014	7839	1422789 at	-0.045	6805	101707 at	0.010	8163	1422789 at	-0.276	2296	6275.75	2715.6324	FALSE	aldehyde dehydrogenase family 1, subfamily A2	207015 s at	-0.035	32539	6.483E-01	FALSE
92258 at	0.132	4092	1429597 at	-0.002	8436	92258 at	0.016	7330	1429597 at	0.091	5247	6276.25	1966.8259	FALSE	developmental pluripotency associated 4	NA	NA	NA	NA	
93336 at	-0.083	5505	1424708 at	-0.097	4977.5	93336 at	0.007	8049	1424707 at	-0.054	6576	6276.875	1355.7371	FALSE	transmembrane emp24-like trafficking protein 10 (yeast)	238886 at	0.324	1735	2.350E-06	FALSE
103875 at	-0.025	7798	1416709 a at	0.180	1569.5	103875 at	-0.031	7398	1416709 a at	-0.008	8343	6277.125	3162.2246	FALSE	neugrin, neurite outgrowth associated	224281 s at	-0.357	4128	1.005E-04	FALSE
94618 at	0.089	3912	1422267 at	0.001	8490.5	94618 at	-0.059	4972	1422267 at	-0.036	7734	6277.125	2184.6953	FALSE	forkhead box B2	NA	NA	NA	NA	
103879 at	0.076	3715	1451354 at	0.044	6206	103879 at	-0.025	6706	1451354 at	0.002	8484	6277.75	1968.3981	FALSE	FAD-dependent oxidoreductase domain containing 1	223128 at	-0.027	31029	5.962E-01	FALSE
104399 at	0.008	8294	1419645 at	-0.065	6549.5	104399 at	0.124	6476	1455523 at	-0.216	3793	6278.125	1857.6327	FALSE	cleavage stimulation factor, 3' pre-RNA subunit 2	238821 at	-0.051	22924	2.989E-01	FALSE
104710 at	0.037	6532	1425716 s at	0.095	4749.5	104710 at	-0.003	8351	1418991 at	0.096	5483	6278.875	1563.1357	FALSE	BCL2-antagonist/killer 1	203728 at	0.004	42582	9.494E-01	FALSE
93216 at	0.071	4153	1449826 a at	0.049	6104	93216 at	-0.034	6655	1449826 a at	0.010	8204	6279	1673.0712	FALSE	fibroblast growth factor 2	204422 s at	0.711	5486	4.394E-04	FALSE
93193 at	-0.022	7704	1437302 at	0.043	6508	93193 at	-0.017	7353	1437302 at	-0.147	3554	6279.75	1885.2201	FALSE	adrenergic receptor, beta 2	206170 at	0.125	12313	2.937E-02	FALSE
94729 r at	0.088	4133	1422352 at	-0.001	8470	94729 r at	-0.121	4104	1422352 at	-0.005	8412	6279.75	2495.7369	FALSE	mast cell protease 1	NA	NA	NA	NA	
97144 at	-0.085	4107	1447981 at	0.042	7146.5	97144 at	0.052	5547	1447981 at	0.010	8324	6281.125	1842.8213	FALSE	expressed sequence C78441	NA	NA	NA	NA	
102802 at	-0.068	4919	1417932 at	-0.002	8485.5	102802 at	0.087	3425	1417932 at	-0.009	8296	6281.375	2512.0924	FALSE	interleukin 18	206295 at	0.052	19487	1.846E-01	FALSE

100995 at	0.150	2274	1448779 at	-0.043	6213	100995 at	0.001	8454	1448779 at	0.013	8191	6283	2853.6927	FALSE	CDKN1A interacting zinc finger protein 1	241524 at	0.060	17509	1.269E-01	FALSE
160349 at	-0.021	7736	1460177 at	0.083	3387.5	160349 at	0.020	7176	1448263 a at	0.076	6848	6286.875	1967.3792	FALSE	CNDP dipeptidase 2 (metallopeptidase M20 family)	217752 s at	0.212	6502	1.046E-03	FALSE
104737 at	-0.040	6659	1435639 at	0.116	4290	104737 at	-0.038	6244	1435639 at	-0.028	7961	6288.5	1519.9242	FALSE	RIKEN cDNA 2610528A11 gene	NA	NA	NA	NA	
94219 at	0.038	6940	1448262 at	-0.009	8197	94219 at	0.017	7312	1444377 at	0.253	2707	6289	2445.5073	FALSE	proteasome (prosome, macropain) subunit, beta type 2	238425 at	0.075	13572	4.501E-02	FALSE
92742 at	-0.026	6987	1417789 at	-0.034	7033	92742 at	0.079	3616	1417789 at	0.030	7523	6289.75	1798.9277	FALSE	small chemokine (C-C motif) ligand 11	210133 at	-0.075	20905	2.305E-01	FALSE
98318 at	0.018	7580	1449926 at	0.058	5948.5	98318 at	-0.066	4975	1449926 at	0.076	6657	6290.125	1102.2154	FALSE	tumor necrosis factor (ligand) superfamily, member 7	206508 at	-0.015	39346	8.607E-01	FALSE
95244 at	0.032	7059	1421251 at	0.083	4332	95244 at	-0.050	6379	1421251 at	0.079	7396	6291.5	1373.1075	FALSE	zinc finger protein 40	NA	NA	NA	NA	
161867 f at	-0.079	5022	1450775 at	0.033	7508	96521 at	-0.048	5940	1450775 at	-0.066	6697	6291.75	1061.3646	FALSE	Moloney sarcoma oncogene	221367 at	-0.023	32608	6.507E-01	FALSE
102772 at	0.017	7637	1423999 at	-0.025	7258.5	102772 at	-0.022	7321	1445153 at	0.160	2951	6291.875	2233.4032	FALSE	v-abl Abelson murine leukemia oncogene 1	202123 s at	0.397	806	2.798E-07	FALSE
94439 at	-0.025	7660	1455534 s at	-0.116	4196	94439 at	-0.011	8127	1455534 s at	0.107	5187	6292.5	1902.0067	FALSE	oxysterol binding protein-like 11	218304 s at	0.745	2239	5.995E-06	FALSE
95043 at	0.053	5946	1424273 at	0.091	5593.5	95043 at	-0.044	5687	1424273 at	0.023	7945	6292.875	1111.4629	FALSE	cytochrome P450, family 2, subfamily c, polypeptide 70	NA	NA	NA	NA	
92907 at	0.043	6128	1448873 at	-0.019	7696	92907 at	0.022	6979	1448873 at	-0.240	4375	6294.5	1431.1936	FALSE	occludin	227492 at	0.181	15884	8.818E-02	FALSE
103340 at	-0.017	7954	1417049 at	-0.095	4300.5	103340 at	0.028	6686	1417049 at	0.080	6239	6294.875	1515.0719	FALSE	Rh blood group, D antigen	216317 x at	0.038	28802	5.133E-01	FALSE
96289 at	-0.086	4433	1448774 at	0.064	6185	96289 at	0.007	8103	1448774 at	0.069	6460	6295.25	1502.801	FALSE	stomatin (Epb7.2)-like 2	215416 s at	-0.104	19275	1.769E-01	FALSE
103808 at	-0.037	6593	1418447 at	-0.006	8273	103808 at	0.101	3514	1418447 at	-0.051	6804	6296	1999.5271	FALSE	golgi autoantigen, golgin subfamily a, 5	218241 at	0.103	17703	1.325E-01	FALSE
96549 at	0.043	6749	1420761 at	-0.008	8247	96549 at	-0.070	4750	1420761 at	-0.086	5440	6296.5	1542.1263	FALSE	cholinergic receptor, nicotinic, delta polypeptide	207024 at	0.023	34620	7.193E-01	FALSE
160567 at	0.016	7632	1448120 at	0.087	3453.5	160567 at	-0.026	6594	1448120 at	0.035	7509	6297.125	1951.4841	FALSE	growth differentiation factor 9	221314 at	-0.042	30278	5.664E-01	FALSE
104212 at	0.028	7459	1424353 at	-0.093	3932	104212 at	0.070	6437	1424353 at	-0.034	7361	6297.25	1642.6772	FALSE	leucine-rich PPR-motif containing	211615 s at	-0.348	5644	4.999E-04	FALSE
93787 f at	-0.054	6362	1448373 at	0.007	8347	93787 f at	0.109	4728	1448373 at	0.079	5755	6298	1523.4004	FALSE	mitochondrial ribosomal protein L18	217907 at	-0.066	24310	3.474E-01	FALSE
103756 at	0.004	8298	1435228 at	-0.082	4104	103756 at	-0.067	4782	1435228 at	-0.015	8013	6299.25	2164.3406	FALSE	cDNA sequence BC023829	NA	NA	NA	NA	
102380 s at	0.096	4310	1450209 at	0.038	6975.5	102380 s at	0.030	6895	1450209 at	-0.050	7017	6299.375	1327.2167	FALSE	homeo box D4	205522 at	0.087	20688	2.227E-01	FALSE
95059 at	-0.016	7947	1416186 at	-0.045	6450.5	95059 at	-0.015	7751	1416187 s at	-0.235	3061	6302.375	2260.6606	TRUE	proline-rich nuclear receptor coactivator 2	217779 s at	0.201	9389	7.271E-03	FALSE
160512 at	0.021	7479	1423678 at	0.047	6507	160512 at	-0.085	3356	1460087 at	-0.024	7878	6305	2048.5776	FALSE	cDNA sequence BC017643	218130 at	0.227	7014	1.601E-03	FALSE
160245 at	0.049	5736	1453013 at	-0.092	5032.5	160245 at	0.036	6882	1453013 at	-0.028	7579	6307.375	1140.0292	FALSE	RIKEN cDNA 1110034O07 gene	NA	NA	NA	NA	
103729 at	0.089	4528	1418153 at	0.007	8181.5	103729 at	0.000	8506	1418153 at	0.107	4016	6307.875	2363.8154	FALSE	laminin, alpha 1	227048 at	0.261	5401	4.002E-04	FALSE
98140 at	0.066	5951	1448261 at	-0.035	7184.5	98140 at	0.046	5145	1448261 at	0.047	6962	6310.625	944.45023	FALSE	cadherin 1	201131 s at	0.063	29757	5.485E-01	FALSE
96767 at	-0.048	5830	1451099 at	-0.025	7643	162079 at	0.069	4057	1451099 at	-0.040	7713	6310.75	1737.019	FALSE	membrane bound C2 domain containing protein	208858 s at	0.288	2686	1.358E-05	FALSE
102357 at	-0.031	6817	1454977 at	-0.004	8338	102357 at	0.026	7316	1442964 at	-0.258	2774	6311.25	2441.6633	FALSE	expressed sequence AU020772	36552 at	0.128	5336	3.756E-04	FALSE
95046 s at	-0.007	8126	1449940 a at	0.075	4402	95046 s at	-0.009	7861	1449940 a at	0.102	4856	6311.25	1954.3141	FALSE	eukaryotic translation initiation factor 2B, subunit 4 delta	209429 x at	0.124	7555	2.407E-03	FALSE
104574 at	0.027	7327	1415730 at	-0.037	6491	104574 at	-0.054	4924	1415730 at	-0.059	6511	6313.25	1004.723	FALSE	RIKEN cDNA 5730453I16 gene	217866 at	0.127	7185	1.847E-03	FALSE
94202 at	-0.026	7251	1427628 at	0.025	7493	94202 at	-0.036	6140	1445895 at	0.148	4376	6315	1420.5781	FALSE	T-cell receptor beta, variable 8.2	NA	NA	NA	NA	
96956 at	-0.137	2116	1416381 a at	0.015	7987	96956 at	0.040	7024	1416381 a at	-0.018	8144	6317.75	2844.59	FALSE	peroxiredoxin 5	222994 at	0.039	34662	7.206E-01	FALSE
92810 at	0.067	6581	1426410 at	-0.014	7996	92810 at	0.060	7100	1426410 at	-0.125	3603	6320	1903.2942	FALSE	pyruvate dehydrogenase kinase, isoenzyme 3	221957 at	-0.160	11684	2.267E-02	FALSE
98334 at	0.084	3099	1449903 at	0.016	7974	98334 at	-0.016	7474	1449903 at	0.056	6735	6320.5	2207.1473	FALSE	cytotoxic and regulatory T cell molecule	206914 at	0.002	43076	9.617E-01	FALSE
92354 at	-0.003	8363	1447945 at	-0.056	6396	92354 at	0.023	7071	1444073 at	-0.220	3453	6320.75	2078.7266	FALSE	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	209348 s at	0.286	6051	7.276E-04	FALSE
99583 at	-0.055	6666	1449575 a at	0.016	7927	99583 at	-0.071	5557	1449575 a at	0.133	5133	6320.75	1250.7732	FALSE	glutathione S-transferase, pi 1	200824 at	0.198	7510	2.325E-03	FALSE
93801 at	0.015	7793	1418173 at	0.055	5347.5	93801 at	0.026	6671	1418173 at	-0.094	5472	6320.875	1148.5915	FALSE	RIKEN cDNA 4631426H08 gene	237905 at	-0.042	27831	4.741E-01	FALSE
160978 at	0.069	5667	1451481 s at	0.034	6616	160978 at	-0.009	7901.5	1451481 s at	-0.095	5100	6321.125	1225.2295	FALSE	organic solute transporter alpha	229230 at	0.001	44110	9.868E-01	FALSE
102918 at	0.053	6231	1449199 at	0.088	4734	102918 at	-0.022	7333	1449199 at	0.070	6990	6322	1154.4652	FALSE	mucin 1, transmembrane	215927 at	0.064	17432	1.251E-01	FALSE
99168 at	0.058	4996	1433429 at	-0.062	5149	99168 at	-0.031	6914	1433429 at	0.011	8230	6322.25	1541.1179	FALSE	phosphatidylinositol glycan, class S	223148 at	-0.041	24735	3.631E-01	FALSE
160162 at	0.052	6081	1426529 a at	0.061	6093.5	160162 at	-0.041	5933	1426529 a at	-0.059	7190	6324.375	581.66877	FALSE	transgelin 2	200916 at	0.489	3611	5.334E-05	FALSE
98858 at	0.073	4766	1449908 at	0.096	4508	98858 at	0.017	7572	1449908 at	0.003	8452	6324.5	1984.1965	TRUE	gastric inhibitory polypeptide	207899 at	-0.011	37022	7.915E-01	FALSE
95684 at	0.039	6519	1415735 at	0.013	8022	95683 a at	-0.162	3819	1415735 at	-0.051	6946	6326.5	1787.2803	FALSE	damage specific DNA binding protein 1	208619 at	0.082	18606	1.581E-01	FALSE
100889 at	-0.038	6299	1460034 at	-0.082	4437.5	100889 at	-0.005	8180	1460034 at	-0.087	6396	6328.125	1528.5461	TRUE	sterile alpha motif domain containing 4B	229871 at	0.170	6877	1.433E-03	FALSE
102896 at	0.096	2584	1417790 at	0.038	6983	102896 at	-0.030	7287	1417790 at	0.004	8460	6328.5	2576.2806	FALSE	docking protein 1	211121 s at	0.129	6212	8.409E-04	FALSE
100671 at	0.051	6456	1422332 at	0.136	3300.5	100671 at	0.023	7568	1422332 at	-0.021	7996	6330.125	2121.4732	FALSE	interferon alpha family, gene 11	NA	NA	NA	NA	
97220 at	0.045	6560	1448307 at	0.013	8031.5	97220 at	0.109	3084	1448307 at	0.034	7646	6330.375	2252.1378	TRUE	Down syndrome critical region homolog 2 (human)	203405 at	-0.057	28585	5.049E-01	FALSE
102645 at	0.024	7715	1438045 at	-0.006	8348	102645 at	-0.153	2202	1438045 at	-0.046	7057	6330.5	2802.3479	FALSE	early endosome antigen 1	204841 s at	0.051	18623	1.585E-01	FALSE
96196 i at	-0.054	5779	1436049 at	0.013	7906	161187 f at	-0.028	6513	1436049 at	-0.151	5129	6331.75	1192.0927	FALSE	RIKEN cDNA 5730589K01 gene	217448 s at	-0.112	7848	2.962E-03	FALSE
104117 at	-0.065	6690	1449197 at	0.082	5037	104117 at	0.017	7945	1449197 at	0.086	5655	6331.75	1273.4843	FALSE	RIKEN cDNA 2310040A13 gene	227693 at	0.230	11019	1.734E-02	FALSE
99827 at	0.027	7406	1429999 at	-0.035	7205	99827 at	-0.016	7548	1429999 at	0.166	3170	6332.25	2112.8578	FALSE	RIKEN cDNA 4933403M19 gene	NA	NA	NA	NA	
160176 at	0.035	6618	1418229 s at	0.169	1813	160176 at	0.001	8495	1418228 at	0.007	8413	6334.75	3136.466	TRUE	histone cell cycle regulation defective interacting protein 5	218946 at	-0.047	35760	7.542E-01	FALSE
98420 at	0.018	7541	1459983 at	0.033	6998.5	98420 at	-0.011	7789	1459983 at	0.156	3015	6335.875	2238.3909	FALSE	inositol (myo)-1(or 4)-monophosphatase 2	203126 at	0.152	11560	2.157E-02	FALSE
97156 at	-0.012	7818	1422409 at	0.069	5400	97156 at	0.063	5463	1422409 at	-0.075	6665	6336.5	1146.4131	FALSE	hairy and enhancer of split 3 (Drosophila)	NA	NA	NA	NA	
96985 at	0.003	8408	1422385 at	0.024	7552.5	96985 at	-0.023	7301	1422385 at	0.247	2087	6337.125	2872.7616	FALSE	olfactory receptor 1264	NA	NA	NA	NA	
102648 at	0.018	7439	1420378 at	0.067	5231	102648 at	0.089	4399	1420378 at	0.012	8280	6337.25	1822.8853	TRUE	surfactant associated protein D	214199 at	0.007	41536	9.214E-01	FALSE
98286 at	0.043	7008	1450774 at	0.041	6265.5	98286 at	-0.055	4713	1450774 at	-0.040	7366	6338.125	1176.3737	FALSE	lymphocyte antigen 6 complex, locus G6D	207457 s at	-0.057	25258	3.818E-01	FALSE
94193 at	0.127	3270	1450490 at	0.020	7956.5	94193 at	0.033	6263	1450490 at	0.025	7867	6339.125	2189.0353	TRUE	potassium voltage-gated channel, shaker-related subfamily, member 7	232936 at	0.016	35017	7.308E-01	FALSE
104740 at	0.143	3475	1424427 at	-0.043	7244	104740 at	-0.011	7943	1459380 at	0.057	6701	6340.75	1976.9816	FALSE	transcriptional adaptor 1 (HFI1 homolog, yeast) like	225455 at	-0.115	19353	1.795E-01	FALSE
101083 s at	0.101	3018	1451884 a at	-0.029	7666	101083 s at	0.018	7210	1451884 a at	-0.031	7471	6341.25	2223.3619	FALSE	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	209449 at	0.105	15505	7.978E-02	FALSE
99349 at	0.060	4758	1421672 at	-0.011	8192	99349 at	-0.069	4006	1421672 at	0.005	8410	6341.5	2285.1021	FALSE	interleukin 17A	208402 at	-0.063	19179	1.743E-01	FALSE
98794 at	0.016	7663	1449287 at	0.133	4266.5	98794 at	0.063	5061	1449287 at	-0.004	8383	6343.375	1988.2468	FALSE	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	234514 at	0.045	30718	5.832E-01	FALSE
101537 at	0.064	5778	1416913 at	0.069	5107.5	101537 at	-0.006	8317	1416913 at	-0.081	6175	6344.375	1386.9124	FALSE	esterase 1	NA	NA	NA	NA	
97782 at	0.089	4991	1450554 at	0.044	6436	97782 at	0.050	6067	1450554 at	0.020	7887	6345.25	1196.7518	TRUE	defensin beta 2	NA	NA	NA	NA	
96708 at	-0.023	7425	1416108 a at	-0.055	7598.5	96708 at	0.119	4624	1441846 x at	0.093	5741	6347.125	1421.7713	FALSE	transmembrane emp24 domain containing 3	208837 at	0.106	17606	1.295E-01	FALSE
104485 at	-0.007	8260	1452523 a at	-0.001	8510	104485 at	-0.022	7422	1452523 a at	0.224	1198	6347.5	3464.3885	FALSE	RIKEN cDNA 4930527D15 gene	208094 s at	0.088	12620	3.286E-02	FALSE
101192 at	0.026	7131	1420348 at	0.112	3903	101192 at	-0.019	7403	1420348 at	0.054	6958	6348.75	1640.7556	FALSE	LIM homeobox protein 5	208333 at	-0.040	27030	4.440E-01	FALSE
160802 at	0.109	3600	1423703 at	-0.003	8421.5	160802 at	0.051	5162	1423703 at	-0.011	8212	6348.875	2361.6375	FALSE	peter pan homolog (Drosophila)	221649 s at	-0.040	32753	6.560E-01	FALSE
160595 at	-0.028	7129	1448555 at	-0.025	7571	160595 at	0.001	8478	1448555 at	-0.187	2223	6350.25	2808.2138	FALSE	DNA segment, Chr 15, ERATO Doi 682, expressed	218842 at	0.051	29953	5.555E-01	FALSE
99041 at	0.061	5129	1431345 a at	-0.037	6750	99041 at	-0.025	6603	1431345 a at	0.053	6923	6351.25	825.26213	FALSE	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, B	214690 at	0.080	8441	4.206E-03	FALSE
160801 at	-0.005	8204	1430125 s at	-0.061	5875	160801 at	-0.004	8241	1430125 s at	-0.169	3085	6351.25	2442.6107	TRUE	PO loop repeat containing 1	218208 at	-0.168	12530	3.164E-02	TRUE
93980 at	-0.038	7164	1426426 at	0.059	5706	93980 at	0.056	5566	1426426 at	-0.042	6971	6351.75	832.18923	FALSE	RNA binding motif protein 13	211686 s at	-0.213	6907	1.472E-03	FALSE
97053 at	0.093	5477	1422294 at	0.002	8462	97053 at	0.075	4296	1422294 at	0.048	7174	6352.25	1836.7131	TRUE	chemokine (C motif) receptor 1	221468 at	0.022	32577	6.493E-01	FALSE
97742 s at	-0.056	6228	1451882 a at	0.024	7575	97742 s at	-0.033	6913	1451882 a at	0.156	4695	6352.75	1234.4328	FALSE	fibroblast growth factor 8	208449 s at	0.045	22797	2.948E-01	FALSE
97001 r at	-0.034	6674	1460312 at	0.062	5987	97001 r at	0.016	7743	1460312 at	-0.088	5011	6353.75	1150.3708	FALSE	olfactory receptor 157	NA	NA	NA	NA	
103689 at	-0.050	5429	1428988 at	-0.001	8513.5	103689 at	-0.036	5908	1443206 at	0.096	5572	6355.625	1452.5259	FALSE	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	242553 at	0.145	7131	1.764E-03	FALSE
160852 at	0.023	7443	1422667 at	0.130	3009	160852 at	0.024	7564	1422667 at	-0.038	7414	6357.5	2233.2784	FALSE	keratin complex 1, acidic, gene 15	204734 at	0.048	20940	2.315E-01	FALSE
94531 at	0.000	8518	1428134 at	0.075	4990.5	94531 at	-0.086	5503	1440183 x at	-0.099	6422	6358.375	1556.7891	FALSE	coenzyme Q9 homolog (yeast)	235822 at	0.070	17047	1.156E-01	FALSE
160226 at	0.044	6251	1416570 s at	0.054	6014	160226 at	-0.020	6901	1416570 s at	0.070	6270	6359	379.63755	FALSE	G elongation factor, mitochondrial 1	225161 at	-0.149	16705	1.065E-01	FALSE
95490 at	-0.043	7043	1460211 a at	0.066	5285	95490 at	0.139	4757	1460211 a at	0.010	8354	6359.75	1650.0261	FALSE	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	200922 at	-0.074	19994	2.005E-01	FALSE
100924 at	0.022	7306	1448886 at	0.028	7492	100924 at	0.034	6288	1448886 at	-0.120	4357	6360.75	1436.8404	FALSE	GATA binding protein 3	209602 s at	-0.051	14590	6.289E-02	FALSE
102576 at	-0.004	8323	1419210 at	-0.056	5489	102576 at	0.020	7471	1419210 at	0.304	4168	6362.75	1884.2474	FALSE	histamine receptor H 1	216735 x at	0.087	18278	1.482E-01	FALSE
101388 at	0.044	6071	1416784 at	-0.029	7238	101388 at	-0.070	4131	1416784 at	0.019	8018	6364.5	1690.3381	FALSE	phosphoglycerate kinase 2	217009 at	0.022	32777	6.571E-01	FALSE
94178 at	-0.032	6699	1421586 a at	0.059	6136	94178 at	-0.005	8209	1421586 a at	0.145	4425	6367.25	1562.894	FALSE	CD46 antigen, complement regulatory protein	208783 s at	0.306	14080	5.392E-02	FALSE
98912 at	-0.069	6752	1434598 at	-0.097	4243.5	98912 at	0.022	7901.5	1434597 at	-0.061	6578	6368.75	1533.6967	FALSE	La ribonucleoprotein domain family, member 5	208954 s at	0.064	22077	2.708E-01	FALSE
101318 at	0.074	4711	1450527 at	0.027	7733	101318 at	0.066	4906	1450527 at	0.021	8127	6369.25	1811.1132	TRUE	somatostatin receptor 1	235591 at	-0.121	10326	1.217E-02	FALSE
99363 at	0.024	7304	1443317 at	0.038	6934	99363 at	0.057	5054	1443317 at	-0.071	6196	6372	992.06317	FALSE	DNA segment, Chr 6, ERATO Doi 47, expressed	NA	NA	NA	NA	
96236 at	0.028	7467	1425554 a at	-0.099	5539	96236 at	0.025	7114	1425554 a at	0.099	5373	6373.25	1071.0544	FALSE	CDC16 cell division cycle 16 homolog (S. cerevisiae)	209658 at	0.195	2733	1.450E-05	FALSE
104198 at	0.028	7344	1427095 at	0.009	8145	104198 at	0.111	2455	1427095 at	-0.033	7553	6374.25	2634.7639	FALSE	CUB domain containing protein 1	218451 at	0.117	10651	1.440E-02	FALSE
93337 at	0.040	7256	1417007 a at	-0.001	8503	93337 at	0.039	7556	1457067 at	0.218	2186	6375.25	2842.9461	FALSE	vacuolar protein sorting 4b (yeast)	218171 at	0.183	14914	6.912E-02	FALSE
94962 a at	-0.058	5820	1423447 at	0.010	8186	94961 at	-0.038	6218	1423447 at	-0.083	5280	6376	1266.4144	FALSE	Caseinolytic peptidase X (E.coli)	204809 at	0.073	23585	3.233E-01	FALSE
93002 r at	0.079	3859	1450989 at	0.033	6811	93002 r at	-0.012	8052	1450989 at	0.067	6783	6376.25	1779.4324	FALSE	teratocarcinoma-derived growth factor	NA	NA	NA	NA	
103240 f at	0.024	7405	1449846 at	0.075	4166	103240 f at	0.007	8131	1449846 at	-0.147	5806	6377	1765.2065	FALSE	eosinophil-associated, ribonuclease A family, member 2	NA	NA	NA	NA	
92607 at	-0.135	3633	1423294 at	-0.106	5810	92607 at	0.008	8037	1423294 at	0.019	8032	6378	2109.1583	FALSE	mesoderm specific transcript	202016 at	-0.189	14344	5.881E-02	FALSE
102167 at	0.015	7890	1422383 at	0.152	3037	102167 at	-0.033	6517	1422383 at	-0.018	8070	6378.5	2333.1387	FALSE	vomeronasal 1 receptor, B6	NA	NA	NA	NA	
103078 at	0.001	8435	1424726 at	0.118	2719	103078 at	0.030	6808	1424726 at	-0.031	7560	6380.5	2529.9229	FALSE	transmembrane protein 150	226239 at	0.053	24529	3.551E-01	FALSE
95381 at	0.057	6427	1425437 a at	-0.039	6699	95381 at	0.050	5239	1425437 a at	-0.047	7161	6381.5	819.71601	FALSE	potassium channel, subfamily K, member 7	224055 x at	0.022	32614	6.511E-01	FALSE
102875 at	-0.148	2420	1434563 at	0.003	8415	102875 at	-0.006	8338	1434563 at	-0.058	6356	6382.25	2808.1515	FALSE	ribosomal protein S6 kinase polypeptide 1	218909 at	-0.131	16542	1.027E-01	FALSE
160890 at	0.077	5337	1415829 at	-0.003	8444	160890 at	0.052	5433	1415829 at	-0.086	6316	6382.5	1443.24	FALSE	lamin B receptor	201795 at	0.428	2352	7.475E-06	FALSE
94053 at	0.067	6049	1423964 at	-0.084	4541	94053 at	0.023	7108	1423964 at	-0.030	7835	6383.25	1430.4369	FALSE	cleavage and polyadenylation specific factor 3-like	217994 x at	0.227	1867	3.072E-06	FALSE
98416 at	0.023	7159	1451233 at	0.059	5939.5	98416 at	0.038	5664	1451233 at	0.052	6773	6383.875	699.50606	TRUE	Tnf receptor-associated factor 2	204413 at	0.008	41535	9.214E-01	FALSE
104651 at	0.062	6310	1456039 at	0.064	6365.5	104651 at	0.081	4800	1456039 at	-0.017	8062	6384.375	1332.9863	FALSE	sorting nexin 14	230759 at	0.036	33092	6.683E-01	FALSE
94125 at	0.020	7273	1416236 a at	0.024	7183	94125 at	-0.036	6296	1416237 at	-0.122	4786	6384.5	1153.2662	FALSE	epithelial V-like antigen 1	203780 at	0.081	10363	1.234E-02	FALSE
97922 at	-0.132	4838	1426307 at	0.055	5773	97922 at	0.042	6467	1426307 at	-0.003	8467	6386.25	1539.3933	FALSE	cytochrome b5 reductase 4	219079 at	-0.113	15366	7.745E-02	FALSE
103200 at	-0.022	7754	1460555 at	0.028	7984	103200 at	-0.018	7195	1434359 at	-0.228	2612	6386.25	2537.8853	FALSE	RIKEN cDNA 6330500D04 gene	209829 at	-0.108	27384	4.576E-01	FALSE
101041 at	-0.010	7960	1460347 at	0.120	3764.5	101041 at	-0.010	7912	1455573 at	0.071	5914	6387.625	1991.7486	FALSE	keratin complex 1, acidic, gene 14	209351 at	-0.034	30157	5.615E-01	FALSE
94724 at	-0.017	7734	1420450 at	0.054	5881.5	94724 at	0.088	4351	1420450 at	0.043	7586	6388.125	1597.1674	FALSE	matrix metallopeptidase 10	205680 at	-0.038	26075	4.068E-01	FALSE
99186 at	0.098	4967	1417911 at	0.039	6713	99186 at	-0.013	7567	1417910 at	-0.102	6308	6388.75	1083.4059	FALSE	cyclin A2	213226 at	0.127	5470	4.334E-04	FALSE
102854 s at	0.109	4926	1418774 a at	0.047	5980	102854 s at	0.035	6958	1436921 at	-0.037	7699	6390.75	1203.8132	FALSE	ATPase, Cu++ transporting, alpha polypeptide	205197 s at	0.139	11989	2.582E-02	FALSE
97308 at	-0.034	6546	1454669 at	0.054	6572	97308 at	0.030	6207	1454669 at	0.083	6241	6391.5	194.20007	FALSE	transmembrane protein 11	203437 at	-0.009	37867	8.179E-01	FALSE
160095 at	0.029	6939	1448228 at	-0.046	5830	160095 at	0.017	7373	1448228 at	0.118	5425	6391.75	915.15076	FALSE	lysyl oxidase	215446 s at	0.056	18313	1.493E-01	FALSE
93538 at	-0.012	8179	1448706 at	-0.010	8153	93538 at	0.148	1836	1448706 at	-0.041	7400	6392	3058.741	FALSE	Traf and Tnf receptor associated protein	202266 at	-0.111	22559	2.869E-01	FALSE
95391 at	0.027	7261	1421774 at	0.052	6024.5	95391 at	-0.067	5092	1421774 at	0.044	7195	6393.125	1036.8255	FALSE	ventral anterior homeobox containing gene 1	NA	NA	NA	NA	
104660 at	0.029	7117	1418751 at	0.088	3939	104660 at	-0.025	7169	1418751 at	0.033	7356	6395.25	1640.7129	FALSE	suppression inducing transmembrane adaptor 1	205484 at	-0.006	42628	9.504E-01	FALSE
99954 at	0.043	6137	1451293 at	0.030	7302.5	99954 at	-0.073	4304	1451293 at	0.023	7841	6396.125	1565.6002	FALSE	RNA, U3 small nucleolar interacting protein 2	204133 at	-0.003	43155	9.640E-01	FALSE
94874 at	-0.030	6861	1416134 at	-0.070	5525	94874 at	0.036	6078	1416134 at	-0.059	7122	6396.5	730.9959	FALSE	amyloid beta (A4) precursor-like protein 1	209462 at	-0.245	10864	1.612E-02	FALSE
102035 at	0.042	5870	1419121 at	-0.034	7138	102035 at	0.010	7858	1419121 at	-0.105	4723	6397.25	1386.0744	FALSE	thiopurine methyltransferase	203672 x at	-0.297	2771	1.538E-05	FALSE
92722 f at	0.062	5312	1427277 at	-0.013	8086.5	92722 f at	-0.068	6044	1427277 at	-0.069	6148	6397.625	1185.783	FALSE	sine oculis-related homeobox 1 homolog (Drosophila)	230911 at	0.063	21752	2.598E-01	FALSE
94784 at	0.047	6893	1434850 at	0.043	6491	94784 at	0.058	4648	1459405 at	-0.040	7568	6400	1249.6744	FALSE	IQ motif containing GTPase activating protein 3	241939 at	-0.058	23073	3.037E-01	FALSE
103079 at	-0.057	7132	1426525 at	0.020	7814.5	103079 at	0.067	5437	1426525 at	0.083	5225	6402.125	1270.7754	FALSE	AT rich interactive domain 2 (Arid-rfx like)	225490 at	0.235	3271	3.312E-05	FALSE
98023 r at	0.001	8488	1460217 at	0.012	8054.5	98023 r at	0.035	5874	1460217 at	0.156	3192	6402.125	2426.5913	TRUE	proliferin related protein	NA	NA	NA	NA	
103710 at	-0.064	6033	1455433 at	0.041	7657	103710 at	-0.027	7503	1455433 at	-0.210	4417	6402.5	1512.5708	FALSE	hypothetical protein LOC383216	NA	NA	NA	NA	
96367 at	0.003	8405	1427163 at	-0.049	6544	96367 at	-0.052	5403	1427163 at	-0.167	5260	6403	1453.0811	FALSE	Ubiquitin protein ligase E3 component n-recognin 2	212756 s at	0.059	21840	2.626E-01	FALSE
101144 at	0.096	5324	1421628 at	-0.007	8325.5	101144 at	-0.094	3737	1421628 at	-0.012	8226	6403.125	2257.6634	FALSE	interleukin 18 receptor 1	206618 at	-0.004	42484	9.462E-01	FALSE
101971 at	0.011	8137	1423729 a at	0.059	5130	101971 at	0.075	6512	1423729 a at	0.081	5834	6403.25	1286.1994	TRUE	RIKEN cDNA 2500002L14 gene	223064 at	-0.006	42923	9.581E-01	FALSE
96905 at	-0.154	1650	1418444 a at	-0.007	8303.5	96905 at	0.017	7447	1418444 a at	0.012	8220	6405.125	3193.4473	FALSE	membrane interacting protein of RGS16	202593 s at	-0.495	5197	3.358E-04	FALSE
92593 at	0.026	7448	1423606 at	-0.025	7619	92593 at	0.035	6918	1423606 at	-0.186	3640	6406.25	1868.1571	FALSE	periostin, osteoblast specific factor	228481 at	-0.030	28143	4.864E-01	FALSE
94696 at	-0.017	7529	1421655 a at	-0.035	6877	94696 at	-0.046	5456	1421655 a at	0.078	5764	6406.5	965.68335	FALSE	chemokine (C-C motif) receptor 4	208376 at	0.030	35064	7.323E-01	FALSE

96568 at	-0.076	5274	1420739 at	-0.019	7838	96568 at	-0.015	7825	1440657 at	-0.213	4702	6409.75	1658.2288	TRUE	contactin 3	229831 at	0.151	28648	5.074E-01	FALSE
103017 at	0.073	4128	1423164 at	0.001	8506	103017 at	0.024	7137	1423164 at	0.073	5869	6410	1863.8625	TRUE	similar to transmembrane 7 superfamily member 1		NA	NA	NA	NA
100713 at	-0.169	3807	1449546 a at	-0.010	8221	100713 at	-0.036	6852	1449546 a at	0.063	6764	6411	1859.7496	FALSE	zinc finger protein 617	219854 at	0.019	36061	7.642E-01	FALSE
160434 at	0.057	6599	1448867 at	0.050	6308.5	160434 at	-0.031	7324	1448867 at	0.076	5426	6414.375	785.19609	FALSE	TMEM9 domain family, member B	218065 s at	0.172	9493	7.768E-03	FALSE
100081 at	-0.029	7572	1415909 at	0.041	6225	100081 at	-0.045	6912	1415909 at	0.139	4956	6416.25	1118.0985	FALSE	stress-induced phosphoprotein 1	213330 s at	0.128	20968	2.324E-01	FALSE
102029 at	0.059	6981	1417391 a at	-0.015	8009.5	102029 at	-0.016	7869	1448686 at	-0.146	2808	6416.875	2448.628	FALSE	interleukin 16	209827 s at	0.052	27789	4.721E-01	FALSE
100719 f at	0.078	4540	1420490 at	0.007	8296	100719 f at	0.078	4427	1420490 at	0.007	8405	6417	2233.5334	TRUE	kallikrein 1-related peptidase b16		NA	NA	NA	NA
97384 at	0.001	8455	1419193 a at	0.082	3512	97384 at	0.009	8045	1419193 a at	-0.084	5662	6418.5	2295.8563	FALSE	glia maturation factor, gamma	204220 at	0.067	24218	3.447E-01	FALSE
93509 at	-0.032	7509	1423107 at	0.048	6992.5	93509 at	0.027	7196	1430177 at	-0.839	3984	6420.375	1638.0831	FALSE	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	202334 s at	-0.312	2717	1.401E-05	FALSE
102001 at	0.020	7787	1434437 x at	0.086	5341.5	102001 at	0.068	5521	1448226 at	-0.047	7034	6420.875	1185.6145	FALSE	ribonucleotide reductase M2	201890 at	0.033	27555	4.638E-01	FALSE
92352 at	0.001	8481	1460661 at	0.008	8271	92352 at	-0.037	6487	1437173 at	0.258	2454	6423.25	2793.297	FALSE	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	228176 at	0.445	5123	3.114E-04	FALSE
103476 at	0.004	8354	1454796 at	0.041	6333.5	103476 at	-0.084	2768	1454796 at	0.013	8246	6425.375	2608.9016	FALSE	DNA segment, Chr 5, ERATO Doi 40, expressed	219910 at	0.149	4559	1.645E-04	FALSE
161214 r at	-0.111	4927	1454820 at	-0.002	8443	103738 at	0.051	5255	1454820 at	-0.042	7084	6427.25	1645.1432	FALSE	cDNA sequence BC037034	220659 s at	-0.015	39406	8.616E-01	FALSE
92987 at	-0.084	5498	1418485 at	-0.002	8463	92987 at	0.119	4759	1418485 at	-0.080	6994	6428.5	1644.3885	FALSE	solute carrier family 4 (anion exchanger), member 3	205918 at	-0.731	809	2.801E-07	FALSE
96955 at	0.044	6002	1448211 at	-0.028	7441.5	96955 at	0.013	7638	1448211 at	0.098	4638	6429.875	1399.6243	FALSE	ATPase, H+ transporting, lysosomal V0 subunit E2	213587 s at	-0.076	27549	4.636E-01	FALSE
97659 r at	0.069	4333	1422447 at	-0.026	7537	97658 f at	-0.048	5774	1422447 at	-0.019	8076	6430	1709.0455	FALSE	insulin I		NA	NA	NA	NA
103328 at	0.071	7075	1421640 a at	0.040	6754	103328 at	-0.149	4763	1459668 at	0.056	7131	6430.75	1124.1721	FALSE	TRAF family member-associated Nf-kappa B activator	207616 s at	-0.093	10448	1.291E-02	FALSE
92746 at	0.062	5483	1449981 a at	0.078	5215	92746 at	-0.012	7838	1449981 a at	-0.087	7188	6431	1281.9332	FALSE	N-acetyltransferase 2 (arylamine N-acetyltransferase)	214440 at	0.043	21373	2.460E-01	FALSE
97652 at	0.042	6458	1427611 at	0.063	6553.5	97652 at	-0.013	7762	1427611 at	-0.127	4962	6433.875	1146.7671	FALSE	growth hormone releasing hormone receptor	211545 at	-0.024	33593	6.856E-01	FALSE
96620 at	-0.005	8345	1417550 a at	0.018	7913	96620 at	0.019	7670	1417550 a at	0.173	1809	6434.25	3096.1095	FALSE	germ cell-specific gene 1	241553 at	-0.035	30538	5.770E-01	FALSE
101025 f at	0.009	8158	1439016 x at	0.109	3760	101025 f at	-0.028	7542	1450618 a at	0.115	6278	6434.5	1947.1733	FALSE	small proline-rich protein 2A	236119 s at	-0.031	28522	5.025E-01	FALSE
103201 at	0.054	6230	1449171 at	0.061	6739	103201 at	0.042	6101	1449171 at	-0.055	6672	6435.5	317.36677	FALSE	Ttk protein kinase	204822 at	-0.013	36880	7.882E-01	FALSE
161455 r at	-0.013	8062	1429528 at	0.018	7720	160466 at	-0.170	2399	1444256 at	-0.032	7564	6436.25	2699.5237	FALSE	RAE1 RNA export 1 homolog (S. pombe)	211318 s at	-0.047	27681	4.684E-01	FALSE
94663 at	0.021	7382	1440874 at	0.057	5941.5	94663 at	0.071	4634	1439588 at	0.028	7794	6437.875	1441.157	TRUE	solute carrier organic anion transporter family, member 5A1	220984 s at	-0.090	19114	1.723E-01	FALSE
161958 at	0.013	7762	1417364 at	-0.033	7278	161958 at	-0.109	3693	1458955 at	0.050	7019	6438	1855.7265	FALSE	Eukaryotic translation elongation factor 1 gamma	241164 at	-0.064	13446	4.307E-02	FALSE
160410 at	-0.001	8442	1416254 a at	-0.031	7163.5	160410 at	-0.051	4960	1416254 a at	-0.105	5195	6440.125	1660.5101	TRUE	vacuolar protein sorting 16 (yeast)	203459 s at	0.100	15759	8.533E-02	FALSE
100884 at	0.077	5452	1448894 at	0.075	4800	100884 at	-0.009	7836	1448894 at	-0.029	7676	6441	1542.9681	FALSE	aldo-keto reductase family 1, member B8		NA	NA	NA	NA
102693 f at	0.029	7186	1419090 x at	0.104	3528	102693 f at	0.021	7501	1419090 x at	0.029	7565	6445	1951.7092	TRUE	kallikrein 1-related petidase b26		NA	NA	NA	NA
162153 i at	0.017	7881	1417167 at	-0.021	7557.5	162153 i at	-0.032	6281	1417167 at	0.160	4074	6448.375	1727.0634	FALSE	exosome component 5	218481 at	-0.172	2666	1.310E-05	FALSE
93139 at	0.040	6309	1418490 at	-0.019	7818	93139 at	-0.056	5135	1418490 at	0.123	6532	6448.5	1099.5825	FALSE	serine dehydratase-like	228274 at	0.225	1938	3.416E-06	FALSE
101693 f at	0.121	4025	1447997 s at	0.022	7452	101693 f at	0.028	7110	1447997 s at	-0.040	7222	6452.25	1624.4171	FALSE	translocase of inner mitochondrial membrane 8 homolog a2 (yeast)		NA	NA	NA	NA
93077 s at	0.010	7932	1421571 a at	-0.008	8323	93077 s at	0.017	7244	1421571 a at	-0.415	2313	6453	2795.8077	FALSE	lymphocyte antigen 6 complex, locus C		NA	NA	NA	NA
99843 at	0.044	6404	1449917 at	0.017	8002	99843 at	0.013	7938	1449917 at	0.121	3469	6453.25	2122.2066	TRUE	paired-like homeodomain transcription factor 3	208277 at	0.021	38219	8.280E-01	FALSE
100451 at	-0.022	7287	1424622 at	-0.010	8112	100451 at	-0.093	3424	1424622 at	-0.066	7006	6457.25	2075.9267	TRUE	heat shock factor 1	202344 at	0.090	16954	1.127E-01	FALSE
95012 at	0.010	8106	1448209 a at	-0.061	6177	95012 at	-0.120	4290	1448209 a at	0.045	7257	6457.5	1646.561	FALSE	solute carrier family 22 (organic cation transporter), member 17	218675 at	-0.257	5656	5.042E-04	FALSE
99811 at	0.037	6834	1422347 at	0.061	6003	99811 at	0.042	5496	1438086 at	-0.038	7499	6458	886.4773	FALSE	neuropeptide Y receptor Y6		NA	NA	NA	NA
95346 at	0.003	8390	1426137 at	0.064	5990.5	95346 at	-0.013	7500	1426137 at	-0.121	3952	6458.125	1942.2479	FALSE	reduced expression 2		NA	NA	NA	NA
95893 at	0.082	5024	1422775 at	0.090	5428	92359 at	-0.039	6915	1422775 at	0.003	8472	6459.75	1568.6819	FALSE	B lymphoid kinase	244394 at	-0.041	26469	4.237E-01	FALSE
102213 at	0.038	6821	1419220 at	0.004	8419	102213 at	0.100	2820	1419220 at	0.023	7781	6460.25	2514.1362	TRUE	cardiomyopathy associated 1	235042 at	-0.002	43669	9.763E-01	FALSE
96087 at	0.095	3109	1423609 a at	-0.011	8045.5	96087 at	0.027	6408	1423609 a at	-0.008	8284	6461.625	2385.5594	FALSE	mannoside acetylglucosaminyltransferase 1	201126 s at	0.158	5733	5.426E-04	FALSE
104699 at	-0.071	5648	1425580 a at	-0.101	4367	104699 at	-0.034	7441	1425580 a at	0.007	8391	6461.75	1801.0277	FALSE	phosphoinositide-3-kinase, class 3	232086 at	-0.288	3423	4.177E-05	FALSE
93611 at	0.040	6399	1449868 at	0.063	5647	93611 at	0.040	6641	1449868 at	-0.049	7163	6462.5	630.24731	FALSE	T-box 6	215122 at	0.040	25440	3.875E-01	FALSE
103593 at	0.136	3958	1456062 at	0.022	7285	103593 at	-0.017	7547	1456062 at	-0.050	7065	6463.75	1682.0787	FALSE	natriuretic peptide precursor type A	209957 s at	-0.001	44235	9.899E-01	FALSE
101073 at	0.010	8068	1448655 at	-0.039	6689.5	101073 at	-0.013	7903	1448655 at	-0.140	3200	6465.125	2261.8634	FALSE	low density lipoprotein receptor-related protein 1	200785 s at	-0.046	27149	4.483E-01	FALSE
93376 at	-0.009	8095	1437419 at	-0.034	7326	93376 at	0.000	8510	1437419 at	-0.387	1930	6465.25	3063.0307	FALSE	BMP2 inducible kinase	226853 at	0.583	1468	1.321E-06	FALSE
92335 at	0.075	4186	1418061 at	0.063	5611	92335 at	0.004	8236	1418061 at	-0.032	7834	6466.75	1909.0789	FALSE	latent transforming growth factor beta binding protein 2	204682 at	0.088	21705	2.582E-01	FALSE
104446 f at	-0.069	6337	1426253 at	0.035	7431	104446 f at	-0.049	5206	1443403 at	-0.051	6895	6467.25	952.10307	FALSE	RIKEN cDNA 4933428G09 gene	235259 at	0.274	4082	9.391E-05	FALSE
96757 at	0.090	3202	1449000 at	0.037	6860.5	96757 at	-0.017	7653	1449000 at	0.014	8167	6470.625	2244.3715	FALSE	DNA segment, Chr 10, Johns Hopkins University 81 expressed	210667 s at	-0.083	22565	2.871E-01	FALSE
94331 at	0.050	5746	1421708 a at	0.061	6185	94331 at	0.055	6732	1421708 a at	0.046	7220	6470.75	642.01317	TRUE	signal transducer and activator of transcription 6	201332 s at	-0.103	15561	8.112E-02	FALSE
101772 r at	-0.012	7854	1425613 at	0.072	5341.5	101772 r at	0.021	7645	1425613 at	0.106	5051	6472.875	1481.3419	FALSE	protocadherin alpha 11		NA	NA	NA	NA
98871 at	0.034	6603	1420581 at	0.106	3944.5	98871 at	-0.002	8440	1420581 at	-0.056	6906	6473.375	1867.8677	FALSE	G protein-coupled receptor 143	206696 at	-0.015	38204	8.277E-01	FALSE
100753 at	0.019	7759	1423111 at	-0.089	4610.5	100753 at	0.014	7725	1420037 at	0.116	5800	6473.625	1543.0634	FALSE	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	213738 s at	-0.321	7611	2.492E-03	FALSE
96038 at	0.011	8051	1422603 at	0.022	7972	96038 at	-0.054	5507	1422603 at	-0.181	4367	6474.25	1835.3447	FALSE	ribonuclease, RNase A family 4	213397 x at	0.578	2110	4.610E-06	FALSE
104681 at	-0.020	7283	1421143 at	-0.036	7228.5	104681 at	-0.066	5420	1437821 at	0.111	5968	6474.875	929.28291	FALSE	diaphanous homolog 1 (Drosophila)	209190 s at	-0.166	5746	5.520E-04	FALSE
104443 at	0.040	6714	1423466 at	0.027	7641	104443 at	0.020	7427	1423466 at	-0.116	4120	6475.5	1619.5684	FALSE	chemokine (C-C motif) receptor 7	206337 at	-0.077	23517	3.209E-01	FALSE
102139 at	-0.038	6922	1420105 at	-0.072	4792	102139 at	-0.058	5858	1420105 at	0.009	8332	6476	1512.3307	FALSE	DNA segment, Chr 13, ERATO Doi 205, expressed		NA	NA	NA	NA
94190 at	0.163	2396	1420782 at	-0.018	8053	94190 at	-0.001	8466	1420782 at	0.050	6993	6477	2790.5026	FALSE	tumor necrosis factor receptor superfamily, member 17	206641 at	-0.043	25841	3.983E-01	FALSE
104072 at	0.057	5219	1419059 at	0.019	7726	104072 at	-0.032	6364	1419059 at	-0.065	6605	6478.5	1028.22	FALSE	serum amyloid P-component	206350 at	-0.012	39422	8.621E-01	FALSE
94188 at	0.111	2288	1451023 at	0.028	7281	94188 at	0.008	8133	1451023 at	-0.013	8216	6479.5	2826.1027	FALSE	hyperpolarization-activated, cyclic nucleotide-gated K+ 3	228741 s at	-0.098	13269	4.080E-02	FALSE
102785 at	0.067	4998	1418477 at	-0.001	8511	102785 at	0.056	5104	1418477 at	0.040	7310	6480.75	1722.7457	FALSE	matrilin 1, cartilage matrix protein 1	206905 s at	0.024	31979	6.305E-01	FALSE
102931 at	0.038	6901	1448386 a at	0.075	4256	102931 at	0.029	6587	1448386 a at	0.014	8182	6481.5	1636.2214	TRUE	whey acidic protein		NA	NA	NA	NA
103737 at	-0.023	7369	1418753 at	0.096	3419	103737 at	-0.009	7862	1418753 at	0.033	7279	6482.25	2058.1826	FALSE	glutamine fructose-6-phosphate transaminase 2	205100 at	0.140	13912	5.087E-02	FALSE
94089 at	0.105	3537	1444160 at	0.037	7247.5	94089 at	0.018	7261	1444160 at	-0.031	7889	6483.625	1987.0828	FALSE	Polycystic kidney disease 1 like 3		NA	NA	NA	NA
101123 at	-0.020	7821	1418000 a at	-0.072	5560	101123 at	-0.015	7972	1418001 at	-0.104	4585	6484.5	1679.4532	TRUE	integral membrane protein 2B	217731 s at	0.139	8837	5.299E-03	FALSE
103259 at	0.045	5934	1417679 at	0.033	7066.5	103259 at	0.015	7722	1417679 at	-0.115	5217	6484.875	1122.458	FALSE	growth factor independent 1	206589 at	-0.014	39399	8.615E-01	FALSE
96838 at	-0.051	5962	1418779 at	-0.010	7963	96838 at	-0.072	3734	1418779 at	-0.009	8282	6485.25	2102.0009	TRUE	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	205333 s at	-0.063	27407	4.581E-01	FALSE
104172 at	0.069	5798	1451648 a at	0.035	6819	104172 at	-0.037	6662	1451648 a at	-0.052	6667	6486.5	464.74688	FALSE	folate receptor 2 (fetal)	229619 at	0.045	26661	4.303E-01	FALSE
99906 at	0.085	4348	1420602 a at	0.036	7073	99906 at	0.028	7161	1420602 a at	0.035	7371	6488.25	1432.2992	TRUE	extraembryonic, spermatogenesis, homeobox 1		NA	NA	NA	NA
92318 at	-0.039	6330	1430297 a at	0.054	6124	92318 at	-0.044	5353	1419773 at	-0.013	8148	6488.75	1183.3966	FALSE	RIKEN cDNA 2010301N04 gene	241379 at	-0.027	26269	4.144E-01	FALSE
96962 at	-0.052	6785	1416546 a at	-0.001	8512	96962 at	0.121	2348	1416546 a at	-0.008	8315	6490	2867.1878	FALSE	ribosomal protein L6	200034 s at	-0.155	10443	1.290E-02	FALSE
97165 r at	-0.014	7741	1458414 at	0.086	4862	97165 r at	-0.097	5367	1458414 at	-0.022	7991	6490.25	1605.1495	FALSE	DNA segment, Chr 2, ERATO Doi 93, expressed		NA	NA	NA	NA
160855 at	-0.024	7114	1434345 at	0.030	7653.5	160855 at	0.057	4605	1434345 at	-0.061	6594	6491.625	1330.055	FALSE	transmembrane protein 12	229777 at	0.003	43505	9.724E-01	FALSE
93680 at	-0.023	7135	1417751 at	0.005	8366.5	93680 at	-0.039	5757	1459736 at	0.165	4716	6493.625	1593.904	FALSE	serine/threonine kinase 10	40420 at	0.151	4391	1.345E-04	FALSE
104292 at	0.125	2479	1424127 at	-0.012	8063	104292 at	0.000	8523	1445755 at	-0.050	6920	6496.25	2761.6591	FALSE	eyes absent 2 homolog (Drosophila)	209692 at	0.262	4633	1.817E-04	FALSE
94154 at	0.025	7323	1450790 at	0.050	6778	94154 at	-0.035	6693	1450790 at	0.103	5200	6498.5	909.55172	FALSE	thyroglobulin	244492 at	-0.056	21564	2.522E-01	FALSE
99479 at	-0.092	4253	1418287 a at	0.036	7481	99479 at	0.040	6803	1418287 a at	0.041	7458	6498.75	1529.8079	FALSE	deleted in malignant brain tumors 1	208250 s at	0.001	44198	9.888E-01	FALSE
95695 at	0.006	8227	1423109 s at	0.024	7787	95695 at	0.001	8448	1423109 s at	-0.255	1535	6499.25	3320.8847	FALSE	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	203658 at	0.175	6166	8.031E-04	FALSE
97757 at	0.058	5253	1420359 at	0.077	5431	97757 at	0.017	7809	1420359 at	-0.030	7504	6499.25	1344.0318	FALSE	seminal vesicle antigen		NA	NA	NA	NA
93556 at	0.058	5730	1427365 at	-0.067	6604	93555 at	0.034	6474	1427118 at	0.042	7203	6502.75	605.13655	FALSE	keratin complex 2, basic, gene 10	215189 at	0.010	39748	8.710E-01	FALSE
100568 at	0.065	6320	1416014 at	0.060	6040	100568 at	0.008	8132	1416014 at	-0.091	5521	6503.25	1135.1685	FALSE	ATP-binding cassette, sub-family E (OABP), member 1	201873 s at	-0.194	13422	4.279E-02	FALSE
96787 at	0.089	4117	1424758 s at	0.032	7106	96787 at	-0.016	7455	1424758 s at	0.036	7339	6504.25	1598.1029	FALSE	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	220626 at	-0.027	35308	7.405E-01	FALSE
103047 at	0.010	8125	1420711 a at	0.015	8132.5	103047 at	0.031	7084	1420711 a at	-0.199	2676	6504.375	2599.3356	FALSE	peroxisomal membrane protein 3	210296 s at	0.058	32070	6.338E-01	FALSE
93591 at	0.029	7202	1448644 at	-0.029	6844	93591 at	-0.077	4066	1448644 at	0.022	7908	6505	1685.0183	FALSE	penta-EF hand domain containing 1	217923 at	-0.180	13098	3.833E-02	FALSE
97372 at	-0.008	8268	1419275 at	-0.041	6805	97372 at	0.080	3195	1419275 at	-0.027	7754	6505.5	2288.6873	FALSE	DAZ associated protein 1	229813 x at	0.264	2405	8.187E-06	FALSE
101604 at	0.014	7752	1446379 at	-0.057	5957	101604 at	0.037	5763	1446379 at	-0.081	6562	6508.5	896.11699	FALSE	expressed sequence C79296		NA	NA	NA	NA
160576 at	0.003	8389	1452697 at	0.056	6282	160576 at	0.012	7668	1452697 at	-0.120	3710	6512.25	2062.6495	FALSE	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	205035 at	0.097	13673	4.638E-02	FALSE
101864 at	0.022	7264	1424678 at	-0.012	8050	101864 at	-0.012	7816	1424678 at	0.198	2921	6512.75	2417.0673	FALSE	actin-like 7b	220498 at	0.006	41248	9.143E-01	FALSE
99950 at	-0.022	7246	1426469 a at	0.054	5747	99950 at	-0.021	7275	1426470 at	-0.083	5791	6514.75	861.38662	FALSE	TATA box binding protein	203135 at	0.022	35393	7.432E-01	FALSE
95693 at	0.023	7331	1450048 a at	0.057	6168	95693 at	0.010	7826	1450048 a at	-0.132	4737	6515.5	1374.3203	FALSE	isocitrate dehydrogenase 2 (NADP+), mitochondrial	210046 s at	-0.083	25671	3.935E-01	FALSE
160366 at	-0.116	4989	1415752 at	0.055	6789.5	160366 at	0.053	6273	1415752 at	-0.018	8012	6515.875	1252.1443	FALSE	cDNA sequence BC031181		NA	NA	NA	NA
98137 at	0.052	5495	1419525 at	0.112	4314	98137 at	0.016	7806	1419525 at	0.003	8451	6516.5	1940.7532	TRUE	carbonic anhydrase 5a, mitochondrial	207421 at	-0.053	26279	4.151E-01	FALSE
94440 at	0.101	2650	1435007 s at	-0.024	7255.5	94440 at	0.013	7925	1435007 s at	-0.016	8238	6517.125	2610.4518	FALSE	expressed sequence AI132487	237765 at	0.019	35126	7.342E-01	FALSE
103509 at	0.050	5522	1421481 at	0.063	6423	97683 at	-0.030	6180	1460469 at	0.021	7947	6518	1025.886	FALSE	tumor necrosis factor receptor superfamily, member 9	211786 at	-0.028	26314	4.167E-01	FALSE
95467 at	0.120	5161	1416267 at	-0.019	8253.5	95467 at	0.057	6826	1416267 at	-0.108	5832	6518.125	1343.9828	FALSE	short coiled-coil protein	223341 s at	-0.587	7237	1.909E-03	FALSE
92803 at	-0.019	7775	1429287 a at	-0.663	5694.5	92803 at	0.009	7934	1429287 a at	-0.262	4672	6518.875	1599.0591	FALSE	prolactin	205445 at	-0.037	31352	6.074E-01	FALSE
96245 at	0.016	7480	1423815 at	-0.014	7985	96245 at	0.031	6308	1423815 at	0.135	4304	6519.25	1635.382	FALSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	217754 at	0.035	26926	4.407E-01	FALSE
94108 at	0.116	3743	1421704 a at	-0.003	8425	94108 at	-0.015	7559	1421704 a at	0.071	6363	6522.5	2036.7375	FALSE	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide	215129 at	0.006	41554	9.223E-01	FALSE
102631 at	0.100	4050	1448953 at	0.041	6928	102631 at	-0.037	6606	1448953 at	0.001	8516	6525	1849.2049	FALSE	Bloom syndrome homolog (human)	205733 at	0.001	44260	9.903E-01	FALSE
104449 at	0.058	5786	1422504 at	-0.101	5964	104449 at	-0.020	7513	1459850 x at	0.069	6838	6525.25	803.10953	FALSE	glycine receptor, beta subunit	205279 s at	-0.896	1896	3.221E-06	FALSE
93752 at	-0.017	7836	1452154 at	-0.085	3740	93752 at	-0.015	7993	1426705 s at	0.058	6537	6526.5	1968.9341	FALSE	isoleucine-tRNA synthetase	204744 s at	-0.349	4285	1.190E-04	FALSE
97917 at	-0.028	7365	1422614 s at	0.184	2426	97917 at	0.002	8465	1422614 s at	-0.033	7861	6529.25	2772.2328	FALSE	biogenesis of lysosome-related organelles complex-1, subunit 1	202592 at	0.119	14938	6.970E-02	FALSE
160985 at	-0.020	7366	1453265 at	-0.040	6364	160985 at	0.038	6647	1429721 s at	-0.076	5742	6529.75	673.56879	FALSE	RIKEN cDNA 4930579C15 gene		NA	NA	NA	NA
99377 at	0.004	8357	1453644 at	0.093	3906	99377 at	0.039	5855	1453644 at	0.019	8001	6529.75	2069.0393	TRUE	odorant binding protein Ia		NA	NA	NA	NA
95294 at	0.018	7755	1419789 at	-0.004	8406	95294 at	-0.065	4084	1419789 at	-0.068	5875	6530	1952.0879	FALSE	Centaurin, gamma 1		NA	NA	NA	NA
97679 at	-0.031	7090	1421770 a at	-0.022	7443	97679 at	-0.042	6275	1421770 a at	-0.085	5315	6530.75	946.64614	TRUE	T-cell leukemia, homeobox 2	207410 s at	-0.038	23271	3.111E-01	FALSE
96092 at	0.038	6762	1448881 at	-0.089	4127	96092 at	0.023	7104	1448881 at	-0.021	8134	6531.75	1705.9223	FALSE	haptoglobin	208470 s at	0.289	10205	1.131E-02	FALSE
103903 at	-0.020	7427	1433881 at	0.084	3848	103903 at	0.001	8452	1433881 at	-0.055	6400	6531.75	1975.5763	FALSE	DnaJ (Hsp40) homolog, subfamily C, member 11	215792 s at	-0.097	10937	1.667E-02	FALSE
99462 at	-0.053	7122	1448458 at	-0.032	7080	99462 at	-0.077	6584	1456688 at	0.097	5346	6533	828.1908	FALSE	topoisomerase (DNA) II beta	211987 at	0.152	18010	1.409E-01	FALSE
102554 at	0.095	4525	1422382 at	-0.022	7750	102554 at	0.031	6657	1422382 at	0.049	7204	6534	1411.7089	FALSE	olfactory receptor 16		NA	NA	NA	NA
101968 at	0.038	6873	1422585 at	0.042	7111	101968 at	0.042	6071	1422585 at	0.060	6083	6534.5	537.15888	TRUE	outer dense fiber of sperm tails 1	214485 at	-0.031	31573	6.155E-01	FALSE
103581 at	0.060	5762	1449065 at	-0.039	6774.5	103581 at	-0.083	5107	1449065 at	-0.003	8497	6535.125	1476.8793	FALSE	acyl-CoA thioesterase 1		NA	NA	NA	NA
98832 at	0.042	7064	1420600 at	0.008	8269	98832 at	-0.054	6050	1420600 at	-0.097	4763	6536.5	1490.1674	FALSE	thyroid peroxidase	210342 s at	-0.029	31906	6.277E-01	FALSE
98850 at	0.022	7557	1420753 at	-0.013	8027	98850 at	0.039	6382	1420753 at	-0.135	4183	6537.25	1715.2105	FALSE	tolloid-like	206415 at	-0.025	26453	4.226E-01	FALSE
100932 at	0.076	4574	1417228 at	-0.019	7627.5	100932 at	-0.024	7063	1417229 at	0.059	6891	6538.875	1347.1621	FALSE	calpain 1	232012 at	0.091	8461	4.247E-03	FALSE
93096 at	0.109	3915	1416025 at	0.049	5948.5	93096 at	0.008	8035	1416025 at	0.014	8259	6539.375	2035.5574	TRUE	fibrinogen, gamma polypeptide	219612 s at	0.009	38255	8.297E-01	FALSE
98598 at	-0.074	5487	1458854 at	0.044	6579	98598 at	0.027	7064	1458854 at	-0.051	7032	6540.5	736.42583	FALSE	expressed sequence C78891		NA	NA	NA	NA
93228 at	0.042	6097	1417541 at	0.010	8181.5	93228 at	0.054	4594	1430139 at	0.048	7291	6540.875	1553.6715	TRUE	helicase, lymphoid specific	220085 at	0.076	18853	1.651E-01	FALSE
92653 at	-0.075	4198	1437917 at	-0.049	6866	92653 at	0.021	7022	1437917 at	0.024	8086	6543	1654.6544	FALSE	RIKEN cDNA D530037H12 gene		NA	NA	NA	NA
103608 at	0.020	7636	1439406 x at	0.033	6900	103608 at	-0.046	5845	1431354 a at	-0.084	5794	6543.75	888.87583	FALSE	phenylalanine-tRNA synthetase 2 (mitochondrial)	204283 at	-0.150	5753	5.589E-04	FALSE
160850 at	0.009	8150	1460673 at	0.036	7020	160850 at	0.128	2967	1460673 at	-0.016	8042	6544.75	2438.9029	FALSE	folylpolyglutamyl synthetase	202945 at	0.101	16149	9.422E-02	FALSE
104541 at	0.032	6916	1419669 at	-0.005	8378	104541 at	0.098	4284	1419669 at	-0.080	6601	6544.75	1694.3816	FALSE	proteinase 3	207341 at	-0.036	29951	5.555E-01	FALSE
100559 at	0.058	5607	1423925 at	-0.030	7639	100559 at	0.004	8381	1423925 at	-0.150	4557	6546	1770.0957	FALSE	DEAH (Asp-Glu-Ala-His) box polypeptide 16	203694 s at	-0.002	43601	9.751E-01	FALSE
161696 f at	0.043	6497	1433775 at	0.009	8157	160697 at	0.070	4221.5	1433775 at	0.044	7329	6551.125	1694.5015	TRUE	expressed sequence C77080	224746 at	-0.066	15002	7.104E-02	FALSE
93754 at	0.064	5748	1448491 at	0.051	6946.5	93754 at	0.011	8108	1448491 at	-0.117	5404	6551.625	1230.3232	FALSE	enoyl coenzyme A hydratase 1, peroxisomal	200789 at	0.151	5992	6.867E-04	FALSE
98881 at	-0.043	6479	1428507 at	0.002	8481	98881 at	-0.055	6843	1441208 at	0.247	4418	6555.25	1669.8268	FALSE	haloacid dehalogenase-like hydrolase domain containing 2	223155 at	0.202	10138	1.085E-02	FALSE
102675 at	0.111	3733	1419007 at	-0.038	6880	102675 at	0.007	8149	1419007 at	0.063	7459	6555.25	1951.6968	FALSE	zona pellucida glycoprotein 3	204148 s at	0.147	24477	3.537E-01	FALSE
102020 at	0.041	6315	1425342 a at	-0.068	5509	102020 at	-0.010	7985	1426058 a at	-0.058	6413	6555.5	1035.4997	FALSE	potassium channel, subfamily K, member 3	205952 at	-0.151	14119	5.467E-02	FALSE
102308 at	0.000	8508	1418251 at	0.045	6712	102308 at	-0.006	8158	1418251 at	-0.177	2847	6556.25	2592.15	FALSE	tubby-like protein 3	205854 at	0.422	1868	3.080E-06	FALSE

92315 at	-0.015	7882	1427102 at	0.015	8009.5	92315 at	0.075	4046	1427102 at	0.093	6294	6557.875	1847.4909	FALSE	schlafen 4	231241 at	0.079	17055	1.159E-01	FALSE
98789 at	0.069	4762	1450140 a at	0.065	6311.5	98789 at	0.005	8224	1450140 a at	-0.043	6934	6557.875	1437.9743	FALSE	cyclin-dependent kinase inhibitor 2A		NA	NA	NA	NA
104605 at	0.046	7160	1434329 s at	0.001	8484	104605 at	-0.035	6380	1434329 s at	0.192	4208	6558	1791.2811	FALSE	adiponectin receptor 2	201346 at	0.520	871	3.270E-07	FALSE
101774 at	0.020	7492	1425772 at	0.068	5710.5	101774 at	0.020	6955	1440250 at	-0.089	6080	6559.375	811.72608	FALSE	procollagen, type IV, alpha 4	214602 at	0.017	35869	7.576E-01	FALSE
96154 at	-0.013	7815	1450107 a at	0.093	4341	96154 at	0.035	5788	1450107 a at	-0.010	8301	6561.25	1837.2121	FALSE	renin binding protein	206617 s at	0.009	41194	9.128E-01	FALSE
101175 at	-0.014	7753	1422250 at	0.082	4388.5	101175 at	0.026	6619	1422250 at	-0.036	7485	6561.375	1527.2808	FALSE	mitogen activated protein kinase kinase kinase 2	226979 at	0.263	4510	1.591E-04	FALSE
102619 at	0.053	6992	1450235 at	0.009	8274	102619 at	0.054	5641	1433398 at	-0.114	5340	6561.75	1348.7486	FALSE	FYVE, RhoGEF and PH domain containing 3	227811 at	0.061	20556	2.180E-01	FALSE
94384 at	-0.108	4588	1419647 a at	-0.031	7339	94384 at	0.044	6532	1419647 a at	0.044	7789	6562	1415.0187	FALSE	immediate early response 3	201631 s at	0.269	9287	6.914E-03	FALSE
95794 f at	0.102	4690	1422963 at	0.052	6009	95794 f at	-0.018	7320	1422963 at	0.009	8233	6563	1546.7163	FALSE	small proline-rich protein 2I		NA	NA	NA	NA
98578 at	0.005	8308	1455041 at	0.096	4480.5	98578 at	-0.013	7759	1455041 at	-0.081	5707	6563.625	1783.721	FALSE	oocyte maturation, beta		NA	NA	NA	NA
100698 at	-0.003	8382	1450361 at	0.113	3585	100698 at	0.035	6155	1450361 at	-0.013	8133	6563.75	2221.7566	FALSE	paired like homeodomain factor 1	211223 at	-0.016	40288	8.859E-01	FALSE
94630 at	0.055	6151	1421643 at	0.019	7901	94630 at	0.058	5914	1421643 at	0.087	6291	6564.25	904.6485	TRUE	zinc finger protein, subfamily 1A, 2 (Helios)	220567 at	0.043	27180	4.491E-01	FALSE
103686 at	0.124	2097	1431705 a at	0.006	8383	103686 at	0.004	8198	1431705 a at	0.027	7584	6565.5	2998.5106	TRUE	mucolipin 2	230110 at	-0.055	25425	3.873E-01	FALSE
103790 at	-0.047	6101	1460742 at	-0.013	8005.5	162337 f at	-0.058	4374	1460742 at	-0.036	7790	6567.625	1692.278	TRUE	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase)	207396 s at	-0.078	14151	5.532E-02	FALSE
103641 at	0.072	4634	1455587 at	-0.012	8036.5	103641 at	-0.055	5921	1455587 at	-0.029	7685	6569.125	1587.7805	FALSE	cDNA sequence BC030183	223657 at	0.113	12263	2.877E-02	FALSE
95410 s at	0.049	7042	1450567 a at	0.050	6636	95410 s at	0.050	5198	1450567 a at	0.059	7410	6571.5	968.69586	TRUE	procollagen, type II, alpha 1	217404 s at	0.017	35314	7.406E-01	FALSE
92963 at	0.046	6056	1460234 at	0.029	7150	92963 at	0.039	5642	1460234 at	-0.030	7438	6571.5	859.30107	FALSE	WD repeat domain 81		NA	NA	NA	NA
93875 at	-0.058	5877	1452388 at	-0.004	8362	93875 at	0.010	8101	1452388 at	0.211	3957	6574.25	2070.6819	FALSE	heat shock protein 1A		NA	NA	NA	NA
93132 at	-0.010	8138	1427676 a at	0.048	6780.5	93132 at	0.020	7505	1427676 a at	0.127	3875	6574.625	1883.2683	FALSE	glutamate receptor, ionotropic, kainate 1	207242 s at	-0.074	16479	1.012E-01	FALSE
160101 at	0.068	5841	1448239 at	0.008	8195.5	160101 at	-0.065	4420	1448239 at	-0.039	7848	6576.125	1772.8814	FALSE	heme oxygenase (decycling) 1	203665 at	0.230	9598	8.175E-03	FALSE
98851 at	0.026	7255	1421409 at	0.023	7682	98851 at	-0.010	8112	1444306 at	0.164	3258	6576.75	2239.9922	FALSE	Musashi homolog 1(Drosophila)	206333 at	0.007	39854	8.735E-01	FALSE
160213 at	0.043	5894	1415905 at	0.029	7192	160213 at	-0.039	5926	1415905 at	-0.043	7296	6577	771.46527	FALSE	regenerating islet-derived 1	209752 at	-0.018	36759	7.851E-01	FALSE
98397 at	0.030	7378	1418973 at	0.007	8229	98397 at	-0.036	6559	1442164 at	-0.102	4149	6578.75	1757.4793	FALSE	basic leucine zipper nuclear factor 1	32088 at	-0.029	17712	1.327E-01	FALSE
104334 at	0.001	8489	1450987 a at	0.068	6035	104334 at	0.046	5952	1450987 a at	0.094	5840	6579	1275.8378	TRUE	RIKEN cDNA 2310004I24 gene	220606 s at	-0.055	24712	3.621E-01	FALSE
160753 at	0.012	8192	1427115 at	0.024	7419	160753 at	-0.085	5232	1427115 at	0.235	5474	6579.25	1454.0521	FALSE	myosin, heavy polypeptide 3, skeletal muscle, embryonic	205940 at	0.036	22126	2.725E-01	FALSE
160583 at	-0.001	8466	1429379 at	-0.021	7609.5	160583 at	-0.143	2649	1429379 at	0.028	7603	6581.875	2653.0575	FALSE	extra cellular link domain-containing 1	231595 at	-0.056	17192	1.197E-01	FALSE
97867 at	0.020	7462	1449038 at	0.010	8126	97867 at	-0.151	3284	1449038 at	0.086	7456	6582	2221.037	FALSE	hydroxysteroid 11-beta dehydrogenase 1	205404 at	0.046	34903	7.275E-01	FALSE
99430 at	0.058	5188	1422942 at	-0.005	8400	99430 at	0.037	6142	1422942 at	0.072	6598	6582	1346.8749	FALSE	galanin receptor 2	211226 at	-0.008	40723	8.995E-01	FALSE
98823 at	0.010	7958	1450503 at	0.018	7802.5	98823 at	0.091	3476	1450503 at	-0.053	7093	6582.375	2104.8636	FALSE	potassium inwardly-rectifying channel, subfamily J, member 2	206765 at	0.096	25880	3.999E-01	FALSE
97966 at	-0.015	7794	1424055 at	-0.042	6077	97966 at	-0.014	7620	1456997 at	0.195	4841	6583	1394.3326	FALSE	nuclear receptor coactivator 5	239815 at	0.065	17511	1.270E-01	FALSE
162325 f at	0.050	6171	1417464 at	0.029	7330	93259 at	-0.083	4437	1417464 at	-0.005	8399	6584.25	1696.1642	FALSE	troponin C2, fast	205388 at	-0.213	8688	4.864E-03	FALSE
95956 at	-0.031	7085	1459926 at	0.018	7810	95956 at	0.053	5810	1459926 at	-0.088	5635	6585	1041.4333	FALSE	expressed sequence C77068		NA	NA	NA	NA
92471 i at	-0.020	7771	1450165 at	0.022	7688.5	92471 i at	0.132	2394	1450165 at	0.002	8487	6585.125	2816.9956	FALSE	schlafen 2		NA	NA	NA	NA
103741 at	0.069	5856	1418606 at	-0.035	6627.5	103741 at	-0.061	5482	1418606 at	0.005	8380	6586.375	1287.3582	FALSE	homeo box D10	229400 at	0.186	1664	2.019E-06	FALSE
97869 at	0.060	5609	1451084 at	0.063	5751	97869 at	0.004	8375	1451084 at	-0.061	6620	6588.75	1271.9278	FALSE	electron transferring flavoprotein, dehydrogenase	33494 at	0.146	8770	5.092E-03	FALSE
104098 at	0.007	8240	1417841 at	0.015	7883	104098 at	0.036	5937	1417841 at	-0.162	4307	6591.75	1828.7368	FALSE	peroxisomal membrane protein 2	219076 s at	0.092	15146	7.355E-02	FALSE
99903 at	0.042	6671	1426005 at	0.039	7134.5	99903 at	-0.021	7172	1443745 s at	-0.187	5401	6594.625	827.72795	FALSE	dentin matrix protein 1	217067 s at	-0.032	31051	5.970E-01	FALSE
93837 at	0.019	7581	1426045 at	0.078	6178	93837 at	0.007	8087	1426045 at	-0.100	4533	6594.75	1594.1552	FALSE	kininogen 1	206054 at	0.019	33852	6.941E-01	FALSE
160929 at	0.057	5402	1423099 a at	0.005	8351	160929 at	-0.062	4581	1423099 a at	0.018	8054	6597	1887.8247	FALSE	methyltransferase-like 3		NA	NA	NA	NA
103378 at	0.087	5473	1448572 at	0.050	6315.5	103378 at	-0.013	7630	1448572 at	-0.071	6987	6601.375	924.07263	FALSE	prolactin-like protein A		NA	NA	NA	NA
93040 at	0.012	7921	1421374 a at	-0.013	8066	93040 at	-0.001	8499	1421374 a at	-0.460	1925	6602.75	3128.1514	FALSE	FXYD domain-containing ion transport regulator 1	205384 at	0.495	3644	5.639E-05	FALSE
98830 at	0.003	8348	1418307 a at	0.047	6003	98830 at	-0.022	6922	1418307 a at	-0.096	5138	6602.75	1372.7115	FALSE	spermine binding protein		NA	NA	NA	NA
103270 at	0.072	5669	1416969 at	0.076	5439.5	103270 at	-0.022	7081	1416969 at	0.011	8225	6603.625	1301.9799	FALSE	G two S phase expressed protein 1	211040 x at	0.134	8323	3.998E-03	FALSE
93104 at	-0.202	3565	1437455 a at	0.035	7590	93104 at	0.016	7966	1426083 a at	-0.040	7294	6603.75	2044.412	FALSE	B-cell translocation gene 1, anti-proliferative	200920 s at	0.286	6882	1.446E-03	FALSE
97082 at	0.091	4061	1418211 at	0.003	8438.5	97082 at	0.054	5480	1418211 at	0.009	8439	6604.625	2195.6653	TRUE	pink-eyed dilution	206498 at	-0.081	19887	1.974E-01	FALSE
99000 at	0.033	6537	1418060 a at	0.007	8341	99000 at	0.044	6530	1418060 a at	-0.130	5015	6605.75	1360.3973	FALSE	mitogen activated protein kinase 7	207292 s at	-0.039	26196	4.112E-01	FALSE
96950 at	0.008	8226	1449277 at	0.037	6514.5	96950 at	-0.069	4450	1449277 at	-0.039	7239	6607.375	1600.1864	FALSE	chemokine (C-C motif) ligand 19	210072 at	0.115	19021	1.697E-01	FALSE
95620 at	-0.065	6291	1426440 at	0.093	4375.5	95620 at	0.050	7381	1426440 at	-0.005	8385	6608.125	1716.5666	FALSE	dehydrogenase/reductase (SDR family) member 7	236332 at	-0.084	12008	2.600E-02	FALSE
94151 at	-0.014	7686	1449212 at	0.074	4898	94151 at	-0.004	8218	1427614 at	-0.092	5639	6610.25	1593.4475	FALSE	prolactin induced protein	206509 at	0.046	26101	4.073E-01	FALSE
99881 at	-0.015	7693	1420360 at	0.099	3474.5	99881 at	-0.021	7054	1458232 at	-0.012	8224	6611.375	2145.2563	FALSE	dickkopf homolog 1 (Xenopus laevis)	204602 at	0.069	20541	2.177E-01	FALSE
161002 at	0.091	4662	1434514 at	-0.006	8278.5	161002 at	0.045	5710	1434514 at	-0.031	7799	6612.375	1712.921	FALSE	RNA binding motif protein 15	219286 s at	0.214	7642	2.552E-03	FALSE
93371 at	0.019	7763	1424890 at	0.089	5489	93371 at	0.050	5516	1424890 at	-0.026	7688	6614	1283.8621	FALSE	basonuclin 1	206581 at	0.041	25503	3.889E-01	FALSE
96741 at	0.015	7981	1434922 at	-0.019	7671	96741 at	0.020	7998	1434922 at	-0.349	2809	6614.75	2541.6148	FALSE	PHD finger protein 12	231815 at	0.178	8629	4.708E-03	FALSE
160504 at	-0.045	6505	1416777 at	0.014	8092	160504 at	-0.030	6497	1416777 at	-0.094	5367	6615.25	1120.2763	FALSE	CEA-related cell adhesion molecule 12		NA	NA	NA	NA
160908 r at	0.061	5330	1423672 at	0.020	7945	160908 r at	-0.012	8011	1423672 at	-0.110	5176	6615.5	1574.7657	FALSE	RIKEN cDNA 2510042P03 gene	243413 at	0.100	19162	1.736E-01	FALSE
99184 at	-0.001	8458	1427981 a at	0.011	8187	99184 at	-0.023	7037	1427981 a at	-0.158	2786	6617	2627.2382	FALSE	cysteine sulfinic acid decarboxylase	221139 s at	0.094	17020	1.149E-01	FALSE
160955 at	-0.057	6932	1417075 at	0.047	6467	160955 at	0.027	6994	1457611 x at	0.066	6077	6617.5	430.29176	FALSE	RIKEN cDNA 2010309E21 gene	215947 s at	-0.182	5995	6.883E-04	FALSE
102978 at	-0.016	7795	1448010 at	0.067	4986	102978 at	0.024	7336	1448010 at	0.067	6357	6618.5	1242.6312	FALSE	RIKEN cDNA A430104N18 gene		NA	NA	NA	NA
103442 at	-0.142	2050	1424869 at	0.006	8320	103442 at	-0.006	8259	1424869 at	-0.024	7846	6618.75	3053.1017	FALSE	dehydrogenase/reductase (SDR family) member 7B	239191 at	0.035	26311	4.167E-01	FALSE
94295 at	0.038	7030	1425628 a at	-0.051	6592	94295 at	0.103	5307	1425628 a at	-0.027	7547	6619	957.80617	FALSE	similar to General transcription factor II-I (GTFII-I) (TFII-I) (Bruton tyrosine kinase-associated protein 135) (BTK-assc		NA	NA	NA	NA
92332 at	-0.051	6398	1448877 at	-0.023	7843.5	92332 at	-0.017	7479	1448877 at	-0.180	4764	6621.125	1381.8886	TRUE	distal-less homeobox 2	207147 at	0.077	17545	1.278E-01	FALSE
93296 at	0.063	5990	1422458 at	-0.011	8173.5	93296 at	-0.028	6970	1422458 at	0.092	5358	6622.875	1228.1929	FALSE	T-cell lymphoma breakpoint 1	39318 at	-0.006	41804	9.292E-01	FALSE
160639 at	0.052	6108	1420712 a at	0.030	7244	160639 at	-0.046	6238	1420712 a at	-0.050	6905	6623.75	541.1755	FALSE	hepsin	237397 at	-0.043	22982	3.009E-01	FALSE
98041 at	0.130	4581	1416523 at	0.007	8299	98041 at	0.036	6691	1416523 at	0.064	6928	6624.75	1535.836	TRUE	ribonuclease, RNase A family, 1 (pancreatic)	201785 at	-0.049	37174	7.958E-01	FALSE
93950 at	0.009	8090	1422833 at	0.107	5032.5	93950 at	-0.057	5027	1422833 at	0.007	8353	6625.625	1845.8844	FALSE	forkhead box A2	210103 s at	-0.052	32689	6.538E-01	FALSE
101726 at	0.029	7380	1422342 at	0.062	5974.5	101726 at	0.022	6878	1422342 at	-0.220	6275	6626.875	627.07527	FALSE	neuromedin B receptor	207333 at	-0.022	35543	7.476E-01	FALSE
93702 at	-0.056	5809	1427128 at	0.021	7660.5	93702 at	-0.046	5806	1427128 at	0.036	7233	6627.125	962.37955	FALSE	protein tyrosine phosphatase, non-receptor type 23	223149 s at	-0.049	25661	3.934E-01	FALSE
102074 at	-0.001	8478	1422285 at	0.076	4869	102074 at	-0.071	4871	1422285 at	0.009	8292	6627.5	2030.8065	FALSE	orthopedia homolog (Drosophila)	223835 x at	0.099	9894	9.554E-03	FALSE
103244 at	-0.039	6812	1418796 at	-0.001	8508	103244 at	-0.043	6421	1418796 at	0.135	4778	6629.75	1531.1861	FALSE	C-type lectin domain family 11, member a	211709 s at	0.138	7838	2.938E-03	FALSE
103498 at	0.099	4014	1450127 a at	0.030	6869	103498 at	-0.012	7851	1450127 a at	0.027	7792	6631.5	1802.0038	FALSE	glucagon receptor		NA	NA	NA	NA
98061 at	0.026	7241	1428049 a at	-0.035	6838	98061 at	-0.080	5108	1437624 x at	0.037	7343	6632.5	1039.4571	FALSE	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	224477 s at	0.090	11828	2.407E-02	FALSE
103050 at	0.021	7403	1417447 at	0.014	8028	103050 at	-0.034	6558	1458887 at	0.150	4541	6632.5	1518.8826	FALSE	transcription factor 21	229529 at	-0.045	22239	2.765E-01	FALSE
92307 at	-0.035	6980	1422952 at	0.118	2608	92307 at	0.001	8501	1422952 at	0.004	8447	6634	2774.9505	FALSE	Ng23 protein		NA	NA	NA	NA
98811 at	0.062	6131	1427313 at	0.020	7582.5	98811 at	0.059	5655	1427313 at	0.040	7180	6637.125	896.136	TRUE	prostaglandin I receptor (IP)	206187 at	0.005	41886	9.318E-01	FALSE
104702 at	0.047	5585	1422709 a at	0.028	7278	104702 at	0.019	7411	1422709 a at	0.059	6286	6640	864.0652	TRUE	WD repeat domain 46	209196 at	-0.056	23977	3.374E-01	FALSE
94373 at	0.072	4592	1428072 a at	0.006	8314	94373 at	-0.028	6681	1428072 a at	-0.049	6980	6641.75	1539.897	FALSE	dolichyl pyrophosphate phosphatase 1	221817 at	-0.001	44098	9.865E-01	FALSE
95651 at	0.013	7824	1424088 at	0.049	5530	95651 at	-0.037	6020	1430729 at	-0.059	7197	6642.75	1053.3399	FALSE	melanocyte proliferating gene 1	218220 at	-0.218	10944	1.673E-02	FALSE
93518 at	0.012	7899	1437851 x at	0.041	7095.5	93518 at	-0.037	6370	1448324 at	0.100	5212	6644.125	1140.8443	FALSE	ribonucleic acid binding protein S1		NA	NA	NA	NA
92436 at	-0.010	7957	1432139 at	-0.046	6027.5	92436 at	-0.002	8359	1447806 s at	0.174	4240	6645.875	1899.5147	FALSE	serine/threonine kinase 23	206216 at	0.108	13693	4.656E-02	FALSE
92626 at	-0.053	6610	1415919 at	-0.038	6925	92626 at	-0.049	7047	1415919 at	0.076	6003	6646.25	466.68574	FALSE	neural proliferation, differentiation and control gene 1	218086 at	-0.060	20186	2.065E-01	FALSE
103089 at	-0.081	5451	1427301 at	0.017	7897	103089 at	-0.002	8364	1427301 at	-0.221	4879	6647.75	1738.4693	FALSE	CD48 antigen	204118 at	0.063	22827	2.958E-01	FALSE
103198 at	-0.017	7512	1455239 at	0.005	8335	103198 at	-0.083	3599	1455239 at	0.050	7158	6651	2093.556	FALSE	RIKEN cDNA 6330512M04 gene		NA	NA	NA	NA
95631 at	-0.029	7057	1460288 a at	0.043	6503	95631 at	0.026	6806	1445350 at	-0.082	6261	6656.75	347.72247	FALSE	protein phosphatase 4, catalytic subunit	208932 at	0.118	11145	1.834E-02	FALSE
95976 at	0.046	6400	1420690 at	0.025	7586	95976 at	0.004	8346	1420690 at	-0.154	4298	6657.5	1765.0959	FALSE	fibroblast growth factor 10	231762 at	-0.049	22647	2.895E-01	FALSE
99463 at	0.019	7842	1419523 at	0.075	5931	99463 at	0.072	4636	1419523 at	0.012	8222	6657.75	1679.7782	TRUE	cytochrome P450, family 3, subfamily a, polypeptide 13	205998 x at	0.122	12644	3.306E-02	TRUE
104152 at	0.000	8512	1429650 at	0.031	7350	104152 at	-0.018	7345	1454543 at	0.119	3432	6659.75	2220.7516	FALSE	serine/threonine kinase 40	223852 s at	0.051	24229	3.450E-01	FALSE
94623 at	0.029	7271	1421699 at	0.056	6502	94623 at	-0.081	4660	1421699 at	-0.017	8207	6660	1504.6034	FALSE	enamelin	240586 at	-0.027	26889	4.390E-01	FALSE
99516 at	-0.019	7671	1422522 at	0.014	7841	99516 at	0.110	5134	1422522 at	0.149	6006	6663	1313.1689	FALSE	fragile X mental retardation gene 2, autosomal homolog	35265 at	-0.086	16196	9.519E-02	FALSE
97707 at	0.087	5120	1448073 at	0.027	7373	97707 at	0.023	7010	1448073 at	-0.055	7153	6664	1040.1048	FALSE	hypothetical LOC541456		NA	NA	NA	NA
93838 at	0.008	8181	1428381 a at	0.075	4215.5	93838 at	0.014	7486	1428381 a at	0.046	6777	6664.875	1730.5964	TRUE	RIKEN cDNA 2700038C09 gene	227994 x at	0.051	32940	6.633E-01	FALSE
94940 at	0.011	8118	1417227 at	0.086	4168.5	94940 at	-0.044	6054	1417227 at	-0.011	8325	6666.375	1955.5591	FALSE	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	218440 at	-0.100	15540	8.066E-02	FALSE
95386 at	-0.089	4448	1434690 at	-0.017	7740	95386 at	-0.014	7726	1434690 at	-0.093	6752	6666.5	1549.6231	TRUE	lysocardiolipin acyltransferase	226996 at	-0.018	38271	8.303E-01	FALSE
98950 at	-0.031	7483	1415749 a at	0.029	7533	98950 at	0.132	4727	1415749 a at	0.047	6924	6666.75	1322.3036	FALSE	Ras-related GTP binding C	218088 s at	0.131	10987	1.710E-02	FALSE
160923 at	0.087	4384	1424600 at	0.053	6853	160923 at	0.013	7752	1424600 at	0.043	7704	6673.25	1581.0464	TRUE	amiloride binding protein 1 (amine oxidase, copper-containing)	229156 s at	-0.438	898	3.460E-07	FALSE
103786 at	0.007	8160	1435946 at	-0.012	8057	103786 at	-0.023	7109	1435946 at	0.175	3369	6673.75	2253.3778	FALSE	DNA segment, Chr 5, ERATO Doi 135, expressed	235516 at	0.068	14609	6.317E-02	FALSE
92685 at	0.043	6370	1419222 at	0.008	8178	92685 at	-0.033	6226	1419222 at	-0.093	5924	6674.5	1019.4173	FALSE	thromboxane A2 receptor	336 at	0.060	20865	2.284E-01	FALSE
98469 at	-0.025	7120	1424128 x at	0.030	7319.5	98469 at	-0.074	5006	1451246 s at	-0.046	7261	6676.625	1116.8933	FALSE	aurora kinase B	209464 at	-0.023	34982	7.294E-01	FALSE
96125 at	0.005	8277	1419026 at	0.018	7828	96125 at	0.015	7405	1419026 at	0.147	3203	6678.25	2344.0318	TRUE	Fas death domain-associated protein	201763 s at	0.080	10420	1.271E-02	TRUE
97150 at	-0.023	7213	1450245 at	0.006	8240.5	97150 at	0.100	3509	1450245 at	0.027	7753	6678.875	2154.5157	FALSE	solute carrier family 10, member 2	207095 at	-0.026	31985	6.308E-01	FALSE
99849 at	0.063	6624	1452418 at	-0.084	4162.5	99849 at	0.022	7608	1452418 at	-0.016	8323	6679.375	1816.7346	FALSE	RIKEN cDNA 1200016E24 gene		NA	NA	NA	NA
102194 at	-0.043	6118	1427085 at	0.067	5160	102194 at	0.009	7841	1427085 at	0.034	7599	6679.5	1267.3759	FALSE	RIKEN cDNA 2810432D09 gene	225403 at	-0.018	33334	6.767E-01	FALSE
103839 at	0.062	5109	1451596 a at	0.035	6841.5	103839 at	0.036	6900	1451596 a at	0.024	7874	6681.125	1150.0948	TRUE	sphingosine kinase 1	219257 s at	0.176	9235	6.665E-03	TRUE
96792 at	0.055	6395	1455593 at	0.032	7573	96792 at	0.005	8195	1455593 at	0.102	4563	6681.5	1597.4541	TRUE	apolipoprotein B	223579 s at	0.021	34301	7.079E-01	FALSE
93724 at	0.028	7170	1423428 at	-0.030	7035	93723 at	-0.045	6156	1446780 at	0.084	6370	6682.75	495.57063	FALSE	receptor tyrosine kinase-like orphan receptor 2	205578 at	0.002	43547	9.737E-01	FALSE
96924 at	0.192	1967	1452189 at	-0.011	8261	96924 at	0.014	8009	1452189 at	-0.002	8501	6684.5	3151.4087	FALSE	WD repeat domain containing 82		NA	NA	NA	NA
103404 at	-0.091	4298	1454670 at	-0.032	7150	103404 at	0.044	6902	1454670 at	-0.005	8395	6686.25	1720.9665	FALSE	arginine glutamic acid dipeptide (RE) repeats	242407 at	0.145	7330	2.044E-03	FALSE
160473 at	0.052	6004	1416798 a at	0.053	5282.5	160473 at	0.022	7467	1416798 a at	-0.019	7995	6687.125	1259.4143	FALSE	expressed in non-metastatic cells 4, protein	212739 s at	0.103	19723	1.916E-01	FALSE
101797 at	0.010	8065	1419408 at	-0.155	4711	101797 at	0.055	6220	1419408 at	-0.032	7755	6687.75	1545.1182	FALSE	sine oculis-related homeobox 6 homolog (Drosophila)	207250 at	0.023	33045	6.665E-01	FALSE
160457 at	0.049	6706	1416496 at	0.072	5317	160457 at	0.023	7285	1416496 at	-0.034	7451	6689.75	969.28337	FALSE	Morf4 family associated protein 1	226091 s at	0.053	28138	4.863E-01	FALSE
94226 at	0.030	6961	1425068 a at	0.023	7691.5	94226 at	-0.052	5014	1442543 at	0.111	7101	6691.875	1162.5154	FALSE	testis expressed gene 264	226624 at	0.102	8943	5.605E-03	FALSE
95953 at	-0.021	7539	1442531 at	0.099	4936	95953 at	-0.057	6352	1442531 at	-0.026	7954	6695.25	1355.1318	FALSE	DNA segment, Chr 12, ERATO Doi 123, expressed		NA	NA	NA	NA
96389 at	0.012	8148	1447978 at	-0.069	4815.5	96389 at	-0.022	7498	1447978 at	0.063	6320	6695.375	1463.9174	FALSE	expressed sequence C80719		NA	NA	NA	NA
100987 f at	0.028	6810	1416894 at	0.016	7826	100987 f at	-0.015	7531	1416894 at	-0.102	4617	6696	1450.214	FALSE	RIKEN cDNA 1500019G21 gene	202415 s at	-0.308	560	1.255E-07	FALSE
94657 at	-0.033	6421	1447130 at	-0.005	8406	94657 at	0.090	4157	1447130 at	-0.029	7806	6697.5	1886.6493	FALSE	DNA segment, Chr 8, Wayne State University 26, expressed		NA	NA	NA	NA
160745 at	-0.053	6301	1422971 at	0.038	6755.5	160745 at	0.006	8201	1426783 at	-0.105	5534	6697.875	1121.7279	FALSE	GCN5 general control of amino acid synthesis-like 2 (yeast)	202182 at	0.108	17769	1.341E-01	FALSE
95438 at	0.028	7429	1423533 a at	0.023	7640	95438 at	-0.035	6612	1423533 a at	0.083	5116	6699.25	1144.82	FALSE	ras homolog gene family, member T1	222148 s at	-0.170	11069	1.769E-02	FALSE
104711 at	-0.045	6225	1417510 at	0.055	6767	104711 at	-0.046	6917	1417510 at	-0.045	6890	6699.75	323.16288	FALSE	vacuolar protein sorting 4a (yeast)	217913 at	-0.065	22622	2.889E-01	FALSE
161561 r at	0.061	7307	1421528 a at	-0.024	7498	161561 r at	0.059	4868	1421528 a at	0.053	7133	6701.5	1231.3891	FALSE	Surfeit gene 5	206593 s at	0.077	16680	1.058E-01	FALSE
94625 at	0.036	7127	1420797 at	-0.031	7446	94625 at	0.033	6397	1420797 at	0.092	5844	6703.5	721.88203	FALSE	otogelin		NA	NA	NA	NA
101600 at	0.056	6582	1444887 at	0.007	8236	101600 at	-0.042	5750	1444887 at	-0.059	6252	6705	1076.464	FALSE	expressed sequence C79015		NA	NA	NA	NA
93703 at	0.060	5860	1417845 at	-0.026	7358	93703 at	0.024	6846	1417845 at	-0.068	6762	6706.5	622.77738	FALSE	claudin 6	208474 at	-0.067	27519	4.619E-01	FALSE
92325 at	0.052	6259	1452589 at	0.006	8263	92325 at	0.103	4444	1452589 at	-0.020	7862	6707	1739.4476	FALSE	PTK7 protein tyrosine kinase 7	207011 s at	0.032	33836	6.935E-01	FALSE
94910 at	0.058	7091	1435737 a at	-0.115	4334	94910 at	0.036	7450	1435737 a at	0.029	7960	6708.75	1622.8196	FALSE	nuclear distribution gene E homolog 1 (A nidulans)		NA	NA	NA	NA
104227 at	-0.045	6340	1417894 at	-0.016	7858	104227 at	0.007	8042	1417894 at	-0.165	4600	6710	1600.1175	FALSE	G protein-coupled receptor 97	220404 at	-0.029	34703	7.224E-01	FALSE
103771 at	0.013	7729	1435105 at	0.048	6772	103771 at	0.063	4848	1435105 at	-0.066	7495	6711	1307.0922	FALSE	RIKEN cDNA 1110061N23 gene	221273 s at	-0.454	743	2.281E-07	FALSE
99437 at	-0.016	7823	1450562 at	0.073	5159	99437 at	0.045	5878	1450562 at	0.025	7989	6712.25	1410.9589	FALSE	lymphocyte antigen 6 complex, locus F		NA	NA	NA	NA
102329 at	0.063	5217	1418976 s at	0.012	8106	102329 at	0.028	7229	1418976 s at	-0.073	6298	6712.5	1240.557	FALSE	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	221188 s at	0.113	17518	1.272E-01	FALSE
103995 at	-0.025	7320	1419086 at	0.032	7714	103995 at	-0.014	7452	1419086 at	0.109	4368	6713.5	1572.2166	FALSE	fibroblast growth factor binding protein 1	205014 at	0.000	44538	9.972E-01	FALSE

103948 at	-0.007	8291	1450806 at	0.117	4415.5	103948 at	0.027	6954	1450806 at	-0.041	7196	6714.125	1639.1009	FALSE	T-cell leukemia, homeobox 3	208495 at	-0.040	28704	5.096E-01	FALSE
98304 at	-0.025	7511	1421352 at	0.056	5553	98304 at	0.045	5789	1421352 at	0.022	8009	6715.5	1226.8892	FALSE	toll-like receptor 6	207446 at	0.029	31564	6.152E-01	FALSE
92393 at	-0.004	8296	1423018 at	-0.065	5798	92393 at	0.000	8507	1423018 at	0.164	4271	6718	2043.2665	FALSE	potassium voltage-gated channel, shaker-related subfamily, member 3	207237 at	-0.040	28791	5.130E-01	FALSE
160447 at	-0.021	7966	1450898 at	-0.058	4552	160447 at	0.054	6740	1450898 at	0.033	7619	6719.25	1534.2032	FALSE	hippocampus abundant gene transcript 1	230868 at	0.208	3541	4.886E-05	FALSE
92421 at	0.069	4530	1453113 at	0.018	7667	92421 at	-0.002	8409	1453113 at	0.087	6295	6725.25	1705.4955	FALSE	WD repeat, SAM and U-box domain containing 1	238892 at	0.107	12991	3.684E-02	FALSE
160784 r at	0.016	7562	1428483 a at	0.004	8337	160784 r at	0.019	7245	1453314 x at	-0.130	3766	6727.5	2026.9163	FALSE	RIKEN cDNA 2610039C10 gene	219004 s at	-0.143	6852	1.398E-03	FALSE
101412 at	-0.028	6962	1432103 a at	-0.075	5312	101412 at	-0.014	7879	1432103 a at	-0.051	6770	6730.75	1062.4416	TRUE	SH3-domain GRB2-like 3	211565 at	-0.075	19726	1.917E-01	FALSE
161159 r at	0.089	4177	1417945 at	-0.012	8086.5	161159 r at	-0.030	7136	1417945 at	-0.052	7544	6735.875	1749.7805	FALSE	POU domain, class 5, transcription factor 1	208286 x at	0.054	23353	3.148E-01	FALSE
96553 at	-0.059	5898	1449175 at	0.039	6708	96553 at	0.038	5913	1449175 at	0.007	8427	6736.5	1188.8141	FALSE	G-protein coupled receptor 65	214467 at	0.039	21594	2.536E-01	FALSE
101635 f at	0.075	5247	1426166 at	0.019	7903	101635 f at	0.042	6251	1426166 at	0.034	7545	6736.5	1220.4801	TRUE	major urinary protein 5	NA	NA	NA	NA	
92976 at	0.058	5566	1449251 at	0.054	5722	92976 at	-0.011	7843	1449251 at	0.044	7826	6739.25	1266.3073	FALSE	Norrie disease homolog	206022 at	0.230	11292	1.944E-02	FALSE
104018 at	0.002	8464	1439479 at	-0.033	7209	104018 at	-0.252	3523	1439479 at	0.040	7775	6742.75	2206.9905	FALSE	lactase	206945 at	0.034	32647	6.523E-01	FALSE
161263 f at	0.032	7102	1448165 at	-0.024	7591	161263 f at	0.030	6668	1448165 at	-0.095	5612	6743.25	843.16285	FALSE	caspase 2	226032 at	0.163	7267	1.950E-03	FALSE
100899 s at	-0.007	8115	1448705 at	-0.029	7470	100899 s at	-0.002	8456	1448705 at	0.134	2932	6743.25	2573.5192	FALSE	zinc finger and BTB domain containing 22	213081 at	-0.024	31954	6.295E-01	FALSE
98800 at	0.061	6158	1460042 at	0.089	4353	161149 r at	-0.022	8251	1460042 at	-0.015	8211	6743.25	1869.3504	FALSE	solute carrier family 23 (nucleobase transporters), member 3	NA	NA	NA	NA	
92699 at	0.047	6096	1448783 at	0.073	5444	92699 at	0.013	7744	1448783 at	-0.032	7691	6743.75	1155.669	FALSE	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	220135 s at	0.063	24870	3.678E-01	FALSE
95071 at	0.018	7670	1418695 a at	0.027	7252	95071 at	-0.014	7717	1418695 a at	0.096	4354	6748.25	1609.7926	FALSE	potassium channel modulatory factor 1	217938 s at	-0.289	1362	1.033E-06	FALSE
103591 at	-0.023	7484	1418593 at	-0.004	8380	103591 at	-0.069	5275	1418593 at	-0.072	5859	6749.5	1433.5458	TRUE	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	203572 s at	-0.109	12573	3.228E-02	TRUE
97131 at	-0.061	5460	1431792 a at	-0.056	6442	97131 at	-0.019	7456	1431792 a at	-0.034	7660	6754.5	1014.1366	TRUE	serine/threonine kinase 11 interacting protein	225713 at	0.020	35601	7.496E-01	FALSE
99373 at	-0.019	7816	1422179 at	0.016	8060.5	99373 at	-0.089	4043	1422179 at	-0.048	7099	6754.625	1853.2252	FALSE	gap junction membrane channel protein beta 4	216579 at	0.004	43459	9.715E-01	FALSE
96883 at	-0.051	6767	1417718 at	0.047	6647.5	96883 at	0.032	6990	1417718 at	0.066	6618	6755.625	169.00955	FALSE	eukaryotic translation initiation factor 3, subunit 4 (delta)	208887 at	0.180	6887	1.450E-03	FALSE
103455 at	-0.011	7922	1436048 at	-0.028	7772	103455 at	-0.042	5616	1436048 at	0.159	5713	6755.75	1262.1755	FALSE	exocyst complex component 8	227577 at	-0.258	11907	2.491E-02	FALSE
94826 at	0.044	6590	1427578 a at	0.026	7346	94826 at	-0.025	7443	1431582 at	0.100	5650	6757.25	830.83387	FALSE	integrin beta 4 binding protein	228016 s at	0.028	33897	6.954E-01	FALSE
92181 at	0.129	3446	1420428 at	0.001	8473.5	92181 at	-0.012	7833	1441958 s at	-0.040	7277	6757.375	2261.0668	FALSE	advanced glycosylation end product-specific receptor	217046 s at	0.028	34138	7.033E-01	FALSE
104366 at	0.008	8242	1435087 at	0.007	8290.5	104366 at	-0.100	6409	1445610 at	0.136	4089	6757.625	1982.9417	FALSE	cDNA sequence BC039093	228957 at	0.074	16549	1.029E-01	FALSE
95293 at	0.011	7900	1419843 at	0.031	6973	95293 at	0.012	7880	1419843 at	-0.190	4279	6758	1708.2851	FALSE	Calreticulin 4	NA	NA	NA	NA	
95373 at	-0.017	7547	1418770 at	0.062	5913.5	95373 at	-0.019	7394	1418770 at	0.081	6181	6758.875	831.2888	FALSE	CD2 antigen	205831 at	-0.003	43801	9.796E-01	FALSE
103415 at	0.005	8340	1448376 at	0.114	3640	103415 at	-0.003	8450	1448376 at	0.061	6611	6760.25	2244.1851	FALSE	Werner helicase interacting protein 1	227619 at	-0.040	23807	3.310E-01	FALSE
104603 at	-0.033	6710	1417883 at	0.063	5065.5	104603 at	0.016	7376	1417883 at	0.044	7898	6762.375	1231.3012	FALSE	glutathione S-transferase, theta 2	205439 at	0.140	23536	3.213E-01	FALSE
93423 at	0.013	7786	1423673 at	0.018	7606	93423 at	-0.083	3325	1423673 at	-0.009	8350	6766.75	2316.2854	FALSE	leucine zipper, down-regulated in cancer 1-like	223228 at	-0.048	26080	4.069E-01	FALSE
102264 at	0.044	6611	1418612 at	0.037	7086	102264 at	0.001	8462	1418612 at	-0.109	4915	6768.5	1463.9008	FALSE	schlafen 1	NA	NA	NA	NA	
103321 at	-0.013	8206	1455184 at	-0.032	7514.5	103321 at	0.132	4085	1455184 at	-0.057	7278	6770.875	1833.3632	FALSE	MOB1, Mps One Binder kinase activator-like 1A (yeast)	225997 at	0.313	8922	5.529E-03	FALSE
93449 at	0.041	6724	1416650 at	-0.006	8324	93449 at	0.083	3829	1416650 at	0.010	8232	6777.25	2097.9154	FALSE	ret finger protein-like 4	NA	NA	NA	NA	
100997 at	0.007	8228	1426731 at	0.004	8368	100997 at	0.099	3251.5	1426731 at	0.050	7276	6780.875	2402.4136	TRUE	desmin	NA	NA	NA	NA	
99361 at	0.043	6768	1422228 at	0.087	4704.5	99361 at	0.025	7360	1422228 at	0.008	8306	6784.625	1524.5584	TRUE	wingless-related MMTV integration site 8A	224259 at	-0.003	42590	9.497E-01	FALSE
98094 f at	0.019	7384	1450102 a at	-0.050	6420.5	98094 f at	0.090	4842	1450102 a at	-0.002	8496	6785.625	1548.594	FALSE	autocrine motility factor receptor	202204 s at	0.038	30842	5.884E-01	FALSE
94813 at	-0.020	7360	1448494 at	0.037	6934	94813 at	-0.023	7201	1416855 at	0.098	5651	6786.5	777.1377	FALSE	growth arrest specific 1	204457 s at	0.236	5970	6.787E-04	FALSE
160314 at	-0.075	5532	1416939 at	-0.043	6647.5	160314 at	-0.028	6920	1416939 at	-0.023	8048	6786.875	1033.1659	TRUE	pyrophosphatase (inorganic) 1	217848 s at	-0.255	7412	2.154E-03	TRUE
95297 at	0.108	4489	1420565 at	-0.005	8320	95297 at	-0.026	6886	1420565 at	-0.042	7467	6790.5	1643.4765	FALSE	homeo box A1	214639 s at	-0.018	37657	8.104E-01	FALSE
94836 at	-0.030	7044	1419965 at	0.057	6288	94836 at	0.051	6064	1419965 at	0.029	7770	6791.5	775.45406	FALSE	expressed sequence C79445	NA	NA	NA	NA	
95602 at	0.002	8410	1460720 at	-0.027	7166	95602 at	-0.037	6745	1441184 at	0.109	4852	6793.25	1474.6302	FALSE	transient receptor potential cation channel, subfamily C, member 4 associated protein	212059 s at	0.071	16040	9.179E-02	FALSE
160161 at	-0.009	8132	1451981 at	-0.055	5447	160161 at	-0.042	6630	1451981 at	0.063	6966	6793.75	1104.707	FALSE	gene trap ROSA b-geo 22	243600 at	0.120	8110	3.512E-03	FALSE
100562 at	0.040	6066	1448740 at	0.021	7677	100562 at	-0.018	7361	1448740 at	-0.102	6076	6795	845.90819	FALSE	RIKEN cDNA 2400006H24 gene	218526 s at	-0.175	8080	3.450E-03	FALSE
93425 at	-0.011	8151	1460231 at	0.060	6672	93425 at	0.051	5944	1460231 at	-0.092	6415	6795.5	952.62182	FALSE	interferon regulatory factor 5	239412 at	0.111	17659	1.311E-01	FALSE
101095 at	-0.015	7770	1417359 at	-0.002	8465.5	101095 at	0.021	7487	1447833 x at	0.140	3471	6798.375	2256.0282	FALSE	microfibrillar-associated protein 2	203417 at	0.008	40301	8.862E-01	FALSE
101151 at	0.004	8324	1450215 at	0.041	7255.5	101151 at	-0.073	5804	1450215 at	0.081	5813	6799.125	1224.2328	FALSE	recoverin	206203 at	0.010	40428	8.906E-01	FALSE
94686 at	0.009	8123	1448078 at	0.012	8044	94686 at	0.025	7085	1448078 at	-0.121	3949	6800.25	1958.5106	FALSE	expressed sequence C76533	NA	NA	NA	NA	
100939 at	-0.007	8104	1424297 at	-0.017	7930	100939 at	-0.061	5421	1424298 at	-0.101	5750	6801.25	1412.0258	TRUE	zinc finger protein 282	212892 at	0.026	32477	6.466E-01	FALSE
99394 at	0.034	7031	1420589 at	-0.059	6011	99394 at	0.012	8031	1420589 at	-0.071	6133	6801.5	937.39408	FALSE	hyaluronan synthase 3	223541 at	0.038	31470	6.114E-01	FALSE
95977 at	0.080	5367	1419774 at	0.045	6163.5	95977 at	0.014	7484	1419774 at	0.011	8198	6803.125	1275.5185	TRUE	DNA segment, Chr 2, ERATO Doi 239, expressed	NA	NA	NA	NA	
92415 at	0.033	7079	1422924 at	0.087	5163	92415 at	0.032	6593	1422924 at	-0.009	8382	6804.25	1329.5501	FALSE	tumor necrosis factor (ligand) superfamily, member 9	NA	NA	NA	NA	
102923 at	-0.015	7713	1425892 a at	-0.038	7302.5	102923 at	0.057	5320	1425892 a at	0.193	6903	6809.625	1046.6954	FALSE	preponociceptin	205901 at	0.025	32103	6.352E-01	FALSE
96035 at	0.035	7104	1416647 at	0.003	8397	96035 at	-0.035	5883	1416647 at	-0.093	5855	6809.75	1207.8022	FALSE	branched chain ketoacid dehydrogenase E1, alpha polypeptide	202331 at	0.060	18001	1.407E-01	FALSE
94172 at	0.043	6594	1455335 at	0.040	6830	94172 at	0.014	7499	1453950 a at	-0.062	6331	6813.5	500.38951	FALSE	X-ray repair complementing defective repair in Chinese hamster cells 2	207598 x at	0.143	12810	3.498E-02	FALSE
103389 at	-0.032	6630	1423523 at	-0.015	8255	103389 at	-0.005	8255	1423523 at	-0.094	4463	6817.125	1718.7051	TRUE	aminoadipate-semialdehyde synthase	214829 at	0.277	3279	3.377E-05	FALSE
102291 at	0.012	8008	1427393 at	0.033	7275	102291 at	-0.049	5130.5	1427393 at	-0.077	6855	6817.125	1221.1977	FALSE	coagulation factor IX	207218 at	-0.050	22340	2.800E-01	FALSE
160839 at	0.066	5711	1416639 at	0.020	7762	160839 at	0.022	7116	1416639 at	-0.068	6692	6820.25	860.47366	FALSE	solute carrier family 2 (facilitated glucose transporter), member 5	204430 s at	0.248	13131	3.879E-02	FALSE
101414 at	0.062	4934	1451849 a at	0.051	6845.5	101414 at	0.022	7219	1451849 a at	0.014	8283	6820.375	1397.2849	TRUE	lamin B2	216952 s at	0.015	36381	7.740E-01	FALSE
103714 at	0.043	6766	1451547 at	0.061	5969.5	103714 at	0.029	6789	1451547 at	-0.029	7765	6822.375	734.89902	FALSE	RIKEN cDNA 0610009A07 gene	231070 at	-0.009	35445	7.446E-01	FALSE
103446 at	0.001	8500	1426276 at	0.001	8492	103446 at	0.058	5709	1426276 at	-0.392	4589	6822.5	1985.7527	FALSE	interferon induced with helicase C domain 1	219209 at	0.153	13621	4.564E-02	FALSE
96360 at	-0.049	6208	1451168 a at	-0.006	8272	96360 at	-0.027	6850	1451168 a at	-0.119	5965	6823.75	1035.1677	TRUE	Rho GDP dissociation inhibitor (GDI) alpha	201167 x at	-0.602	3004	2.219E-05	TRUE
97005 at	0.058	5496	1422367 at	0.033	7086	97005 at	-0.014	7632	1422367 at	0.065	7081	6823.75	922.16064	FALSE	olfactory receptor 70	NA	NA	NA	NA	
101928 at	0.027	7233	1417498 at	0.045	6543	101928 at	0.028	6807	1417498 at	-0.073	6722	6826.25	292.64014	FALSE	serine (or cysteine) peptidase inhibitor, clade F, member 2	205075 at	-0.020	36896	7.884E-01	FALSE
95552 at	0.081	5033	1417991 at	-0.021	7703.5	95552 at	0.036	6176	1417991 at	-0.005	8398	6827.625	1514.2136	FALSE	deiodinase, iodothyronine, type I	206457 s at	0.015	38758	8.432E-01	FALSE
93755 at	0.050	6756	1418368 at	-0.060	6201	93755 at	-0.023	6855	1418368 at	0.031	7518	6832.5	540.08055	FALSE	resistin like beta	NA	NA	NA	NA	
160817 at	0.063	6045	1451546 s at	-0.008	8157	160817 at	0.017	7714	1424966 at	-0.145	5415	6832.75	1311.59	FALSE	transmembrane protein 40	219503 s at	0.038	25306	3.831E-01	FALSE
160958 at	-0.037	7051	1424075 at	-0.029	7816.5	160958 at	0.031	7203	1424075 at	0.107	5262	6833.125	1098.4439	FALSE	RIKEN cDNA 9430016H08 gene	219176 at	-0.147	15054	7.193E-02	FALSE
99407 at	-0.024	7263	1422199 at	0.047	5860	99407 at	0.013	7659	1422200 at	0.071	6558	6835	793.62334	FALSE	olfactory marker protein	221361 at	0.010	39300	8.596E-01	FALSE
92919 at	-0.001	8467	1418268 at	0.013	8096	92919 at	-0.060	4883	1418268 at	0.096	5901	6836.75	1725.9	FALSE	5-hydroxytryptamine (serotonin) receptor 3A	216615 s at	-0.049	29529	5.398E-01	FALSE
96796 f at	0.021	7404	1419622 at	0.083	4610.5	96796 f at	-0.022	7241	1419622 at	-0.014	8093	6837.125	1529.6561	FALSE	UDP glucuronosyltransferase 2 family, polypeptide B5	NA	NA	NA	NA	
161012 at	0.053	5941	1417640 at	0.039	7027	161012 at	-0.013	7894	1417640 at	-0.078	6514	6844	828.71346	FALSE	CD79B antigen	205297 s at	-0.023	36413	7.750E-01	FALSE
101676 at	0.032	7422	1449106 at	-0.320	4934	101676 at	-0.024	7113	1449106 at	-0.062	7910	6844.75	1315.4085	FALSE	glutathione peroxidase 3	201348 at	-0.348	12344	2.970E-02	FALSE
94786 at	0.100	5283	1443605 at	0.043	7066.5	94786 at	0.016	7356	1443605 at	0.024	7675	6845.125	1070.6582	TRUE	expressed sequence C81272	NA	NA	NA	NA	
92469 at	0.059	5281	1451031 at	0.007	8266	92469 at	-0.048	5836	1451031 at	0.028	7998	6845.25	1506.9646	FALSE	secreted frizzled-related sequence protein 4	204051 s at	0.079	22154	2.736E-01	FALSE
96551 at	-0.008	8102	1420330 at	0.044	6038	96551 at	0.015	7660	1420331 at	0.075	5597	6849.25	1218.326	FALSE	C-type lectin domain family 4, member e	222934 s at	0.086	19286	1.773E-01	FALSE
103279 at	-0.024	7502	1449393 at	0.009	8203	103279 at	0.075	3931	1449393 at	-0.023	7763	6849.75	1967.2182	FALSE	SH2 domain protein 1A	210116 at	0.057	13983	5.202E-02	FALSE
101463 at	0.005	8334	1418708 at	0.084	5501	101463 at	-0.039	6390	1418708 at	-0.054	7176	6850.25	1202.7653	FALSE	apolipoprotein C-IV	206738 at	-0.007	42218	9.396E-01	FALSE
100347 at	0.032	7028	1447986 at	-0.031	6853	100347 at	-0.015	7733	1447986 at	-0.121	5792	6851.5	802.23376	FALSE	expressed sequence D17892	NA	NA	NA	NA	
160684 at	0.007	8116	1423786 at	0.028	6919	160684 at	-0.003	8295	1423786 at	0.142	4081	6852.75	1946.182	FALSE	RIKEN cDNA 8430410A17 gene	201677 at	-0.433	1890	3.187E-06	FALSE
95029 at	0.009	7990	1417475 at	0.051	6049	95029 at	-0.028	6660	1417475 at	-0.050	6714	6853.25	815.62956	FALSE	ATPase type 13A1	218052 s at	-0.022	33156	6.707E-01	FALSE
97699 at	0.061	5739	1421232 at	0.013	8152	97699 at	0.004	8264	1428623 at	0.116	5263	6854.5	1575.5855	TRUE	plexin A1	221538 s at	0.245	8669	4.812E-03	TRUE
92977 s at	-0.051	5959	1422150 at	0.028	7632.5	92977 s at	0.067	5327	1422150 at	0.001	8506	6856.125	1468.3213	FALSE	H6 homeo box 3	NA	NA	NA	NA	
160201 r at	-0.045	6640	1423621 a at	-0.017	7719	160201 r at	0.026	7412	1423621 a at	-0.117	5663	6858.5	917.20318	FALSE	solute carrier family 33 (acetyl-CoA transporter), member 1	203164 at	0.142	15316	7.678E-02	FALSE
98150 at	-0.118	4000	1423448 at	-0.019	7663	98150 at	0.003	8443	1423448 at	0.032	7336	6860.5	1962.7254	FALSE	RAB11B, member RAS oncogene family	34478 at	-0.168	7608	2.481E-03	FALSE
160756 at	-0.017	7532	1435517 x at	0.063	5927	160756 at	-0.027	6995	1417744 a at	0.056	6991	6861.25	672.6695	FALSE	v-ral simian leukemia viral oncogene homolog B (ras related)	202100 at	-0.113	8661	4.795E-03	FALSE
94102 at	0.077	5215	1422152 at	-0.034	7010	94102 at	-0.014	8106	1422152 at	0.047	7126	6864.25	1204.3982	FALSE	H6 homeo box 1	NA	NA	NA	NA	
101194 at	0.081	4440	1420568 at	0.058	6731	101194 at	0.002	8423	1420568 at	0.020	7866	6865	1763.3251	TRUE	stimulated by retinoic acid gene 8	NA	NA	NA	NA	
100459 at	0.039	6325	1425939 at	-0.010	8150	100459 at	0.032	6170	1422630 at	0.054	6820	6866.25	899.60524	FALSE	RAD50 homolog (S. cerevisiae)	230405 at	0.197	2945	1.972E-05	FALSE
160197 at	-0.004	8310	1416400 at	0.105	3409	160197 at	0.003	8334	1416400 at	0.068	7412	6866.25	2344.4349	FALSE	pyrroline-5-carboxylate reductase-like	218944 at	0.008	41451	9.190E-01	FALSE
160630 at	0.047	6622	1428699 at	0.049	5807	160630 at	0.002	8418	1434190 at	0.053	6626	6868.25	1102.6182	TRUE	spermine synthase	202043 s at	0.046	33022	6.660E-01	FALSE
101807 at	0.016	7949	1450594 at	0.091	5253	101807 at	-0.057	5795	1450594 at	0.002	8478	6868.75	1583.268	FALSE	melanoma antigen, family A, 4	NA	NA	NA	NA	
102356 at	-0.016	7841	1460189 at	-0.062	6980	102356 at	-0.038	5861	1448418 s at	-0.048	6796	6869.5	812.09544	TRUE	WD repeat domain 23	216389 s at	-0.111	11782	2.369E-02	TRUE
100679 at	0.042	6205	1421701 at	0.033	7453	100679 at	-0.017	7611	1421701 at	-0.071	6216	6871.25	765.70333	FALSE	vomeronasal 2, receptor, 16	NA	NA	NA	NA	
101234 at	-0.008	8172	1458862 at	-0.001	8501.5	101234 at	0.059	5483	1458862 at	0.085	5332	6872.125	1697.6642	FALSE	expressed sequence C78704	NA	NA	NA	NA	
100408 at	0.035	6684	1421015 s at	0.005	8310	100408 at	0.001	8483	1421015 s at	0.116	4022	6874.75	2067.2831	TRUE	polymerase (DNA directed), epsilon 3 (p17 subunit)	208828 at	-0.119	22547	2.867E-01	FALSE
103837 at	0.000	8514	1418748 at	0.113	3046	103837 at	0.013	7619	1443787 x at	0.008	8330	6877.25	2583.1572	TRUE	caspase 14	231722 at	-0.051	25728	3.949E-01	FALSE
97550 at	-0.032	6503	1420812 at	-0.034	7387.5	97550 at	-0.014	7482	1420812 at	0.080	6158	6882.625	654.05038	FALSE	histone deacetylase 7A	244263 at	0.029	31324	6.064E-01	FALSE
97428 at	0.072	3982	1423116 at	0.022	7620.5	97428 at	0.007	8071	1423116 at	-0.021	7877	6887.625	1945.8504	FALSE	DOM-3 homolog Z (C. elegans)	204522 at	-0.071	18748	1.623E-01	FALSE
94243 at	-0.082	5564	1437349 at	-0.023	7489	94243 at	-0.017	7719	1437349 at	-0.048	6781	6888.25	968.88024	TRUE	cytoskeleton associated protein 5	212832 s at	0.003	43234	9.658E-01	FALSE
96021 at	-0.061	5652	1424154 a at	-0.006	8246	96021 at	0.053	5249	1424154 a at	-0.007	8408	6888.75	1670.1875	FALSE	HESB like domain containing 1	226007 at	-0.054	26752	4.337E-01	FALSE
98796 at	0.050	5939	1435447 at	0.031	6877	98796 at	0.021	7159	1435447 at	0.037	7602	6894.25	703.27869	TRUE	major intrinsic protein of eye lens fiber	220863 at	-0.035	29285	5.309E-01	FALSE
100484 at	0.076	5671	1417256 at	0.029	7374	100484 at	-0.007	8223	1417256 at	-0.055	6310	6894.5	1130.4018	FALSE	matrix metallopeptidase 13	205959 at	-0.031	28486	5.003E-01	FALSE
98760 at	0.156	3643	1421433 at	0.007	8335	98760 at	0.008	8126	1421433 at	0.045	7487	6897.75	2199.6135	TRUE	zinc finger homeodomain 4	233257 at	0.088	19586	1.869E-01	FALSE
99412 at	0.055	5986	1422957 at	0.003	8403	99412 at	0.030	6535	1422957 at	-0.063	6674	6899.5	1045.4194	FALSE	chemokine (C-C motif) receptor 3	208304 at	-0.045	29539	5.400E-01	FALSE
95685 at	0.034	6848	1416890 at	-0.020	7781.5	95685 at	-0.002	8417	1416890 at	0.121	4554	6900.125	1691.6216	FALSE	WD repeat domain 74	221712 s at	-0.089	13963	5.183E-02	FALSE
161132 at	-0.006	8256	1422837 at	-0.041	6576	161132 at	0.040	5749	1459426 at	-0.049	7021	6900.5	1046.1283	FALSE	sciellin	206884 s at	-0.005	40453	8.912E-01	FALSE
101711 at	0.016	7840	1422295 at	0.052	6394	101711 at	0.011	7823	1422295 at	-0.095	5548	6901.25	1128.3414	FALSE	myelodysplasia syndrome 1 homolog (human)	208434 at	-0.017	37672	8.106E-01	FALSE
160152 at	-0.075	6476	1416005 at	0.007	8391	160152 at	0.103	4684	1416005 at	0.017	8058	6902.25	1698.4755	FALSE	protease (prosome, macropain) 26S subunit, ATPase 1	204219 s at	-0.032	31900	6.274E-01	FALSE
95098 at	0.012	7941	1423650 at	0.060	5729	95098 at	0.037	5680	1423650 at	0.015	8289	6909.75	1399.0786	TRUE	ring finger protein 26	NA	NA	NA	NA	
97957 at	0.028	7242	1424441 at	-0.039	6674	97957 at	-0.016	7798	1424441 at	0.075	5932	6911.5	798.11006	FALSE	solute carrier family 27 (fatty acid transporter), member 4	225779 at	0.014	38157	8.266E-01	FALSE
93175 at	0.046	6247	1454678 s at	-0.058	5809	93175 at	0.006	8249.5	1454678 s at	-0.039	7358	6915.875	1102.5117	FALSE	RIKEN cDNA A130022J15 gene	NA	NA	NA	NA	
103484 at	0.027	6982	1423856 at	0.029	7109	103484 at	-0.003	8347	1423856 at	-0.125	5241	6919.75	1277.3586	FALSE	popeye domain containing 3	219926 at	0.009	41113	9.103E-01	FALSE
97470 at	0.031	6663	1427366 at	0.020	7930	97470 at	-0.051	4982	1427366 at	0.018	8117	6923	1446.2326	FALSE	keratin associated protein 3-1	233537 at	0.018	37588	8.081E-01	FALSE
103666 at	0.089	3802	1418415 at	0.030	7049.5	103666 at	0.003	8388	1418415 at	0.003	8455	6923.625	2179.4411	TRUE	homeo box B5	205601 s at	0.094	11580	2.170E-02	TRUE
96492 at	-0.033	6482	1449600 at	-0.062	6275.5	96492 at	-0.015	7588.5	1449600 at	0.047	7359	6926.25	644.63976	FALSE	gene model 1683, (NCBI)	NA	NA	NA	NA	
92468 at	0.010	7992	1423421 at	0.008	8218.5	92468 at	-0.041	6656	1423421 at	-0.118	4840	6926.625	1552.547	FALSE	ankyrin repeat domain 49	219069 at	-0.014	38637	8.403E-01	FALSE
96694 at	0.029	6926	1448981 x at	-0.016	7970	96694 at	0.078	4434	1448981 x at	-0.006	8389	6929.75	1773.914	FALSE	T-cell leukemia/lymphoma 1B, 1	NA	NA	NA	NA	
104068 at	-0.063	5055	1426209 at	-0.031	7176	104068 at	-0.015	7553	1426209 at	-0.026	7944	6932	1290.0194	TRUE	Striatin, calmodulin binding protein 4	217903 at	-0.327	1708	2.232E-06	TRUE
102302 at	-0.017	8100	1427153 at	-0.067	6174.5	102302 at	0.101	5479	1427153 at	0.030	7975	6932.125	1308.5728	FALSE	branched chain ketoacid dehydrogenase E1, beta polypeptide	243302 at	-0.124	7702	2.678E-03	FALSE
101688 at	0.043	6245	1448089 at	-0.003	8440	101688 at	-0.039	6249	1448089 at	-0.053	6801	6933.75	1037.5726	FALSE	DNA segment, Chr 4, ERATO Doi 58, expressed	NA	NA	NA	NA	
101763 at	0.036	7106	1450346 at	0.080	5203	101763 at	0.014	7579	1450346 at	-0.023	7856	6936	1196.1101	FALSE	G-protein-coupled receptor 50	208311 at	-0.030	31827	6.257E-01	FALSE
103503 at	0.034	7017	1426926 at	0.028	7545	103503 at	0.032	6828	1426926 at	-0.097	6361	6937.75	489.80226	FALSE	phospholipase C, gamma 2	204613 at	0.016	40215	8.834E-01	FALSE
100895 at	0.075	4645	1437630 at	0.046	6452	100895 at	0.000	8508	1437630 at	-0.015	8147	6938	1772.0634	FALSE	large subunit GTPase 1 homolog (S. cerevisiae)	223200 s at	0.099	14828	6.727E-02	FALSE
97153 at	-0.058	5497	1422144 at	0.029	7556	97153 at	0.025	7223	1422144 at	0.045	7488	6941	973.3266	FALSE	inhibin beta E	210587 at	0.024	25851	3.988E-01	FALSE
95411 at	-0.014	7980	1423335 at	0.108	4178	95411 at	0.031	7729	1423335 at	-0.022	7879	6941.5	1845.217	FALSE	RIKEN cDNA 1110004F10 gene	200084 at	-0.188	10657	1.450E-02	FALSE
93709 at	0.006	8314	1449952 s at	0.092	4290	93709 at	0.019	7359	1449952 s at	-0.029	7804	6941.75	1810.3794	FALSE	transmembrane protease, serine 8 (intestinal)	NA	NA	NA	NA	
99150 at	-0.020	7593	1460308 a at	0.035	7622	99150 at	0.003	8390	1444276 at	0.131	4164	6942.25	1888.5787	FALSE	immature colon carcinoma transcript 1	204868 at	0.077	21063	2.355E-01	FALSE
93617 at	0.011	7993	1427736 a at	-0.034	6891	93617 at	0.035	6093	1427736 a at	-0.055	6809	6946.5	784.3492	FALSE	chemokine (C-C motif) receptor-like 2	211434 s at	-0.007	41556	9.224E-01	FALSE



104561 at	0.021	7276	1423998 at	0.051	5701	104561 at	-0.004	8268	1423998 at	-0.021	7943	7297	1141.3171	FALSE	general transcription factor IIIC, polypeptide 5	233173 x at	0.165	2165	5.141E-06	FALSE
93991 at	0.053	6331	1433984 a at	0.012	8195.5	93991 at	0.004	8407	1433984 a at	0.071	6265	7299.625	1160.1084	TRUE	malate dehydrogenase 2, NAD (mitochondrial)	213333 at	-0.418	2878	1.796E-05	FALSE
94554 at	0.020	7498	1448999 at	0.026	7562.5	94554 at	0.011	7721	1448999 at	0.080	6426	7301.875	591.38628	TRUE	trafficking protein particle complex 5		NA	NA	NA	NA
102309 at	-0.064	6114	1419181 at	0.034	7386	102309 at	-0.029	7515	1419181 at	-0.021	8195	7302.5	868.18143	FALSE	zinc finger protein 326	227680 at	0.408	4169	1.053E-04	FALSE
92340 at	0.039	6349	1422183 a at	0.063	6682	92340 at	0.012	7913	1422183 a at	-0.009	8268	7303	930.78497	FALSE	adrenergic receptor, alpha 1b	207589 at	0.024	28946	5.189E-01	FALSE
97119 at	-0.026	6995	1447976 at	0.051	6491	97119 at	-0.017	7440	1447976 at	-0.012	8288	7303.5	762.27751	FALSE	expressed sequence AI596198		NA	NA	NA	NA
94282 at	-0.064	5823	1416735 at	0.002	8447	94282 at	0.002	8422	1416735 at	-0.064	6528	7305	1335.6529	FALSE	N-acylsphingosine amidohydrolase 1	213902 at	-0.067	19729	1.918E-01	FALSE
93469 at	-0.049	6328	1451550 at	-0.002	8472	93469 at	0.043	6453	1451550 at	-0.026	7978	7307.75	1079.3857	FALSE	Eph receptor B3	204600 at	0.026	32549	6.487E-01	FALSE
101907 s at	0.019	7827	1421603 a at	0.028	6838	101907 s at	-0.028	7199	1421603 a at	0.036	7373	7309.25	410.83685	FALSE	CEA-related cell adhesion molecule 2	216605 s at	0.027	32415	6.448E-01	FALSE
101159 at	0.006	8235	1455214 at	-0.083	5564.5	101159 at	-0.021	7046	1422025 at	0.005	8402	7311.875	1312.0647	FALSE	microphthalmia-associated transcription factor	207233 s at	0.096	18255	1.477E-01	FALSE
100128 at	0.010	8067	1448314 at	0.036	7203	100128 at	-0.039	6489	1448314 at	0.045	7497	7314	656.61861	FALSE	cell division cycle 2 homolog A (S. pombe)	203213 at	0.045	17830	1.360E-01	FALSE
160336 at	0.002	8407	1426500 at	-0.035	6663	160336 at	0.046	5735	1426500 at	0.002	8480	7321.25	1350.4366	FALSE	isoprenylcysteine carboxyl methyltransferase	201611 s at	-0.258	5417	4.070E-04	FALSE
94294 at	-0.036	7215	1450920 at	-0.005	8364.5	94294 at	-0.046	5672	1450920 at	0.015	8100	7337.875	1214.5001	FALSE	cyclin B2	232768 at	0.105	11331	1.972E-02	FALSE
99162 at	-0.013	8127	1429043 at	0.036	7146.5	99162 at	-0.055	6717	1452999 at	-0.048	7365	7338.875	590.35588	FALSE	survival motor neuron domain containing 1	200071 at	0.135	20667	2.222E-01	FALSE
101940 at	-0.020	7522	1416999 at	-0.021	7584.5	101940 at	0.040	6134	1416999 at	0.019	8183	7355.875	867.36789	FALSE	sphingomyelin phosphodiesterase 2, neutral	205622 at	0.117	10994	1.713E-02	FALSE
102316 at	0.002	8420	1449165 at	0.011	8199	102316 at	0.028	6602	1449165 at	-0.091	6213	7358.5	1113.2063	FALSE	calpain 5	205166 at	0.065	18523	1.558E-01	FALSE
97168 at	0.016	7843	1421456 at	0.010	8191	97168 at	0.044	5234	1421456 at	0.016	8210	7369.5	1433.6277	TRUE	purinergic receptor P2Y, G-protein coupled 1	207455 at	-0.078	11190	1.862E-02	FALSE
96855 at	0.015	7705	1450907 at	-0.039	7268	96855 at	0.011	7794	1450907 at	0.054	6729	7374	487.58657	FALSE	signal peptidase complex subunit 2 homolog (S. cerevisiae)	201240 s at	0.187	8444	4.210E-03	FALSE
97969 at	-0.026	7508	1419105 at	0.046	6693.5	97969 at	0.024	7029	1419105 at	0.009	8275	7376.375	686.01256	FALSE	nuclear receptor subfamily 1, group H, member 4	243800 at	-0.065	13458	4.330E-02	FALSE
96738 at	-0.002	8421	1416094 at	-0.051	6903	96738 at	0.083	6394	1416094 at	0.024	7810	7382	907.06303	FALSE	a disintegrin and metallopeptidase domain 9 (meltrin gamma)	202381 at	0.199	19967	1.996E-01	FALSE
100893 at	0.010	7895	1460243 at	-0.020	7674	100893 at	0.013	7783	1454257 at	0.084	6179	7382.75	807.55614	FALSE	serine palmitoyltransferase, long chain base subunit 2	232867 at	0.100	18333	1.499E-01	FALSE
99644 at	0.015	7584	1439460 a at	-0.042	7068	99644 at	0.012	7694	1439460 a at	0.061	7200	7386.5	299.88164	FALSE	zinc finger protein 289	238161 at	0.117	12746	3.421E-02	FALSE
99359 at	0.022	7534	1440499 at	0.051	6006	99359 at	-0.016	7607	1440499 at	0.005	8416	7390.75	1005.9746	FALSE	DNA segment, Chr 9, ERATO Doi 26, expressed		NA	NA	NA	NA
102219 at	0.027	7194	1417332 at	0.018	7796.5	102219 at	0.027	7212	1417332 at	0.044	7382	7396.125	280.03344	TRUE	regulatory factor X, 2 (influences HLA class II expression)	226872 at	0.345	6603	1.132E-03	TRUE
100984 at	-0.058	6494	1417296 at	0.010	8176	100984 at	0.009	8121	1417296 at	0.056	6797	7397	876.81735	FALSE	activating transcription factor 1	222103 at	0.213	7084	1.677E-03	FALSE
100921 at	-0.014	7697	1422536 at	0.019	7981.5	100921 at	-0.030	6631	1422536 at	-0.036	7284	7398.375	586.27573	FALSE	troponin I, cardiac	205742 at	-0.011	38392	8.338E-01	FALSE
92639 at	0.010	8039	1424511 at	-0.013	8130	92639 at	-0.025	6773	1440129 at	-0.049	6749	7422.75	765.08839	FALSE	aurora kinase A	208080 at	0.049	21767	2.604E-01	FALSE
161137 r at	0.048	6936	1452954 at	-0.011	8086.5	161137 r at	-0.035	6356	1452954 at	0.009	8361	7434.875	947.83441	FALSE	ubiquitin-conjugating enzyme E2C	202954 at	0.023	36709	7.834E-01	FALSE
102569 at	0.027	7121	1449822 at	0.025	7881.5	102569 at	-0.009	7882	1449822 at	-0.062	6863	7436.875	524.38446	FALSE	atonal homolog 1 (Drosophila)	221336 at	-0.045	31267	6.050E-01	FALSE
99324 at	0.021	7221	1421510 at	0.009	8234	99324 at	-0.033	6126	1421510 at	0.013	8172	7438.25	990.08497	FALSE	protease, serine, 7 (enterokinase)	207638 at	-0.019	32868	6.607E-01	FALSE
160909 at	-0.013	8079	1449133 at	0.054	6661.5	160909 at	0.026	7165	1449133 at	0.028	7965	7467.625	673.93884	FALSE	small proline-rich protein 1A	213796 at	0.047	24938	3.697E-01	FALSE
101172 at	0.042	6830	1421710 at	0.002	8476	101172 at	0.023	7122	1421710 at	0.056	7445	7468.25	717.25234	TRUE	zinc finger protein 92		NA	NA	NA	NA
93836 at	0.048	6156	1422470 at	0.004	8434	93836 at	0.035	7763	1422470 at	-0.028	7521	7468.5	956.4401	FALSE	BCL2/adenovirus E1B interacting protein 1, NIP3		NA	NA	NA	NA
97154 f at	0.035	6897	1439065 x at	0.030	7041	97154 f at	-0.009	7852	1439065 x at	-0.014	8103	7473.25	594.12141	FALSE	Similar to zinc finger protein 665		NA	NA	NA	NA
97451 at	0.013	8072	1424024 at	0.020	7915	97451 at	-0.055	6704	1424024 at	-0.042	7217	7477	635.34715	FALSE	multiple coagulation factor deficiency 2	212246 at	-0.091	19128	1.728E-01	FALSE
102989 at	0.014	7651	1450645 at	-0.015	7861	102989 at	0.036	7423	1450645 at	-0.041	6989	7481	373.59872	FALSE	metallothionein 4	217395 at	0.134	9181	6.488E-03	FALSE
101591 at	-0.012	7851	1422443 at	-0.015	7842	101591 at	0.031	7070	1422443 at	0.043	7181	7486	418.74495	FALSE	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	208453 s at	-0.168	9910	9.629E-03	FALSE
92702 at	0.093	5222	1418615 at	0.015	7972	92702 at	-0.002	8477	1418615 at	-0.009	8293	7491	1526.9929	FALSE	astrotactin 1	213197 at	-0.302	6634	1.167E-03	FALSE
102231 at	0.042	6493	1419295 at	0.030	7199	102231 at	-0.004	8270	1419295 at	-0.028	8008	7492.5	807.33904	FALSE	cAMP responsive element binding protein 3-like 1	213498 at	-0.044	29097	5.242E-01	FALSE
103952 at	0.016	7739	1452317 at	-0.018	7926	103952 at	-0.004	8357	1452317 at	0.067	5974	7499	1049.0818	FALSE	Homeo box B9	226461 at	0.057	15547	8.078E-02	FALSE
102657 at	0.032	6952	1418939 at	0.023	7441.5	102657 at	-0.012	7890	1418939 at	0.028	7730	7503.375	411.77692	FALSE	H2.0-like homeo box 1 (Drosophila)	214438 at	0.156	6804	1.332E-03	FALSE
160716 at	0.005	8281	1451118 a at	0.000	8516	160716 at	-0.027	6836	1451118 a at	-0.064	6383	7504	1053.6821	FALSE	RIKEN cDNA 2410018C17 gene	236206 at	-0.035	31643	6.181E-01	FALSE
101278 at	-0.001	8453	1432032 a at	-0.015	7822.5	101278 at	-0.038	6701	1432032 a at	0.056	7049	7506.375	786.09895	FALSE	artemin	216052 x at	0.025	33017	6.660E-01	FALSE
101606 at	0.026	7268	1459085 at	0.013	8104.5	101606 at	0.021	6988	1459085 at	-0.032	7737	7524.375	495.03558	FALSE	DNA segment, Chr 1, ERATO Doi 259, expressed		NA	NA	NA	NA
94849 at	-0.007	8214	1416335 at	0.035	7705	94849 at	0.007	7990	1433109 at	-0.076	6217	7531.5	900.74802	FALSE	Macrophage migration inhibitory factor	217871 s at	-0.412	2156	4.975E-06	FALSE
102412 at	0.020	7267	1426751 s at	0.000	8516	102412 at	0.019	7187	1426751 s at	-0.048	7185	7538.75	652.61851	FALSE	nucleoporin 107	218768 at	0.139	15212	7.463E-02	FALSE
101827 at	-0.011	8078	1422424 at	0.063	5821	101827 at	0.032	7741	1422424 at	0.000	8524	7541	1190.6662	FALSE	human papillomavirus 18 E5 central sequence motif gene 2		NA	NA	NA	NA
104184 at	-0.001	8492	1450791 at	0.017	7944	104184 at	-0.005	8166	1450791 at	-0.087	5591	7548.25	1324.1003	FALSE	natriuretic peptide precursor type B		NA	NA	NA	NA
160275 at	-0.032	7052	1418888 a at	0.005	8357.5	160275 at	0.015	7583	1418888 a at	0.049	7232	7556.125	577.96286	FALSE	selenoprotein X 1	217977 at	0.056	23027	3.022E-01	FALSE
94478 at	0.070	6568	1416426 at	-0.024	7890	94478 at	0.032	7704	1416426 at	-0.017	8078	7560	678.73019	FALSE	RAB5A, member RAS oncogene family	206113 s at	-0.304	11204	1.874E-02	FALSE
97916 at	-0.007	8251	1452773 at	0.032	7168	97916 at	0.019	7919	1452773 at	-0.057	6931	7567.25	620.60636	FALSE	RIKEN cDNA 5730494N06 gene	220477 s at	-0.196	18505	1.554E-01	FALSE
95401 at	-0.040	6214	1452164 at	-0.024	7658	95401 at	-0.011	7885.5	1452164 at	0.000	8526	7570.875	976.37991	TRUE	cDNA sequence BC038286	222129 at	-0.128	11483	2.089E-02	TRUE
95555 at	0.035	6635	1418123 at	0.053	6734	95555 at	-0.001	8472	1418123 at	-0.005	8477	7579.5	1034.249	FALSE	unc-119 homolog (C. elegans)	203271 s at	-0.036	29204	5.278E-01	FALSE
101599 at	0.002	8441	1419941 at	0.047	5954	101599 at	0.014	7867	1419940 at	-0.029	8091	7588.25	1114.8116	FALSE	RIKEN cDNA C030018P15 gene		NA	NA	NA	NA
160582 at	-0.016	7862	1418551 at	-0.034	6895.5	160582 at	-0.021	7385	1418551 at	-0.006	8366	7627.125	631.13712	TRUE	myosin binding protein C, cardiac	208040 s at	-0.016	37399	8.019E-01	FALSE
98295 at	0.020	7834	1421363 at	0.004	8390	98295 at	0.034	6703	1421363 at	0.043	7640	7641.75	701.9242	TRUE	cytochrome P450, family 2, subfamily c, polypeptide 39	215103 at	-0.033	29115	5.250E-01	FALSE
96499 at	0.001	8469	1449603 at	-0.012	8211.5	96499 at	0.048	5531	1449603 at	0.005	8384	7648.875	1415.975	FALSE	expressed sequence AI594671		NA	NA	NA	NA
97332 at	-0.011	7832	1416378 at	0.001	8481	97332 at	-0.021	7340	1416378 at	-0.054	6953	7651.5	659.69311	FALSE	polynucleotide kinase 3'- phosphatase	218961 s at	-0.051	24724	3.627E-01	FALSE
92224 at	0.043	6417	1449466 at	0.008	8256	92224 at	0.014	7711	1449466 at	-0.009	8256	7660	867.57939	FALSE	C-type lectin domain family 3, member b	205200 at	0.386	14096	5.430E-02	FALSE
93380 at	0.002	8397	1449570 at	0.071	5305.5	93380 at	0.002	8455	1449570 at	-0.001	8522	7669.875	1577.0773	FALSE	killer cell lectin-like receptor subfamily B member 1C		NA	NA	NA	NA
92276 at	0.047	6335	1449901 a at	-0.021	7781.5	92276 at	-0.003	8288	1449901 a at	-0.007	8328	7683.125	932.5335	FALSE	mitogen-activated protein kinase kinase kinase 6	229960 at	-0.105	13964	5.188E-02	FALSE
96029 at	-0.049	7034	1423811 at	-0.011	8127.5	96029 at	-0.008	8004	1423811 at	-0.030	7614	7694.875	491.94146	TRUE	splicing factor 3a, subunit 3	203818 s at	0.171	7257	1.939E-03	FALSE
102674 at	-0.024	7311	1450476 at	0.031	7322	102674 at	-0.006	8104	1450476 at	0.013	8092	7707.25	451.24818	FALSE	cannabinoid receptor 2 (macrophage)	206586 at	0.009	41636	9.243E-01	FALSE
95330 at	-0.002	8454	1423529 at	0.035	6499	95330 at	-0.011	8050	1423529 at	-0.023	7832	7708.75	846.66695	FALSE	glucose-6-phosphatase, catalytic, 2	221453 at	0.039	29675	5.452E-01	FALSE
94785 at	0.007	8232	1447957 at	-0.001	8493	94785 at	-0.034	7083	1447957 at	0.039	7071	7719.75	749.80948	FALSE	DNA segment, Chr 7, ERATO Doi 128, expressed		NA	NA	NA	NA
101648 at	0.000	8510	1422318 at	-0.022	7555	101648 at	0.032	6738	1422318 at	-0.020	8089	7723	764.14964	FALSE	forkhead box D4	217032 at	-0.080	27200	4.502E-01	FALSE
93550 at	-0.008	8108	1420731 a at	0.059	6689.5	93550 at	0.015	7663	1420731 a at	-0.004	8503	7740.875	780.3993	FALSE	cysteine and glycine-rich protein 2	207030 s at	1.258	842	3.001E-07	FALSE
93383 at	-0.015	7761	1419613 at	-0.027	7302.5	93383 at	-0.016	7507	1419613 at	-0.005	8419	7747.375	485.44127	TRUE	procollagen, type VII, alpha 1	217312 s at	0.059	21149	2.383E-01	FALSE
99820 f at	-0.015	7692	1424816 at	-0.019	7820	99820 f at	0.004	8354	1440664 at	-0.042	7298	7791	436.14218	FALSE	cat eye syndrome chromosome region, candidate 5 homolog (human)	218592 s at	0.129	13289	4.105E-02	FALSE
98515 at	0.004	8284	1448884 at	0.017	8086.5	98515 at	-0.024	6962	1448884 at	-0.026	7869	7800.375	584.04985	FALSE	general transcription factor II E, polypeptide 2 (beta subunit)	202680 at	0.080	24100	3.413E-01	FALSE
104762 r at	-0.001	8437	1432462 a at	-0.003	8454	104762 r at	0.041	5964	1432462 a at	0.001	8519	7843.5	1253.4982	FALSE	cofactor required for Sp1 transcriptional activation, subunit 8	221598 s at	-0.099	14461	6.066E-02	FALSE
104644 at	0.068	5889	1450692 at	0.001	8504	104644 at	0.000	8525	1450692 at	0.004	8466	7846	1304.8951	FALSE	kinesin family member 4	218355 at	0.054	29397	5.355E-01	FALSE
94843 at	0.014	7853	1427885 at	-0.020	7721	94843 at	-0.013	7624	1427885 at	0.009	8397	7898.75	345.17085	FALSE	polymerase (DNA-directed), delta 4	202996 at	0.028	32306	6.416E-01	FALSE
93281 at	-0.004	8388	1422449 s at	0.002	8483	93281 at	0.025	7923	1422449 s at	0.052	6816	7902.5	764.54627	FALSE	reticulocalbin 2	201486 at	-0.105	26164	4.098E-01	FALSE
101384 at	0.012	7820	1424549 at	-0.016	8062	101384 at	-0.007	8170	1424549 at	0.033	7694	7936.5	218.06039	FALSE	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	236496 at	-0.022	35775	7.547E-01	FALSE
160731 at	-0.017	7639	1417738 at	0.021	7685.5	160731 at	0.011	7948	1417738 at	-0.001	8520	7948.125	404.79262	FALSE	RAB25, member RAS oncogene family	218186 at	0.016	35814	7.555E-01	FALSE
99357 at	0.019	7631	1447956 at	0.003	8438.5	99357 at	-0.018	7351	1447956 at	-0.004	8417	7959.375	552.8507	FALSE	expressed sequence C76614		NA	NA	NA	NA
94634 at	0.023	7385	1422234 at	0.009	8240.5	94634 at	0.003	8363	1422234 at	0.025	8040	8007.125	435.59583	TRUE	tachykinin receptor 2	244069 at	-0.269	2193	5.411E-06	FALSE
161085 r at	0.002	8472	1455338 at	0.017	7785	161085 r at	0.020	8190	1455338 at	0.018	7913	8090	305.65667	TRUE	alpha 1,4-galactosyltransferase	219488 at	0.023	37177	7.961E-01	FALSE
101828 at	0.002	8399	1421359 at	-0.018	7960	101828 at	-0.008	8063	1421359 at	0.004	8489	8227.75	255.87155	FALSE	ret proto-oncogene	215771 x at	-0.077	21209	2.401E-01	FALSE